MAKERERE  UNIVERSITY

MORPHOLOGICAL DIVERSITY, PERFORMANCE AND GENE ACTION FOR TRAITS AMONG HOT PEPPER GENOTYPES IN UGANDA

BY

VALLENCE NSABIYERA
B.Sc. AGRIC (HONS) (MUK)

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DECLARATION

I hereby declare that the research work presented in this thesis is my original research, which has not been submitted to any other university for any academic award.

Signed..... Date..31/07/2012.....

Mr. Vallence Nsabiyera,

Makerere University

This thesis has been submitted to the Directorate of Graduate Research and Training for examination with our approval as supervisors.

Signed..... Date..July..31, 2012.

Dr. Mildred Ochwo-Ssemakula

B.Sc. Agric (Mak), M.Sc. Crop Science (Molecular Plant Mycology) (Mak), PhD (Molecular Plant Virology) (Mak)

Makerere University

Signed..... Date....31/07/2012

Dr. Peter Sseruwagi

B.Sc. Agric (Mak), M.Sc. Crop Science (Plant Virology) (Mak), PG. Dip (Biotechnology), PhD (Molecular Plant Virology) (University of the Witwatersrand)

Mikocheni Agricultural Research Institute, P. O. Box, Dar es Salaam, Tanzania

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DEDICATION

To my brother, Dennis Mugisha, who has encouraged and helped me during this study. And to all present and future hot pepper growers in Uganda who will benefit from this work.

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ABSTRACT

Pepper (*Capsicum* spp.) production is constrained by poor quality cultivars and various biotic stresses, among which diseases are prominent. Lack of information on diversity, yield, disease resistance and a narrow genetic base for the existing *Capsicum* cultivars hinder pepper improvement in Uganda. The main objective of this study was to establish the performance and morphological characteristics among a diverse collection of hot pepper germplasm, as a basis for contributing towards the improvement of pepper production in Uganda. To achieve this, studies were carried out between April 2008 and October 2010 in Wakiso district to: a) characterize the morphological diversity of hot exotic and local *Capsicum annuum* genotypes, b) identify pepper genotypes with superior agronomic (growth), yield and quality traits for use in pepper cultivar improvement efforts in Uganda and/or for direct release to farmers, c) establish levels of disease resistance among various pepper genotypes and select parents for disease improvement efforts, d) analyze the nature of gene action among pepper genotypes through combining ability studies, in order to identify parents that produce offspring with superior fruit yield and associated traits.

Thirty-seven local and introduced genotypes were characterized for morphological traits in a screen-house at the National Agricultural Research Laboratories (NARL), Kawanda. Thirty-five genotypes were evaluated for growth, yield, quality and disease resistance traits for two seasons in a high disease pressure site at the National Crops Resources Research Institute (NaCRRI), Namulonge. Detection and diagnosis of field disease causative organisms (viruses) was done in the Virology laboratory at the International Institute of Tropical Agriculture (IITA) in Namulonge, Uganda and in the Molecular Biology laboratory at the Department of Agricultural Production, Makerere University for fungal and bacterial diseases. Combining ability studies for yield and yield-contributing traits was done at NaCRRI.

Findings indicated significant morphological differences among pepper germplasm for most characterized quantitative traits ($P<0.001$) and for days to fruit maturity ($P=0.003$) except in the case of primary branch numbers. Local genotypes were characterized by smaller fruits and later maturing types compared to exotic accessions, with the exception of local accessions CA-EASC-

09-1 and CA-UGKA 09-3. However, local types performed better in plant height, width and fruit numbers per plant. On the other hand, very little diversity was detected among genotypes for qualitative traits (Diversity index, $e^{H'} = 1.83$). Higher diversity indices were observed for stem pubescence type (3.20), leaf pubescence type and density (2.77), anther colour (2.56), calyx margin and fruit surface (2.90), and immature fruit colour intensity (2.80). Cluster analyses using 20 quantitative and 28 qualitative traits showed diversity among the genotypes at phenotypic level but with some level of genotypic relatedness and closeness.

Very highly significant differences were observed in all plant growth ($P<0.001$), most yield ($P<0.001$) and most quality ($P<0.001$) traits in the two seasons. The performance of pepper genotypes during season 2009B was far higher than in season 2009A for majority of the traits. Local genotypes performed better in season 2009A than in 2009B in number of fruits per plant, percentage of non-marketable fruits, number of seeds per fruit, fruit seed yield (t/ha) and 200 seed weight (g). A pooled analysis across seasons showed that local genotypes performed worse than exotic genotypes in all scored parameters except plant width. The commercial local check genotype CA-UGKA 09-3 performed better than all the local genotypes and most of the AVRDC genotypes in terms of fruit yield and early maturity. The local genotype CA-EASC-09-1from the East African Seed Company was the earliest maturing among all genotypes, and could be used as a donor parent for earliness, even though it was also the poorest yielding type. An AVRDC check genotype PP97-7195-1 performed best of all the exotic genotypes in all traits except fruit size. With the exception of number of seeds per fruit, highly significant genotype by season (GxE) ($P<0.001$) interactions was observed in other traits, an indication of lack of trait stability among genotypes across seasons. Eight of the agronomic traits showed significant correlations between seasons indicating some degree of stability for these traits. Correlation analyses indicated that fruit size (weight and length) and numbers per plant were the most important determinants of total and marketable yield (t/ha) suggesting that selecting genotypes that produce many and/or bigger fruits during the hot pepper breeding programme can consequently lead to increased yields. However, fruit weight contributed more compared to number of fruits per plant.

Disease assessment confirmed field infection with viral diseases, wilts, *Phytophthora* blight, *Cercospora* leaf spot, anthracnose and bacterial spot. Viral diseases and *Cercospora* leaf spot were the most predominant and severe diseases, followed in descending order by anthracnose, *Phytophthora* blight and wilt diseases. Results showed highly significant genotypic differences ($P<0.001$) for most scored diseases. No genotype was found to be resistant to all observed field diseases apart from the AVRDC genotype PP97-7195-1, which was resistant to fungal and bacterial diseases, and only moderately resistant to viral diseases. Field disease correlation analysis across seasons indicated significant severity indices for viral disease and *Phytophthora* blight implying some stability in these scores across seasons with the viral disease severity index being the most consistently scored disease. In 2009A, all disease incidences and severities correlated negatively with both total and marketable fruit yields except for the viral disease severity index, implying that all except viral diseases contributed to the loss of both total and marketable fruit yields. Anthracnose contributed most to the loss in yield. *Cercospora* leaf spot contributed more to total fruit yield loss in 2009B.

Laboratory analysis found *Phytophthora capsici*, *Fusarium oxysporum* f.sp. *capsici* and *Ralstonia solanacearum* associated with wilt disease. *Colletotrichum* sp. was associated with anthracnose diseases on stems while *Xanthomonas campestris* pv. *vesicatoria* caused bacterial spot on leaves. Species confirmed to cause viral diseases included: *Tomato spotted wilt virus* (TSWV), *Chilli veinal mottle virus* (ChiVMV), *Tobacco mosaic virus* (TMV), *Potato virus Y* (PVY), *Pepper mottle virus* (PepMoV), *Pepper veinal mottle virus* (PVMV), *Alfalfa mosaic virus* (AMV) and *Cucumber mosaic virus* (CMV). Of these PVY, ChiVMV *and* CMV were the most prevalent.

Evaluation of F1 hybrids and their parents indicated significant differences in heterotic, general combining ability (GCA) and specific combining ability (SCA) effects among the studied traits. Additive gene action was predominant in viral and wilt disease incidences and a few quantitative traits. The AVRDC genotype PP9852-115 and local genotype CA-UGKI 09-4, demonstrated highly significant and desirable GCA effects for most of the studied traits. These were followed by local parents CA-UGKI 09-6 and CA-UGCE 09-3 that were thus considered good combiners.

However, for wilt disease, only the AVRDC parent PP0537-7504 showed significant desirable GCA. Three hybrids; CA-UGCE 09-3 x CA-UGKI 09-6, CA-UGKI 09-6 x PP9852-115 and CA-UGCE 09-3 x PP0337-7562 were the top-most performers among all crosses with several significant best SCAs for measured traits. Two hybrids; CA-UGCE 09-3 x PP9852-115 and CA-UGKI 09-6 x PP9852-115 were better performers for *Cercospora* leaf spot resistance while PP9852-115 x PP0537-7504 was the best for viral disease resistance. Some of these hybrids performed well compared to their best parent for various traits, suggesting that obtaining transgressive segregants should be possible in later generations.

The introduction of exotic pepper genotypes has the potential to diversify the existing *Capsicum* genetic base in Uganda. Sources of improved traits have been identified that can be used in the pepper breeding program. In order to enhance *Capsicum* improvement and production in Uganda, the identified genotypes should be further evaluated and then released to farmers. Alternatively, these genotypes could be used by breeders to introgress superior traits into cultivars being grown by farmers and therefore improve specific traits for enhanced productivity.

CHAPTER ONE

INTRODUCTION

1.1 Background

1.1.1 Taxonomy and nomenclature of hot peppers (*Capsicum* spp)

Pepper (*Capsicum* spp.) is one of the most varied and widely used foods in the world (Terry & Boyhan, 2006). It ranks third in importance among important vegetables, after peas and tomato (Ochoa-Alejo & Ramirez-Malagon, 2001; Ali, 2006) and is the world's second most important Solanaceous vegetable, after tomato (Yoon *et al.*, 1989). There are about 28 species of *Capsicum* peppers (McMullan & Livsey, 2007), but only five have been domesticated and are currently cultivated, namely: *Capsicum annuum* (Linnaeus), *Capsicum baccatum* (Linnaeus), *Capsicum chinense* (Jacquin), *Capsicum frutescens* (Linnaeus) and *Capsicum pubescens* (Ruiz & Pavon) (Ochoa-Alejo & Ramirez-Malagon, 2001; Ali, 2006; McMullan & Livsey, 2007). Of the five domesticated *Capsicum* species *C. annuum* is the most widely cultivated (Katoh *et al.*, 2004; Singh *et al.*, 2006) with both pungent and sweet types (Ochoa-Alejo & Ramirez-Malagon, 2001).

Capsicum terminology is quite confusing with pepper, chilli, chile, chili, aji, paprika and capsicum all used interchangeably as vernacular terms in various geographical regions to describe the plants and pods of the genus *Capsicum* (Bosland, 1996; McMullan & Livsey, 2007). The term '*Capsicum*' is used for taxonomic discussions and the rest generally refer to plants that have pungent pods that attract worldwide use of hot peppers as spices (Bosland, 1996, CAP, 2009). The word "chili" is mainly spoken in central Mexico, "aji" among Caribbean countries (Bosland, 1996), chile in European countries (Bosland, 1996; McMullan & Livsey, 2007) whereas, chilli is mainly used in India (Stephens, 2009).

Considerable confusion also exists over the scientific names of the domesticated *Capsicum* peppers and some of their wild relatives (AVRDC, 1989; Bosland, 1996). The taxonomic

confusion is blamed on Bailey (1923) for considering all the domesticated peppers known to him as a single species (AVRDC, 1989). For example, some publications from the early 20th century and later, use *C. frutescens* for what is now called *C. annuum*, though they were domesticated independently, incorporate different samples of the ancestral gene pool, belong to different chromosomal races and offer different resources to the plant breeder (AVRDC, 1989). In Uganda, all peppers are called the same common name whether sweet or hot, regardless of the species and the level of capsaicin responsible for the pungency in which various cultivars differ markedly (Terry & Boyhan, 2006). Therefore, in this thesis, the commonly used name for all pungent *Capsicum* peppers (hot pepper), and the scientific name of hot pepper species (*Capsicum anuum L.*) involved in this study are used interchangeably. Genotypes are differentiated based on the codes they were assigned during collection.

1.1.2 World pepper production and trade

Hot pepper is increasingly becoming an economic crop worldwide, with cultivation on more than 3.7 million hectares (ha) annually (FAO, 2003) across the tropics, subtropics, and temperate regions (Pickersgill, 1997). In 2004, a total production of over 24million tonnes (m t) was reported for all hot pepper species (FAO, 2004). It is estimated that world production of hot pepper (*Capsicum annuum* L) is about 2.5m t with paprika accounting for one-third of the total world consumption of chilli (Zacharich & Gobinath, 2008). India is the leading producer, with about 1m t from acreage of 8.3 million ha (Zacharich & Gobinath, 2008). Other major producers include: China (0.4m t), Pakistan (0.3m t), Mexico (0.3m t), South Korea (0.15m t) and Bangladesh (0.1m t) (Thampi, 2003). Mexico is the world's largest exporter, with a global market share of 23% (Singh *et al.*, 2006) while Canada, USA and the European Union (EU) are leading importers of the world's chillies (Singh *et al.*, 2006). In 2002, the EU imported 24,615t fresh hot peppers valued at $ 28.6million, up from 20,779t valued at $26.2 million, in 1999 (UEPB, 2005a).

1.1.3 The nutrient content and uses of hot pepper

Hot peppers contain steam-volatile oils, fatty oils, capsaicinoids, carotenoids, vitamins, protein, fibre and mineral elements (Bosland & Votava, 2003). They are cholesterol-free and low in sodium. Hot peppers are, however, rich in vitamins A (carotene), C (ascorbic acid), vitamin E (tocopherol) and mineral nutrients such as potassium phosphorus, and calcium (Simon *et al.*, 1984; Terry & Boyhan, 2006). Fresh green chilli peppers are reported to contain more vitamin C than citrus fruits while fresh red chillies have more vitamin A than carrots (Marin *et al.*, 2004). Chillies contain ß-carotene and ß-cryptoxanthin pigments that have vitamin A activity (Hornero-Mendez *et al.*, 2000) and capsaicinoids that are responsible for pungency or the spicy hot flavour (Garcés-Claver *et al.*, 2006).

Capsicum peppers may be used as vegetables, spices, medicinal herbs or ornamental plants with the non-pungent varieties being an economically important 'green' crop used as vegetables (Eshbaugh, 1993) in fresh form, fried or grilled and used as a garnish or added to traditional dishes. The steam-volatile oils, fatty oils, capsaicinoids, carotenoids, vitamins, protein, fibre and mineral elements found in hot peppers are responsible for its medicinal and nutritional uses (Palevitch & Cracker, 1995). Hot peppers are used as red ripe, fresh, or dried, to add heat to curries, marinades, soups, stir-fries and pizza. Capsaicinoids have strong physiological and pharmacological benefits. They are used as a neuro-pharmacological tool in medicine to treat painful ailments such as rheumatic diseases, cluster headaches, painful diabetic neuropathy, post-herpetic neuralgia, arthritis, cystitis and human immunodeficiency virus (Simon *et al.*, 1984; Perucka & Materska, 2001; Tsuchiya, 2001). Capsaicinoids have antioxidant and antibacterial effects on some bacteria such as *Helicobacter pylori* (Jones *et al.*, 1997) and *Salmonella enteritidis* (Vicente *et al.*, 2007) and are also effective in reducing myocardial and aortic cholesterol levels (Hussain & Chandrasekhara, 1993; Manjunatha & Srinivasan, 2007).

Capsaicin exhibits antigen toxicity, anti-mutagenic, and anti-carcinogenic effects (Surh *et al.*, 1998) and also plays many roles in digestion (Simon *et al.*, 1984; Palevitch & Cracker, 1995). Many carotenoids in hot peppers have a high nutritional value (Pérez-Gálvez *et al.*, 2003) and

because of their antioxidant and free-radical scavenging effect, these carotenoids play a role in preventing some types of cancer, cardiovascular disease, eye disorders, skin degeneration and aging (Topuz & Ozdemir, 2007). Vitamin C in the *Capsicum* species acts as an antioxidant.

1.1.4 Hot pepper production and export trends in Uganda

Capsicum chinense was introduced into Uganda in the late 1990's to diversify cash crops and improve household livelihoods (Tusiime *et al.*, 2010). The other two hot chilli species; *C. annuum* and *C. frutescens* (preferably termed *Capsicum annuum* var. *glabriusculum*) (Valenzuela, 2011) were probably introduced into Uganda in the later part of the 19th century by early Arab traders and explorers at the East African who proceeded to Uganda (Anonymous, 2012).

Currently, hot peppers varying in colour, appearance, taste, and pungency are cultivated on small scale in Uganda, with out-grower schemes working together with exporters (ADC/IDEA, 2001) although, aggregate acreage under production is not documented. Red bird's eye chilli, a relative of Tabasco (*C. frutescens*), is produced mainly in the western region (Bundibugyo, Kasese, Kibaale, Rukungiri and Mbarara Districts); northern region (Arua, Apac, Lira and Gulu Districts); central region (Mubende, Mukono and Kayunga Districts) and eastern region (Iganga and Kamuli Districts), (UEBP, 2005b; Anonymous, 2010a). Other hot pepper types are largely grown in the central region (Wakiso, Mukono, Mubende, Mpigi, Masaka and Luwero Districts) but may also be found in the western region (Kasese and Hoima districts) and eastern region (Jinja, Kamuli and Iganga Districts) (UEPB, 2005a). However, Kasese district is by far the largest producing district in Uganda (Ssonko *et al.*, 2005). The 'Caribbean' Scotch Bonnet is the most widely produced commercial variety. It belongs to the *Capsicum chinense* species and is a major high-value crop export from Uganda (ADC/IDEA, 2001; UEPB, 2005a). Another unidentified dark green Indian cultivar of the *Capsicum annuum* species is also popular and is mainly grown for local consumption via fresh market sale and processing (Otim-Nape *et al.*, 1999 as quoted by Buyinza & Kabi, 2008; Buyinza & Mugagga, 2010).

The domestic market for hot peppers in Uganda is small and consists mainly of foreigners, who are mostly of Indian ethnicity (Ssonko *et al.*, 2005). The bulk of *Capsicum* peppers produced in Uganda are, therefore, targeted for the EU and Holland while green chillies are exported to the UK (ADC/IDEA, 2001; Mr. James Kanyije, 2010; Director of ICEMARK, a major Horticultural Export Company in Uganda, *personal communication*). The quality attributes emphasized for export of hot peppers include pungency (hotness due to a chemical capsaicin), colour (red or yellow, long chilli types are exported when green), fruit size (large); and pest and disease status (free) (Mr. James Kanyije, 2010; *personal communication*).

Export of hot pepper from Uganda increased from 394 tons in 2004 to 817 tons in 2005, then dropped sharply to 218tons (2006), 194 tons (2007) and increased to 320 tons in 2009 (FAO, 2009; UBOS, 2009; 2010). Production was almost stagnant in 2000, 2001 and 2002 at 3800, 3904, and 3867 tons (t), respectively. It increased to 5264t (2003), 5840t (2004), declined to 4342t in 2005 and subsequently increased slightly to 4596t (2006) and further to 6162t (2007) then declined to 5052t (2008), 4679t (2009) and 3700t (2010) (FAO, 2012; Statistics derived by imputation methodology). This level of production however, remains lower than in other countries producing hot peppers worldwide where annual production exceeds 200,000 tons (dry equivalent) (Singh *et al.*, 2006). Compared to other traditional and non-traditional export crops, the volume of exported peppers remains relatively low although its value per kg is high (Appendix 1).

1.2 Problem statement

Uganda realised a general increase in hot pepper production, from 3800-6162t between 2000 and 2009 albeit with fluctuations. More recently, though, a sharp decline in production was recorded in 2010 at 3700t (FAO, 2012). However, production remains lower than the average annual global production of 28m t (FAO, 2009). In addition, the quality of produce realized does not meet the stringent standards of the international market where Uganda already faces fierce competition from major producing countries such as India and China (Thampi, 2003). The poor quality of produce has mainly been attributed to biotic and abiotic stresses in the field and the

poor quality of cultivars grown by farmers (ADC/IDEA, 2001; UEPB, 2005a; Douglas, 2008; Buyinza & Mugagga, 2010; Tusiime *et al.*, 2010). Biotic stresses that affect pepper include insect pests (spider mites, thrips, fruit flies, aphids and leaf miners), nematodes and diseases caused by fungal, bacterial and viral pathogens (ADC/IDEA, 2001; UEPB, 2005a; Buyinza & Mugagga, 2010), which are prevalent in tropical environments (Black *et al.*, 1991). While losses from biotic stresses have not been quantified in Uganda, yield losses of up to 100% have been realised from anthracnose in the USA (Melanie & Sally, 2004). Viral diseases are also reported to cause 60 to 100% yield loss in Taiwan (Green, 1993) while leaf spots are known to cause severe defoliation resulting in reduced yields and loss of fruit quality (Sun *et al.*, 2002; Mohamed & Shymaa, 2008). In addition, insect pests alone account for about 20% yield loss (Asawalam *et al.*, 2007).

In order to control the pests and diseases that affect hot pepper in Uganda, farmers largely use pesticides (Karungi *et al.*, 2010) which are quite expensive and are often applied in large quantities that expose produce to potential retentions beyond the acceptable threshold (Aubertot *et al.*, 2005). The indiscriminate application of pesticide has also over time resulted in a buildup of resistance among target pests and pathogens (Flint, 1999). Pests and diseases are best managed using host resistance, which is a cheap option for farmers (Byoung-Cheorl *et al.* 2005; Duveiller *et al.*, 2007). However, inadequate and poorly-described germplasm collections, such as exist in Uganda, make the search for improved genotypes limited (Nass & Paterniani, 2000). There is, therefore, need to collect new hot pepper germplasm, characterize and evaluate it before breeding can be initiated for the development of superior and adapted genotypes.

1.3 Justification of the study

Breeding for yield and disease resistance among cultivars of many important crops is hindered by the narrow genetic diversity that exists among their cultivated landraces (Persley, 1986; Okello *et al.*, 2010; Scotti, 2011). In Uganda, the same can be said about pepper, which in addition to experiencing a scarcity of improved seed (Douglas, 2008) largely depends on non-improved local varieties (Buyinza & Mugagga, 2010) that have suffered inbreeding depression or on expensive imported hybrid seeds that cannot be regenerated (Derera *et al.*, 2005; Rosendal

et al., 2005). Provision of high-yielding and disease-resistant cultivars would enhance pepper crop yields.

Breeding for resistance also offers the most efficient, cost effective and environmentally friendly approach for integrated disease management (Byoung-Cheorl *et al.*, 2005). In order to breed and make available to farmers better performing cultivars, there is need for a pool of germplasm with desirable traits to draw on. In the absence of this pool, exotic genotypes are the next viable source of resistance for developing commercial varieties. This study identified hot pepper cultivars that performed well under Ugandan conditions, in order to understand the diversity that existed among them. In addition the nature of gene action and combining abilities that influenced fruit yield and associated traits were identified. With the information generated, it will be possible to identify materials for further evaluation before either being released as varieties to farmers, or for further improvement of pepper varieties in Uganda.

1.4 Objectives of the study

The overall objective of this study was to establish the performance and phenotypic characteristics among a diverse collection of hot pepper germplasm, as a basis for contributing towards the improvement of pepper production in Uganda.

1.4.1 Specific objectives

The study specifically:

1. Characterized the morphological diversity of exotic and local *Capsicum annuum* genotypes.
2. Identified pepper genotypes with superior horticultural (growth), yield and quality traits for use in cultivar improvement in Uganda.
3. Evaluated disease resistance of various pepper genotypes for disease resistance improvement efforts.

4. Determined the nature of gene action to identify parents that produced offspring with superior fruit yield, and associated traits.

1.4.2 Hypotheses of the study

- Local and exotic pepper genotypes differ in morphological traits, yield and resistance to field diseases in Uganda.
- Pepper genotypes that are hybridized differ in combining ability, and hence gene action, for diseases, fruit yield and associated traits.

CHAPTER TWO

LITERATURE REVIEW

2.1 Composition and characteristics of species in the genus *Capsicum*

The genus *Capsicum* has about 28 species of which, only five have been domesticated and are currently cultivated, namely: *Capsicum annuum* (Linnaeus), *Capsicum pubescens* (Ruiz & Pavon), *Capsicum baccatum* (Linnaeus), *Capsicum chinense* (Jacquin), and *Capsicum frutescens* (Linnaeus) (DeWitt & Bosland, 1996; Ochoa-Alejo & Ramirez-Malagon, 2001; McMullan & Livsey, 2007). *Capsicum chinense* (Jacquin) means from China (this is misleading as the species originated in the Amazon Basin). *Capsicum chinense* includes the extremely hot varieties including the Habanero, Scotch Bonnet and the legendary Red Savina. *Capsicum frutescens* (Linnaeus) means shrubby and includes the well known tabascos and the famous variety Malagueta. *Capsicum pubescens* (Ruiz & Pavon) means hairy and includes Peruvian 'Rocoto' and the Mexican 'Manzano' *rocotos* from South America. *Capsicum annuum* (Linnaeus) means annual (which is inaccurate as *Capsicum* species are perennial plants) (Berke *et al.*, 2005; McMullan & Livsey, 2007).

The *Capsicum* species involved in this study, *Capsicum annuum*, is the most commonly cultivated and economically important species worldwide (AVRDC, 1989; DeWitt & Bosland, 1996; Ochoa-Alejo & Ramirez-Malagon, 2001; McMullan & Livsey, 2007). The species was domesticated in Mexico, where it is the most popular cultivated pepper. It includes all the commercially important sweet peppers and many types of spice peppers such as Ancho, Bell Pepper, Cayenne, Cherry, Cuban, De Arbol, Jalapeno, Mirasol, Ornamental, New Mexican, Paprika, Pimiento, Pequin, Serrano, Squash and Wax peppers (McMullan & Livsey, 2007). Each type named above has its own unique characteristics of pungency, flavour and colour (McMullan & Livsey, 2007). This species is distinguished from other domesticated species by its solitary flowers and fruits, and its clear white corollas (Fig. 1).

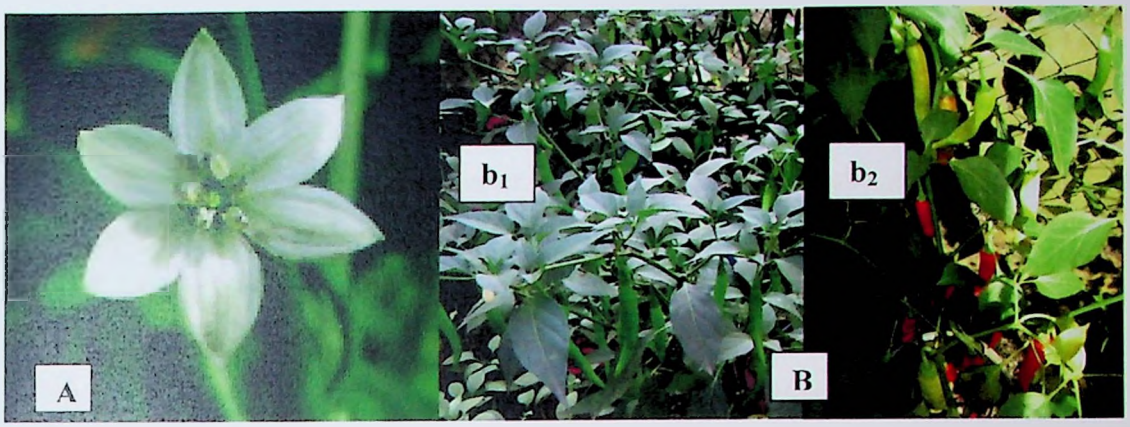

Figure 1. Some distinguishing characteristics of hot chilli pepper (*Capsicum annuum* L.) (A) clear solitary white corollas; B) variation in fruit types of *Capsicum annuum*: b_1) dark green immature type, b_2) light green immature type.

Each domesticated species varies in fruit colour, size, shape and pungency, with non-pungent cultivars that are eaten as vegetables rather than as a spice having been established in most, if not all, of the cultivated species (AVRDC, 1989). Species are further distinguished by their flower and seed colour, shape of the calyx, number of flowers per node, and flower orientation. The size and shape of the fruit pods range from erect, short, and pointed, to pendant and elongated pods. During the ripening process, the fruit colour can change from green to orange, red, yellow or brown. Pods may be conical, cylindrical or bell shaped (IBPGR, 1993; IPGRI *et al.*, 1995).

2.1.1 Quality attributes of *Capsicum sp.* hot peppers

Hot peppers have numerous constituent chemicals that provide quality, nutritional value, flavour, aroma, texture and colour. These include steam-volatile oils, phenols, flavonoids, fatty oils, capsaicinoids, carotenoids, vitamins, protein, fibre and mineral elements (Rosa *et al.*, 2002; Bosland & Votava, 2003). Carotenoids are mainly synthesized during the ripening stage and confer the various fruit colours, with variability in colour being due to differences in the components of the carotenoid pigment (Rosa *et al.*, 2002). Hirasa & Takemasa (1998) identify a number of carotenoid components and their associated colours in chilli pepper: ß-carotene (reddish-orange), Cryptoxanthin (red), Lutein (dark red), Zeaxanthin (yellow), Capsanthin (dark-

red), Capsorbin (purple-red), Neoxanthin (orange-yellow) and Violaxanthin (orange). Among the morphological traits that give these fruits their quality are size, colour and shape (in both fresh and dry states) (AVRDC, 1989; Bozokalfa & Kilic, 2010). *Capsicum* peppers also differ in flavour. Several aromatic substances present in very small quantities but not connected with pungency contribute to flavour in peppers (Bosland, 1993). The highest concentration of these was found in the outer walls, with lesser amounts in the cross walls and placenta, and none in the seeds (De Witt & Bosland, 1996).

Capsicum is the only genus that has a specific capacity to synthesize and accumulate lipophylic alkaloids called capsaicinoids. These secondary metabolite compounds are the ones responsible for the spicy hot flavour (pungency). Pepper cultivars differ significantly in their level of pungency (Terry & Boyhan, 2006), with those of *C. chinense* among the highest (Singh *et al.*, 2006) and then *C. frutescens* (Bosland, 1993). There are nine known capsaicinoids in pepper: capsaicin, dihydrocapsaicin, norcapsaicin, nordihydrocapsaicin, homocapsaicin I, homodihydrocapsaicin I, homocapsaicin II, homodihydrocapsaicin II, N-vaninnyl nonanamide, N-vanillyl octanamide, and N-vanillyl decanamide (Garcés-Claver *et al.*, 2006). Among the capsaicinoids, capsaicin and dihydrocapsaicin together account for about 90% of pungency (Rosa *et al.*, 2002; Garcés-Claver *et al.*, 2006). Capsaicin ($C_{18}H_{27}NO_3$) is a fat-soluble, flavourless, odourless, and colourless compound whose distribution in fresh jalapeno peppers was highest in the cross walls, followed by placenta, seeds, and outer walls (Rashid *et al.*, 2007).

2.2 Origin, distribution and domestication of *Capsicum annuum*

The *Capsicum* species are thought to have originated from Central and South America (Ochoa-Alejo & Ramirez-Malagon, 2001; Grubben & Mohamed, 2004). Mexico is thought to be the centre of origin of the hot (Chilli) and sweet peppers (*Capsicum annuum* in the narrow sense), while aromatic hot pepper (*Capsicum chinense*) originated in the Amazonian region and bird pepper (*Capsicum frutescens*) in the coastal regions of the southern part of tropical South America (Grubben & Mohamed, 2004). Native Americans have used *Capsicum* for more than 9000 years and cultivated it for 5000 years (Ochoa-Alejo & Ramirez-Malagon, 2001; Terry &

Boyhan, 2006). However, during his first voyage to the Americas in 1492, Christopher Columbus is accredited with having accidentally discovered a plant (now described as *Capsicum annuum*) whose fruit, it was said, had a pungent taste similar to that of black pepper, *Piper nigrum* L. (Bosland, 1996). He introduced the crop to Europe in 1493, from where it subsequently spread to Africa and Asia through subsequent voyages by the early explorers (Terry & Boyhan, 2006). *Capsicum* was quickly established in local cuisines and used as a substitute for the more expensive black pepper that, in those times, only the wealthy could afford (Bosland, 1996). Today hot chilli peppers are widely domesticated as a crop in many parts of the world, including Africa, Europe, and Asia, with tropical countries, such as Malaysia, Indonesia, West Indies, Central, East and West Africa, and the Philippines (AVRDC, 1993).

2.3 Growth requirements of *Capsicum* peppers

Capsicum species are perennial crops in suitable environments (DeWitt & Bosland 1996; Thampi, 2003). Unlike sweet peppers, hot *Capsicum* peppers are photoperiod-insensitive and are better adapted to hot weather with an optimum temperature range of 20-30°C. Generally, higher night temperatures are not conducive for fruit set, thus, temperatures above 32°C and below 15°C for extended periods often result in poor growth and low yields (Berke *et al.*, 2005). It is reported that the lowest temperature peppers can tolerate is 15°C and the highest is 35°C (AVRDC, 1989). Though young seedlings are cold-sensitive, mature plants can tolerate a light frost. Hot peppers are shallow rooted and do not withstand flooding for more than 48 hours.

Hot *Capsicum* peppers prefer sandy loam to clay loam soil with high moisture and a pH range of 5.5-7.5 (AVRDC, 1989). Fruit yield is greatest when plants receive daily rainfall or have an adequate water supply through irrigation, as they are not particularly drought-tolerant. In the case of irrigation, furrow or drip types are recommended (Berke *et al.*, 2005). The seedbeds or fields should be well prepared before planting with organic fertilizers such as cow manure, but soil analyses should be conducted prior to planting to prevent inadequate or excessive fertilizing (Kelly *et al.*, 2009). Seedlings are transplanted when they are somewhat hardy, 40-45 days after planting. Hot peppers require a high level of fertility early in the growing cycle plus frequent

side dressing to supplement nitrogen. Berke *et al.* (2005) suggested N:P:K at a rate of 450:220:400 kg/ha, depending on soil fertility tests and a target yield of 5 t/ha under Taiwan conditions. Almost three months after planting, the plants flower and, depending on the variety, produce fruits that are harvested for two months, from which six to ten pickings are done. Hot, dry weather is desirable when the fruit is ripening. The fruits should be harvested by cutting the stem rather than tearing the fruit off, as the latter leads to damage to the plant. Some pepper varieties require staking as they lodge when the fruit set is high. Yields tend to be higher when staked. Under good management and suitable conditions, total yields of 5.6-38.45 t/ha have been reported (AVRDC-RCA, 2003; AVRDC, 2004).

2.4 Factors that limit pepper production

Chilli pepper production, like any other crop of economic importance, is affected by various biotic and abiotic factors that diminish the yields (DeWitt & Bosland, 1993).

2.4.1 Biotic factors

Several infections can cause significant losses in pepper, including fungal, bacterial or viral diseases, nematodes, mites and many insect pests (Yoon *et al.*, 1989; Wien *et al.*, 1989; Ochoa-Alejo & Ramirez-Malagon, 2001). These infections result in extensive losses in the yield and quality of peppers (Black *et al.*, 1991; ADC/IDEA, 2001; UEPB, 2005a), and thus severely reduce the production and profitability of this crop even further by reducing the period in which the crop can be harvested. The major limiting diseases of most chilli peppers are phytopathogenic fungi, bacteria, and viruses (Yoon *et al.*, 1989; Wien *et al*, 1989; Black *et al.*, 1991; Green & Kim, 1991). A number of bacterial, fungal, and viral diseases that reduce the yield and degenerate the quality of *Capsicum* peppers are mentioned in Black *et al.* (1991). For example, 60 to 100% losses of marketable fruit have been reported from virus infection (Green, 1993), up to 100% loss from pepper anthracnose (Melanie & Sally, 2004) while bacterial spot caused by a seedborne bacterial pathogen (*Xanthomonas campestris* pv. *vesicatoria*) is also capable of causing severe defoliation of plants, resulting in reduced yield and loss of quality of

harvested fruit when severe damage occurs on enlarging fruits (Sun *et al.,* 2002; Mohamed & Shymaa, 2008). More than 35 viruses including *Pepper veinal mottle virus* (PVMV), *Potato Virus* Y (PVY), *Tobacco mosaic virus* (ToMV), *Cucumber mosaic virus* (CMV), *Pepper mottle virus* (PepMoV) and many others infect peppers, significantly affecting production and causing low yields and reduced fruit quality (Alanso *et al.,* 1989; Green & Kim, 1991). These viruses cause a number of symptoms, including mottling, mosaic, discolorations, deformation of pepper leaves, malformation of fruit, and stunting of plants (Yoon *et al.*, 1989).

Insect damage significantly affects the quality and production of hot peppers. Several pests, such as pepper weevils (*Anthonomus eugenii*), flea beetles, aphids, cut worms, leaf worms, fruit worms, thrips, and whiteflies are considered to be the most important arthropod pests of peppers (Black *et al.*, 1991; Kelly *et al.*, 2009). These insects not only suck plant sap, but some such as whiteflies and aphids also transmit viral diseases and produce sticky honeydew during feeding, which often attracts the growth of a black sooty mold fungus (*Cladosporum sp*) on foliage and fruits that interferes with the normal functioning of the leaves (Jeppson, 1989). This reduces both the photosynthesis capacity of the plant and market value of the fruits. Other important pepper pests are the broad mite [*Polyphagotarsonemus latus* (Banks)] and gall midges [*Contarinia lycopersci* (det. Gagné) and *Prodiplosis longifila* Gagné]. It is reported that insect pests alone account for about 20% of yield loss of *Capsicum* species (Asawalam *et al.*, 2007).

2.4.1.1 Management of biotic constraints of *Capsicum* peppers

Conventional pepper growers control pests using cultural measures such as soil amendments including compost manure, poultry manure, animal manure and inorganic fertilizers (Asawalam *et al.,* 2007), reflective mulches like aluminium foil or silver coloured mulches (Flint, 1999; Berke *et al.*, 2005) and use of an expensive therapeutic approach of killing pest organisms with various toxic pesticides (Hausbeck & Lamour, 2004). Nematodes are managed by planting *Brassica* cover crops that act as natural bio-fumigants and thus, reduce both infestations and the need for chemical fumigation (Kokalis-Buerrell & Dickson, 2003). For a long time plant viruses have been controlled using conventional measures like crop rotation, cross protection, sanitation

(roguing infected plants and using virus-free planting materials) and chemicals against virus vectors such as aphids, whiteflies, thrips, and leafhoppers (Green & Kim, 1991; Bos, 2000; Hull, 2002). In addition to these traditional methods of virus control, biotechnological approaches have recently come into play.

Chemical treatments have proved ineffective against some diseases such as those caused by bacteria (Jones, 2001). Chemical control has also become unpopular because a number of chemicals have lost their efficacy due to the development of pest resistance. In addition, there are growing widespread concerns over food safety, human health, and environmental pollution that call for safe and economically-sustainable practices. Cultural methods are often tedious and generally inefficient, especially under heavy disease pressure. Adaptability of viruses to new hosts makes them difficult to control. The safety of transgenic plant products is an important factor because these genetically modified (GM) crops may also express foreign proteins with unknown allergenicity and effects on the gastrointestinal system of humans (Pusztai & Bardocz, 2011).

The most efficient and simplest way to fight diseases is breeding for disease resistance by introducing a gene or genes from a resistant species or cultivar into a susceptible variety. The development of disease-resistant cultivars can provide an economical and environmentally-friendly approach, which could potentially form the basis of integrated disease management in peppers.

2.4.2 Abiotic factors

The most frequently cited abiotic factors that cause stress in pepper production and result in dropping of flower and fruit include extreme temperatures, too much moisture, and lack of moisture, low light conditions, and imbalance of mineral nutrients (Wien *et al.*, 1989; Barke *et al.*, 2005; Dahal *et al.*, 2006). A number of physiological disorders also hinder pepper production, such as blossom drop with reduced fruit set, blossom end rot, sun scald, poor colour development, pepper stippling and nutrient disorders (Black *et al.*, 1991; Terry & Boyhan, 2006).

Blossom drop in pepper is primarily associated with high night temperatures (above 70°F) and inadequate moisture in the soil. Blossom-end rot is associated with calcium deficiency and characterized by a dark brown to black necrotic region on the blossom end of the developing fruit. Fruit losses from this disorder vary from negligible to economically devastating levels (Terry & Boyhan, 2006). Pepper stippling is associated with calcium and potassium deficiency, and is characterized by brown or black spots inside the fruit wall as the pepper reaches maturity, expressed also on the fruit surface as green or yellow spots (Terry & Boyhan, 2006). Sunscald, which occurs when ripening fruit is not adequately shaded by the plant's leaf canopy, produces large sections of gray or brown paper-thin areas on the exposed fruit. This disorder can be managed by planting pepper varieties that produce a large canopy and are resistant to defoliating diseases (Black *et al.*, 1991; Terry & Boyhan, 2006). Poor colour development results from insufficient light entering the canopy during the period when peppers are grown to full maturity beyond the initial immature fruit colour (Terry & Boyhan, 2006). Nutrient disorders other than blossom end rot occur when peppers do not receive adequate nutrients, and when the soil pH is low, resulting in stunted growth and aluminium toxicity (Black *et al.*, 1991; Terry & Boyhan, 2006).

2.5 Breeding in *Capsicum* peppers

2.5.1 Diversity as a basis for improvement of *Capsicum* peppers

The basis for any plant breeding program is the existence of variation among the different varieties from which selection is done to gain superior genotypes of interest (AVRDC, 1990). Wide genetic diversity offers a wide range of sources of genes for crop improvement (Nass & Paterniani, 2000). The existence of genetic diversity among crops has special significance for maintaining and enhancing productivity of agricultural crops in countries that are characterized by highly varied agro-climates and diverse growing conditions. Such genetic diversity provides security for the farmer against diseases, pests, drought, and other stress conditions. Genetic diversity also allows farmers to exploit the full range of highly varied micro-environments differing in characteristics such as soil composition, water availability, temperature, altitude,

slope, and fertility (Hawkes, 1991). Variation among individual plants is influenced by genotype, environment and their interaction. Considerable variation among pepper lines has been noted in flowering ability, fruit set, yield and other qualitative traits under different agro-ecological climates (Rani, 1996; AVRDC, 2004; Adetula & Olakojo, 2006; Seleshi, 2011).

Varieties available for use by farmers include traditional and improved varieties. Traditional varieties (or landraces) are those that have been used by farmers for many generations. They usually start as a farmer's selection that is later reproduced and maintained by the farmers themselves. Improved varieties, on the other hand, result from systematic plant breeding and seed multiplication by trained personnel. Variety improvement has been proved to increase productivity in many crops, including wheat (Evenson & Gollin, 2003). For variety improvement, significant variation for important traits is important, including variation in yield, fruit traits, and tolerance to environmental stresses, (Bosland, 1993; DeWitt & Bosland, 1996).

2.5.2 Breeding principles and practices in *Capsicum* peppers

Successful breeding involves developing genotypes that are genetically superior to those currently available (Lynch & Walsh, 1998). Breeders achieve this through combining the desired alleles into a single target genotype. Though *Capsicum* is a self-pollinating plant, the rate of out-crossing associated with natural insect pollinators varies from 7 to 91% (Bosland, 1996). This affects breeding methods, necessitating precautions by plant breeders to eliminate pollination by insects and promote self-pollination if they are to develop true-to-type seeds (DeWitt & Bosland 1996). Inter-specific crosses have been made successfully between *C. annuum* and *C. chinense*. Hybridization of chillies has been commercially successful using hand-emasculation, genetic male-sterility and cytoplasmic male-sterility techniques. Backcross, mass, single plant and pedigree selection methods, as well as single seed descent and haploid breeding are being practiced (Bosland, 1996). Genetic transformation research on *Capsicum* has been attempted with success (Ochoa-Alejo & Ramirez-Malagon, 2001; BoShou, 2005).

The breeding methodology adopted depends considerably upon the nature and magnitude of gene action controlling the genetic behavior of traits of interest (El-Bramawy & Shaban, 2007). Selection and improvement of these traits requires knowledge on the magnitude of useful genetic variances present in the pepper cultivars, in terms of combining ability and heterosis. Exploitation of hybrid vigor and selection of parents on the basis of combining ability and gene action have been important breeding approaches in crop improvement (Chowdhary *et al.*, 2007). Combining ability can be general (GCA) or specific (SCA) where GCA is a measure of the additive gene action, while the SCA is due to non-additive (dominant or epistatic) gene action (Chowdhary *et al.*, 2007). Genetic studies of this nature have been examined using the diallel analysis techniques and have proved to be useful to obtain precise information about the types of gene actions involved in the expression of various traits and to predict the performance of the progenies in the latter segregating generations (Marame *et al.*, 2008).

2.6 Evaluation and characterization of pepper germplasm

Germplasm collection and assembling avail plant breeders with a broad genetic base for crop improvement. Characterization and evaluation of the collected and assembled materials enhance their utilization towards increasing yield potential and adaptation to environmental stresses (AVRDC, 1989; Engle, 2001). This effort involves recording characters that are highly heritable, can be easily seen by the eye, and are expressed in all environments (IBPGR, 1993; Engle, 2001). Phenotypic and genetic diversity among genotypes can be assessed using morphological descriptors and biochemical and/or molecular markers. Characterization with morphological descriptors enables easy and quick discrimination among cultivars. Evaluative descriptors such as yield, agronomic performance, susceptibility to stress, and biochemical and cytological traits are susceptible to environmental differences, though useful in crop improvement (IBGPR, 1993)

2.6.1 Morphological markers as tools for assessing plant diversity

Morpho-agronomic characterization, using standard descriptors, in most breeding programmes is the first step in conservation of germplasm, and the use and study of genetic relationships (Van

ningen & Busch, 1997; Engle, 2001). Morphological characterization does not require any
nisticated equipment or complex experiments, but is generally simple, rapid and inexpensive.
vever, many traits that are important in breeding programmes, such as yield performance and
ity characters, are controlled by multiple genes and thus are subject to varying degrees of
ronmental modification and interaction (IBPGR, 1993). In addition, most morphological
riptors are recessive and therefore expressed only in the homologous condition. Thus, to
quately describe the genotypes under study using morphological markers, extensive
icated tests are needed (Lin & Binns, 1994). Smith & Smith (1989) argue that valid
parisons of genotypes with morphological descriptors are possible only when those
riptors are recorded at the same location during the same season. Hence, information that is
vided by morphological descriptors is often limited and may not accurately indicate the
ting genetic diversity among genotypes. Such results should be complemented by molecular
iochemical studies (Karp *et al.*, 1997).

2 Biochemical and molecular markers as tools for plant diversity assessment

chemical markers use isozymes, which are enzymes that share a common substrate but differ
lectrophoretic mobility. These markers have been used to determine genetic similarity among
ıy crops (Cabrita *et al.*, 2001; Veasey *et al.*, 2002). Use of isozymes is simple because
acting and running protein extracts is simple on agarose gels; a large number of samples can
un in a very short time and the bands are expressed co-dominantly. In recent years, molecular
kers (DNA-based) have been the most popularly type of marker used to genetically
racterise a wide range of crop species at the levels of species and subspecies (Karp *et al.*,
6; Kumar, 1999; Melake-Berhan, 2000). These markers include: Restriction Fragment
gth Polymorphism (RFLP), Randomly Amplified DNA Polymorphism (RAPD), Amplified
gment Length Polymorphism (AFLP), and Simple Sequence Repeats (SSR's), or
rosatellites. Molecular markers are advantageous in determining the genetic diversity in traits
are controlled by many genes and influenced by the environment, thus being difficult to
ermine by conventional methods (Engle, 2001). These markers allow a direct comparison of
etic diversity at the DNA level, have the potential to identify a large number of polymorphic

loci with excellent coverage of an entire genome, are phenotypically neutral, allow scoring of plants at any developmental stage and are not modified by environment and management practices (Messmer *et al.,* 1993). However, for molecular markers to be effective, they must be polymorphic, co-dominant in nature, evenly distributed throughout the genome, easy, fast and inexpensive to detect as well as highly reproducible or transferable (Karp *et al.*, 1997; Kumar *et al.*, 2009).

2.7 Chapter summary

Pepper production in Uganda is constrained by pests and diseases that necessitate an integrated approach to management. An integral part of this approach would be resistant varieties. Apart from some viruses, most of the diseases that affect pepper in Uganda have not been identified (Ssekyewa, 2007; Dafalla, 2008; Nono-Womdim, 2008, Mukasa *et al.*, unpublished). These diseases need to be identified and appropriate improved germplasm evaluated for resistance. Cultivars that combine high yield, good horticultural traits and resistance to diseases under local conditions would be most desirable for the farmers. The AVRDC has developed pepper varieties that have improved horticultural traits (Gniffke, 2008). There was need to compare these cultivars with local Ugandan germplasm collections for yield, horticultural traits and reaction to field diseases under Ugandan environmental conditions so as to identify the most suitable cultivars to recommend for *Capsicum* improvement. Through breeding and selection from a wide array of germplasm with considerable diversity, better performing pepper cultivars will be identified to provide improved cultivars for the hot pepper sub-sector in Uganda. This study attempted to determine the diversity that existed within a selection of collected germplasm in order to identify better-performing cultivars in terms of disease resistance, good horticultural and yield traits. The genetics of control over yield and its associated traits was also studied as a basis for initiating pepper improvement in Uganda that has been lacking. It is expected that the output from this research will boost farmers' livelihood income through improved productivity.

CHAPTER THREE

MORPHOLOGICAL CHARACTERIZATION OF HOT PEPPER (*C. annuum*) GENOTYPES IN UGANDA

Introduction

provement of hot pepper requires genetically-diverse materials from which breeders can ntinuously develop improved varieties that can stand environmental stresses, which evolve h time. In order for this assembly of diverse germplasm to be fully utilized, it would need to characterized for highly-heritable characters that can be easily seen by the eye, and are pressed in all environments (IBPGR, 1993; Engle, 2001). Phenotypic and genetic diversity ong genotypes can be assessed using morphological descriptors and biochemical and/or lecular markers. Morphological characterization, using standard descriptors, in most breeding grammes is the first step in conservation of germplasm, and the use or study of genetic ationships (Van Beuningen & Busch, 1997; Engle, 2001). Besides, characterization with rphological descriptors enables easy and quick discrimination among cultivars. Researchers e recorded wide variation in pepper germplasm using morphological markers (Munshi *et al.*, 00; Hallidri & Tome, 2000; Denton *et al.*, 2000). Differences between pepper landraces due to notype, environments or genotype-environment interaction have also been observed (Zewdie Bosland, 2000). In order to enhance the diversity of pepper germplasm in Uganda, a collection elite genotypes from the Asian Vegetable Research and Development Centre (AVRDC) in wan, China were evaluated. In this chapter, the morphological traits of this collection were racterized, alongside local pepper germplasm, and the morphological diversity among them s determined.

Materials and Methods

.1 Study area

t pepper germplasm was characterized in a screen-house trial at the National Agricultural search Laboratories Institute (NARL) from March to July 2010. The Institute is located 15km th of Kampala in Kyadondo county, Wakiso district and stands at an elevation of 1,200m ve sea level. The area has sub-humid climate and receives mean annual precipitation of 50mm that has a bimodal distribution. Mean maximum air temperatures vary between 25°C d27°C, while minimum temperatures range between 15°C and17°C.

.2 Source of hot pepper genotypes

irty seven (37) hot pepper (*Capsicum annuum*) genotypes were characterized in this study, luding 11 local accessions and 26 exotic introductions predominantly from the AVRDC ible 1). The local germplasm were collected from four districts in Central and Western anda, which are among the major hot pepper growing regions (ADC/IDEA, 2001; UEPB, 05a,b). The districts were Kampala and Wakiso in the Central region; and Kasese and Kisoro he Western region (Fig. 2). Local genotypes were collected from around farmer homesteads. e local genotype, CA-EASC-09-1 was collected from East African Seed Company and ther one, CA-UGCE 09-3 from ICEMARK, a local company that exports fresh fruits and getables from Uganda. The local varieties were coded by the name of the species, year of lection and a collection number. All genotypes were sourced between November 2008 and rch 2009.

.3 Propagation of germplasm and experimental design

or to sowing in a screen-house on August 10, 2009, seeds were treated in order to inactivate d-borne tobamoviruses: *Tobacco mosaic virus* (TMV), *Tomato mosaic virus* (ToMV), *Pepper d mottle virus* (PMMV) (Rashid *et al.*, 2007). In this process, seeds were soaked in a 10%

Table 1. Hot pepper (*Capsicum annuum*) genotypes characterized for morphological traits in the screen house at NARL, Uganda from 2009-2010

Genotype No.	Code /Name	Country of Origin	Region
1	PBC 375	Taiwan	AVRDC
2	PBC 535	Taiwan	AVRDC
3	PP97-7195-1	Taiwan	AVRDC
4	PP9848-4996	Taiwan	AVRDC
5	PP9852-110	Taiwan	AVRDC
6	PP9852-149	Taiwan	AVRDC
7	PP9852-173	Taiwan	AVRDC
8	PP9955-15	Taiwan	AVRDC
9	PP0007-2247	Taiwan	AVRDC
10	PP0007-2259	Taiwan	AVRDC
11	PP0007-2269	Taiwan	AVRDC
12	PP0042-17	Taiwan	AVRDC
13	PP0237-7502	Taiwan	AVRDC
14	PP0237-7508	Taiwan	AVRDC
15	PP0337-7065	Taiwan	AVRDC
16	PP0337-7545	Taiwan	AVRDC
17	PP0337-7546	Taiwan	AVRDC
18	PP0337-7562	Taiwan	AVRDC
19	PP0437-7506	Taiwan	AVRDC
20	PP0537-7513	Taiwan	AVRDC
21	PP0537-7528	Taiwan	AVRDC
22	PP0537-7539	Taiwan	AVRDC
23	PP0537-7541	Taiwan	AVRDC
24	PP0537-7558	Taiwan	AVRDC
25	PP0537-7504	Taiwan	AVRDC
26	CA-EASC-09-1	Uganda	EASC[a]
27	CA-PPCHI-08-1	China	Seed company
28	PP9852-115	TZ	AVRDC-RCA
29	CA-UGKI 09-6[c]	Uganda	Kisoro
30	CA-UGKI 09-5	Uganda	Kisoro
31	CA-UGCE 09-3	Uganda	Wakiso[b]
32	CA-UGKA 09-3	Uganda	Kasese
33	CA-UGKI 09-1	Uganda	Kisoro
34	CA-UGKI 09-2	Uganda	Kisoro
35	CA-UGKI 09-4	Uganda	Kisoro
36	CA-UGKI 09-7	Uganda	Kisoro
37	CA-UGKA 09-4	Uganda	Kasese

[a]East African Seed Company, Kampala
[b]Commercial variety (ICEMARK)
[c]Locally collected genotypes were arbitrary designated names based on the place of origin with prefixes "CE", "KI", "KA", EASC

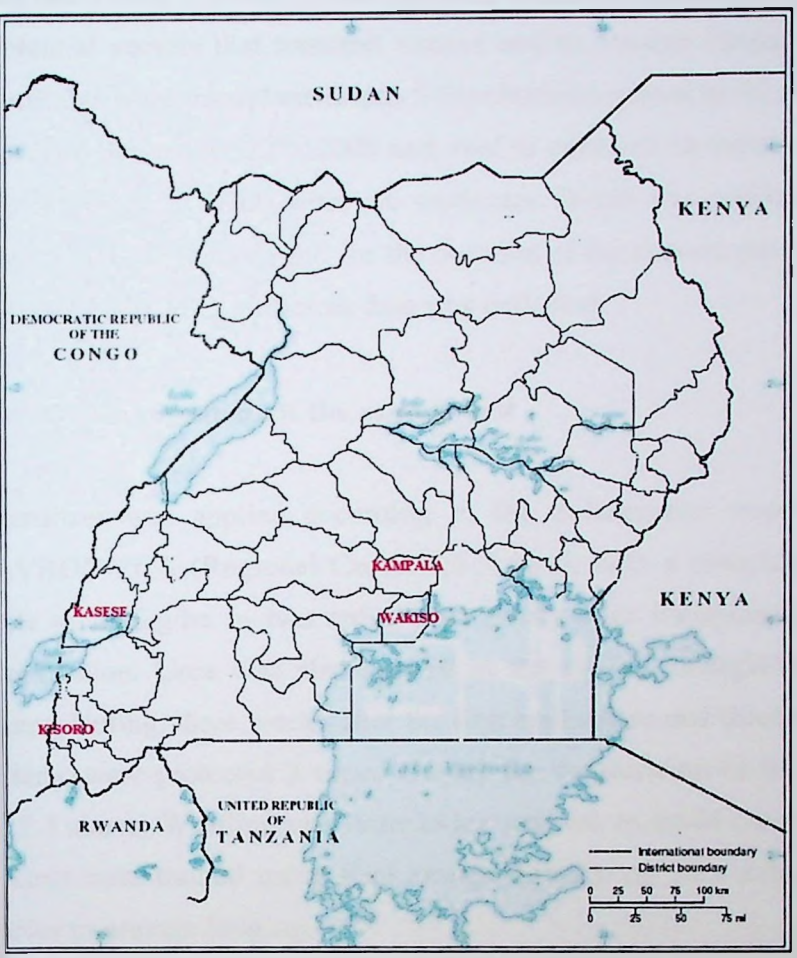

Figure 2. Map of Uganda showing districts where the characterized local hot pepper genotypes were collected.

w/v) solution of trisodium phosphate (TSP) for 30 minutes and transferred to a fresh solution of he same reagent for a further two hours before rinsing in running water for 45 minutes. Seed were then soaked in water for 24 hours in order to facilitate germination (Rashid *et al.*, 2007) and planted in growth media made up of sterilized soil in the ratio 3:1:1 (soil: sand: decomposed dried cow dung). In addition, the organic fertilizer vegimax (trace minerals, vitamins and amino acids produced from plant products, at the rate 35mls/15lts) was applied twice a week for two weeks at the two-leaf stage. After germination, seedlings were protected 3 times a week for four weeks using one protective fungicide, Ridomil (Metalaxyl-M 40g/kg + Mancozeb 640g/kg ai, at

the rate 60g/15lts) to control fungal infection and two pesticides Tafgor 40 EC (Dimethoate 40% EC ai, at the rate 30mls/15lts) and Alfapor spray and dip (50 mg/ml alpha-cypermethrine EC, at the rate 15mls/15litres) interchangeably to protect against insect pests and mites, and to eliminate potential vectors that transmit viruses and to manage fungal pathogens. Five-weeks old single seedlings were transplanted into 5-litre buckets spaced at 45 cm within rows and 60 cm between rows on September 22nd, 2009 and used to establish an experiment using a randomized complete block design (RCBD) with two replicates. Water was applied twice a day, in the morning and evening in the nursery and for the duration of the experiment. The experiment was terminated on May 1, 2010, after sufficient data was collected.

3.2.4 Management of the experiment

Fertilizer was applied according to the Solanaceous vegetable evaluation protocols of the AVRDC-RCA (Regional Center for Africa), with a complete fertilizer NPK (20:10:10) at the rate of 400kg/ha in two splits: two weeks after transplanting and three weeks after the first application. Urea was also applied at the rate of 100kgN/ha in three splits: two weeks after transplanting, three weeks after the first application and three weeks after the second application. Plants were protected 3 times a week for the duration of the experiment using as described in 3.2.3 above. Weeding was done twice a month to avoid competition for nutrients. At flowering, plants were trained using sisal strings fastened on wire strings to produce a grid of support in order to prevent lodging.

3.3 Data collection and analyses

3.3.1 Data collection

Data were collected on morphological traits, covering the vegetative parts of the plant, the inflorescence, fruit and seed in a protocol adapted from IPGRI *et al.* (1995) and Engle (2001). These traits included:

1. Vegetative descriptors (15) such as nodal anthocyanin, stem pubescence type, stem pubescence density, plant height, plant growth habit, plant canopy width, stem length, stem diameter, primary branch numbers, secondary branch numbers, leaf shape, leaf surface, lamina margin, leaf pubescence type and leaf pubescence.
2. Inflorescence descriptors (9) that included days to flowering, pedicel position, corolla colour, corolla length, anther colour, anther length, stigma exertion, calyx margin and calyx annular constriction.
3. Fruit descriptors (21) including days to fruiting, days to fruit maturity, presence of anthocyanin spots or stripes, fruit colour at intermediate stage, intermediate fruit colour intensity, fruit colour at mature stage, mature fruit colour intensity, fruit shape, fruit length, fruit width, fruit weight, fruit pedicel length, fruit wall thickness, fruit shape at pedicel attachment, neck at base of fruit, fruit shape at blossom end, fruit blossom end appendage, fruit cross-sectional corrugation, fruit surface, number of fruit per plant and number of seeds per fruit.
4. Seed descriptors (3) such as seed diameter, 300-seed weight and number of seeds per fruit.

The detailed descriptor list used in this characterisation study is presented in Appendix 2. For quantitative characters, data were collected on all the five plants in a replicate and the mean values considered. Qualitative descriptors were scored from all the 10 plants per genotype in the whole experiment.

3.3.2 Data analyses

Quantitative data were subjected to Analysis of Variance (ANOVA) using GenStat computer package (12th edition, Version 12.2; VSN International Ltd, 2010). Two multivariate analysis methods were used, principal component analysis (PCA) and hierarchical cluster analysis. Mean values of all quantitative traits were standardized so as to assume values from the same interval according to Kalbarczyk (2010) as follows:

$$Z_i = [X_i - \text{Min}(X_i)]/\text{Max}(X_i) - \text{Min}(X_i)$$

Where; Min (X_i) = lowest value of the i^{th} factor.

Max (X_i) = Highest value of the i^{th} factor

Standardized trait values were subjected to principal component analysis (PCA) using the appropriate options of the XLSTAT statistical computer package (Version 2011.3.01) to determine the traits most effective in discriminating between genotypes basing on Pearson (n-1) Correlation Coeffients Matrix procedure generated by the package. Principal components coefficients, eigenvalues, and relative and cumulative proportions of the total variance expressed by single traits were calculated. Principal components with eugenvalues >1 were extracted for interpretation as recommended by Kaiser (1960) and Wuensch (2010). The first two components explaining the maximum variance were rotated by Varimax method for uncorrelated components with Kaiser Normalization to reduce the complexity of the components by making the large loadings larger and the small loadings smaller within each component and plotted together to generate trait and genotype graphs and a bi-plot for ease of interpretation (Wuensch, 2010; Anonymous, 2010b). Euclidean distance coefficient (EDC) was estimated to generate a matrix for assessing the level of dissimilarity between genotypes using cluster analysis on both quantitative and qualitative traits based on Complete Link method of the GenStat computer package (12th edition, Version 12.2; VSN International Ltd, 2010). The generated phenograms were used to determine clusters with high similarity coefficients. The phenotypic diversity among genotypes by qualitative traits was further assessed using Shannon-Weaver diversity

index (Shannon & Weaver, 1949), calculated based on phenotypic frequency of alleles controlling each qualitative trait category of descriptors as follows:

Shannon-Weaver diversity index = $e^{H'}$

$$H' = -\sum_{i=1}^{S}(p_i \ln p_i)$$

Where; H′ = diversity index

S = total number of descriptor states in the i-th descriptor

P_i = fraction of individuals belonging to the i-th descriptor state (number of observations/descriptor state in the i-th descriptor divided by the total number of characterized plants)

3.4 Results

3.4.1 Analysis of quantitative morphological traits

3.4.1.1 Variability in quantitative morphological traits among hot pepper genotypes characterized under protected environment

Analysis of variance showed highly significant variability among genotypes in 19 traits ($P<0.01$ for days to fruiting, and $P<0.001$ for the rest of traits), except number of primary branches ($P=0.579$) (Table 2). In general, the local genotypes were taller, matured later, had smaller fruit size and produced lower yields compared to the improved exotic genotypes, except for the East African seed company genotype 26 that was the earliest maturing, was shorter and produced medium fruit size genotype (Appendix 3). The AVRDC genotypes 8, 19 and 16 and the Chinese seed company genotypes 27 had the largest fruits. However, genotype 27 was shorter and yielded fewer fruits per plant (Appendix 3).

Table 2. Analysis of variance, mean and range of quantitative traits of 37 hot pepper genotypes characterized in the screen house at NARL in Uganda from 2009-2010

Parameter	Genotype (df =36)	Residual (df=36)						
	Mean Squares		Fpr (Genotype)	Mean	Range	SED±	LSD (0.05)	CV (%)
Days to flowering (days)	201.74	29.04	<0.001	41.7	14.0-60.5	5.39	10.93	12.9
Days to fruiting (days)	184.3	71.01	0.003	46.1	19.5-65.0	8.43	17.09	18.3
Days to fruit maturity (days)	229.9	61.01	<0.001	90.8	58.5-108.5	7.81	15.84	8.6
Fruit length (cm)	28.79	1.703	<0.001	9.4	2.2-16.1	1.31	2.65	13.9
Fruit width (cm)	0.302	0.021	<0.001	1.7	0.96-3.0	0.15	0.30	8.7
Fruit pedicel length (cm)	0.920	0.123	<0.001	3.4	2.3-5.1	0.35	0.71	10.4
Fruit wall thickness (cm)	5.57×10^{-3}	1.17×10^{-3}	<0.001	0.17	0.08-0.3	0.03	0.07	19.6
300 seed weight (g)	0.106	9.89×10^{-3}	<0.001	1.6	1.1-2.0	0.10	0.20	6.4
Number of seeds per fruit	1147.9	124.8	<0.001	71.7	31.1-149.1	11.17	22.66	15.6
Number of fruit per plant	95.64	22.18	<0.001	13.0	4.0-44.5	4.71	9.55	36.3
Stem diameter (cm)	0.069	0.0134	<0.001	1.1	0.7-1.3	0.12	0.23	10.9
Stem height (cm)	201.94	12.59	<0.001	27.0	6.7-55.0	3.55	7.20	13.1
Secondary branch numbers	5.894	0.7421	<0.001	6.0	4.0-9.8	0.86	1.75	14.3
Primary branch numbers	0.022	0.023	0.579	2.1	2.0-2.4	0.15	0.31	7.3
Plant width (cm)	353.03	40.54	<0.001	69.4	44.1-108.5	6.37	12.91	9.2
Plant height (cm)	677.23	54.82	<0.001	78.9	47.1-129.1	7.40	15.02	9.4
Seed diameter (cm)	3.53×10^{-3}	7.07×10^{-4}	<0.001	0.4	0.3-0.5	0.03	0.05	6.9
Fruit weight (g)	105.21	3.709	<0.001	8.7	1.2-37.4	1.93	3.91	22.2
Corolla length (cm)	0.178	1.13×10^{-3}	<0.001	1.2	0.5-1.8	0.03	0.07	2.8
Anther length (cm)	4.52×10^{-3}	3.01×10^{-5}	<0.001	0.3	0.2-0.4	0.01	0.01	1.8

3.4.1.2 Principal component analysis for 20 hot pepper quantitative traits

Results obtained for principal component (PC) analysis grouped the twenty quantitative traits into 20 principal components, with eugenvalues in the range of 0.12 (PC 20) and 8.328 (PC1) (Data not shown). The analysis showed the first five components to have eigenvalues greater than 1, accounted for 76.46% of original total variability with uneven positive and negative loadings (Table 3) and were thus, considered important (Kaiser, 1960; Wuensch, 2010; Anonymous, 2010b). However, the first two components accounted for 55.4% of the total variance and hence were the most meaningful components for variability as indicated by a scree test (Appendix 4). The first five PCs with eigenvalues >1 are maintained for purposes of interpretation. In this interpretation, a vector loading is considered responsible for variability to a given component if its absolute value is >0.40 or more for that component and the other components (Wuensch, 2010; Anonymous, 2010b).

Based on this measure, high positive loadings that accounted for variability on the first PC (41.64%) in the descending order were: fruit length, fruit weight, fruit wall thickness, fruit width, number of seeds per fruit, seed diameter, 300 seed weight and anther length while those that contributed negatively in the descending order were plant height, stem diameter, plant width, day to flowering, stem height, days to fruiting, number of fruits per plant, days to fruit maturity, and secondary branch numbers. The high positive loadings in decreasing order of importance were of days to flowering, days to fruiting, days to fruit maturity, fruit width, fruit wall thickness, primary branch numbers and fruit weight account for more variability on PC2 (13.76%). Three high positive loadings of corolla color, anther length, number of seeds per fruit and 300 seed weight contributed most on variability of PC3 (8.41%). Two high positive loadings of fruit pedicel length and secondary branch numbers and one high negative loading of primary branch numbers contributed most to the variability on fourth PC (7.37 %) while the positive loadings of primary branch numbers, secondary and pedicel length contributed mostly to PC5.

Table 3. Principal component (PC) analysis of 20 quantitative characters from 37 *C. annuum* hot pepper genotypes characterized in the screen house at NARL in Uganda from 2009-2010

	Eigenvectors (principal components)					
Trait	**PC1**	**PC2**	**PC3**	**PC4**	**PC5**	**PC6**
Eigen values (Variance)	8.328	2.751	1.682	1.475	1.055	0.852
Proportion of variance (%)	41.64	13.76	8.41	7.37	5.28	4.26
Cumulative variance (%)	41.64	55.4	63.81	71.18	76.46	80.72
	Factor loadings (correlation coefficients)					
Days to flowering	-0.712	0.595	-0.011	-0.178	0.032	0.021
Days to fruiting	-0.679	0.516	0.002	-0.200	-0.020	-0.076
Days to fruit maturity	-0.670	0.544	0.022	-0.096	-0.017	0.091
Fruit length (cm)	0.872	0.199	-0.068	0.029	0.000	-0.100
Fruit width (cm)	0.697	0.525	0.089	0.186	-0.180	0.222
Fruit pedicel length (cm)	0.226	0.327	-0.080	0.638	0.406	0.046
Fruit wall thickness (cm)	0.721	0.521	-0.038	-0.010	-0.040	0.026
300 seed weight (g)	0.545	0.076	-0.631	0.117	0.072	0.277
Average number of seeds per fruit	0.618	0.372	0.437	-0.008	-0.113	-0.286
Average number of fruits per plant	-0.676	-0.342	0.281	0.090	0.200	-0.118
Stem diameter (cm)	-0.811	0.278	-0.011	0.232	-0.042	0.286
Stem height (cm)	-0.704	0.324	0.009	0.343	-0.070	-0.302
Secondary branch numbers	-0.625	-0.260	0.185	0.422	0.294	0.045
Primary branch numbers	-0.105	0.440	-0.045	-0.490	0.544	-0.274
Plant width (cm)	-0.773	0.149	-0.114	0.315	-0.177	0.021
Plant height (cm)	-0.825	0.372	-0.161	0.114	-0.061	-0.074
Stem diameter (cm)	0.553	0.029	-0.347	0.161	0.496	-0.139
Average fruit weight (g)	0.762	0.509	0.121	0.122	-0.096	0.016
Corolla length (cm)	0.005	0.126	0.641	-0.222	0.343	0.542
Anther length (cm)	0.491	0.003	0.610	0.370	-0.016	-0.183

PC1-6: Principal components 1-6

On the five important extracted principal components, many variables load on more than one component making interpretation difficult since they seemed to measure similar constructs across components (Anonymous, 2010b). Results of the rotation indicate that the first two PCs account for 28.16% and PC2 27.23%, respectively of the total variance (Table 4).

Table 4. Factor loadings, variability and cumulative variability of total variance for each trait characterized in hot pepper in Uganda during 2009-2010with respect to the first two principal components after Varimax rotation

Trait	Factor loadings[a]	
	PC1[b]	PC2[c]
Days to flowering	-0.097	0.923
Days to fruiting	-0.129	0.843
Days to fruit maturity	-0.103	0.856
Fruit length (cm)	0.765	-0.463
Fruit width (cm)	0.866	-0.107
Fruit pedicel length (cm)	0.390	0.078
Fruit wall thickness (cm)	0.880	-0.127
300 seed weight (g)	0.445	-0.324
Average number of seeds per fruit	0.703	-0.163
Average number of fruits per plant	-0.724	0.224
Stem diameter (cm)	-0.389	0.764
Stem height (cm)	-0.280	0.723
Secondary branch numbers	-0.630	0.247
Primary branch numbers	0.231	0.390
Plant width (cm)	-0.452	0.644
Plant height (cm)	-0.335	0.841
Stem diameter (cm)	0.418	-0.364
Average fruit weight (g)	0.901	-0.164
Corolla length (cm)	0.091	0.087
Anther length (cm)	0.355	-0.339
Eigen values (Variance)	5.632	5.447
Proportion of variance (%)	28.16	27.23
Cumulative variance (%)	28.16	55.39

[a]Correlation coefficients
[b]PC1: Principal components 1
[c]PC2: Principal component 2

Both fruit length and plant width load on both components with loadings above 0.4, and are dropped from interpretation since they are not pure measures of any one construct (Anonymous, 2010b). Consequently, the meaningful positive loadings for PC1 after Varimax rotation in the descending order are fruit weight, fruit width, fruit wall thickness, number of seeds per fruit, 300 seed weight and seed diameter while meaningful negative loadings were number of fruits per plant and secondary branch numbers. This component is thus related to yield traits whose genotypes with big fruits and seeds, few numbers of secondary branch numbers and fruits per plant contributed more to its variability. The meaningful traits that loaded highly on PC2 in

descending order were positive values of days to flowering, days to fruit maturity, days to fruiting, plant height, stem diameter, stem height and plant width which are related to growth traits. Genotypes with late maturity, taller plants and wider canopies contributed more to the variability of this component.

Principal component analysis (PCA) bi-plots show how traits and genotypes cluster according to similarity (Fig. 3 and 4). The bi-plots of all genotypes grouped by PC1 and PC2 delineated genotypes according to similarities in traits, regardless of place of origin, into four quadrants. The PCA bi-plot before Varimax rotation shows genotypes and traits scattered without a clear pattern of delineation to the component axes (Fig. 3) and are thus hard to interpret. The PCA bi-plot after Varimax rotation gives a clear picture (Fig. 4) for interpretation. Genotypes on the negative side of horizontal axis (PC1) have small fruits and seeds, many primary branch numbers and number of fruits per plant while genotypes on the positive side have big fruits and seeds, few primary branch numbers and number of fruits per plant. Genotypes on the positive side of vertical axis (PC2) are late maturing, have tall plants with wide canopies and stems while genotypes on the negative side of the vertical axis are early maturing, have short plants with narrow canopies and stems.

Apart from the AVRDC genotypes 14 and 8 that did not fall clearly in any group, all other genotypes clustered into four quadrants I, II, III, and IV (Fig. 4). Genotype 14 shares characteristics of both quadrants 1 and 2 while, genotype 8 shares characteristics of both quadrants 2 and 4. Genotypes 31, 20, 36, 29, 33, 37, 34, 30 and 35 grouped in quadrant I of the bi-plot are characterized by late maturity, tall plants with wide plants and stem, small fruits and seeds, many secondary branch numbers and fruits per plant. Genotypes 20, 36, 29 and 33 are intermediate in these traits. The local genotype 35 was the most late maturing, the tallest with widest plant canopies and stems while the local check commercial genotype 31 had the smallest fruits and seeds and most number of fruits and secondary branch numbers.

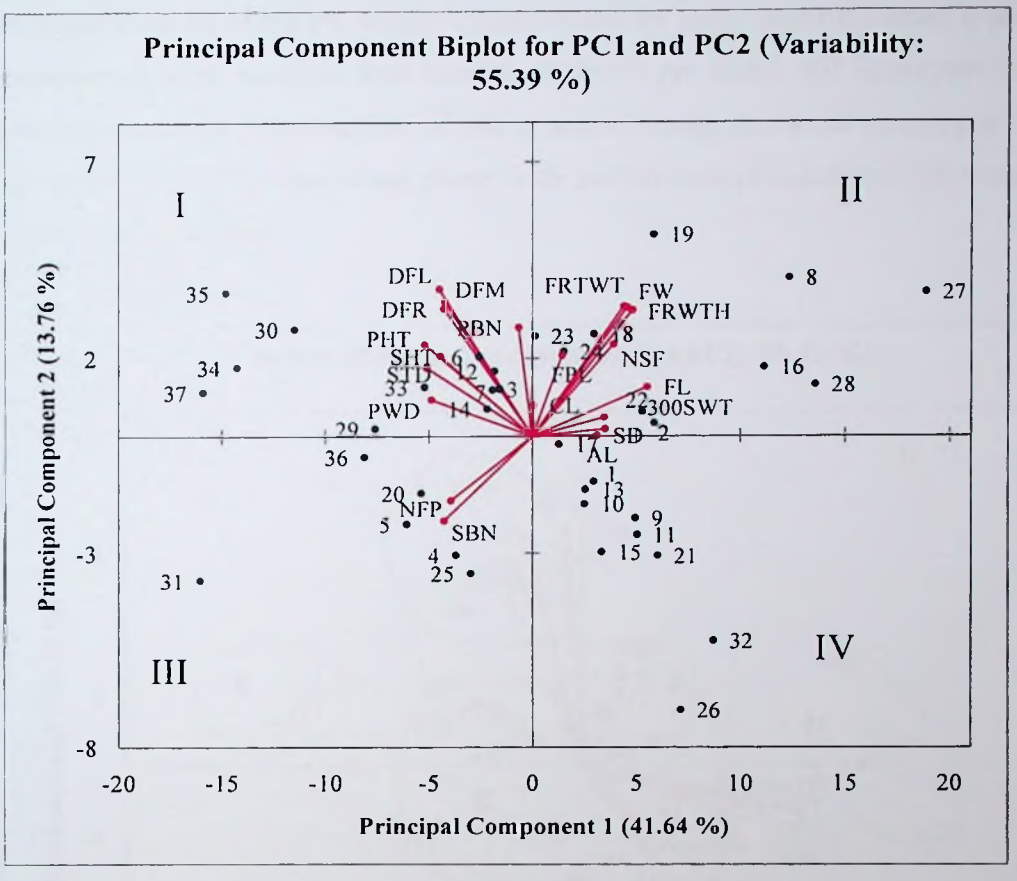

Figure 3. ***Capsicum annuum*** **morphological characterization biplot based on Principal Component 1 and 2 values using 20 quantitative descriptors before Varimax rotation. 1-37 refer to genotypes. Abbreviated words refer to descriptors.**

The AVRDC genotypes 3, 12, 6, 23, 24, 18 and 19 delineated in quadrant II of the bi-plot characterized by late maturity, tall and wide plant canopies with big stems, big fruits and seeds and few secondary branch numbers and number of fruits per plant. All genotypes in this group have intermediate traits for this quadrant except genotype 19 that exhibited big fruits and seeds, few secondary branch numbers and number of fruits per plant.

Genotypes 5, 4, 25, 10, 1, 15, 9, 11, 21, 32 and 26 isolat

ed in quadrant III of the PC bi-plot characterized by early maturity, small fruits and seeds, many secondary branch numbers and number of fruits per plant. All genotypes in this group have intermediate traits characteristic of this quadrant except the local genotypes 32 and 26 that are the earliest maturing, have short plants with narrow canopies and narrow stems that make them susceptible to lodging.

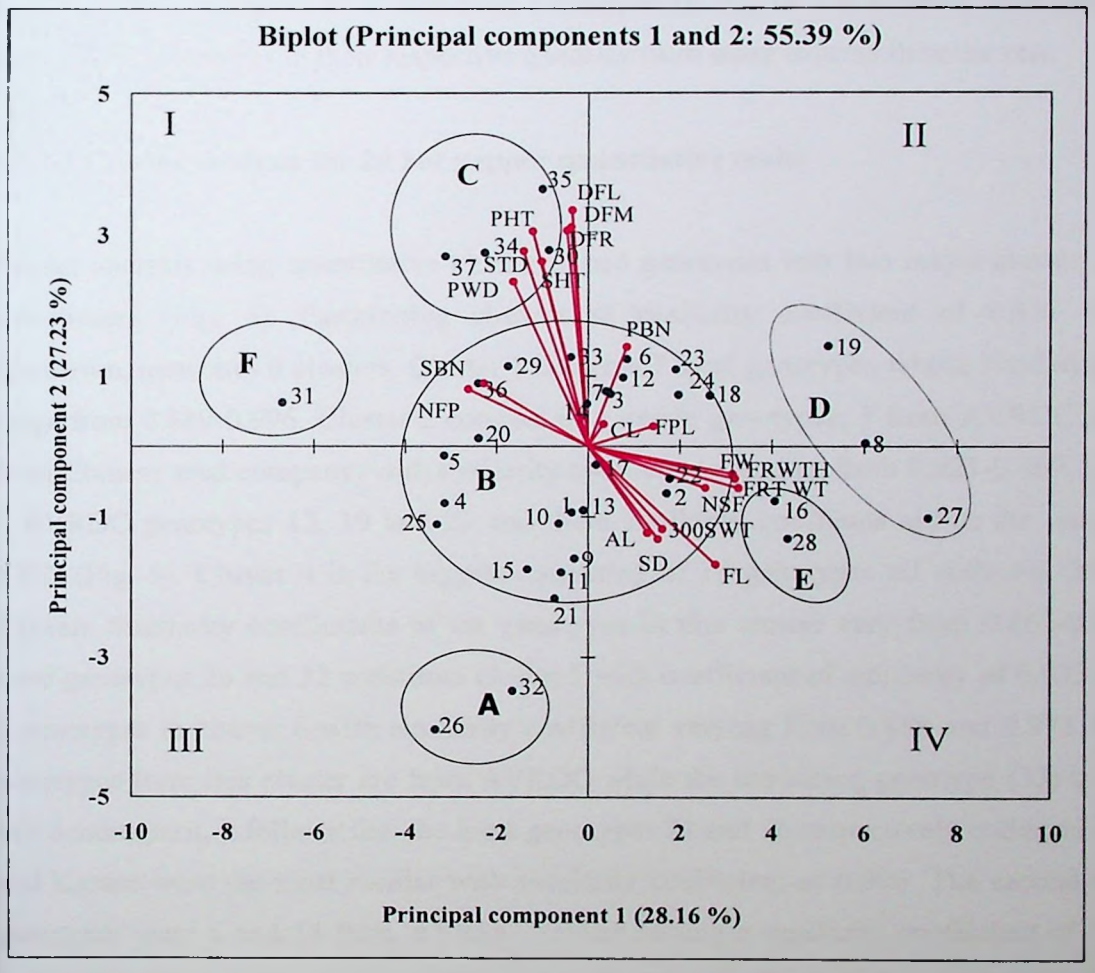

Figure 4. *Capsicum annuum* morphological characterization biplot based on the Principal Component 1 and 2 values using 20 quantitative descriptors after Varimax rotation. 1-37 refer to genotypes. Abbreviated words refer to descriptors.

this cluster have intermediate traits characterizing this quadrant apart from the Chinese seed company genotype 27 that had the biggest fruits and seeds and the fewest secondary branch numbers and number of fruits per plant.

The PC bi-plot also grouped genotypes into 6 sub-clusters A-F. Cluster A (26, 32) has negative loadings of PC2, cluster B (most traits) has intermediate loadings of both PC1 and PC2, cluster C (30, 35, 35, 37) has high positive loadings of PC2, cluster D (19, 8, 27) has high positive loadings of PC1, cluster E (16, 28) has intermediate loadings of PC1) while cluster F (31) has high negative loadings of PC1. However, genotypes 26, 32, 35, 19, 8, and 27 that separated more from all the genotypes in their respective quadrats were more diverse than the rest.

3.4.1.3 Cluster analysis for 20 hot pepper quantitative traits

Cluster analysis using quantitative traits grouped genotypes into two major clusters and several sub-clusters (Fig. 5). Partitioning clusters at similarity coefficient of 0.857, for ease of discussion, generates 6 clusters. Cluster 1 contains 7 local genotypes whose similarity coefficient range from 0.889-0.996. Cluster 2 consists of 4 exotic genotypes, 3 from AVRDC and one (27) from Chinese seed company, with similarity coefficients ranging from 0.921-0.969. Cluster 3 has 3 AVRDC genotypes 12, 19 and 23 and there similarity coeffients are in the range of 0.928-0.957 (Fig. 5). Cluster 4 is the biggest consisting of 12 genotypes all collected from AVRDC Taiwan. Similarity coefficients of the genotypes in this cluster vary from 0.867-0.985. Only 2 local genotypes 26 and 32 constitute cluster 5 with coefficient of similarity of 0.933. There were 9 genotypes in cluster 6 with similarity coefficient varying from 0.888 and 0.975. Eight of the genotypes from this cluster are from AVRDC while the remaining genotype (33) is local. From this dendrogram, it follows that the local genotypes 29 and 36 respectively collected from Kisoro and Kasese were the most similar with similarity coefficient of 0.996. The second most similar genotypes were 6 and 14 from AVRDC-Taiwan having a similarity coefficient of 0.985. Of all genotypes that sub-clustered together in a pair, 26 and 32 were the most dissimilar with the similarity coefficient of 0.933.

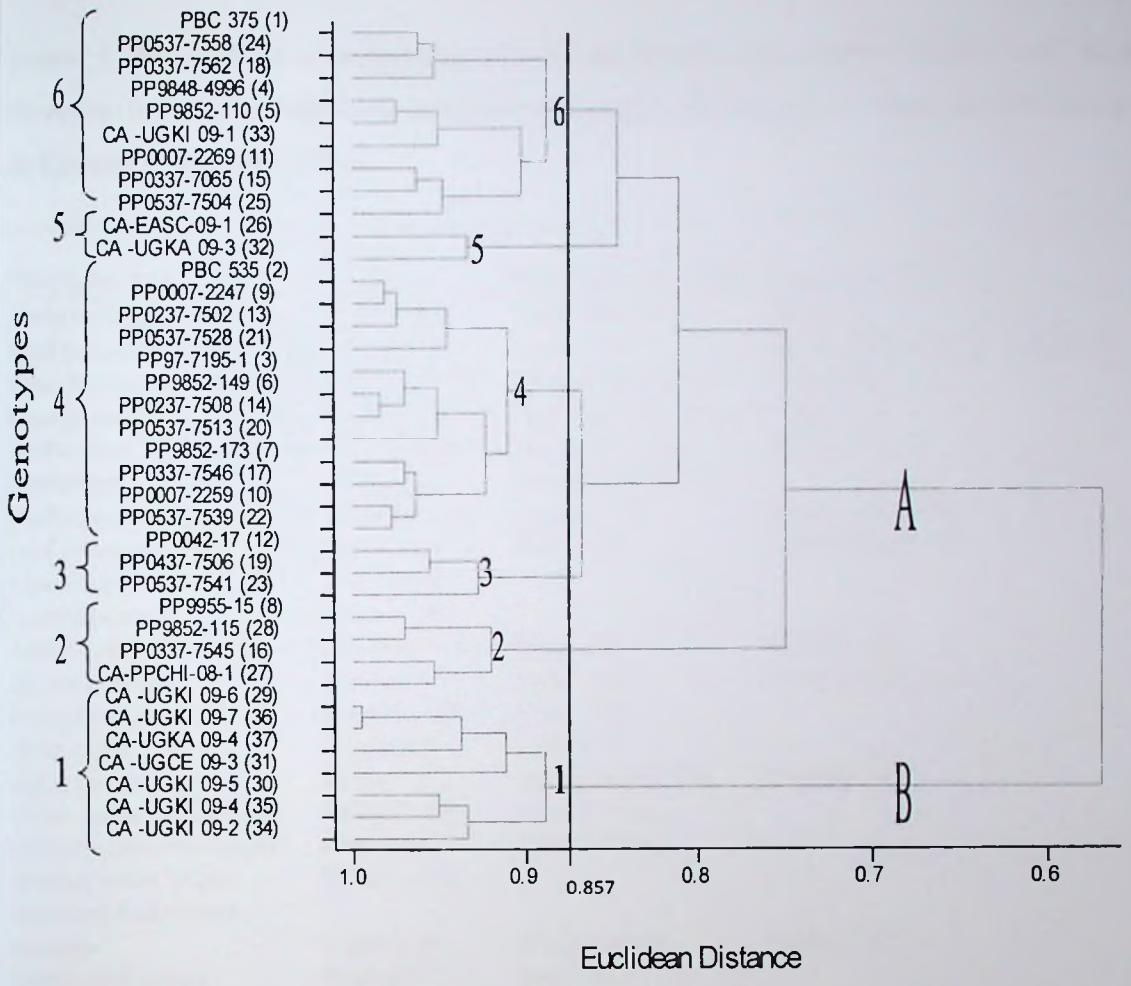

Figure 5. Dendrogram generated by hierarchical cluster analysis showing the interrelationships observed among local and exotic chilli pepper genotypes characterized using 20 quantitative traits in 2010 in Uganda. The vertical axis represents genotypes (codes in brackets). Euclidean Distance = Coefficient of similarity.

3.4.2 Analysis of morphological qualitative traits

3.4.2.1 Shannon-Weaver diversity index analysis of 28 morphological qualitative traits

Based on the frequency of 28 qualitative traits distribution among characterized genotypes, a wide range of variation was observed (Table 5). The predominant qualitative traits included

Table 5. Percentage distribution of 28 qualitative descriptor traits and their derived diversity indices in *Capsicum annuum* genotypes characterized in a screen house at NARL in Uganda from 2009-2010.

Descriptor trait	Descriptor occurrence frequency (%)				$e^{H'}$
Nodal anthocyanin	Green = 81	Light purple = 11	Purple=8		1.85
Stem pubescence type	Absent = 22	Short = 54	Intermediate = 8	Long = 16	3.20
Stem Pubescence density	Grabrous = 78	5 Intermediate = 11	dense =11		1.96
Plant growth habit	Prostate = 8	Intermediate = 78	Erect = 14		1.94
Leaf surface	Smooth = 76	Intermediate = 11	Rough=14		2.06
Leaf shape	Ovate = 43	Lanceolate = 57			1.44
Leaf pubescence density	Glabrous = 46	Sparse = 38	Intermediate =16		2.77
Leaf pubescence type	Absent = 46	Short = 38	Intermediate = 16		2.77
Leaf margin	Entire =100				1.00
Corolla colour	White = 100				1.00
Anther colour	Pale-Blue = 11	Blue = 54	Purple = 35		2.56
Stigma exersion	Inserted = 3	Same = 16	Exerted = 81		1.76
Pedicel position	Pendant = 84	Erect = 16			1.56
Style colour	White=95	Purple=5			1.23
Calyx margin	Entire = 22	Intermediate = 38	Dentate = 41		2.90
Calyx annular constriction	Absent = 46	Present = 54			1.99
Anthocyanin spots/stripes	Absent = 89	Present = 11			1.41
Immature fruit colour	Green = 100				1.00
Immature fruit colour intensity	Light = 19	Medium = 49	Dense = 32		2.80
Mature fruit colour	Orange = 5	Red = 95			1.23
Mature fruit colour intensity	Medium = 54	Dense = 46			1.99
Fruit shape	Elongate = 89	Triangular = 11			1.41
Fruit shape at pedicel attachment	Acute = 24	Obtuse = 68	Truncate = 8		2.25
Fruit neck at pedicel attachment	Absent = 100				1.00
Fruit shape at blossom end	Pointed = 95	Blunt = 5			1.23
Fruit blossom end appendage	Absent = 100				1.00
Fruit wall corrugation	Absent = 100				1.00
Fruit surface	Smooth = 38	Semi-wrinkled = 22	Wrinkled = 40		2.90
Mean					**1.83**

$e^{H'}$ = Shannon-Weaver Diversity Index

green nodal anthocyanin and exerted stigma (81%), obtuse fruit shape at pedicel attachment (68%), grabrous stem pubescence density and intermediate growth habit (78%), smooth leaf surface (76%), entire leaf margin, white corolla colour and medium green immature fruits (100%), pendant pedicel position (84%), white styles, medium red mature fruits and pointed fruits at blossom end (95%) and elongate fruits (89%). The detailed collected qualitative trait data for various genotypes are shown in Appendix 5.

Analysis of the Shannon-Weaver diversity index (H') showed significant diversity in the scored qualitative traits (Table 5). Although the overall mean index was moderately high (1.83), the index was high in stem pubescence type (3.20), leaf pubescence density and leaf pubescence type (2.77); anther colour (2.56), calyx margin and fruit surface (2.90), and immature fruit colour intensity (2.80). The lowest diversity was recorded in style colour, mature fruit colour and fruit shape at blossom end (1.23) while no diversity was detected among genotypes for leaf margin, corolla colour, immature fruit colour, fruit neck at pedicel attachment, fruit blossom end appendage and fruit wall corrugation traits (Table 5). All the genotypes had mature red fruit colour apart from local genotypes 29 and 35 that were orange at maturity. Similarly, only AVRDC genotypes 8 and 16 had pink style colour while the rest had white style colour (Appendix 5).

3.4.2.2 Cluster analysis of 28 morphological qualitative traits

The generated dendrogram from cluster analysis of qualitative traits clearly clusters genotypes into two major clusters A and B, with coefficients of similarity of 0.698 and 0.605, respectively which further subdivided into several sub-clusters (Fig. 6). Partitioning clusters at a similarity coefficient of 0.8, for ease of discussion, generates 8 clusters. Qualitative characteristics of genotypes within these clusters are shown in Appendix 5. Genotypes did not cluster together on the basis of the geographical origin. The biggest cluster 3 subdivided at similarity coefficient 0.808 has 12 genotypes with 17 and 20 being the most similar at 0.952 similarity coefficient. Cluster 1, at similarity coefficient of 0.806, contained 7 genotypes including local genotypes 26 and 32 that are the most similar with a coefficient of 0.968. Cluster 2 at similarity coefficient of

0.866 had 6 genotypes all from AVRDC, of which 23 and 26 were the most similar at 0.965 similarity coefficient.

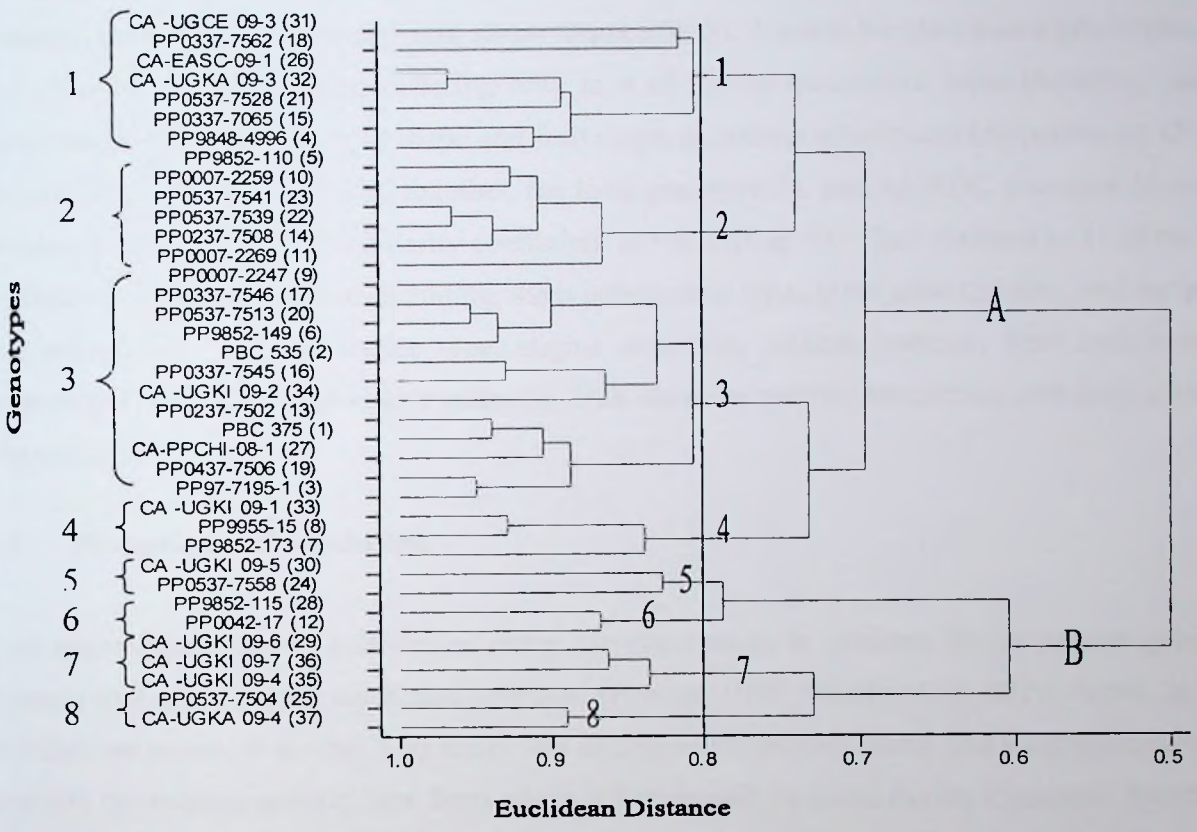

Figure 6. Dendrogram generated by hierarchical cluster analysis showing the interrelationships observed among local and exotic chilli pepper genotypes characterized using 28 quantitative traits in 2010 in Uganda. The vertical axis represents genotypes (codes in brackets). Euclidean Distance = Coefficients of similarity.

Cluster 4 at similarity coefficient of 0.841 has one local genotype and 2 exotic genotypes with local genotype 33 and AVRDC genotype 8 being the most similar at similarity coefficient of 0.929. Each of the clusters 5, 6 and 8 has 2 genotypes at similarity coefficients of 0.829, 0.869 and 0.892, respectively while cluster 7 has 3 local genotypes only at similarity coefficient of

0.837 with 29 and 36 being the most similar at similarity coefficient of 0.864. Like quantitative traits, genotypes 29 and 39 collected from Kisoro and Kasese, respectively are the most similar based on qualitative traits. They only differ in 7 of the 28 traits studied including, stem pubescence, stem pubescence density, anther colour, pedicel position, immature fruit colour intensity, mature fruit colour and fruit shape (Appendix 5). Among the introduced genotypes, 22 and 23 were the most similar differing only in 4 of the 28 qualitative traits including, nodal anthocyanin, calyx margin, fruit shape and fruit shape at pedicel attachment (Appendix 5). Of all the two genotypes that clustered together, the local genotype 31 and AVRDC genotype 18 were the most dissimilar with the similarity coefficient of 0.816 (Fig. 6). They differed in 11 of the 28 qualitative traits characterized including; stem pubescence type, plant growth habit, leaf surface, leaf pubescence, leaf pubescence type, stigma exsertion, pedicel position, fruit anthocyanin spots/stripes, immature fruit colour intensity, fruit shape at pedicel attachment and fruit surface (Appendix 5).

3.5 Discussion and conclusion

Crop improvement among cultivars of many important crops is hindered by the narrow genetic diversity that exists among cultivated landraces (Persley, 1986; Okello *et al.*, 2010; Scotti, 2011) of which hot pepper is among. This study was undertaken to collect exotic and local genotypes to diversify the existing genetic base from which selection will be made during *Capsicum* breeding programmes. Selected local and exotic pepper genotypes from Uganda, Tanzania and China were characterized using recommended qualitative and quantitative morphological descriptors (IPGRI *et al.*, 1995; Engle, 2001) to determine the extent of morphological diversity existing among them.

Most of the qualitative traits evaluated were found variable, indicating that these traits may be used to discriminate among genotypes. These traits included: fruit colour, size and shape; nodal anthocyanin, stem pubescence type and density, pedicel position and stigma exersion. However, no variability was found for leaf margin, corolla colour, immature fruit colour, fruit neck at pedicel attachment, fruit blossom end appendage and fruit wall corrugation. All the quantitative traits exhibited highly significant differences among genotypes apart from primary branch

numbers, implying high genetic diversity that can be used in pepper improvement programmes. Pepper genotypes elsewhere have recorded variations in growth, quality and yield traits (Manju & Sreelathakumary, 2002; Adetula & Olakojo, 2006; Sharma *et al.*, 2010). In this study particularly, high coefficients of variation were obtained for traits such as fruit weight (22.2%) and number of fruit per plant (36.3%), supporting occurrence of high levels of variability among genotypes for these traits (Nandadev & Hosaman, 2003; Rodríguez *et al.*, 2008; Manyasa *et al.*, 2009; Sharma *et al.*, 2010). Morphological diversity found existing among landraces and introduced germplasm in this study may be indicative of genetic variation among genotypes and consequently provide more scope for trait improvement through selection. However, morphological traits such as fruit size and color have been reported not to necessarily measure genetic variability in Seabuckthorn (Rongsen, 1992). Since qualitative traits are controlled by many genes and are thus subject to genotype by environmental interaction, the diversity recorded for this collection would only be linked to genetic diversity on confirmation with molecular markers (Karp *et al.*, 1997; Galović *et al.*, 2006).

Principal component analysis (PCA) results further supported the diversity found by the ANOVA, with the first two PCs accounting for 55.4% of the total variance, in line with the results of Madu & Uguru (2006) although Portis *et al.* (2006) reported higher values for PCs 1 and 2, at 82.9% of the total variability. Such differences in percent contribution may be attributed to differences in the genotypes used and/or environmental conditions as was the case with mustard where contribution by components was influenced by environmental differences (Rabbani *et al.*, 1998). In this study a high level of similarity was observed among genotypes that grouped together as demonstrated by local genotypes (35, 30, 34, 37), (26, 32), (36, 33, 29) and exotic genotypes (16, 28) and (19, 8, 27) and most exotic genotypes around the centre. This suggests that none of the genotypes in their category can be used to improve the other. The grouping of local genotypes 36, 33 and 29 with most AVRDC genotypes around the centre of the bi-plot regardless of place of origin suggests some level of relatedness among these genotypes. Similar observations were reported by Madu & Uguru (2006) in hot pepper, Rabbani *et al.* (1998) in mustard and Manyasa *et al.* (2009) in pigeon pea. The fact that most of the exotic

genotypes grouped together (Fig 4) indicated that a high level of diversity existed among local genotypes compared to the exotic genotypes.

Nevertheless, genotypes 26, 32, 35, 19, 8, and 27 separated more from the rest suggesting that they are more diverse from the rest and can be used for pepper improvement in their respective superior traits. Genotypes 32 and 26 were short and early maturing and could provide good sources of genes for earliness. Genotypes 35, 30, 34, 37 35 were tall, with wide canopy and stems and could provide good sources of genes for tallness and bigger stems that can resist lodging in susceptible genotypes such as 26 and 32 with weak stems. Genotypes 27, 18, and 19 produced particularly big fruits and could be good sources of genes for bigger fruits which are an essential market quality (AVRDC, 1989; Bozokalfa & Kilic, 2010). However, these genotypes would require improvement by enhancement of the number of fruits produced per plant. In this case, the local commercial genotype 31 would be a prime candidate since it produced the highest number of fruits per plant and secondary branch numbers. Fruit weight and number of fruits per plant have been found to be major traits that directly contribute to yield (Hanson *et al.*, 2007; Rodríguez *et al.*, 2008; Bozokalfa & Kilic, 2010). Combining both traits into a single genotype would improve hot pepper yields in Uganda. Nevertheless, integration of both traits into a single genotype would be challenging because big fruited types tend to abort flowers to allow for maturity of other fruits while the small fruited genotypes compensate for yields by having several fruits per cluster (Rodríguez *et al.*, 2008). The same was observed in this study.

Like in the PCA bi-plot, separation of genotypes in cluster analyses was not influenced by the place of origin even though, collection sites were not considered during clustering. Votala *et al.* (2005) had a similar observation when he studied the relationship among *C. annuum* genotypes from northern New Mexico, Colorado and Mexico using RAPD markers. However, this was more pronounced for qualitatitive traits where most clusters contained both local and exotic probably implying that local and exotic genotypes were more diverse in quantitative than qualitative traits. However, the fact that clusters stemmed from the same place supported the occurrence of genotypic relationship probably because the genotypes belong to the same species (*Capsicum annuum*) or originated from the same ancestral gene pool before distribution to

various places. Close genotypic relationship is further evidenced by the narrow range of coefficients of similarity for both quantitative traits (0.889-0.996) and qualitative traits (0.806-0.968).

Capsicum annuum is believed to have originated from Central and South America and spread to Europe and other parts of the world including Asia and Africa where the germplasm used in this study was collected (Bosland, 1996; Ochoa-Alejo & Ramirez-Malagon, 2001; Terry & Boyhan, 2006). However, the observed and/or detected diversity could have arisen from pepper germplasm improvement and systematic farmer selection for desirable fruit traits. The lowest diversity for quantitative traits was observed in local genotypes 29 and 36; characterized by the same growth habits, fruit shapes and sizes although they differ in fruit position and colour, with genotype 29 being orange with erect fruits while genotype 36 is red with pendant fruits. These two genotypes were sourced from Chahi and Nyakabande sub-counties in Kisoro District. Their close proximity may have facilitated possible gene flow between them (Waines & Hegde, 2003; Portis *et al.*, 2006; Thul *et al.*, 2009). On the other hand, the low diversity for qualitative traits was observed between local genotypes 26 (from East African seed company) and 32 (local genotype from Kasese). They could have simply originated from the same genetic source but developed along different morphological lines due to out-crossing with other related genotypes.

Local genotypes were characterized mostly by small fruit size, late maturity and tallness compared with the introduced cultivars. This shows that these being landraces, little and/or no selection or improvement, has been done on them. The improvement of introduced genotypes explains why they are early maturing with bigger fruit sizes. This may also explain why most of them are closely related since pepper improvement is directed towards market demand driven by qualities such as big fruit size. Generally, this study has shown morphological diversity among the collected exotic and local germplasm, with very little existing especially among exotic compared to local genotypes. However, most genotypes were closely related to one or more genotypes apart from a few that were at the extremes such as commercial local genotype 31 and the Chinese seed company genotype 27. This can possibly be attributed to their close genetic background and narrow genetic base (fewer samples) characterized. This may also have resulted

rom limitations in morphological markers in determining genetic diversity among genotypes. The low genetic diversity within genotypes grouped together may further be attributed to homozygous and true breeding cultivars resulting from continued inbreeding for uniformity and selection for desirable traits (Bisognin, 2002; Gichimu *et al.,* 2009). Molecular markers may be handy in discriminating among these genotypes.

For any crop improvement program to take off genetically-diverse materials should be available that can be used to produce improved varieties with acceptable traits. This study has identified genotypes with superior agronomic traits, which may be used as breeding lines. The genetic integrity of the base materials should be protected through long term preservation techniques in a gene bank such as seed banks and field gene banks that will allow for regeneration when seed viability has started to decline (Engle, 2001). In order to facilitate the initiation of breeding, it is also essential that the expected gains from utilization of the improved materials be established.

The type of hot pepper fruit preferred by the market, from Uganda, is that which is pungent, disease and pest-free; and possesses big fruit that is, red or orange at maturity (Mr. James Kanyije, 2010; *personal communication*). The local commercial genotype 31 produced many fruit per plant though of a small size. The exotic introductions with bigger fruits could enhance farmer productivity by improving the fruit size of this and other local varieties. All genotypes had red mature fruits apart from two local genotypes 29 and 35 that had orange fruit colours. Since hot pepper is mainly grown for commercial purposes, when presented with varieties for selection, farmers would often prefer high yielding and early maturing varieties to provide quick and high income and also free land for other crops in rotation (Roy-Macauley, 2002; Simtowe *et al.*, 2009). Locally adaptable genotypes that are resistant to pests and diseases are most ideal to farmers (Beronio & Tizon, 2007; Buyinza & Mugagga, 2010). These traits were investigated in the two proceeding chapters.

CHAPTER FOUR

FIELD EXPRESSION OF GROWTH, YIELD AND QUALITY TRAITS IN HOT PEPPER (*C. annuum* L.) GENOTYPES

4.1 Introduction

Hot pepper was probably introduced into Uganda in the nineteenth century by early European explorers and Arab traders when they entered (Anonymous, 2012). Even though diverse cultivars of the crop have since been grown by farmers mainly at the subsistence scale, little breeding work has been undertaken (Anonymous, 2010a). With the Government of Uganda initiating an export diversification program that targeted horticultural crops as a means of boosting national revenue (Dijkstra, 2001), commercial production of hot pepper began in the 1990s (Tusiime *et al.*, 2010). Since then the yield potential of this crop in Uganda has been limited by abiotic and biotic stresses as well as lack of improved cultivars (Anonymous, 2010a). The local genotypes are of poor quality probably due to their inherent genetic factors in diverse cross combinations as observed for similar types elsewhere (Hannan *et al.*, 2007). There is, therefore, need to identify potential genotypes for hot pepper improvement in order to increase production and meet growing market demand. These objectives could be achieved by evaluating local and introduced improved types for yield and yield contributing traits.

In order to develop a crop improvement program, pepper germplasm is usually screened to identify desired genotypes with traits of importance to the farmers and the target markets. These types would exhibit traits such as big pungent fruit, high yielding and disease resistant genotypes (Singh *et al.*, 2006; Makoka *et al.*, 2010; Valenzuela, 2011). This study was initiated to evaluate local and exotic pepper genotypes as a means to identifying superior types with desirable growth, quality and yield traits under natural environmental conditions.

4.2 Materials and Methods

4.2.1 Study area

Field experiments were conducted at the National Crops Resources Research Institute (NaCRRI), which is located 27km from Kampala city at the coordinates 0°32'N and 32°7'E of the equator and at an elevation of 1150m a.s.l. The soils are ferralitic (red sandy clay loams) and have a pH range of 4.9-5.0. The area has a bi-modal rainfall pattern with one short rainy season (March-May) and one long rainy season (August-November). Its climate is of a tropical wet and mild dry type, with slightly humid conditions (averaging 65%). The average annual rainfall and temperature are 1,270mm and 22.2^{0}C per year, respectively with mean minimum and maximum temperatures of 16^{0}C and 28^{0}C, respectively.

4.2.2 Source and character of hot pepper genotypes evaluated at Namulonge

Thirty five (35) hot pepper genotypes were evaluated in this study, including 26 exotic and 9 local genotypes (Table 6). Twenty five exotic genotypes were imported from the Asian Vegetable Research and Development Centre (AVRDC) in Taiwan. The remaining one exotic genotype was provided by Dr. Sophy Musaana of the National Horticultural Research Programme of NARO, Uganda and had been originally sourced from a seed company in China. The local pepper germplasm was mainly obtained from homesteads in Kisoro and Kasese districts (western region), one commercial variety from a farmer's field in Wakiso district (central region) and one from a commercial seed company in Kampala. Three checks were included in the trials including two varieties from AVRDC: genotype 12 (PP97-7195-1); small fruit size, resistant to *Chilli veinal mottle virus* (ChiVMV), *Pepper virus* Y (PVY), bacterial wilt, *Phytophthora* blight and susceptible to *Cucumber mosaic virus* (CMV), *Tobacco mosaic virus* (ToMV) and Anthracnose, genotype 11 (PP0437-7506; big fruit size, resistant to ChiVMV, CMV, PVY, bacterial wilt and susceptible to *Phytophthora* blight, ToMV and anthracnose and one commercial variety: genotype 3 (CA-UGCE 09-3) whose performance is not known. The

traits of local genotypes were not known at the time of collection, while some for the AVRDC genotypes are shown (Table 7).

Table 6. *Capsicum annuum* genotypes evaluated for growth and yield traits at Namulonge, Uganda for two seasons in 2009A and 2009B

Genotype No.	Code/Name	Country of Origin	Source
1	CA-PPCHI-08-1	China	Seed company
2	CA-EASC-09-1	Uganda	EASC[a]
3	CA-UGCE 09-3[c]	Uganda	Wakiso[b]
4	CA-UGKI 09-1	Uganda	Kisoro
5	CA-UGKI 09-5	Uganda	Kisoro
6	CA-UGKI 09-4	Uganda	Kisoro
7	CA-UGKI 09-2	Uganda	Kisoro
8	CA-UGKA 09-3	Uganda	Kasese
9	CA-UGKI 09-6	Uganda	Kisoro
10	CA-UGKA 09-4	Uganda	Kasese
11	PP0437-7506	Taiwan	AVRDC
12	PP97-7195-1	Taiwan	AVRDC
13	PP0537-7513	Taiwan	AVRDC
14	PP0237-7508	Taiwan	AVRDC
15	PP9848-4996	Taiwan	AVRDC
16	PP0537-7539	Taiwan	AVRDC
17	PP0337-7545	Taiwan	AVRDC
18	PP9852-149	Taiwan	AVRDC
19	PP0337-7065	Taiwan	AVRDC
20	PP0007-2269	Taiwan	AVRDC
21	PP0337-7562	Taiwan	AVRDC
22	PP0537-7504	Taiwan	AVRDC
23	PP0537-7528	Taiwan	AVRDC
24	PP0007-2259	Taiwan	AVRDC
25	PP0337-7546	Taiwan	AVRDC
26	PBC 375	Taiwan	AVRDC
27	PBC 535	Taiwan	AVRDC
28	PP9852-110	Taiwan	AVRDC
29	PP9852-173	Taiwan	AVRDC
30	PP9955-15	Taiwan	AVRDC
31	PP0007-2247	Taiwan	AVRDC
32	PP0042-17	Taiwan	AVRDC
33	PP0237-7502	Taiwan	AVRDC
34	PP0537-7541	Taiwan	AVRDC
35	PP0537-7558	Taiwan	AVRDC

[a]East African Seed Company
[b]Commercial variety
[c]Locally collected genotypes were arbitrary designated names based on the place of origin with prefixes "CE", "KI", "KA", EASC

Table 7. Fruit and disease traits for *Capsicum annuum* genotypes evaluated for growth and yield traits at Namulonge, Uganda

Genotype No.[a]	Genotype	DF	FL (cm)	FW (cm)	FW (g)	CMV	CVMV	PVY	ToMV	BW	PB	Anthr
1	CA-PPCHI-08-1	-[b]	-	-	-	-	-	-	-	-	-	-
2	CA-EASC-09-1	-	-	-	-	-	-	-	-	-	-	-
3	CA-UGCE 09-3	-	-	-	-	-	-	-	-	-	-	-
4	CA-UGKI 09-1	-	-	-	-	-	-	-	-	-	-	-
5	CA-UGKI 09-5	-	-	-	-	-	-	-	-	-	-	-
6	CA-UGKI 09-4	-	-	-	-	-	-	-	-	-	-	-
7	CA-UGKA 09-3	-	-	-	-	-	-	-	-	-	-	-
8	CA-UGKI 09-2	-	-	-	-	-	-	-	-	-	-	-
9	CA-UGKI 09-6	-	-	-	-	-	-	-	-	-	-	-
10	CA-UGKA 09-4	-	-	-	-	-	-	-	-	-	-	-
11	PP0437-7506	67	14.8	2.0	21	R	R	R	S	R	S	S
12	PP97-7195-1	65	8.0	1.0	5	S	R	R	S	R	R	S
13	PP0537-7513	68	6.5	1.1	3	R	R	R	S	MR	S	S
14	PP0237-7508	57	10.2	1.3	8	R	S	R	S	R	MR	
15	PP9848-4996	61	8.0	1.0	3	R	MR	R	R	R	S	S
16	PP0537-7539	68	10.9	1.4	11	R	R	R	S	R	S	S
17	PP0337-7545	57	11.8	2.3	19	MR	S	R	S	R	MR	-
18	PP9852-149	60	14.5	2.0	15	S	S	MR	S	S	S	-
19	PP0337-7065	53	12.8	1.2	8	R	S	R	S	R	R	-
20	PP0007-2269	68	8.0	1.0	5	R	MR	MR	S	R	MR	S
21	PP0337-7562	55	13.3	1.6	13	MR	S	MR	S	R	S	-
22	PP0537-7504	75.5	8.6	1.2	4	-	MR	-	-	S	S	S
23	PP0537-7528	67	12.5	1.4	10	R	S	R	S	MR	R	S
24	PP0007-2259	69	7.0	1.0	6	MR	R	R	S	MR	S	S
25	PP0337-7546	55	10.7	1.7	10	R	S	MR	S	R	MR	-
26	PBC 375	61	10.6	1.6	10	S	S	S	S	R	MR	-
27	PBC 535	70	14.0	2.0	15	S	S	R	S	R	R	-
28	PP9852-110	59	6.8	1.3	4	R	S	R	S	MR	S	-
29	PP9852-173	66	9.0	1.7	10	S	S	R	S	R	S	FR
30	PP9955-15	62	15.3	2.3	27	MR	S	R	S	MR	S	S
31	PP0007-2247	63	12.0	1.0	8	S	MR	R	S	R	S	S
32	PP0042-17	63	11.0	1.0	7	R	S	R	S	R	S	S
33	PP0237-7502	61	12.0	1.6	12	MR	S	R	S	R	R	-
34	PP0537-7541	73	13.1	1.5	13	R	R	R	S	MR	S	S
35	PP0537-7558	69	11.6	1.8	14	R	S	R	S	R	MR	FR

Source: AVRDC Pepper Breeding Program, Taiwan

[a]Genotypes 1-25 evaluated in 2009A; 1-35 evaluated in 2009B

[b]Traits were not evaluated before.

DF = days to flowering, FL = fruit length, FW = fruit width, FW = fruit fresh weight, CMV = *Cucumber mosaic virus*, CVMV = *Chilli veinal mottle virus*, PVY= *Potato virus* Y, ToMV = *Tobacco mosaic virus*, BW = bacterial wilt, PB= *Phytophtora* blight, Anthr = anthracnose, R = resistant, MR = moderately resistant, S = susceptible, FR = field tolerance

4.2.3 Seedling propagation and maintenance

Before raising seedlings in the nursery, seeds were treated as described in section 3.2.3 to inactivate seed-borne tobamoviruses. During 2009A, seedlings were raised under field conditions on soilbeds that had been surface-sterilized by burning a layer of dry grass for one hour to kill soil-borne pathogens. As a result of low germination percentages in 2009A, screen house nursery propagation and management was applied in 2009B as described in section 3.2.2 and protection was done before transplanting as described in 3.2.3. Seedlings were transplanted at 6-8 weeks after planting.

4.2.4 Establishment of field trials

Genotype performance for growth, quality and yield traits under natural field conditions was evaluated in two experiments conducted in two consecutive seasons of 2009A and 2009B. In 2009A, 25 genotypes were evaluated during the dry season from June to November 2009. The evaluation was repeated with 35 genotypes in the rainy season from December 2009 to May 2010. In both seasons, an alpha lattice design was used with 2 replications. In 2009A, a 5x5 (5 incomplete blocks each containing 5 experimental plots with a total of 25 experimental plots) alpha lattice design was used while in 2009B, the alpha lattice design was a 7 x 5 (7 incomplete blocks each containing 5 experimental plots totalling 35 experimental plots). In both designs, each plot was a single row raised bed 1m wide and 5m long with a population of 14 plants. The spacing between plants within rows was 45cm and between rows was 60cm. The distance between plots was 1.5m and between replications 2m. To counteract border effects, guard rows of beans were planted around the trial.

4.2.5 Management of field trials

Plants were fertilized as described in 3.2.4. Seedlings were protected for 5 weeks as described in section 3.2.3 in order to allow proper plant establishment in the field. Weeding was done as often as necessary to avoid competition for nutrients with plants. Watering was done twice a day for 2

weeks after transplanting and thereafter thrice a week during dry conditions until seedlings were fully established.

4.2.6 Data collection

Plant growth traits assessed were days to 50% flowering (only season 2009B because seedlings in 2009A were transplanted at flowering and past flowering in some cases due to delays in accessing resources), days to 50% fruit maturity, plant height and width (cm) at maturity. Quality traits evaluated were fruit size measured as average mature fruit length (cm), width (cm) and weight (g) for 20 mature fruits per plot from the second harvest; non-marketable fruits computed as a percentage (%) of total number of fruits harvested per genotype for the whole experiment and seed weight measured by weighing 200 seeds per genotype. Yield traits evaluated were: fruit numbers per plant; total fruit yield (t/ha) computed from fruit weight and total fruits harvested; marketable fruit yield (t/ha) computed from fruit weight and number of marketable fruits; fruit seed yield averaged from 20 marketable fruits and seed yield (t/ha) computed from fruit seed yield and fruit weight. Mature fruits were harvested 6 times over a period of 8 weeks after maturity and marketability of fresh harvest (pest and disease free) determined.

4.2.7 Data analyses

All data were entered and edited in the Excel computer package (Microsoft Office, 2007) then exported into the GenStat computer package (12^{th} edition, version 2; VSN International Ltd, 2010) to generate analyses of variance (ANOVA) and examine variations among the genotypes (Padi, 2007). For all traits, the ANOVA for the alpha-lattice design using the Linear Mixed Model selection in the Restricted Maximum Likelihood (ReML) procedure resulted in ineffective lattice blocks shown by negative variance components and hence, analysis was done using randomized complete block design. Data collected per season were individually analyzed using one-way analysis of variance (ANOVA). Data on the 25 genotypes common to both seasons were then pooled across seasons to determine the interaction effects between seasons and treatments (genotypes). The ANOVA for single season analysis was based on the linear

mathematical model: $Y_{ij} = \mu + r_i + g_j + e_{ij}$; while the pooled ANOVA across seasons was based on the linear model $Y_{ijk} = \mu + s_i + r(s)j(i) + g_k + (gs)_{ik} + e_{ijk}$, where Yij= observed effect for i^{th} replication and j^{th} genotype μ = grand mean of the experiment, r_i = effect of the i^{th} replication, g_i = effect of the j^{th} genotype, e_{ij} = residual effect or random error of the experiment for single season analysis. Yijk = observed effect for the *i*th season, j^{th} replication within the i^{th} season, and k^{th} genotype, s_i = effect of the *i*th season, r(s)j(i) = effect of the j^{th} replication within the i^{th} season, g_k = effect of the k^{th} genotype, $(gs)_{ik}$ = interaction of the k^{th} genotype with the i^{th} season, and e_{ijk} = residual effect or random error of the experiment for pooled analysis.

Where the ANOVA showed significant differences, treatment means were separated using Fischers' Protected Least Significant Differences (LSD) test at 5% probability level (Gomez & Gomez, 1984). Correlation analyses were performed to assess the relationships for yield and its contributing growth traits in individual seasons. For the purposes of results interpretation, significant correlations were grouped into low ($r<0.4$), intermediate ($r=0.4$-0.64) and high ($r>0.65$). The growth and yield data on 25 genotypes common to both seasons were also correlated to assess their stability (Quilot *et al.*, 2005; AVRDC, 2007; Balkaya & Karraağaç, 2009).

4.3 Results

Results of individual and combined seasons on growth traits are respectively presented in Tables 8-9; those on quality traits in Tables 10-11 while those on yield traits in Tables 12-13. The analysis of variance tables of the traits in individual seasons are presented in appendices 6-9.

4.3.1 Growth traits

4.3.1.1 Days to 50% flowering

Mean squares of days to 50% flowering showed highly significant differences among genotypes ($P<0.001$) (Table 8). However, results show that local genotypes (mean 54 days) flowered later

ıble 8. Mean values of varietal horticultural (growth) traits for hot pepper genotypes 'aluated in an open field at Namulonge, Uganda in 2009A[1] and 2009B[2]

enotype[c]	50 % Days to flowering 2009B[b]	50 % Days to fruit maturity 2009A[a]	2009B	Plant width (cm) 2009A	2009B	Plant height (cm) 2009A	2009B
	24a	54 a	57a	16.4 ab	23.2a	20.4 abc	23.3ab
Control 1	41e-j	73 bcd	80bc	31.7 h-k	54.3r-u	38.7 g-k	57.6n
	48ij	74 cd	85bcd	34.4 kl	43.7h-p	44.6 ijk	41.3g-k
	73l	80 ef	116i	32.7 i-l	52.3q-t	37.1 f-j	43.6kl
	39c-i	70 bc	94d-g	23.7 c-f	60.4tu	47.2 jk	51.8mn
	41e-j	88 ghi	77bc	18.2 bc	56.5stu	33.1 d-h	44.7klm
	59k	69 bc	99gh	26.2 e-i	50.8o-s	30.6 c-g	52.4n
	83l	89 hi	117i	24.9 c-h	51.1p-s	26.5 a-f	43.5jkl
)	82l	106 j	112hi	26.6 f-i	46.6l-r	36.2 e-j	43.9kl
	44g-j	83 efg	86b-e	24.9 c-h	61.7u	28.3 b-g	50.4lmn
1 Control 2	42f-j	68 b	82bcd	30.8 g-k	30.6a-e	38.7 g-k	37.8d-k
2 Control 3	39c-i	74 bcd	85bcd	39.3 l	48.6n-s	48.8 k	41.1g-k
3	38b-i	82 ef	87c-g	26.9 f-j	35.0c-g	30.6 c-g	35.8c-j
4	42e-j	71 bc	82bcd	27.6 f-k	36.0d-h	33.7 e-i	39.1e-k
5	40d-i	92 i	87c-f	10.8 a	37.9d-k	18.4 ab	39.3e-k
6	38b-i	77 de	80bc	24.2 c-g	30.0a-d	25.5 a-e	30.7bcd
7	43f-j	73 bcd	78bc	25.3 d-h	36.8d-j	29.5 b-g	31.9cde
8	29abc	83 efg	74b	34.5 kl	31.7b-f	28.4 b-g	31.4cd
9	32a-f	72 bcd	75bc	19.4 b-e	31.5a-f	21.9 a-d	22.8a
0	30a-d	74 cd	81bc	19.1 bcd	26.9abc	16.6 a	32.1cde
1	33a-f	83 fgh	78bc	33.7 jkl	42.5g-o	43.7 h-k	40.1f-k
2	30a-d	85 fgh	79bc	24.4 c-g	38.6e-l	30.9 c-g	42.7h-k
3	30a-d	72 bcd	76bc	24.3 c-g	36.3d-i	29.6 c-g	32.5c-f
4	28ab	74 bcd	80bc	25.5 d-h	35.1c-g	31.0 c-g	35.6c-i
5	31a-e	69 bc	75bc	14.6 ab	42.4g-o	20.3 abc	41.9g-k
6	36b-g		78bc		44.9j-q		40.3g-k
7	51jk		98fg		36.3d-h		28.7abc
8	47hij		97efg		42.6g-o		43.0i-l
9	29abc		77bc		44.8i-q		41.9g-k
0	34a-g		80bc		45.4k-q		35.2c-h
1	48ij		86b-e		47.4m-r		55.7n
2	37b-h		85b-e		39.8f-m		43.8kl
3	41e-j		87c-f		40.6g-n		32.0cde
4	47hij		87c-f		25.1ab		34.8c-g
5	42f-j		86c-f		43.7h-p		41.5g-k
Mean	41.5	77	84.7	25.6	41.3	31.6	39.3
SD (5%)	10.92	5.54	12.50	6.86	8.59	11.16	7.80
-test	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
V (%)	12.8	3.5	7.2	3.3	10.1	17.1	9.6

Evaluated from June 22nd to November 18th 2009; [b] Evaluated from December 1st 2009 to May 11th, 010; [c]Genotypes; 2-10 = local genotypes; 1, 11-35 = exotic genotypes.

Means within columns followed by same letter are not significantly different at 5% level according to ischer's Protected LSD

Table 9. Analysis of variance for three quantitative growth traits in twenty-five genotypes pooled across two seasons (2009A and 2009B) of evaluation at Namulonge, Uganda

Characters	Source of Variation – df					Mean	SEM±
	Season (E)-1	Replication (R)-2	Genotypes (G)-24	G x E-24	Pooled Error-47		
	Mean squares						
Days to 50% fruit maturity	1354.54***	22.78^{ns}	439.33**	142.15***	12.780	81.0	5.96
Plant height (cm)	4819.15***	13.78^{ns}	147.04^{ns}	89.90***	14.830	32.3	4.74
Plant width (cm)	2511.01***	117.90***	284.87**	96.01***	24.460	36.4	4.89

^{ns}not significant; *significant (P <0.05); **highly significant (P <0.01); ***highly significant (P <0.001)

than exotic genotypes (mean 38 days). Among the local cultivars, genotypes 5, 10 and 11 flowered later than the rest at 73, 82 and 83 days after transplanting (DAT), respectively while, genotype 2 significantly flowered much earlier (24 DAT) followed by genotype 6 at 39 DAT. Among the exotic genotypes, there were no clear cut differences in days to 50% flowering. However, genotypes 24, 18, 29, 20, 22, 23, and 25 flowered earlier (range 28-31 DAT), while genotypes 28, 34, 31 and 27 were the latest flowering (47-51 DAT).

4.3.1.2 Days to 50% fruit maturity

There were highly significant differences among genotypes ($P<0.001$) for days to 50% fruit maturity in both seasons 2009A and 2009B (Table 8). Pooled analysis of variance for the 25 genotypes common to both seasons varied highly significantly with season (E) ($P<0.001$), genotype (G) ($P<0.01$) and genotype by season (GxE) interaction ($P<0.001$) (Table 9). Generally, genotypes in season 2009A matured earlier (mean 77.0 DAT), than genotypes in 2009B (mean 84.7 DAT). However, local genotypes matured later in season 2009A (mean 78.1 DAT) than exotic genotypes (mean 77.0 DAT). The earliest maturing local genotypes were 2 (54 DAT), 8 (69 DAT) and 6 (70 DAT) while, the earliest maturing exotic genotypes were 11 and 25 at 68 and 69 DAT, respectively.

Similarly, in 2009B, exotic genotypes matured significantly earlier (mean 82.5 DAT), than local genotypes (mean 93.0 DAT). The earliest maturing local genotypes were 2 (57 DAT) and 8 (77 DAT) while, the earliest maturing exotic genotypes were 18, 19, 25, 23 and 29 (range 74-77 DAT). The latest maturing local genotypes were 10, 5 and 9 at 112, 116 and 117 DAT, respectively while, the latest maturing exotic genotypes and 27 (98 DAT). Of the local genotypes, 2 and 8 consistently matured earlier whereas genotypes 9 and 10 consistently matured later across the two seasons. Among the introduced genotypes, the AVRDC genotype 25, 23, and 17 consistently matured earlier while, genotypes 13, 1 and 15 systematically matured later across seasons.

4.3.1.3 Plant height (cm)

Plant height differed highly significantly among genotypes (P<0.001) in both seasons 2009A and 2009B (Table 8). Pooled analysis of variance for the 25 genotypes common to both seasons varied highly significantly (P<0.001) with GxE interaction but did not vary significantly with genotype (Table 9). In general, genotypes in season 2009A grew shorter, (mean 25.6cm) than genotypes in 2009B, (mean 39.3cm). However, local genotypes still grew taller (mean 26.1cm) than exotic genotypes (mean 25.3cm) in 2009A. The shortest local genotypes were 2 (16.5cm) and 7 (18.0cm) tall while, the tallest genotypes were 3 (31.7cm), 5 (32.7cm) and 4 (34.4cm). The shortest exotic genotypes were 15 (10.8cm) and 25 (14.6cm) whilst, the tallest were 21, 18 and 12 with 33.7cm, 34.5cm and 39.3cm, respectively.

Similarly, in 2009B, local genotypes grew taller (mean 44.7cm) compared with exotic genotypes (mean 37.8cm). The shortest local genotype was 8 (23.3cm) followed by 4 (41.3cm) whereas, the tallest genotypes were 10, 5 and 2 with 51.2cm, 52.4cm and 57.6cm, respectively. The shortest exotic genotypes were 19 (22.8cm), 27 (28.7cm) and 16 (30.7cm) whereas, the tallest were 1 and 31 with 50.4cm and 55.7cm respectively. Among the local genotypes, 8 and 6 consistently grew shorter while, genotypes 3, 10 and 5 consistently grew taller across the two seasons. Of the introduced genotypes, 19, 16 and 17 consistently grew shorter while, genotypes 11, 21 and 12 consistently grew taller across the two seasons.

4.3.1.4 Plant width (cm)

Plant width differed highly significantly among genotypes (P<0.001) in both seasons 2009A and 2009B (Table 8). Pooled analysis of variance for the 25 genotypes common to both seasons varied highly significantly (P<0.001) with genotype, season and with GxE interaction (Table 9). In general, genotypes in season 2009A had narrower plant canopy (mean 31.6cm) compared with, genotypes in 2009B (mean 41.3cm). On the other hand, local genotypes in 2009A had wider plant canopies (mean 34.9cm) compared with exotic genotypes (mean 29.7cm). Local genotypes 2 (20.4cm) and 9 (26.5cm) had the narrowest plant canopies while; genotypes with the

widest canopies were 4 and 6 with 44.6cm and 47.2cm, respectively. Exotic genotypes with narrowest canopies were 20 (16.6cm wide) and 15 (18.4cm wide) while, genotypes 21 (43.7cm) and 12 (48.8cm) had the widest canopies.

Similarly, in 2009B, local genotypes exhibited wider plant canopies (mean 48.8cm) compared with exotic genotypes (mean 38.9cm). The narrowest local genotype was 2 with 23.2cm of canopy wide while, the widest genotypes were 3, 7 and 6 with 54.3cm, 56.5cm and 60.4cm of canopy, respectively. The narrowest exotic genotypes were 34 (25.1cm) and 20 (26.9cm) while, the significantly widest genotype was the Chinese genotype 1 (61.7cm). Among the local genotypes, 2 consistently had narrower plant canopies whilst, genotypes 3 and 6 consistently exhibited wider plant canopies across the two seasons. Of the introduced genotypes, 19 and 16 consistently exhibited small plant width while genotype 12 consistently grew wider canopies than all genotypes across the two seasons.

4.3.2 Quality traits

4.3.2.1 Fruit length (cm)

There were highly significant differences in fruit length among genotypes ($P<0.001$) in both seasons 2009A and 2009B (Table 10). Pooled analysis of variance for the 25 genotypes common to both seasons highly significantly ($P<0.001$) differed with genotype, season and GxE interaction (Table 11). Overall mean of fruit lengths (7.7cm) in season 2009A were shorter than those of genotypes grown in 2009B (9.59cm). Fruit lengths of local genotypes in 2009A were shorter (4.6cm) compared with those of exotic genotypes (mean 9.4cm). The local genotypes with the shortest fruits were 9 (2.4cm), 6 (3.1cm) and 10 (3.1cm) while, genotypes with longest fruits were 2 and 8 (6.7cm) (8.8cm). Exotic genotypes with shortest fruits were 23 and 24 with 6.2cm and 7.2cm long, respectively while those with the longest fruits were 21 and 1 with 12.4cm and 12.6cm, respectively.

Likewise, fruit lengths of local genotypes in 2009B were shorter (mean 5.0cm) compared with

able 10. Mean values of quality traits for hot pepper genotypes evaluated in an open field Namulonge, Uganda in 2009A and 2009B

enotype[c]	Fruit Length (cm)		Fruit Width (cm)		Average Fruit Weight (g)		Non-marketable Fruit (%)		200 Seed Weight (g)	
	2009A[a]	2009B[b]	2009A	2009B	2009A	2009B	2009A	2009B	2009A	2009B
	6.7 ef	9.6h-k	0.8 ab	1.0ab	1.9 ab	2.4abc	47 b-f	58b-e	1.0 g-j	0.9jk
Control 1	5.4 cd	6.2def	0.9 a-c	1.0ab	1.7 ab	1.9ab	67 h-l	35a	1.1 ij	0.9ijk
	5.0 c	5.8cde	1.3 fg	1.6h-m	3.5 def	5.0b-g	71 i-m	55bcd	1.0 hij	0.7a-e
	3.7 b	3.7ab	1.3 fg	1.6i-m	2.3 bc	2.5abc	74 j-m	63b-f	1.0 e-i	0.6a
	3.1 ab	3.6ab	0.9 ab	0.8a	1.2 a	1.1a	73 i-m	52bc	0.6 a	0.5a
	3.6 b	7.2efg	1.1 c-f	1.3c-g	2.0 abc	3.1a-d	60 e-j	72e-j	1.0 f-i	0.7a-e
	8.8 hij	3.9abc	0.9 a-c	1.3c-g	3.0 cde	2.6a-d	73 i-m	72e-j	0.7 a-c	0.7a-h
	2.4 a	2.4a	1.9 c-h	1.8m	2.1 abc	2.7a-d	82 lm	52bc	0.8 c-g	0.7a-h
0	3.1 ab	2.2a	1.7 hi	1.6j-m	2.4 bc	2.3abc	86 m	62b-f	0.8c-g	0.7a-e
	12.6 p	16.2r	2.1 j	2.6n	16.2 m	14.6i	38 a-d	81h-n	1.0 e-i	0.9h-k
1 Control 2	9.5 jkl	12.1l-q	1.3 fg	1.4f-k	6.1 ijk	9.6jk	49 b-g	90lmn	0.6 a	0.6ab
2 Control 3	8.2 ghi	10.3i-l	0.8 a	1.2b-g	1.8 ab	3.5a-e	65 g-k	71e-j	0.9 d-i	0.9f-k
3	7.7 fgh	6.8d-g	1.2 d-g	1.1a-e	3.8 ef	4.2a-f	54 d-h	64b-g	0.7 a-c	0.6abc
4	8.7 hij	10.9j-n	1.4 g	1.3c-g	5.1 hi	6.9f-k	47 b-f	68d-i	0.9 e-i	0.8d-k
5	10.3klm	10.7j-m	1.3 fg	1.3c-i	5.0 ghi	8.4h-k	34 ab	79g-m	0.6 a	0.8b-j
6	11.4mno	11.5k-p	0.9 a-c	1.3c-g	4.4 fgh	7.2f-k	45 b-e	77f-l	0.7 a-d	0.7a-f
7	11.5 nop	11.2j-o	1.1 c-f	1.8lm	4.2 fgh	9.3jk	64 g-k	94mn	0.9 d-i	0.7a-g
8	9.0 ij	8.4ghi	1.2 efg	1.2b-f	6.4 jk	5.3c-h	77 klm	85j-n	0.9 d-h	0.8e-k
9	8.9 hij	11.5l-p	1.3 fg	1.1b-e	5.6 ij	6.4e-j	66 h-l	67c-h	1.0 e-i	0.7a-i
20	9.1 ijk	9.5hij	1.0 b-d	1.2b-g	3.7def	7.3f-k	53 c-h	84i-n	0.6 ab	0.7a-e
21	10.5 l-n	13.4pq	1.2 d-g	1.3d-j	6.8 k	8.8ijk	37 abc	73e-k	1.2 j	1.0k
22	12.4 op	8.0fgh	1.6 h	1.1b-e	11.5 l	3.3a-e	28 a	72e-j	1.0 hij	0.7a-g
23	6.3 de	13.8q	1.0 a-c	1.3c-h	2.7 bcd	7.1f-k	63 f-k	83i-n	0.8 c-f	0.8c-k
24	7.2 efg	8.2gh	1.0 b-e	1.4e-j	2.4 bc	8.2g-k	57 e-i	60b-e	0.8 b-e	0.7a-f
25	7.7 fgh	9.5hij	1.0 b-e	1.3c-j	4.0 efg	5.5c-h	66 h-k	88k-n	0.8 b-e	0.8e-k
26		10.3i-l		1.4f-k		8.3h-j		86j-n		0.8e-k
27		13.3pq		1.6h-m		9.1jk		77f-l		0.9g-k
28		5.1bcd		1.0abc		1.8a		49ab		0.9jk
29		10.3i-m		1.5g-l		9.1jk		86j-n		0.8c-k
30		16.2r		1.7klm		16.4i		83h-n		0.7a-h
31		12.2m-q		1.2b-g		7.1f-k		83i-n		0.7a-e
32		12.7n-q		1.1a-d		5.7d-i		83i-n		0.6a-d
33		12.2l-q		1.5g-m		7.6g-k		83i-n		0.7a-g
34		12.9opq		1.3c-g		6.8f-k		95n		0.6ab
35		11.2j-o		1.3c-i		9.9k		83i-n		0.8b-k
Mean	7.7	9.59	1.2	1.35	4.4	6.36	59	73.07	0.9	0.75
LSD (5%)	1.17	1.98	0.22	0.30	1.02	3.25	16.44	15.98	0.18	0.20
F-test	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	<.001	0.002
CV (%)	7.3	10.0	8.9	10.8	11.3	24.8	7.96	10.6	10	12.7

[a]Evaluated from June 22nd to November 18th 2009; [b]Evaluated from December 1st 2009 to May 11th, 2010; [c]Genotypes; 2-10 = local genotypes; 1, 11-35 = exotic genotypes.

Means within columns followed by same letter are not significantly different at 5% level according to according to Fischer's Protected LSD.

Table 11. Analysis of variance for five quality traits of twenty-five genotypes pooled across two seasons (2009A and 2009B) of evaluation at Namulonge, Uganda

Characters	Source of Variation - df					Mean	SEM±
	Season (E)-1	Replication (R)-2	Genotypes (G)-24	G x E-24	Pooled Error-47		
	Mean squares						
200 seed weight (g)	0.29***	5.58***	0.06**	0.02***	0.007	0.8	0.07
Average fruit weight	35.13***	5.58***	37.98***	4.51***	1.342	5.0	1.06
Fruit length (cm)	22.16***	0.29^{ns}	42.35***	3.43***	0.399	8.2	0.93
Fruit width (cm)	0.57***	0.10***	0.43***	0.05***	0.011	1.3	0.12
Non marketable fruits (%)	3122.42***	101.99^{ns}	256.90^{ns}	610.55***	64.720^{m}	64.0	12.36

^{m}df = 48 because one variety (34) never gave any yield in replication 2 of season 2009B and thus was given 0 score for these parameters and was considered missing for the rest

^{ns}non significant; *significant ($P < 0.05$) ** highly significant ($P < 0.01$); *** highly significant ($P < 0.001$)

hose of exotic genotypes (mean 11.1cm). The local genotypes with the shortest fruits were 10 nd 9 with 2.2cm and 2.4cm long respectively while genotypes with longest fruits were 7 and 2 vith 7.2cm and 9.6cm, respectively. Exotic genotypes with shortest fruits were 28 and 13 with .1cm and 6.8cm long, respectively while those with the longest fruits were 30 and 1 both with 6.2cm. Within the local genotypes, 9, 6 and 10 consistently displayed shorter fruits while genotypes 2 and 3 consistently showed longer fruits across the two seasons. Among the exotic genotypes, 24, 13 and 25 consistently exhibited shorter fruits whereas; genotypes 21 and 1 consistently had longer fruits across the two seasons.

4.3.2.2 Fruit width (cm)

Fruit width differed highly significantly within genotypes ($P<0.001$) in both seasons 2009A and 2009B (Table 10). Pooled analysis of variance for the 25 genotypes common to both seasons varied highly significantly ($P<0.001$) with genotype, season and GxE interaction (Table 11). Fruits in 2009A had narrower fruits (mean 1.2cm) compared with those in 2009B (mean 1.35cm). Fruit widths of both local and exotic genotypes in 2009A were equally wide (mean 1.2cm). The local genotypes with the narrowest fruits were 2 (0.8cm), 3, 6 and 8 (all 0.9cm) while, genotypes with broadest fruits were 10 and 9 (1.7cm and 1.8cm, respectively). Exotic genotypes with the narrowest fruits were 12 (0.8cm) and 16 (0.9cm) while, genotypes with widest fruits were 1 (2.1cm) followed by 22 (1.6cm).

Conversely, fruits of local genotypes were narrower (mean 1.3cm) compared with those of exotic genotypes (mean 1.4cm) in 2009B. The local genotype with the narrowest fruits was 8 (0.8cm) while, local genotypes with widest fruits were 4, 5, 10 and 9 with the first 3 having 1.6cm and the last with 1.8cm. Most exotic genotypes had intermediate fruit width in the range 1.0-1.8cm with the exception of genotype 1, whose fruits were 2.6cm wide. Among the local genotypes, 2 and 3 consistently displayed thinner fruits while genotypes 10 and 9 consistently showed wider fruits across the two seasons. Among the exotic genotypes, 13 and 20 consistently exhibited narrower fruits whereas; genotype 1 consistently exhibited wider fruits than all genotypes across the two seasons.

4.3.2.3 Average fruit weight (g)

There was a highly significant difference in average fruit weight among genotypes (P<0.001) in both seasons 2009A and 2009B (Table 10). Combined analysis of variance for the 25 genotypes common to both seasons varied highly significantly (P<0.001) with genotype, season and GxE interaction (Table 11). Overall, fruits from season 2009B were heavier (mean 6.36g) than those from 2009A (mean 4.4g). Average fruit weight of local genotypes in 2009A were lighter (mean 2.2g) compared with those of exotic genotypes (mean 5.6g). The local genotypes with the lightest fruits were 6 (1.2g) and 3 (1.7g) while, the heaviest fruits were 8 and 4 (3.0g and 3.5g, respectively). Exotic genotypes with lightest fruits were 12 (1.8g), 24 (2.4g) and 23 (2.7cm) while, those with the heaviest fruits were 22 (11.5g) and 1 (16.2g).

Similarly, fruits of local in 2009B were lighter (mean 2.6g) compared with those of exotic genotypes (mean 7.6g). The local genotypes with the lightest fruits were 6 (1.1g) and 3 (1.9g) while the heaviest fruits were from genotypes 7 and 4 (3.5g and 5.0g, respectively). Exotic genotype with lightest fruits was 28 (1.8g) while, those with the heaviest fruits were 1 (14.6g) and 30 (16.4g). Among the local genotypes, 6 and 3 consistently displayed lighter fruits while genotypes 8 and 4 consistently showed heavier fruits across the two seasons. Among the exotic genotypes, 12 and 13 consistently exhibited lighter fruits whereas; genotype 1 consistently had heavier fruits across the two seasons.

4.3.2.4 Non-marketable fruits (%)

Several factors caused non-marketability of fruits including some shown in Figure 7. There were highly significant differences in percentage non-marketable fruits among genotypes (P<0.001) in both seasons 2009A and 2009B (Table 10). Combined analysis of variance for the 25 genotypes common to both seasons varied highly significantly (P<0.001) with season and GxE interaction while did not vary significantly with genotype (Table 11). More fruits were scored non-marketable in 2009B (mean 73.1%) compared with those in 2009A (mean 58%). Local genotypes in 2009A had more non-marketable fruits (mean 70.3%) as compared with exotic

genotypes (mean 52.7%). Local genotype with lowest percentage of non-marketable fruits was 2 (47%) while those with higher percentage of non-marketable fruits were 9 (82%) and 10 (86%). Exotic genotypes with low percentage of non-marketable fruits were 22, 15, 21 and 1 (range 28-38%) while genotype 18 had significantly higher percentage of non-marketable fruits (77%).

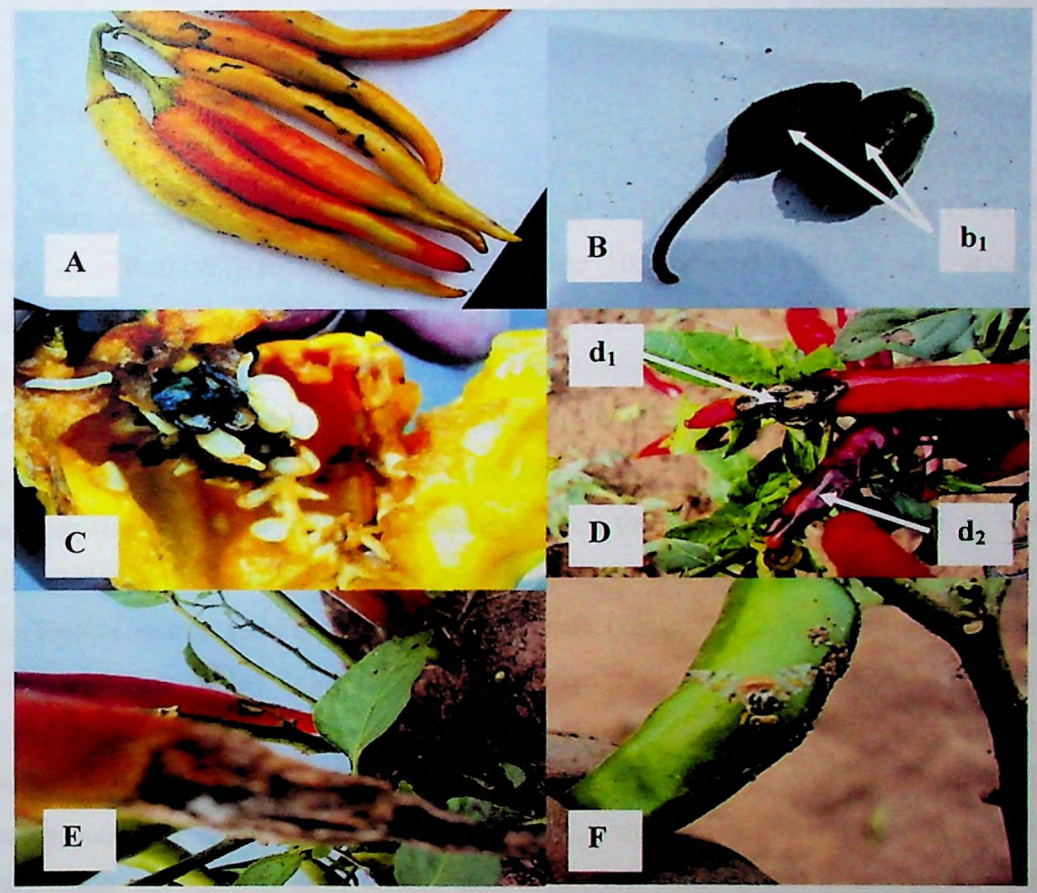

Figure 7. Factors that rendered chilli pepper fruits non marketable during during 2009A and 2009B evaluation seasons at Namulonge, Uganda: A) insect damage (larvae entry); B) bacterial spot infected fruits: b_1) raised spots on fruit due to bacterial spot; C) larvae of fruit fly that lead to fruit soft rot D) fruit rot: d_1 = anthracnose, d_2 = soft rot; E) blossom end rot and F) fruit fly.

In contrast, local genotypes in 2009B had fewer non-marketable fruits (mean 57.9%) as compared with exotic genotypes (mean 78.6%). The local genotype with lowest percentage of

non-marketable fruits was 3 (35%) while genotypes with higher percentage of non-marketable fruits were 7 and 8 (72%). Exotic genotype with the lowest percentage of non-marketable fruits was 28 (49%) while genotypes with significantly higher percentage of non-marketable fruits were 11 (90%), 17 (94%) and 34 (95%). Genotypes 2 and 3 within the local genotypes consistently had lower percentage of non-marketable fruits while genotypes 5 and 8 consistently exhibited higher percentage of non-marketable fruits across the two seasons. Among the exotic genotypes, only 28 had a lower percentage of non-marketable fruits while genotype 19, 25 and 18 consistently had a higher percentage of non-marketable fruits across the two seasons.

4.3.2.5 200 Seed weight (g)

There were highly significant differences in seed weight among genotypes ($P<0.001$) in season 2009A and ($P<0.002$) in season 2009B (Table 10). Shared analysis of variance for the 25 genotypes common to both seasons indicated that seed weight differed highly significantly with genotype ($P<0.01$), season ($P<0.001$) and GxE interaction ($P<0.001$) (Table 11). On the whole, seeds from season 2009A were heavier (mean 0.9g) than those from 2009B (mean 0.75g). Seed weight of local genotypes in 2009A were heavier (mean 0.9g) compared with those of exotic genotypes (mean 0.8g). The local genotypes with the lightest seeds were 6, 8, 9 and 10 (range 0.6-0.8g) while the heaviest seeded genotypes 2, 4, 5, 7 and 3 had seeds ranging from 1.0g to 1.1g. Twelve exotic genotypes had lighter seeds (range 0.6-0.9g) while 4 genotypes produced heavier seeds (range 1-1.2g) with genotype 21 being the heaviest seed yielder. Conversely, seeds of local genotypes in 2009B were lighter (mean 0.7g) compared with those of exotic genotypes (mean 0.8g). Local genotypes 2 and 3 yielded the heaviest seeds (0.9g) whereas, the local genotype with the lightest seeds was 6 (0.5g). Exotic genotype 21 was the heaviest seed yielder (1.0g) while, the lightest seed yielder genotypes had 0.6g. Local genotypes 7 and 3 and exotic genotypes 1 and 21 were consistent with producing heavy seeds across seasons.

4.3.3 Yield traits

4.3.3.1 Number of fruits per plant

Number of fruits per plant differed highly significantly among genotypes (P<0.001) in both seasons 2009A and 2009B (Table 12). Pooled analysis of variance for the 25 genotypes common to both seasons varied highly significantly (P<0.001) with GxE interaction, varied significantly with genotype (P<0.05) and did not vary with season (Table 13). Genotypes in 2009A had more fruits per plant (mean 38 fruits) compared with those in 2009B (mean 34.4 fruits). Local genotypes in 2009A produced more fruits per plant (mean 47.4) compared with exotic genotypes (mean 32.8 fruits). Local genotypes with the fewest fruits per plant were 7 (28 fruits) and 2 (29 fruits) while, genotypes with most fruits per plant were 4 (60 fruits) and 6 (76 fruits). Exotic genotypes with fewer fruits per plant were 1 (12 fruits), 22 (14 fruits) and 25 (18 fruits) while, genotype 12 significantly displayed more fruits per plant than the rest (91 fruits).

On the contrary, local genotypes in 2009B had fewer fruits per plant (mean 28.9 fruits) compared with exotic genotypes (mean 36.5 fruits). Local genotypes with fewer fruits per plant were 8, 2, 4, and 7 (range 12-19 fruits) while, genotypes with more fruits per plant were 5, 6 and 3 with 40, 40 and 56 fruits, respectively. Exotic genotypes with fewer fruits per plant were 1 (16 fruits) and 11 (17 fruits) while genotype 12 significantly displayed more fruits per plant (65 fruits) than the rest followed by genotype 14 (55 fruits). Of the local genotypes, 2 and 7 consistently displayed fewer fruits per plant while genotypes 6, 5 and 3 consistently showed more fruits per plant across the two seasons. Among the exotic genotypes, 1 and 17 consistently exhibited fewer fruits per plant while the AVRDC control genotype 12 consistently exhibited significantly more fruits per plant than all genotypes across the two seasons.

4.3.2.2 Total fruit yield (t/ha)

Mean squares of total fruit yield indicated highly significant differences among genotypes (P<0.001) in both seasons 2009A and 2009B (Table 12). Combined analysis of variance for the

able 12. Mean values of yield traits for hot pepper genotypes evaluated in an open field at amulonge, Uganda in 2009A and 2009B

	NF/P		TFY (t/ha)		TMFY (t/ha)		NSF		FSY (t/ha)	
enotype[c]	2009A[a]	2009B[b]	2009A	2009B	2009A	2009B	2009A	2009B	2009A	2009B
	29 b-h	13ab	2.0 ab	1.3a	0.9 a	0.6ab	72	46a	0.4 abc	0.1a
Control 1	76 kl	58no	4.7 a-h	4.2a-f	3.1 c-h	2.9g-j	93	61abc	1.4 e	0.6ghi
	60 jk	18a-e	7.7 ijk	3.2a-d	5.4 i	1.5a-i	77	101klm	0.9 d	0.2a-d
	52 ij	40g-n	4.4 a-g	3.6a-e	3.3 d-h	1.4a-h	80	100klm	0.7 cd	0.4b-h
	43 ghi	40g-n	1.9 a	1.7ab	1.4 abc	0.9a-e	92	76b-h	0.4 a-d	0.3a-f
	28 a-g	19a-f	2.2 ab	2.2abc	1.3 abc	0.7abc	85	89f-l	0.4 a-d	0.2a-d
	43 ghi	12a	4.9 b-i	1.0a	3.6 fgh	0.3a	95	89g-l	0.5 a-d	0.2ab
	45 hij	39f-n	3.4 a-e	4.0a-f	2.8 b-h	2.0a-i	89	91h-l	0.6 a-d	0.5d-i
0	51 ij	21a-g	4.5 a-g	1.8ab	3.4 d-h	0.7a-d	89	96i-l	0.7 bcd	0.2a-d
	12 a	16abc	7.2 g-k	8.6e-j	2.7 a-h	1.7a-i	109	127n	0.2 ab	0.3a-f
1 Control 2	41 d-i	17a-d	9.1 jk	6.1a-i	4.4 hi	0.5ab	62	71b-g	0.3 abc	0.1ab
2 Control 3	91 l	65o	6.2 e-j	8.5e-j	4.0 ghi	2.5e-i	93	68b-e	1.4 e	0.7i
3	34 c-h	50j-o	4.8 a-i	7.3c-j	2.6 a-h	2.7f-j	53	60ab	0.2 ab	0.3a-f
4	40 d-i	55mno	7.6 h-k	14.2kl	3.5 e-h	4.3j	76	67b-e	0.5 a-d	0.6f-i
5	20 a-c	38e-m	3.8 a-e	12.0jk	1.2 ab	2.5d-i	65	85e-k	0.1 a	0.5d-i
6	25 a-d	41h-n	3.9 a-f	10.9h-k	1.8 a-f	2.4c-i	72	63a-d	0.2 ab	0.3a-f
7	23 abc	25a-h	3.5 a-e	9.1f-k	2.2 a-g	0.5ab	100	78b-i	0.4 a-d	0.2a-d
8	42 f-i	28a-i	9.9 k	5.5a-g	7.6 j	0.9a-e	66	75b-h	0.5 a-d	0.3a-f
9	25 a-e	34c-l	5.2 c-i	7.9d-j	3.3 d-h	2.6e-j	68	79c-j	0.3 abc	0.4a-f
20	26 a-f	41h-n	3.1 a-d	11.0ijk	1.6 a-d	1.9a-i	80	88f-l	0.2 abc	0.5c-i
21	28 a-g	37e-m	6.8 f-j	12.1jk	2.5 a-g	2.9g-j	87	78b-i	0.5 a-d	0.5e-i
22	14 ab	46i-o	5.6 d-i	5.7a-h	1.7 a-d	1.8a-i	75	70b-f	0.2 a	0.4c-h
23	41 e-i	36d-m	4.1 a-f	9.9g-k	2.7 a-h	1.4a-h	87	68b-e	0.6 a-d	0.4b-g
24	45 hij	28a-i	4.0 a-f	8.5e-j	2.2 a-g	3.2ij	83	101klm	0.5 a-d	0.4a-f
25	18 abc	38f-m	2.6 abc	7.9d-j	1.7 a-e	1.1a-f	93	72b-h	0.2 abc	0.4c-h
26		32b-j		9.8g-k		1.3a-h		106lm		0.5e-i
27		24a-h		8.5e-j		2.3b-i		98j-m		0.4b-g
28		52k-o		3.4a-e		1.7a-i		65a-d		0.6f-i
29		53l-o		17.9l		2.6e-j		82d-k		0.7hi
30		30a-i		17.9l		3.0hij		117mn		0.5c-i
31		42h-n		11.1ijk		1.9a-i		86e-k		0.4c-i
32		35c-l		7.4d-j		1.4a-h		68b-e		0.3a-e
33		26a-h		7.2c-j		1.2a-g		98j-m		0.3a-f
34		26a-h		6.6b-i		0.4a		67b-e		0.2abc
35		33c-k		12.1jk		2.1a-i		77b-i		0.4a-g
Mean	38	34.40	4.9	7.69	2.8	1.74	81	81.50	0.5	0.38
LSD (5%)	16.02	19.90	2.91	5.19	1.80	1.79	39.22	19.41	0.49	0.27
F-test	<.001	<.001	<.001	<.001	<.001	0.008	0.547	<.001	<.001	0.005
CV (%)	20.5	28.5	28.7	33.2	31	50.4	23.3	11.7	46.8	34.8

[a]Evaluated from June 22nd to November 18th 2009; [b]Evaluated from December 1st 2009 to May 11th, 2010; [c]Genotypes 2-10 = local genotypes; 1, 11-35 = exotic genotypes.

Means within columns followed by same letter are not significantly different at 5% level according to according to Fischer's Protected LSD

NF/P=number of fruit per plant, TFY=total fruit yield, TMFY=total marketable fruit yield, NSF=number of seeds per fruit, FSY=fruit seed yield.

Table 13. Analysis of variance for five yield traits of twenty-five genotypes pooled across two seasons (2009A and 2009B) of evaluation at Namulonge, Uganda

Characters	Source of Variation - df					Mean	SEM±
	Season (E)-1	Replication (R)-2	Genotypes (G)-24	G x E-24	Pooled Error-47		
	Mean squares						
Number of fruit per plant	357.21^{ns}	127.85^{ns}	759.77*	338.46***	94.790	36.0	9.19
Total fruit yield (t/ha)	79.51***	23.01***	23.08^{ns}	15.03***	4.462^{a}	5.8	1.94
Total marketable fruit yield (t/ha)	30.36***	0.037^{ns}	3.15^{ns}	3.25***	0.709^{a}	2.3	0.90
Number of seeds per fruit	38.80^{ns}	20.5^{ns}	695.90**	260.80^{ns}	220.200	81.0	8.07
Fruit seed yield (t/ha)	0.48***	0.03^{ns}	0.18*	0.09***	0.038^{a}	0.4	0.15

^{a}df = 48 because one variety (34) never gave any yield in replication 2 of season 2009B and thus was given 0 score for these parameters and was considered missing for the rest

^{ns}non significant; *significant ($P < 0.05$) ** highly significant ($P < 0.01$); *** highly significant ($P < 0.001$)

5 genotypes common to both seasons varied highly significantly (P<0.001) with season and GxE interaction but did not vary significantly with genotype (Table 13). Higher fruit yields were ecorded in 2009B (mean 7.69t/ha) compared with those in 2009A (mean 4.9t/ha). Local enotypes in 2009A had lower fruit yield (mean 4.0t/ha) as compared with exotic genotypes mean 5.5t/ha). Local genotypes with lower fruit yields were 6 (1.9t/ha), 2 (2.0t/ha) and 7 2.2t/ha) while, genotypes with higher yields were 8 (4.9t/ha) and 4 (7.7t/ha). Exotic genotype vith significantly lowest total fruit yield was 25 (2.6t/ha) while, genotypes 11 and 18 had higher ruit yields (9.1t/ha and 9.9t/ha, respectively).

imilarly, local genotypes in 2009B had lower fruit yield (mean 2.6t/ha) as compared with exotic enotypes (mean 9.5t/ha). Local genotypes with low fruit yield were 8, 2, 6, 10 and 7 (range 1.0-.2t/ha) while genotypes with higher fruit yield were 9 (4.0t/ha) and 3 (4.2t/ha). Exotic genotype vith significantly low fruit yield was 28 (3.4t/ha) while genotypes 29 and 30 had higher fruit ield (17.9t/ha). Among the local genotypes, 2 and 6 consistently had lower total fruit yield vhile genotypes 5 and 3 consistently exhibited higher total fruit yield across the two seasons. Of ll the exotic genotypes, only 19 and 13 had consistent lower total fruit yields (t/ha) while enotype 1 and 14 consistently produced higher total fruit yields (t/ha) across the two seasons.

3.2.3 Total marketable fruit yield (t/ha)

here was a highly significant difference in total marketable fruit yield (t/ha) among genotypes season 2009A (P<0.001) and 2009B (P=0.008) (Table12). Pooled analysis of variance for the 5 genotypes common to both seasons differed highly significantly (P<0.001) with season and xE interaction but did not vary significantly with genotype (Table 13). Higher marketable fruit elds were recorded in 2009A (mean 2.8t/ha) compared with 2009B (mean 1.74t/ha). Local enotypes in 2009A had lower marketable fruit yield (mean 2.8t/ha) as compared with exotic enotypes (mean 2.9t/ha). Local genotype with the lowest marketable fruit yield was 2 (0.9t/ha) hile genotypes with the highest marketable fruit yield was 4 (5.4t/ha). Exotic genotypes with w marketable fruit yield were 15, 20, 22, 25 and 16 (range 1.2-1.8t/ha) while genotype18 had gnificantly the highest marketable fruit yield (7.6t/ha).

Likewise, local genotypes in 2009B had lower marketable fruit yield (mean 1.2t/ha) as compared with exotic genotypes (mean 2.0t/ha). Local genotypes with low fruit marketable fruit yield were 3, 2, 7, 10 and 6 (range 0.3-0.9t/ha) while genotypes with higher yields were 9 (2.0t/ha) and 3 (2.9t/ha). Exotic genotypes with significantly lower marketable fruit yield were 34, 11, 17 and 18 (range 0.4-0.9t/ha) while genotype 14 had the highest marketable fruit yield with 4.3t/ha. Among the local genotypes, 2, 7 and 6 consistently had lower total marketable fruit yield while genotype 9 consistently exhibited higher total marketable fruit yield across the two seasons. Within the exotic genotypes, it is 20, 22 and 25 that always had lower total marketable fruit yield while genotype 14 consistently produced a higher total marketable fruit yield across the two seasons.

4.3.2.4 Number of seeds per fruit

Number of seeds per fruit were not significantly different among genotypes in season 2009A save for season 2009B where they highly significantly varied among genotypes ($P<0.001$) (Table 12). Pooled analysis of variance for 25 genotypes common to both seasons showed that number of seeds per fruit also differed highly significantly ($P<0.001$) with genotype but did not differ significantly with season and GxE interaction (Table 13). Genotypes in 2009A and 2009B generally produced almost the same number of seeds per fruit with grand means of 80.0 and 80.5 seeds per fruit, respectively (Table 12). Though no significant differences were observed among genotypes in 2009A, local genotypes on average had more seeds per fruit (85.8 seeds) compared with exotic genotypes (79.3 seeds). The highest seed yielding fruits in 2009A were from exotic genotypes 17 (100 seeds per fruit) and 1 (109 seeds per fruit). Fruit seed yield from local genotypes ranged from 72-95 seeds per fruit.

In season 2009B, local and introduced genotypes produced almost the same seeds per fruit with means 83.2 and 81.3 seeds per fruit, respectively. The highest exotic seed yielding fruits came from genotypes 30 (117 seeds per fruit) and 1 (127 seeds per fruit) while, genotypes 5 and 4 had fruits with the highest seeds per fruit among local genotypes. The lowest exotic seed yielding fruits came from genotype 13 (60 seeds per fruit) while the lowest among local genotypes came

rom 2 (46 seeds per fruit). Exotic genotype 1 consistently exhibited high number of seeds per ruit across seasons while, all the local genotypes had no significant variations in the number of eeds per fruit across seasons save for genotype 2.

.3.3.5 Fruit seed yield (t/ha)

Total seed yield (t/ha) varied highly significantly among genotypes (P<0.001) in season 2009A nd (P<0.005) in season 2009B (Table 12). Joint analysis of variance for the 25 genotypes ommon to both seasons varied highly significantly (P<0.001) with season and GxE interaction ut only varied significantly with genotype (P<0.05) (Table 13). More seed yield was recorded in 009A (mean 0.5t/ha) compared with those in 2009B (mean 0.38t/ha). Local genotypes in 2009A ad significantly higher seed yield (mean 0.7t/ha) as compared with exotic genotypes (mean .4t/ha). Local genotype 3 and exotic genotype 12 out yielded all the others (1.4t/ha). In season 009B, exotic genotypes had more seed yield (0.4t/ha) than the local genotypes (0.3t/ha). Among ocal genotypes, 5 and 4 registered the highest seed yield (100t/ha and 101t/ha, respectively) hile, genotypes 24, 26, 30 and 1 were the highest exotic seed yielders with 101t/ha, 106t/ha, 17t/ha and 127t/ha, respectively. The Chinese genotype 1 was a consistent exotic high seed ielder (t/ha) across seasons.

.3.4 Trait correlation and stability analysis

.3.4.1 Relationship between growth and yield parameters in season 2009A and 2009B

n this study, many variables were found significantly related positively and negatively in both eason 2009A and 2009B (Tables 14 and 15). For purposes of results interpretation, significant orrelations below 0.4 were considered low, those in the range 0.4-0.64 were intermediate while orrelations above 0.65 were considered high. In 2009A, no significant low positive correlations

Table 14. Correlation coefficients between growth, quality and yield traits in hot pepper for season 2009A field trial at Namulonge, Uganda

TRAIT	200 SDWT	50 % DMAT	% NMF	AFWT (g)	FL (cm)	FSY (t/ha)	FW (cm)	NF/P	NS/F	PHT (cm)	PWD (cm)	TFY (t/ha)	TMFY (t/ha)
200 SDWT	1.00												
50 % DMAT	0.01	1.00											
% NMF	-0.05	0.09	1.00										
AFWT (g)	0.21	0.18	-0.60**	1.00									
FL (cm)	0.00	-0.13	-0.73***	0.71***	1.00								
FSY (t/ha)	0.40*	-0.05	0.46*	-0.44*	-0.43*	1.00							
FW (cm)	0.17	0.60**	-0.08	0.64***	0.08	-0.24	1.00						
NF/P	0.13	-0.07	0.55**	-0.55**	-0.51**	0.93***	-0.30	1.00					
NS/F	0.27	0.02	0.24	0.07	-0.09	0.33	0.12	0.12	1.00				
PHT (cm)	0.35	0.02	0.28	-0.01	-0.07	0.65***	0.02	0.69***	0.08	1.00			
PWD (cm)	0.25	0.04	0.24	-0.17	-0.31	0.63***	-0.09	0.66***	0.22	0.77***	1.00		
TFY (t/ha)	0.22	0.08	-0.11	0.49*	0.37	0.15	0.33	0.20	-0.24	0.66***	0.33	1.00	
TMFY (t/ha)	0.16	0.07	0.43*	0.07	-0.03	0.37	0.15	0.48*	-0.17	0.71***	0.34	0.82***	1.00

*significant ($P < 0.05$) ** highly significant ($P < 0.01$); *** highly significant ($P < 0.001$); the rest non-significant

SWT = seed weight, AFW = Average fruit weight, FL= fruit length, FM = fruit maturity, FSY = fruit seed yield, FW = fruit width, NF/P = number of fruits per plant, NMF = non marketable fruit, NS/F = number of seeds per fruit, PHT = plant height, PWD = plant width, TFY= total fruit yield, TMKFY= total marketable fruit yield.

Table 15. Correlation coefficients between growth, quality and yield traits in hot pepper for season 2009B evaluation trial at Namulonge, Uganda

TRAIT	200SWT (g)	AFW (g)	50 % days FLW	50 % days FM	FL (cm)	FSY (t/ha)	FW (cm)	NF/P	NMF (%)	NS/F	PHT (cm)	PWD (cm)	TFY (t/ha)
200SWT (g)	1.00												
AFW (g)	0.11	1.00											
50 % days FLW	-0.27*	-0.29*	1.00										
50 % days FM	-0.27*	-0.28*	0.89***	1.00									
FL (cm)	0.22	0.77***	-0.50***	-0.49***	1.00								
FSY (t/ha)	0.45***	0.06	-0.09	0.03	0.01	1.00							
FW (cm)	0.03	0.56***	0.34**	0.25*	0.28*	-0.02	1.00						
NF/P	0.14	-0.21	-0.09	0.05	-0.14	0.83***	-0.33**	1.00					
NMF (%)	-0.10	0.59***	-0.27*	-0.25*	0.62***	-0.20	0.25*	-0.28*	1.00				
NS/F	-0.10	0.49***	0.26*	0.26*	0.11	0.11	0.71***	-0.30*	0.11	1.00			
PHT (cm)	-0.06	-0.16	0.28*	0.29*	-0.32**	0.36**	0.07	0.34**	-0.26*	0.20	1.00		
PWD (cm)	0.03	-0.08	0.36**	0.37**	-0.27*	0.37**	0.30*	0.23	-0.34**	0.45***	0.78***	1.00	
TFY (t/ha)	0.15	0.77***	-0.38**	-0.31**	0.61***	0.50***	0.22	0.35**	0.47***	0.20	-0.05	-0.06	1.00
TMKFY (t/ha)	0.22	0.26*	-0.16	-0.09	0.17	0.67***	0.03	0.60***	-0.33**	0.10	0.08	0.10	0.58***

*significant ($P < 0.05$) ** highly significant ($P < 0.01$); *** highly significant ($P < 0.001$); the rest non-significant

SWT = seed weight, AFW = Average fruit weight, FL= fruit length, FM = fruit maturity, FLW= flowering, FSY = fruit seed yield, FW = fruit width, NF/P = number of fruits per plant, NMF = non marketable fruit, NS/F = number of seeds per fruit, PHT = plant height, PWD = plant width, TFY= total fruit yield, TMKFY= total marketable fruit yield.

were observed (Table 14). In 2009B, most observed significant correlations were low (Table 15). Low positive and significant correlations were between days to 50% flowering and fruit width (r= 0.34**), number of seeds per fruit (r=0.26*), plant height (r=0.28*), plant width (r=0.36**), total fruit yield (r=0.26*); days to 50% fruit maturity and fruit width (r= 0.25*), number of seeds per fruit (r=0.26*), plant height (r=0.29*) and plant width (r=0.37**); fruit length and fruit width (0.28*); fruit seed yield and plant height (r=0.36**), plant width (r=0.37**); fruit width and % non-marketable fruits (0.25*), plant width (r=0.30*); number of fruits per plant and plant height (r=0.34**), total fruit yield (r=0.35**); total marketable fruit yield and average fruit weight (r= 0.26*).

Significant intermediate positive correlations in 2009A were observed for 200 seed weight with fruit seed yield (r=0.40*); days to 50% fruit maturity with fruit width (r=0.60**); % non-marketable fruits NMF with fruit seed yield (r=0.46*), number of fruits per plant (r=0.55**) and total marketable fruit yield (r=0.43*); average fruit weight fruit width (r=0.64***) and total fruit yield (r=0.49*); fruit seed yield with plant width (r=0.63***), number of fruits per plant with total marketable fruit yield (r=0.48*). Significant intermediate positive correlations in 2009B existed between fruit seed yield and 200 seed weight (0.45***), average fruit weight (r=0.56***); % non-marketable fruits and average fruit weight (r=0.59***), fruit length (r=0.62***), number of seeds per fruit (r=0.49***); plant width and number of seeds per fruit (r=0.45***); total fruit yield and fruit length (r=0.61***), fruit seed yield (r=0.50***), % non-marketable fruits (r=0.47***); total marketable fruit yield and number of fruits per plant (r=0.60***) and total fruit yield (r=0.58***)

Significant high positive correlations in 2009A were found between average fruit weight and fruit length (r=0.71***); fruit seed yield and number of fruits per plant, (r=0.93***), plant height (r=0.65***); number of fruits per plant and plant height (r=0.69***), plant width (r=0.66***); plant height and plant width (r=0.77***), total fruit yield (r=0.66***) and total marketable fruit yield (r=0.71***); total fruit yield and total marketable fruit yield(r=0.82***). In 2009B, significant high positive correlations were observed for days to 50% fruit maturity with days to 50% flowering (r=0.89***); fruit length width average fruit weight (r=0.77***); number fruit

ber plant with fruit seed yield (r=0.83***), number of seeds per fruit with fruit width r=0.71***), plant width with plant height (r=0.78***), total fruit yield with average fruit weight r=0.77***); total marketable fruit yield and fruit seed yield (r=0.67***)

For negative correlations, no significant low negative correlation was found among traits in 2009A (Table 14). On the other hand, majority of the observed significant negative trait correlations in 2009B were low (Table 15). Negative low correlations were found between days to 50% flowering and 200 Seed weight (r=-0.27*), average fruit weight (r=-0.29*), % non-marketable fruits (r=-0.27*); days to 50% fruit maturity and 200 seed weight (r=-0.27*), average fruit weight (r=-0.28*), % non-marketable fruits (r=-0.25*), total fruit yield (r=-0.31**); fruit length and plant height (r=-0.32**), plant width (r=-0.27*); fruit width and number of fruits per plant (r=-0.33**); number of fruits per plant and % non-marketable fruits (r=-0.28*), number of seeds per fruit (r=-0.30*); % non-marketable fruits and plant height (r=-0.26*), plant width (r=-0.34**) and total marketable fruit yield (r=-0.33**).

Intermediate negative and significant correlations in 2009A were observed between % non-marketable fruits and average fruit weight (r=-0.60**); average fruit weight and fruit seed yield (r=-0.44*), number of fruit per plant (r=-0.55**); fruit length and fruit seed yield (r=-0.43*) and number of fruits per plant (r=-0.51**). In 2009B, intermediate negative correlations among traits were observed between fruit length and days to 50% flowering (r=-0.50***) and 50% fruit maturity (r=-0.49***). High negative trait correlation in 2009A was only exhibited between % non-marketable fruits and fruit length (r=-0.73***). There was no high negative trait correlation observed in season 2009B (Table 15).

4.3.4.2 Growth, quality and yield trait stability analysis of 25 common genotypes evaluated in both season 2009A and 2009B

Genotype stability in this study was tested by rank correlation analysis performed on all traits studied across the two seasons. The correlations between 2009A and 2009B values were highly significant for average fruit weight (r=0.65; P<0.001), fruit length (r=0.74; P<0.001), fruit width

r=0.71; P<0.001), 200 seed weight (r=0.51; P=0.0089), 50% days to fruit maturity (r=0.55; P<0.0045), plant width (r=0.50; P=0.01) and significant for number of seeds per fruit (r=0.43; P=0.03) hence, these traits were most stable.

Table 16. Correlation coefficients between seasons 2009A and 2009B measured traits for 25 common hot pepper genotypes evaluated in Namulonge, Uganda.

Trait	Correlation coefficient (r)	F-probability
200 Seed weight (g)	0.5117	0.0089
Average fruit weight (g)	0.6534	<0.001
50% days to fruit maturity (days)	0.5493	0.0045
Fruit length (cm)	0.7402	<0.001
Fruit seed yield (t/ha)	0.3216	0.1169
Fruit width (cm)	0.7116	<0.001
Number of fruits per plant (fruits)	0.3493	0.087
Non-marketable fruits (%)	-0.3115	0.1296
Number of seeds per fruit (seeds)	0.4274	0.0331
Plant height (cm)	0.2419	0.2441
Plant width (cm)	0.5049	0.01
Total fruit yield (t/ha)	0.2105	0.3124
Total marketable fruit yield (t/ha)	-0.0627	0.7658

Traits with high positive correlation across seasons were considered stable

4.4 Discussion and conclusion

Hot pepper genotypes available to farmers in Uganda are characterized by low yields and poor quality due to several biotic and abiotic factors that often lead to seasonal availability in the world market (ADC/IDEA, 2001; UEPB, 2005a, 2005b; Buyinza & Mugagga, 2010; Tusiime *et al.*, 2010). While cultivar improvement is necessary to address the biotic constraints sufficient information on growth, yield, and quality traits is generally lacking. This study was carried out under natural field conditions to identify hot pepper genotypes that performed better for growth, quality and yield traits for use by *Capsicum* breeders in cultivar improvement.

Results showed highly significant differences among genotypes for all growth, quality and yield traits in both 2009A and 2009B seasons except for number of seeds per fruit in 2009A indicating genotypic diversity for these traits. For some traits, genotypes performed better in 2009A including number of fruits per plant, days to fruit mature, seed weight, and number of marketable fruits or 2009B such as in the case of plant height and width, and total fruit yield, an observation attributed to GxE interaction. Inconsistencies in cultivar performance and trait expression (such as for fruit width, non-marketable fruit, 200-seed weight, fruit seed yield and number of fruits per plant) across seasons were also attributed to the effect of GxE interaction. In the case of trait expression, suitable cropping seasons would have to be identified for optimal performance of most traits except for number of seeds per fruits that performed well across seasons. Factors such as rainfall, evaporation, sunshine duration, temperature and relative humidity are known to affect the growth and yield of hot pepper (Omonijo & Afuye, 2009).

Results from this study were in agreement with findings obtained from the characterization studies in the preceding chapter where exotic genotypes performed better in most quantitative traits than local genotypes. For traits such as flowering and maturity periods, fruit sizes and yield, this trend in performance could be explained by the fact that exotic cultivars were most probably improved for these traits. On the other hand, local genotypes seemed to offer good sources of genes for tallness and wide canopies that are associated with many fruits per plant due to high number of primary, secondary and tertiary branch numbers where fruits are formed which in turn, translate into high yields (Seleshi, 2011). Tall plants also have long main stem lengths which can help improve short genotypes whose fruits are exposed to the soil there by acquiring fruit rots from fungal and bacterial soil pathogens (Rodríguez *et al.*, 2008). The higher number of seeds per fruit of local genotypes than exotic genotypes could be exploited for improved seed yield, especially to target the seed industry.

Earliness among growth traits is an important trait in hot pepper because early maturing genotypes can be grown in short rainy seasons and fit well in the intensive and multiple cropping systems that are characteristic of Ugandan situation. Traits that defined earliness were, days to 50% flowering and fruit maturity. Number of days to 50% flowering ranged from 24 to 83 days

while days to 50% fruit maturity in both seasons ranged from 54 to 119 days. Results on days to 50% flowering agreed with those reported in Taiwan (63-81 days) except in the case of days to 50% fruit maturity (111-132 days) (AVRDC, 2004). This variation could be attributed to genotypic differences or the influence of environmental factors and cultural practices that could have caused genotypes in 2009A to mature earlier than genotypes in 2009B. While there was a small difference in average temperature in both seasons, 22.7°C (2009A) and 22.9°C (2009B), there were wide variations in rainfall amounts received (92.9mm and 132.68mm in season 2009A and 2009, respectively) (Appendix 16). Late transplanting also seemed to affect the time to flowering, with a delay of 2weeks in the case of 2009A. Maturity length has been reported to be influenced by differences in environmental factors and cultural practices elsewhere (Seleshi, 2011).

Plant height and width are also important growth traits in hot pepper because they determine the number of branch numbers which define numbers of fruits per plant. Plant height and width (canopies) ranges observed in this study were lower and narrower than what has been reported elsewhere (Qaryouti *et al.*, 2003; AVRDC, 2004, DeMasi *et al.*, 2007). Much as the variation in this study may have been due to differences in genotype, it is worth noting that seedlings were transplanted at flowering in 2009A and could have suffered stress that may have delayed shoot re-growth, causing plants to reach maturity at shorter height and narrower canopy. The lower precipitation levels in this season (2009A) probably contributed even more by affecting the plant vigor.

Quality traits are important for both the farmer and the market. In addition to being an important quality trait for the market (AVRDC, 1989; Mr. James Kanyije, 2010; *personal communication*), fruit size measured by fruit length, width and weight have been reported to contribute to capsicum fruit yields (Rodríguez *et al.*, 2008; Bozokalfa & Kilic, 2010). Bigger fruits are also easy to harvest, transport and process (Akinci & Akinci, 2004). Marketable fruits are most desirable since increased marketable fruit means much more economic gain for a farmer involved in *Capsicum* production. A number of previously documented physiological and biotic factors were observed to reduce marketability of fruits (Black *et al.*, 1991; Fouché & Boelk,

2006; Terry & Boyhan, 2006). Blossom end rot in particular, has been associated with calcium imbalance due to intermittent uptake of water (Black *et al.*, 1991; Terry & Boyhan, 2006) while vegetable fruit cracking has been linked with the genetics of the plants, intermittent water uptake as well as variations in humidity, temperature, soluble solids (sugars), calcium nutrition and standing water on the fruits ("UMass Extension", 2009). These results therefore, indicate that, envorinmental differences caused nutrition imbalances resulting in these disorders. The role of genetics in expression for such traits should be investigated to identify resistant genotypes against the disorders.

The important quality traits evaluated in this study included; fruit length, fruit width, average fruit weight, non-marketable fruits (%), and seed weight. The ranges observed for fruit length were reported in other production environments: Tanzania (AVRDC-RCA, 2003), Jordan (Qaryouti *et al.*, 2003), Taiwan (AVRDC, 2004), Turkey (Akinci & Akinci, 2004), Mediterranean (Sermenli & Mavi, 2010) and Nigeria (Idowu-Agida *et al.*, 2010). Fruit width ranges also agreed with those previously reported from the above production environments but totally disagree with the observations made by Idowu-Agida *et al.* (2010). The variation observed for fruit weight was also previously reported (AVRDC-RCA, 2003; Qaryouti *et al.*, 2003; Akinci & Akinchi, 2004; AVRDC, 2004). Results on seed weight disagreed with those of Akinci & Akinchi (2004). The fewer non-marketable fruits and heavier seeds in 2009A compared to 2009B might have resulted from favourable environmental conditions that prevailed in 2009A. Much rains observed in 2009B compared to 2009A could have played a role in higher percentage of non-marketable fruits. High humidity provided favorable environment for growth of fungal and bacterial pathogens that resulted into fruit rots causing more fruits non-marketable (Agrios, 2005). On the other hand, the dry weather condition observed in 2009A could have resulted in smaller fruit sizes in 2009A compared to 2009B. This is supported by summer season studies conducted in Taiwan that resulted into summer chilli fruits being shorter, narrower and lighter than those produced in the spring season (AVRDC, 2004). This discrepancy may have also resulted from additional genotypes from AVRDC with improved fruit sizes evaluated in 2009B.

Fruit and seed yield traits are very important for the farmer and seed industry. With the exception of number of seeds per fruit in 2009A, highly significant genotypic differences were observed in all yield traits in both seasons in various ranges. Total and marketable fruit yield were generally lower than reported in Tanzania (AVRDC-RCA, 2003) and Taiwan, respectively (AVRDC, 2004). Results on number of fruits per plant, however, agreed with the findings of Qaryouti *et al.* (2003), Akinchi & Akinci (2004) and Sermenli & Mavi (2010) although higher values had been reported in Tanzania (AVRDC-RCA, 2003). Similarly, number of seeds per fruit were in line with the previous finding of Akinchi & Akinci, (2004) who recorded a range of 25-112 seeds per fruit.

The lower fruit numbers obtained in 2009B may have been due to loss of fruits to dampness and decay because of high levels of precipitation (Idowu-Agida *et al.*, 2010) or abscission of flower buds, flowers and young fruits induced by higher temperatures and excessive moisture from much rains during flowering and fruiting stages (AVRDC, 1989; Dahal *et al.*, 2006). High precipitation levels (330.4mm) were received in 2009B with high temperatures (23.3°C) during flowering and fruiting between January-March, 2010 compared to 193.1mm rainfall and 22.4°C received at flowering and fruiting in 2009A. Such conditions are the most important factors that limit chilli pepper production by inducing abscission of flower buds, flowers and young fruits (AVRDC, 1989; Dahal *et al.*, 2006). Higher total seed yields were observed in 2009A, probably due to the greater number of fruit produced in the season, which fruit also had heavier seed. Nowaczyk & Nowaczyk (1999) noted that the yield of hybrid seeds depends on the number of fruit as well as the weight of seeds included in them. Whereas season 2009A had more average fruits per plant than season 2009B, season 2009B exhibited higher total and marketable fruit yields compared to season 2009A. This could be as a result of bigger fruits: fruit length, fruit width, average fruit weight produced in season 2009B than in season 2009A: fruit length, fruit width (1.2cm), average fruit weight.

Pooled analysis of variance for genotypes common to both seasons indicated seasonal (environmental) variation for all evaluated traits, with the exception of number of fruit per plant and number of seeds per fruit. This indicates that these two traits scored the same in both

seasons. Very high variations due to GxE interaction were also observed in all traits except number of seeds per fruit indicating that genotypic performance was not consistent due to seasonal changes. The differential response of genotypes for various growth quality and yield traits when grown under different seasons has been observed (AVRDC, 2004; Idowu-Agida *et al.*, 2010). Similarly, highly significant variations due to genotypes were observed in most traits except in plant height, total fruit yield, total marketable fruit yield and non marketable fruits indicating that all genotypes performed the same for these traits in both seasons.

Hence, for all traits other than plant height, total fruit yield, non marketable fruits, total and marketable fruit yields, seasonal specific genotypes need to be selected. These results also indicate that for all traits among 25 genotypes pooled together across seasons, only number of fruits per plant and number of seeds per fruits can consistently perform well across seasons. Variation due to GxE interaction in most traits except number of seeds per fruit indicated that genotypes varied significantly with seasons in performance for most traits other than number of seeds per fruit. However, stability analysis indicated that average fruit weight, fruit length, fruit width, seed weight, 50% days to fruit maturity, plant width and number of seeds per fruit were the most stable traits and could be used to select stable genotypes across seasons. The implication of this is that traits that varied with the environment may be improved by using suitable cropping seasons and management practices.

Yield in plants results from the interaction of many correlated characters (Sreelathakumary & Rajamony, 2003). Correlation studies provide information about various yield and yield-contributing traits to identify traits for yield improvement (Irum *et al.*, 2011; Rahimi *et al.*, 2011). Results from this study indicated significant correlation between most traits in season 2009B than in 2009A. The level of significance also differed in both seasons. For example, the lowest significant absolute correlation between traits in 2009B was observed at 0.25 between number of fruits per plant, fruit width, days to 50% fruit maturity and non-marketable fruits while in 2009A, the lowest was at 0.40 between fruit seed yield and 200 seed weight. These observations were attributed to differences in numbers of genotypes used in correlation analyses

in both seasons since the significance of relationships between variables was reported to depend on sample size (StatSoft Inc., 2001).

There were also changes in trait correlations between genotypes and seasons. This is demonstrated in traits whose correlation was either positive and negative or highly positive and lowly positive and/or highly negative and lowly negative in 2009A or 2009B and vice-versa such as total fruit yield, plant height; number of fruit per plant, % non-marketable fruits; average fruit weight, % non-marketable total fruit yield; fruit seed yield, total marketable fruit yield; plant height, average fruit weight; number of seeds per fruit, number of fruit per plant; fruit length, number of fruit per plant; average fruit weight, days to 50 % fruit maturity; fruit length, number of fruits per plant. This observation is attributed to the effect of the environmental differences on genotypes. This finding confirms the ANOVA on GxE interaction and is supported by observations by other researchers on hot pepper elsewhere (Todorova *et al.*, 2003; Rodríguez *et al.*, 2008).

Nevertheless, some traits exhibited consistent positive relationship among genotypes across seasons such as total fruit yield, average fruit weight; total fruit yield, fruit length, total fruit yield, fruit width and number of fruits per plant, total fruit yield among others. This consistency implies that the relationship was stable and one trait could be used to predict and or determine the other. These results agreed with findings from previous studies that reported positive correlation between fruit yield and fruit weight (AVRDC, 2007; Rodríguez *et al.*, 2008), fruit length and fruit width (Hasanuzzaman & Golam, 2011), number of fruits per plant (Kumar *et al.*, 2003; Sreelathakumary & Rajamony, 2003; AVRDC, 2007); seed yield and seed weight in soybean (Iqbal1 *et al.*, 2010), number of pods per plant in lentil (Anjam *et al.*, 2005); average fruit weight and fruit dimensions (Sreelathakumary & Rajamony, 2003; Hasanuzzaman & Golam, 2011); fruit length and fruit width (Hasanuzzaman & Golam, 2011). Total marketable fruit yield among genotypes increased with increase in total fruit yield and number of fruits per plant probably because the more the fruits per plant and consequently the higher total yield, more fruits escaped environmental and biotic factors that caused non-marketability of fruits. The high positive correlation between days to 50% flowering and 50% fruit maturity (r= 0.89) in 2009B

suggested that both traits could be good maturity indices and one would be sufficient in a breeding programme.

On the other hand, number of fruit per plant and average fruit weight, number of fruits per plant and fruit width consistently related with each other negatively in both seasons implying that, an increase in fruit size reduced number of fruits per plant. Similar negative relationships between average fruit weight, number of fruits per plant were reported by earlier studies (Kumar *et al.*, 2003; Nandadevi & Hosamani, 2003; Rodríguez *et al.*, 2008). From consistent negative relationship between plant height and width, plant height and fruit length, it also appeared that tall plants with wide canopies were associated with shorter fruits. Results from this study also suggested that both fruit weight and number of fruits per plant were major yield determinant traits, although fruit weight contributed more to yield determination. This agreed in part with the findings of Rodríguez *et al.* (2008) but, conflicted with those of Nandadev & Hosaman, (2003) who reported that number of fruits per plant was the most important yield determinant trait. This may be due to genotypic differences used in the study.

In summary, results from this study showed that introduced pepper genotypes outperformed local genotypes in flowering and maturity periods, bigger fruits, total and marketable fruit yields. Local genotypes were however better in number of seeds produced per fruit, plant height and width. Genotypes performed better in either 2009A or 2009B and vice versa for most traits due to GxE interaction. Genotypes were most stable for average fruit weight, fruit length, fruit width, seed weight, 50% days to fruit maturity, plant width and number of seeds. Exotic genotypes 12 (PP97-7195-1), 13 (PP0537-7513), 19 (PP0337-7065), 25 (PP0337-7546), 24 (PP0007-2259), 1 (CA-PPCHI-08-1), 17 (PP0337-7545), 23 (PP0537-7528), 16 (PP0537-7539), 20 (PP0007-2269), 15 (PP9848-4996), 21 (PP0337-7562) and 14 (PP0237-7508) produced high yields with other good evaluated attributes across seasons with the AVRDC check genotype 12 (PP97-7195-1) performing better than all exotic genotypes in all traits. Similarly, of the exotic genotypes grown only in season 2009B; 33 (PP0237-7502), 32 (PP0042-17), 27 (PBC 535), 26 (PBC 375), 31 (PP0007-2247), 35 (PP0537-7558), 29 (PP9852-173) and 30 (PP9955-15) had high yields and good attributes of the traits evaluated. However, the commercial local check genotype 3 (CA -

UGCE 09-3) performed better than all the local genotypes and most of the AVRDC genotypes in terms of fruit yield and maturity periods and perhaps this is why it is popular as a commercial variety among farmers. The East African Seed Company local genotype 2 (CA-EASC-09-1) though the poorest yielder was the earliest-maturing variety among all genotypes in both seasons and its genes can be used for early yield improvement in pepper. All better performing exotic genotypes identified in this study could thus be recommended to farmers and or used in crop improvement by breeders. Growth, yield and quality traits reported in this study were evaluated under natural field conditions under the influence of many biotic stresses including diseases. The response of pepper genotypes to field diseases is reported in the next study.

CHAPTER FIVE

EVALUATION OF HOT PEPPER GENOTYPES FOR REACTION TO FIELD DISEASES

5.1 Introduction

In tropical conditions, hot pepper production is limited by diseases caused by viruses, fungi, nematodes, bacteria, mites, and insect pests (Yoon *et al.*, 1989; Wien *et al*, 1989; Black *et al.*, 1991; Ochoa-Alejo & Ramirez-Malagon, 2001; ADC/IDEA, 2001; UEPB, 2005a; Terry & Boyhan, 2006) and environmental abiotic stresses (Black *et al.*, 1991; Terry & Boynan, 2006). In Uganda, these factors also severely reduce the production and profitability of hot pepper as a result of extensive losses in yield and quality (ADC/IDEA, 2001; UEPB, 2005a; Buyinza & Mugagga, 2010; Tusiime *et al.*, 2010). Control of these diseases and their vectors are attempted by application of chemicals and use of various appropriate practices (Karungi *et al.*, 2010). However, breeding for disease resistance offers farmers the most efficient, cost-effective and environmentally-friendly approach for integrated disease management (Byoung-Cheorl *et al.*, 2005).

For any control measure to be effective a proper understanding of the disease is required. This level of understanding is facilitated by proper and accurate diagnosis. Field diagnosis of plant diseases is mainly based on symptoms expressed by diseased plants. However, this method is limited by the fact that several factors can cause similar symptoms on the same crop. For example, in hot peppers, virus-like symptoms may be caused by insect feeding damage, mutations, pH toxicity and nutrient deficiencies (Black *et al.*, 1991; Terry & Boyhan, 2006). In the same crop wilts can be caused by nematodes, bacterial and fungal pathogens (AVRDC, 1990; Black *et al.*, 1991). Field diagnosis therefore, requires the support of laboratory diagnosis in order to establish the causal agent of a particular disease condition. The aim of this study was to evaluate hot pepper germplasm for reaction to field diseases in Uganda in order to identify

potential sources of resistance for use in a disease resistance breeding programme. In addition, pathogens causing field diseases in hot pepper were identified.

5.2 Materials and Methods

The study was carried out at National Crops Resources Research Institute (NaCRRI), Namulonge, for two seasons (2009A and 2009B). The experimental genotypes, design, propagation and management were done as for the previous study in chapter 4.

5.3 Data collection

Assessment of wilt disease began three weeks after transplanting when seedlings were properly established. Assessment of other diseases (*Phytophthora* blight with foliar symptoms, *Cercospora* leaf spot, anthracnose and viral) began seven weeks after transplanting (2 weeks after protection with pesticides was discontinued). Data were taken on disease incidence and severity. Disease incidence (DI) was calculated as the proportion of infected plants per plot and expressed as a percentage (Galanihe *et al.*, 2004; Ssekyewa, 2006; Orawo, 2007). In plots where the disease incidence was 0% or 100% in one replicate and not the other, the 0% incidence value was adjusted by (0+100/4n) and 100% by (100-100/4n) (n = number of plants observed in a plot) to cater for the small sample size (Prof. Paul Gibson, former Professor of Plant breeding, Genetics and Biometry, University of Southern Illinois, USA; *personal communication*).

Disease severity was rated using a rating scale developed for each disease identified (Appendix 10). The disease severity index (DSI) for each disease was calculated according to the formula below (Galanihe *et al.*, 2004):

$$DSI\ (\%) = \Sigma\ \{(P \times Q)\}/\ (M \times N)] \times 100$$

Where P = severity score, Q = number of infected plants having the same score; M = Total number of plants observed, N = Maximum rating scale number.

Disease severity indices and disease incidence scores were used to assess disease resistance according to Pratt *et al.* (1994) and Galanihe *et al.* (2004).

The observed field diseases were identified by symptoms using the AVRDC pepper disease compendium by Black *et al.* (1991). Data on wilted plants, excluding wilts due to *Phytophthora capsici*, were recorded every week throughout the duration of the experiment. Wilts due to *Phytophthora capsici* were identified according to Black *et al.* (1991) and Sanogo & Carpenter (2007) and were scored independently as *Phytophthora* blight disease. Anthracnose, *Cercospora* leaf spot, *Phytophthora* blight and viral diseases were scored three times on each plant in the middle rows of each plot. The data were recorded at the onset of disease symptoms, at the intermediate (fruiting) growth stage and at physiological maturity of plants when the genotype first fruit changed to its respective maturity colour.

Resistance to wilt was determined on the basis of wilt incidence (%) as: Highly resistant (HR): 0% wilting; Resistant (R): 1-10% wilting; Moderately Resistant (MR): 11-20% wilting; Moderately Susceptible (MS): 21-30% wilting; Susceptible (S): 31-50% wilting; Highly susceptible: > 50 % wilting (Modified Bayoumi & El-Bramawy, 2007). Resistance to viral diseases, *Cercospora* leaf spot, *Colletotrichum spp.* and *Phytophthora* blight diseases were based on the Disease Severity Index (DSI) (%) as: Highly resistant (HR) = 0%; Resistant (R) = DSI% < 10%; Moderately resistant (MR) = 10-20%; MS = 21-40%; Susceptible (S) = 41-60 %; Highly susceptible (HS) > 60% (Modified Galanihe *et al*, 2004).

5.4 Data analyses

Data on disease incidence and severity indices were entered into the Excel program (Microsoft Office, 2007) and transformed using the square root function $\sqrt{(X+1)}$ so as to normalise variability. The transformed data were exported into GenStat computer package (12^{th} edition, version 12; VSN International Ltd, 2010) to generate analyses of variance (ANOVA) and examine variations among the genotypes (Padi, 2007). After ANOVA for the alpha-lattice design using the Linear Mixed Model selection in the Restricted Maximum Likelihood (ReML)

procedure resulted ineffective lattice blocks, analysis was done using randomized complete block design using linear models for single and combined seasons as described in section 4.2.7. Where the ANOVA showed significant differences, treatment means were separated using Fischers' Protected Least Significant Differences (LSD) test at 5% probability level (Gomez & Gomez, 1984). Correlation analyses were performed to assess the relationships between yield and scored disease parameters in individual seasons. Disease data for two seasons on 25 genotypes common to both seasons were also correlated to assess the stability (Pratt *et al.*, 1994; Quilot *et al.*, 2005) of disease resistance.

5.5 Laboratory diagnosis to confirm field diseases

5.5.1 Enzyme linked immunorsobent assay for viruses

Sixty-six (66) leaf samples with symptoms characteristic of viral diseases (Fig. 8) were collected together with nine symptomless samples from the pepper field trial in 2009B. Samples were packaged in self-sealing polythene bags and put on ice blocks for transfer to the laboratory for analysis. In the lab, the samples were stored at 4°C within 24hours. Leaf samples from healthy plants maintained under an insect-proof screen house protected experiment at NARL were collected to use as negative controls. Enzyme linked immunorsobent assays were performed for the detection of 8 viruses previously reported to occur in Uganda namely; TSWV (genus: *Tospovirus*), ChiVMV (genus: *Potyvirus*), TMV (genus: *Tobamovirus*) PVY (genus: *Potyvirus*), PepMoV (genus: *Potyvirus*), PVMV (genus: *Potyvirus*), AMV (genus: *Alfamovirus*), and CMV (genus: *Cucumovirus*) (Ssekyewa, 2006; Dafalla, 2008; Nono-Womdim, 2008). Assays were performed using commercial ELISA kits and the manufacturers' recommended protocol (Germany Collection of Microorganisms and Cell Cultures, Braunschweig, Germany). Triple-antibody sandwich ELISA (TAS-ELISA) was used for TSWV, the double antibody-sandwich ELISA (DAS-ELISA) for ChiVMV, TMV, PVY, PepMoV, PVMV, AMV, CMV; and antibody-coated plate ELISA (ACP-ELISA) for general potyvirus kit. All the ELISA kits contained monoclonal antibodies (MAbs). Samples were not replicated except for the negative control that was replicated twice. Absorbance values were read at 405nm using a Benchmark Microplate

Reader (Biorad Laboratories, 1998) with Microplate manager software (version 5.0.1, Bio-Rad Laboratoris Inc.) following development of a yellow colour for positive samples. A sample was considered positive for the test virus when its absorbance value was at least three times the average of the negative control.

Figure 8. Symptoms of viral disease on field pepper plants at Namulonge, Uganda in 2009B. A) Leaf curl, B) Leaf mosaic, C) Vein banding, D) Yellowing and stunted growth.

5.5.2 Microbiology for detection of pathogens associated with bacterial and fungal diseases

Plants exhibiting symptoms typical of infection with fungi and bacteria (Fig. 9) were sampled from the 2009B trial for confirmation of the causal agent in microbiology. Symptoms observed included:

- Plant wilt with no symptoms of collar rot associated with *Phytophthora* blight (Fig. 9B)
- Extensive stem lesions shoot die back and finally death of severely infected plants (Fig. 9E) that were suspected to be *Choanephora* blight.

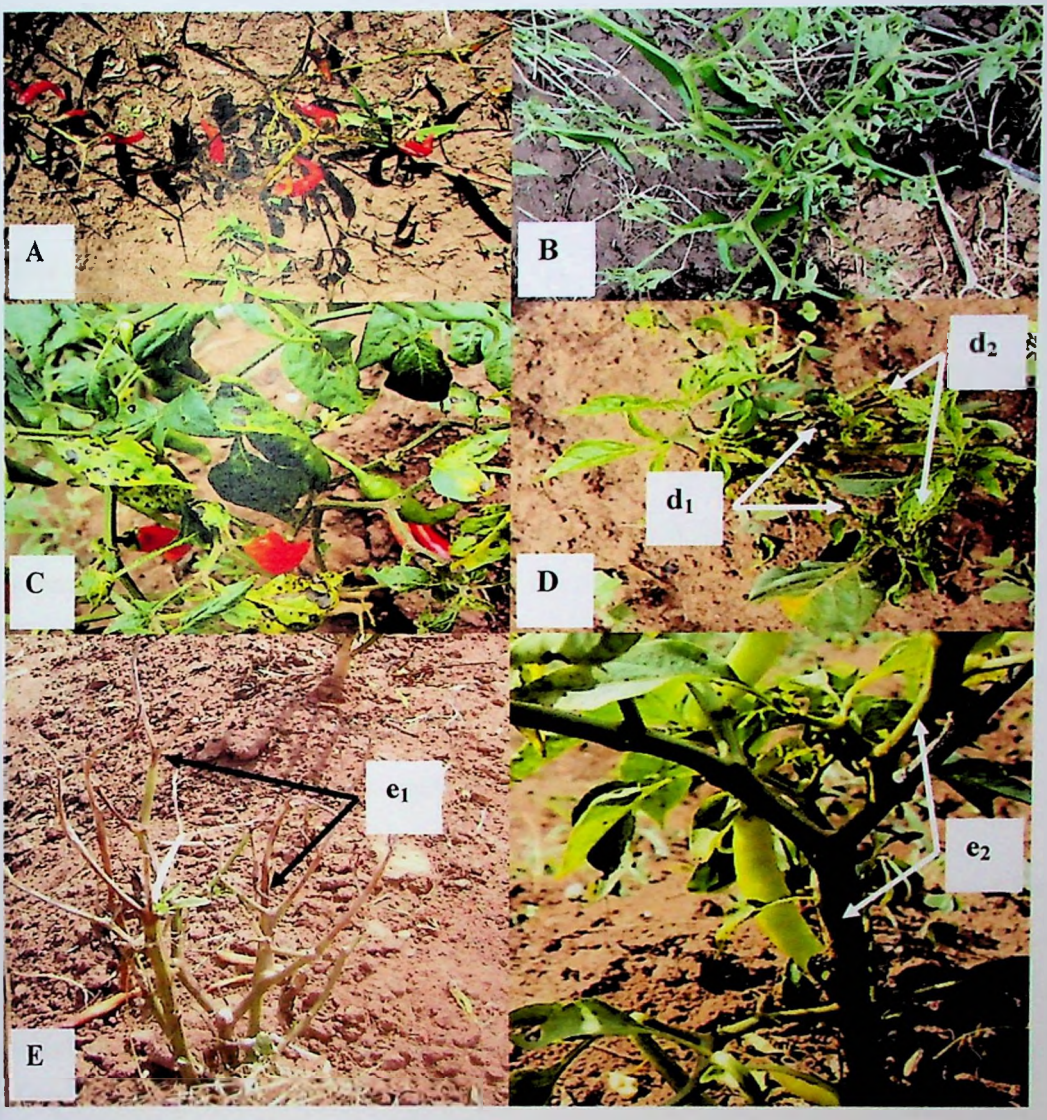

Figure 9. Field disease symptoms observed during season 2009A and 2009B hot pepper evaluation trials at Namulonge, Uganda: A) wilt disease due to *Phytophthora capscisi* with associated collar rot and foliar symptoms; B) wilt disease without collar rot associated with *P. Capscisi*; C) *Cercospora* leaf spot; D) Bacterial spot diseased plant: d_1) shoot die back and leaf defoliation, d_2) numerous water soaked lesions; E) Anthracnose diseased plant: e_1) extensive necrosis and plant death, e_2) stem necrotic lesions.

- Dark water-soaked leaf spots, extensive shoot die-back, defoliation, flower drop, stunting, reduced yield and even death of the plants when infection occurred early after transplanting (Fig. 9D) suspected to be bacterial spot.

5.5.2.1 Sample collection and preparation

Seven samples of each suspected disease were randomly selected and picked. Wilt samples were cleaned under running tap water to remove soil. Under aseptic conditions, these samples were further disinfected according to Sanogo & Carpenter (2007). In this procedure, 3 two-centimeter sections were cut from the base of the stem and the upper part of the tap root for each plant. These sections were surface disinfected for 3 minutes in 1% NaOCl and rinsed thrice in distilled water. Three stem segments per sample suspected to be caused by *Choanephora* blight were prepared. For suspected bacterial spot, five leaves collected from each sample were bulked and prepared alongside five bulked leaves from a *Cercospora* leaf spot diseased genotype 27 (Fig 9C) as a control. Leaf spot samples were washed under running tap water, surface-sterilized by soaking in 1% NaOCl solution for 2 minutes and rinsed in sterile distilled water three times.

5.5.2.2 Sample culture and examination

To identify the causal agent of wilt disease, sections from the root and plant base of each wilted sample were made to stand in sterile distilled water for 30 minutes. The resultant suspension was used to inoculate Kelman triphenyltetrazolium chloride (TTC) nutrient agar prepared according to Kelman (1954). The culture was incubated at 27°C for 48 hours and then checked for pinkish slimy colonies characteristic of *Rhalstonia solanacearum* (Kelman, 1954).

For bacterial spot, sterile samples were obtained as described above and made to stand in sterile distilled water for 1 hour. Aliquots of the resultant suspension were used to inoculate yeast dextrose carbonate (YDC) media (10g yeast extract, 20g dextrose, 20g $CaCO_3$, 20g agar, 1 liter double-distilled water at neutral pH) and were cultured at 27 °C for 48 hours then examined for bacterial growth (Mohamed & Shymaa, 2008).

To isolate fungal pathogens, sterile sections from the roots and base of the stem were plated on water agar and incubated at room temperature. After 4 days, a flamed needle was used to pick samples of mycelia and fruiting bodies for examination under a LEICA M55 stereoscopic microscope (LEICA, Denmark). Photographic micrographs of these fungal tissues were then taken at a magnification of 400X with the aid of a LEICA DLMM235 microscope (LEICA, Denmark) equipped with differential 21 interface contrast optical and digital camera. Fungi were identified by mycelial structure and morphology of fruiting bodies according to Barnett & Hunter (1972).

5.6 Results

5.6.1 Disease traits

5.6.1.1 Disease incidence

Diseases confirmed infecting hot pepper at Namulonge, Uganda during 2009A and 2009B were anthracnose (*Colletotricum spp.*), *Cercospora* leaf spot (*Cercospora capsici*), *Phytophthora* blight (*P. capsici*), wilts and viral diseases (Fig 8 and 9). The ANOVAs for disease incidence in seasons 2009A and 2009B are presented in Appendices 11 and 12, respectively. In both seasons, disease incidences differed highly significantly ($P<0.01$; $P<0.001$, respectively) among predominant diseases (Tables 17 and 18). With the exception of viral disease incidence that differed highly significantly ($P<0.01$) across seasons, the rest of the disease incidences did not vary for the 25 genotypes pooled across seasons. However, genotypes exhibited highly significant ($P<0.001$) variation across seasons with respect to all disease incidences (Table 19). Generally, season 2009B had higher disease incidences compared to season 2009A except for viral diseases and *Phytophthora* blight that were higher in season 2009A (Tables 17 and 18).

Table 17. Mean disease incidence and yield of 25 hot pepper genotypes grown in the open field at Namulonge, Uganda during season 2009A[a]

Genotype No[b]	Anthracnose	*Cercospora* leaf spot	*Phytophthora* blight	Virus disease	Wilt disease	TFY[d] (t/ha)	TMFY[e] (t/ha)
2	2.9[c] (7.7)ef	9.5 (88.8)abc	6.4 (41.2)a-d	9.8 (96.4)	1.0 (0.0)c	2.0ab	0.9a
3 Control 1	4.0 (19.2)def	8.7 (74.2)a-d	4.0 (14.8)d-g	8.3 (71.4)	1.0 (0.0)c	4.7a-h	3.1c-h
4	1.0 (0.0)f	8.0 (65.7)bcd	1.0 (0.0)h	10.0 (100.0)	1.0 (0.0)c	7.7ijk	5.4i
5	5.1 (25.5)cde	9.1 (81.9)a-d	1.0 (0.0)h	10.0 (100.0)	3.8 (14.6)ab	4.4a-g	3.3d-h
6	8.8 (77.5)ab	10.0 (100.0)a	1.0 (0.0)h	10.0 (100.0)	2.8 (7.1)ab	1.9a	1.4abc
7	9.9 (96.4)a	10.0 (100.0)a	1.0 (0.0)h	10.0 (100.0)	2.8 (7.1)ab	2.2ab	1.3abc
8	4.4 (25.0)def	9.8 (96.4)ab	5.7 (32.1)a-e	9.8 (96.4)	1.0 (0.0)c	4.9b-i	3.6fgh
9	2.8 (7.1)ef	9.8 (96.4)ab	1.0 (0.0)h	9.1 (81.3)	1.0 (0.0)c	3.4a-e	2.8b-h
10	5.2 (28.0)b-e	7.2 (50.6)d	3.0 (7.7)e-h	10.0 (100.0)	1.0 (0.0)c	4.5a-g	3.4d-h
1	1.0 (0.0)f	10.0 (100.0)a	4.9 (32.1)b-f	9.6 (92.3)	1.0 (0.0)c	7.2g-k	2.7a-h
11 Control 2	3.4 (10.7)ef	8.3 (71.4)a-d	3.4 (10.7)e-h	10.0 (100.0)	1.0 (0.0)c	9.1jk	4.4hi
12 Control 3	1.0 (0.0)f	7.3 (55.0)d	1.0 (0.0)h	10.0 (100.0)	1.0 (0.0)c	6.2e-j	4.0ghi
13	7.1 (51.7)a-d	10.0 (100.0)a	2.6 (5.0)fgh	10.0 (100.0)	1.0 (0.0)c	4.8a-i	2.6a-h
14	1.0 (0.0)f	7.6 (58.8)cd	1.0 (0.0)h	8.9 (78.8)	1.0 (0.0)c	7.6h-k	3.5e-h
15	9.5 (89.3)a	9.6 (92.3)ab	7.0 (48.6)abc	10.0 (100.0)	2.3 (3.6)bc	3.8a-e	1.2ab
16	5.0 (33.3)cde	9.9 (96.2)ab	4.2 (22.2)c-f	10.0 (100.0)	1.0 (0.0)c	3.9a-f	1.8a-f
17	9.3 (85.7)a	9.7 (95.0)ab	7.5 (55.7)ab	8.8 (75.7)	3.4 (11.1)ab	3.5a-e	2.2a-g
18	1.0 (0.0)f	10.0 (100.0)a	1.0 (0.0)h	9.7 (95.0)	1.0 (0.0)c	9.9k	7.6j
19	7.3 (52.2)a-d	10.0 (100.0)a	2.6 (5.6)fgh	10.0 (100.0)	2.6 (4.5)bc	5.2c-i	3.3d-h
20	8.2 (70.1)abc	10.0 (100.0)a	7.8 (61.7)a	8.1 (69.2)	2.4 (4.5)bc	3.1a-d	1.6a-d
21	2.3 (3.6)ef	10.0 (100.0)a	1.0 (0.0)h	10.0 (100.0)	1.0 (0.0)c	6.8f-j	2.5a-g
22	1.0 (0.0)f	10.0 (100.0)a	1.0 (0.0)h	9.2 (85.0)	1.0 (0.0)c	5.6d-i	1.7a-d
23	1.0 (0.0)f	10.0 (100.0)a	2.2 (5.6)fgh	9.8 (96.2)	2.6 (5.6)bc	4.1a-f	2.7a-h
24	1.0 (0.0)f	9.4 (87.5)abc	1.0 (0.0)h	9.3 (87.5)	4.5 (21.7)a	4.0a-f	2.2a-g
25	9.7 (93.8)a	10.0 (100.0)a	1.0 (0.0)h	10.0 (100.0)	1.0 (0.0)c	2.6abc	1.7a-e
Mean	4.5 (31.1)	9.4 (88.4)	2.9 (13.7)	9.6 (93.0)	1.7 (3.2)	4.9	2.8
LSD (5%)	3.639	1.969	2.858	1.568	1.75	2.91	1.80
F-test	<0.001	0.047	<0.001	0.319	0.003	<0.001	<0.001
CV (%)	39.1	10.2	47	7.9	49.1	28.7	31

[a]Evaluated from June 22nd to November 18th 2009

[b]Genotypes; 2-10 = local genotypes; 1, 11-25 = exotic genotypes

[c]Data transformed by square root $\sqrt{(X+1)}$ function. Actual means are in parenthesis. Mean separation was done by Fischer's Protected LSD on transformed data. Means in the the same column having similar letters are not significantly different from one another.

[d]TFY= Total Fruit Yield, [e] TMFY= Total Marketable Fruit Yield

Table 18. Mean disease incidence and yield of 35 hot pepper genotypes grown in the open field at Namulonge, Uganda during season 2009B[a]

Genotype No[b]	Wilt disease	*Cercospora* leaf spot	Virus disease	Anthracnose	*Phytophthora* blight	TFY[d] (t/ha)	TMFY[e] (t/ha)
2	3.1[c] (8.6)bc	9.0 (80.8)b	10.1 (100.0)k	3.4 (16.7)a-d	8.2 (67.9)	1.3a	0.6ab
3 Control 1	1.0 (0.0)a	8.1 (64.0)a	6.6 (45.1)bcd	1.9 (3.6)ab	3.6 (12.7)	4.2a-f	2.9g-j
4	1.0 (0.0)a	9.3 (84.7)bcd	6.7 (44.2)b-e	1.0 (0.0)a	5.0 (25.3)	3.2a-d	1.5a-i
5	1.0 (0.0)a	7.4 (53.8)a	10.1 (100.0)k	1.0 (0.0)a	1.0 (0.0)	3.6a-e	1.4a-h
6	1.0 (0.0)a	9.1 (82.2)bc	10.1 (100.0)k	7.9 (61.0)d-g	1.0 (0.0)	1.7ab	0.9a-e
7	1.0 (0.0)a	10.1 (100.0)d	9.5 (90.0)ijk	1.0 (0.0)a	3.7 (20.0)	2.2abc	0.7abc
8	1.9 (3.6)ab	9.9 (96.4)cd	8.2 (66.5)d-k	8.2 (66.8)fg	3.0 (11.5)	1.0a	0.3a
9	1.0 (0.0)a	8.1 (64.9)a	9.7 (92.9)ijk	1.0 (0.0)a	4.0 (16.1)	4.0a-f	2.0a-i
10	1.0 (0.0)a	10.1 (100.0)d	8.5 (70.7)d-k	1.0 (0.0)a	3.2 (14.3)	1.8ab	0.7a-d
1	1.0 (0.0)a	9.9 (96.4)cd	7.5 (55.8)b-h	1.0 (0.0)a	3.8 (14.6)	8.6e-j	1.7a-i
11 Control 2	1.0 (0.0)a	9.9 (96.4)cd	9.8 (95.8)jk	5.6 (32.7)b-g	2.6 (8.4)	6.1a-i	0.5ab
12 Control 3	1.0 (0.0)a	10.1 (100.0)d	5.7 (32.1)b	6.8 (46.4)d-g	1.0 (0.0)	8.5e-j	2.5e-i
13	3.6 (12.2)bc	9.5 (90.0)bcd	8.2 (66.7)d-k	6.6 (54.2)c-g	6.0 (43.5)	7.3c-j	2.7f-j
14	1.9 (3.6)ab	10.1 (100.0)d	9.7 (92.3)ijk	8.1 (65.4)fg	1.0 (0.0)	14.2kl	4.3j
15	2.0 (3.8)ab	10.1 (100.0)d	9.7 I92.3)ijk	6.5 (51.2)c-g	4.2 (18.1)	12.0jk	2.5d-i
16	2.5 (7.7)abc	10.1 (100.0)d	8.0 (64.2)d-j	7.9 (63.2)efg	2.5 (7.2)	10.9h-k	2.4c-i
17	1.0 (0.0)a	9.4 (88.5)bcd	5.9 (33.9)bc	1.0 (0.0)a	1.0 (0.0)	9.1f-k	0.5ab
18	1.9 (3.6)ab	10.1 (100.0)d	9.3 (84.6)h-k	6.1 (36.8)b-g	1.0 (0.0)	5.5a-g	0.9a-e
19	3.7 (13.6)bc	10.1 (100.0)d	9.4 (87.9)h-k	9.3 (85.9)g	3.9 (14.5)	7.9d-j	2.6e-j
20	4.4 (18.7)c	10.1 (100.0)d	10.1 (100.0)k	7.3 (53.2)d-g	4.7 (21.4)	11.0ijk	1.9a-i
21	3.9 (14.9)bc	9.5 (89.9)bcd	9.5 (89.4)ijk	2.2 (5.6)abc	4.5 (19.6)	12.1jk	2.9g-j
22	3.5 (11.5)bc	9.8 (95.5)cd	7.8 (61.7)c-i	8.8 (77.3)g	2.9 (10.7)	5.7a-h	1.8a-i
23	3.5 (11.3)bc	9.6 (91.6)bcd	7.1 (53.4)b-g	8.7 (75.0)g	2.5 (7.2)	9.9g-k	1.4a-h
24	4.0 (14.8)bc	9.8 (94.4)bcd	10.1 (100.0)k	5.2 (44.4)a-g	2.9 (10.7)	8.5e-j	3.2ij
25	1.0 (0.0)a	9.9 (96.4)cd	9.6 (91.7)ijk	7.4 (54.2)d-g	2.5 (7.2)	7.9d-j	1.1a-f
26	1.9 (3.6)ab	10.1 (100.0)d	9.9 (96.4)jk	7.2 (53.8)d-g	1.0 (0.0)	9.8g-k	1.3a-h
27	1.0 (0.0)a	10.1 (100.0)d	8.7 (74.8)f-k	3.5 (11.5)a-e	1.9 (3.6)	8.5e-j	2.3b-i
28	2.5 (7.7)abc	10.1 (100.0)d	10.1 (100.0)k	3.6 (11.9)a-e	2.0 (4.2)	3.4a-e	1.7a-i
29	1.9 (3.6)ab	10.1 (100.0)d	8.0 (63.5)d-j	3.8 (14.6)a-f	1.9 (3.6)	17.9l	2.6e-j
30	2.0 (3.8)ab	9.9 (96.2)cd	6.7 (43.9)b-e	1.0 (0.0)a	2.0 (3.9)	17.9l	3.0hij
31	2.9 (7.1)abc	9.8 (95.8)cd	7.0 (48.1)b-f	4.0 (15.7)a-f	3.4 (11.0)	11.1ijk	1.9a-i
32	2.5 (7.7)abc	10.1 (100.0)d	9.0 (81.8)g-k	8.1 (68.2)fg	1.0 (0.0)	7.4d-j	1.4a-h
33	1.0 (0.0)a	10.1 (100.0)d	8.7 (73.9)e-k	1.0 (0.0)a	1.0 (0.0)	7.2c-j	1.2a-g
34	3.9 (14.9)bc	10.1 (100.0)d	10.1 (100.0)k	5.2 (41.3)a-g	2.6 (8.3)	6.6b-i	0.4a
35	2.0 (3.8)ab	10.1 (100.0)d	2.9 (10.3)a	4.1 (16.7)a-f	4.3 (19.2)	12.1jk	2.1a-i
Mean	2.1 (5.1)	9.7 (93.1)	8.5 (74.4)	4.8 (32.2)	2.9 (11.6)	7.69	1.74
LSD (5%)	2.059	0.8319	1.973	4.461	3.622	5.19	1.79
F-test	0.005	<0.001	<0.001	<0.001	0.058	<0.001	0.008
CV (%)	48.2	4.2	11.4	46.1	61.9	33.2	50.4

[a]Evaluated from December 1st 2009 to May 11th, 2010

[b]Genotypes; 2-10 = local genotypes; 1, 11-35 = exotic genotypes

[c]Data transformed by square root $\sqrt{(X+1)}$ function. Actual means are in parenthesis. Mean separation was done by Fischer's Protected LSD on transformed data.Means in the the same column having similar letters are not significantly different from one another.

[d]TFY= Total Fruit Yield, [e] TMFY= Total Marketable Fruit Yield

Table 19. Pooled Analysis of variance for five observed field disease incidences among 25 pepper genotypes evaluated across 2 seasons (2009A and 2009B) at Namulonge, Uganda

Trait	Source of Variation – df					Mean[a]	SEM±
	Season (E)-1	Replication (R)-2	Genotypes (G)-24	G x E-24	Pooled Error-48		
	Mean squares						
Anthracnose incidence (%)	7.39 ^{ns}	0.02 ^{ns}	21.08 ^{ns}	20.14***	3.63	4.8(33.7)	1.91
Cercospora leaf spot incidence (%)	0.54 ^{ns}	0.77 ^{ns}	1.43 ^{ns}	1.43***	0.55	9.4(89.5)	0.74
P. blight incidence (%)	3.43^{ns}	2.45 ^{ns}	11.28 ^{ns}	5.78***	2.46	3.1(13.8)	1.57
Virus incidence (%)	24.36**	0.96 ^{ns}	2.49 ^{ns}	2.06***	0.74	9.1(84.3)	0.86
Wilt incidence (%)	4.35ns	1.33 ^{ns}	3.07 ^{ns}	2.35***	2.35	1.9(4.2)	0.75

^{ns}non significant; **highly significant ($P < 0.01$); ***highly significant ($P < 0.001$)

[a]Square root transformed values, original values in parenthesis

5.6.1.1.1 Anthracnose

Anthracnose incidence varied highly significantly (P<0.001) in both season 2009A and 2009B (Tables 17 and 18). When pooled across seasons for 25 common genotypes, anthracnose incidence was not influenced by season and genotype (P>0.05). However, it was highly influenced by genotype by season (GxE) interaction (P<0.001) (Table 19). More genotypes in season 2009B had higher anthracnose incidence (mean 32.2%) compared with those in 2009A (mean 31.1%). In season 2009A, local genotypes were more infected (mean 88.9%) than exotic genotypes (mean 55.3%). The reverse was true in season 2009B where local genotypes had lower anthracnose incidence (mean 44.4%) than the introduced genotypes (mean 84.6%). High incidences among local genotypes were recorded in genotype 7 (96.4%) followed by 6 (77.5%) and in season 2009B, it was genotype 8 (66.8%) followed by 6 (61.0%). Local genotype 4 was consistently not attacked by anthracnose in both seasons while local genotype 6 consistently had higher anthracnose incidence than other local genotypes.

Nine exotic genotypes had incidences greater than 50% in 2009A while they were 8 genotypes in season 2009B. Introduced genotypes 25 (93.8%), 15 (89.3%), 17 (85.7%) and 20 (70.1%) had the highest anthracnose incidences in that order in 2009A while in 2009B introduced genotypes genotypes 19 (85.9%), 22 (77.3%), 23 (75.0%), 32 (65.4%) and 14 (63.2%) had the highest incidences. The introduced Chinese genotype 1 consistently registerered no anthracnose disease while the AVRDC genotype 21 consistently had lower incidences of the disease. On the other hand, the AVRDC genotypes 15, 20 and 25 consistently registered higher incidences. Of the controls, the local genotype 3 had the lowest incidence in both seasons compared to the AVRDC controls 11 and 12 that had intermediate incidences.

5.6.1.1.2 *Cercospora* leaf spot

Cercospora leaf spot was the most abundant disease in season 2009B and the second most abundant in season 2009A (Tables 17 and and 18). Analysis of variance in season 2009A showed significant differences among genotypes (P<0.05) and in 2009B genotypes varied highly

significantly (P<0.001) among themselves (Appendices 11 and 12). Pooled analysis of variance for the 25 genotypes common to both seasons indicated a highly significant GxE interaction (P<0.001). *Cercospora* leaf spot incidence did not vary significantly with season and genotype (Table 19). All local and exotic evaluated genotypes exhibited high incidences of *Cercospora* leaf spot (Table 17 and 18). Higher incidences of *Cercospora* leafspot recorded in 2009B (mean 93.1%) compared with those in 2009A (mean 88.4%). The introduced genotypes on average had relatively higher *Cercospora* leaf spot incidences in both seasons compared to local genotypes.

In season 2009A, the lowest incidence among local genotypes was recorded on genotype 10 (50.6%) followed by 4 (65.7%) while the highest was recorded on two genotypes 6 and 7 (100% incidence). Only the commercial local check genotype 3 consistently scored relatively low incidences in both seasons 2009A and 2009B at 72.5% and 64.0%, respectively and local genotype 7 consistently had the highest number of plants infected in both seasons (100%). Nine (56.3%) introduced genotypes in 2009A were completely infected with *Cercospora* leaf spot compared to 16 (57.7%) in season 2009B. In season 2009A, the lowest incidence was recorded on control genotype 12 (55.0%) followed by 14 (58.8) and in 2009B, the genotypes least infected were 17 (88.5%) followed by 21 (89.9%).

5.6.1.1.3 *Phytophthora* blight

Analysis of variance for *Phytophthora* blight incidence in 2009A and 2009B seasons are respectively presented in Appendices 11 and 12. Genotypes varied highly significantly (P<0.001) with respect to *Phytophthora* blight incidence for season 2009A (Tables 17 and 18) unlike season 2009B (P>0.05). Overall, genotypes from season 2009A had higher *Phytophthora* blight incidence (mean 13.7%) than those from season 2009B (mean 11.6%). Fewer plants of local genotypes (44.4%) were infected compared to the introduced genotypes (56.3%) in season 2009A. On the other hand, more plants of local genotypes (77.8%) were infected compared to the introduced genotypes (73.1%) in season 2009B. Of the local genotypes, 2 and 8 were more infected at 41.2% and 32.1% incidences, respectively while, the more infected among the

introduced genotypes in descending order were 20 (61.7%), 17 (55.7%) and 15 (48.6%) (Tables 17 and 18).

In season 2009B, the most severely infected local genotype was 2 (67.9%) while the exotic genotype in season 2009B was 13 (43.5%). Pooled analysis of variance for 25 common genotypes across the two seasons indicated no influence of season and genotype on *Phytophthora* blight incidence. However, there was a high significant ($P<0.001$) influence of GxE interaction on *Phytophthora* incidence (Table 19).

5.6.1.1.4 Viral disease

Viral diseases were the most abundant infection in season 2009A and only came second to *Cercospora* leaf spot in season 2009B (Tables 17 and 18). In both seasons, no genotype was found symptomless. Mean squares of viral disease incidence in season 2009A did not indicate significant differences among genotypes ($P>0.05$) while, results for season 2009B clearly indicated highly significant variability ($P<0.001$) among genotypes (Appendices 11 and 12). Pooled analysis of variance for the 25 genotypes common to both seasons indicated a highly significant seasonal difference ($P<0.01$) and GxE ($P<0.001$) interaction for viral disease incidence while it did not vary significantly with genotype across seasons (Table 19). Genotypes in 2009A had higher viral disease incidence (mean 93.0%) compared with those in 2009B (mean 74.4%).

In general season 2009A registered higher viral disease incidences, with means of 93.9% (local genotypes) and 92.5% (introduced genotypes). Season 2009B had relatively lower values at mean incidences of 78.8% (local genotypes) and 72.9% (exotic genotypes). In season 2009A, 55.6% of the local genotypes recorded 100% infected with viral diseases compared to 50% of the introduced genotypes whereas, in 2009B, 33.3% of the local genotypes were 100% infected compared to 15.4% of the exotic genotypes. Of the local genotypes, 5 and 6 consistently exhibited high incidence levels of viral disease infection while only the local commercial check (3) consistently registered low incidences across seasons (71.4% and 45.1% in season 2009A and

2009B, respectively). Among the introduced genotypes, the AVRDC genotype 35 (evaluated only in season 2009B) was the least infected with viral disease (10.3%) (Table 18). However, genotypes 17 and 22 consistently recorded the lowest viral disease incidences over the 2 seasons (Table 17 and 18).

5.6.1.1.5 Wilt disease

Wilt disease was the least abundant of all the five diseases in both 2009A and 2009B seasons (Tables 17 and 18). Analysis of variance for this disease indicated highly significant disease incidence among genotypes in both seasons (Appendices 11 and 12) with genotypes varying significantly at P=0.003 and P=0.005 for season 2009A and 2009B, respectively (Tables 17 and 18). The pooled analysis of variance for 25 common genotypes indicated a highly significant effect (P<0.001) of GxE interaction on wilt disease incidence (Table 19).

Season 2009A had significantly lower wilt disease incidence (mean 3.2%) compared to season 2009B (mean 5.1%). The percentage of local genotypes infected was lower (mean 33.3%) than that for exotic genotypes (mean 37.5%) in 2009A. Similarly, a greater percentage of introduced genotypes (mean 73.1%) were infected than local genotypes (mean 22.2%) in season 2009B. Local genotypes 6 and 7 and introduced genotypes 20, 17, 15 and 25 had higher wilt incidences in season 2009A and the reverse was true in 2009B with significantly lower incidences recorded on genotypes 18 and 15 or no infection on genotypes 6, 7, 17 and 25 (Tables 17 and 18).

5.6.1.2 Disease severity index

Data on disease severity indices on pepper genotypes evaluated in season 2009A and 2009B are presented in Tables 20 and 21, respectively. Their respective analyses of variance are shown in Appendices 11 and 12.

Table 20. Mean diseases severity index (DSI) of 25 hot pepper genotypes evaluated at Namulonge, Uganda during season 2009A[a]

Genotype No[b]	Anthracnose	*Cercospora* leaf spot	*Phytophthora* blight	Virus disease	TFY[d] (t/ha)	TMFY[c] (t/ha)
2	1.5[c] (1.5)fg	5.2 (26.5)e-j	6.3 (39.8)ab	7.4 (54.1)ab	2.0ab	0.9a
3 Control 1	2.6 (8.5)efg	5.6 (30.7)d-i	3.9 (14.1)a-f	5.2 (27.0)d-g	4.7a-h	3.1c-h
4	1.0 (0.0)g	3.8 (15.9)h-k	1.0 (0.0)f	7.2 (51.2)abc	7.7ijk	5.4i
5	3.1 (8.8)efg	4.8 (21.9)f-k	1.0 (0.0)f	7.4 (54.2)ab	4.4a-g	3.3d-h
6	7.3 (53.0)abc	8.3 (68.4)abc	1.0 (0.0)f	7.2 (51.2)abc	1.9a	1.4abc
7	9.3 (85.1)a	8.2 (67.5)abc	1.0 (0.0)f	7.0 (48.6)a-d	2.2ab	1.3abc
8	3.5 (17.9)d-g	5.3 (28.2)e-j	4.5 (20.0)a-d	7.4 (53.5)abc	4.9b-i	3.6fgh
9	1.8 (2.9)fg	6.3 (39.0)b-g	1.0 (0.0)f	5.5 (28.8)c-g	3.4a-e	2.8b-h
10	3.8 (15.4)def	3.1 (8.6)jk	3.0 (7.7)c-e	8.0 (62.9)a	4.5a-g	3.4d-h
1	1.0 (0.0)g	9.0 (79.8)a	4.5 (32.1)a-d	6.5 (42.5)a-g	7.2g-k	2.7a-h
11 Control 2	2.5 (7.9)efg	4.3 (17.5)g-k	3.0 (7.9)c-f	7.3 (52.1)abc	9.1jk	4.4hi
12 Control 3	1.0 (0.0)g	2.7 (6.7)k	1.0 (0.0)f	4.8 (22.0)fg	6.2e-j	4.0ghi
13	6.0 (35.3)bcd	5.8 (33.3)d-i	2.2 (5.0)def	7.3 (51.7)abc	4.8a-i	2.6a-h
14	1.0 (0.0)g	3.4 (11.7)ijk	1.0 (0.0)f	4.8 (23.0)efg	7.6h-k	3.5e-h
15	9.2 (84.2)a	7.8 (60.2)a-d	4.0 (18.4)a-e	6.8 (45.4)a-e	3.8a-e	1.2ab
16	2.8 (10.0)	5.9 (35.0)c-h	3.5 (17.8)b-f	6.7 (44.6)a-f	3.9a-f	1.8a-f
17	8.9 (79.3)a	8.7 (75.0)ab	5.9 (36.6)abc	4.8 (23.1)fg	3.5a-e	2.2a-g
18	1.0 (0.0)g	7.7 (58.9)a-d	1.0 (0.0)f	6.3 (39.0)a-g	9.9k	7.6j
19	5.1 (25.3)cde	6.1 (36.6)c-h	1.1 (1.4)ef	6.6 (43.2)a-g	5.2c-i	3.3d-h
20	8.0 (65.4)ab	7.3 (55.0)a-e	6.6 (44.2)a	5.9 (37.7)b-g	3.1a-d	1.6a-d
21	1.7 (2.1)fg	6.0 (34.5)c-h	1.0 (0.0)f	7.4 (55.1)ab	6.8f-j	2.5a-g
22	1.0 (0.0)g	5.8 (33.0)d-i	1.0 (0.0)f	4.7 (22.0)g	5.6d-i	1.7a-d
23	1.0 (0.0)g	7.5 (57.3)a-e	1.1 (1.4)ef	6.9 (46.4)a-d	4.1a-f	2.7a-h
24	1.0 (0.0)g	5.1 (25.5)e-j	1.0 (0.0)f	5.7 (31.7)b-g	4.0a-f	2.2a-g
25	9.7 (93.8)a	6.7 (46.9)a-f	1.0 (0.0)f	5.8 (33.0) b-g	2.6abc	1.7a-e
Mean	3.8 (23.9)	6.0 (38.9)	2.5 (9.8)	6.4 (41.8)	4.9	2.8
LSD (5%)	2.782	2.4	2.95	1.965	2.91	1.80
F-test	<.001	<.001	0.002	0.029	<.001	<.001
CV (%)	35.5	19.3	57.5	14.8	28.7	31

[a]Evaluated from June 22nd to November 18th 2009

[b]Genotype; 2-10 = local genotypes; 1, 11-25 = exotic genotypes

[c]Data transformed by square root $\sqrt{(X+1)}$ function. Actual means are in parenthesis. Mean separation was done by Fischer's Protected LSD on transformed data. Means in the same column having similar letters are not significantly different from one another.

[d]TFY= Total Fruit Yield, [e] TMFY= Total Marketable Fruit Yield

Table 21. Mean diseases severity index (DSI) and yield of 35 hot pepper genotypes evaluated at Namulonge, Uganda during season 2009B[a]

Genotype No[b]	*Cercospora* leaf spot	Virus disease	Anthracnose	*Phytophthora* blight	TFY[d] (t/ha)	TMFY[e] (t/ha)
2	7.2[c] (56.0)d-j	6.1 (37.3)f-j	2.4 (6.7)ab	7.0 (53.6)	1.3a	0.6ab
3 Control 1	5.5 (29.5)a-d	5.3 (27.2)d-h	1.8 (2.9)ab	3.6 (12.7)	4.2a-f	2.9g-j
4	5.4 (28.4)a-d	3.6 (12.1)abc	1.0 (0.0)a	5.0 (25.3)	3.2a-d	1.5a-i
5	3.5 (11.1)a	7.0 (48.6)ij	1.0 (0.0)a	1.0 (0.0)	3.6a-e	1.4a-h
6	6.3 (38.9)b-g	7.3 (52.7)j	7.2 (50.5)fg	1.0 (0.0)	1.7ab	0.9a-e
7	8.5 (71.3)h-l	6.8 (45.0)hij	1.0 (0.0)a	3.7 (20.0)	2.2abc	0.7abc
8	7.9 (61.6)f-l	5.3 (26.7)d-h	6.4 (40.5)efg	2.9 (10.8)	1.0a	0.3a
9	4.7 (21.4)ab	6.4 (40.1)f-j	1.0 (0.0)a	4.0 (16.1)	4.0a-f	2.0a-i
10	7.7 (59.1)e-k	5.1 (24.7)c-f	1.0 (0.0)a	3.2 (14.3)	1.8ab	0.7a-d
1	7.9 (61.5)f-l	4.4 (18.6)b-e	1.0 (0.0)a	3.8 (14.6)	8.6e-j	1.7a-i
11 Control 2	6.5 (42.3)b-i	6.5 (41.7)f-j	3.5 (12.2)a-d	2.3 (5.8)	6.1a-i	0.5ab
12 Control 3	5.6 (31.0)a-e	3.0 (7.9)ab	3.5 (11.4)a-d	1.0 (0.0)	8.5e-j	2.5e-i
13	6.4 (40.2)b-h	4.4 (20.0)b-e	3.6 (15.8)a-d	5.3 (32.0)	7.3c-j	2.7f-j
14	9.9 (96.6)kl	6.6 (43.1)g-j	5.9 (34.6)c-g	1.0 (0.0)	14.2kl	4.3j
15	6.2 (38.2)b-g	6.4 (40.3)f-j	3.9 (18.7)b-e	3.9 (16.6)	12.0jk	2.5d-i
16	10.0 (99.1)l	4.2 (17.0)b-e	6.2 (38.1)c-g	2.5 (7.1)	10.9h-k	2.4c-i
17	4.9 (23.1)abc	2.3 (4.8)a	1.0 (0.0)a	1.0 (0.0)	9.1f-k	0.5ab
18	8.9 (78.6)jkl	5.4 (27.7)d-h	3.6 (11.8)a-d	1.0 (0.0)	5.5a-g	0.9a-e
19	8.5 (72.7)h-l	5.5 (29.9)d-i	6.3 (38.1)d-g	4.3 (18.8)	7.9d-j	2.6e-j
20	8.6 (74.4)i-l	5.2 (26.3)d-g	5.5 (29.7)c-f	4.7 (21.4)	11.0ijk	1.9a-i
21	5.8 (33.6)b-f	5.4 (28.7)d-h	1.9 (3.3)ab	4.5 (19.6)	12.1jk	2.9g-j
22	5.9 (36.4)b-f	4.2 (17.7)b-e	5.9 (33.6)c-g	2.9 (10.8)	5.7a-h	1.8a-i
23	8.5 (71.4)h-l	3.5 (12.5)ab	5.6 (30.8)c-g	2.5 (7.1)	9.9g-k	1.4a-h
24	8.7 (75.6)jkl	6.5 (40.9)f-j	4.2 (26.7)b-e	2.9 (10.7)	8.5e-j	3.2ij
25	4.4 (19.1)ab	5.6 (30.6)e-i	4.3 (18.0)b-e	2.5 (7.1)	7.9d-j	1.1a-f
26	8.2 (67.5)g-l	7.3 (53.8)j	4.5 (20.0)b-f	1.0 (0.0)	9.8g-k	1.3a-h
27	9.8 (95.7)kl	4.4 (18.5)b-e	2.0 (3.1)ab	1.9 (3.6)	8.5e-j	2.3b-i
28	9.9 (97.2)l	6.1 (36.0)f-j	2.0 (3.1)ab	2.0 (4.2)	3.4a-e	1.7a-i
29	9.4 (86.9)kl	4.0 (15.8)bcd	1.9 (2.9)ab	1.9 (3.6)	17.9l	2.6e-j
30	7.0 (49.6)c-j	3.3 (9.6)ab	1.0 (0.0)a	2.0 (3.8)	17.9l	3.0hij
31	6.0 (36.7)b-f	3.5 (11.3)ab	2.7 (6.5)ab	3.4 (11.0)	11.1ijk	1.9a-i
32	9.5 (89.5)kl	6.1 (38.1)f-j	6.6 (48.2)efg	1.0 (0.0)	7.4d-j	1.4a-h
33	9.7 (92.3)kl	5.0 (24.5)c-f	1.0 (0.0)a	1.0 (0.0)	7.2c-j	1.2a-g
34	10.0 (99.0)l	5.7 (21.4)e-i	8.4 (69.1)g	2.6 (8.3)	6.6b-i	0.4a
35	8.6 (72.2)h-l	3.0 (8.7)ab	2.2 (4.2)ab	3.8 (14.6)	12.1jk	2.1a-i
Mean	7.5 (58.8)	5.2 (27.7)	3.5 (16.6)	2.8 (10.7)	7.69	1.74
LSD (5%)	2.172	1.5258	2.739	3.647	5.19	1.79
F-test	<0.001	<0.001	<0.001	0.159	<0.001	0.008
CV (%)	14.3	14.5	39	64	33.2	50.4

[a]Evaluated from December 1st 2009 to May 11th, 2010

[b]Genotype; 2-10 = local genotypes; 1, 11-35 = exotic genotypes

[c]Data transformed by square root $\sqrt{(X+1)}$ function. Actual means are in parenthesis. Mean separation was done by Fischer's Protected LSD on transformed data. Means in the same column having similar letters are not significantly different from one another.

[d]TFY= Total Fruit Yield, [e] TMFY= Total Marketable Fruit Yield

Table 22. Pooled Analysis of variance for five observed field disease severity indices among 25 pepper genotypes evaluated across 2 seasons (2009A and 2009B) at Namulonge, Uganda

Trait	Source of Variation - df					Mean[a]	SEM ±
	Season (E)-1	Replication (R)-2	Genotypes (G)-24	G x E-24	Pooled Error-48		
	Mean squares						
Anthracnose severity index (%)	1.57ns	0.77ns	15.25ns	13.68***	1.94	3.7(20.4)	1.39
Cercospora leaf spot severity index (%)	20.9***	4.8***	6.65ns	5.83***	1.28	6.5(45.8)	1.13
P. blight severity index (%)	13.95*	6.13ns	8.12*	4.04ns	2.59	2.9(11.4)	1.61
Virus severity index (%)	32.8***	0.93ns	3.50ns	1.97***	0.69	5.9(35.3)	0.83

[ns]non significant; ** highly significant ($P < 0.01$); *** highly significant ($P < 0.001$)
[a]Square root transformed values, original values in parenthesis

5.6.1.2.1 Viral diseases

The severity index for viral diseases significantly (P=0.029) and highly significantly (P<0.001) differed among genotypes in 2009A and 2009B, respectively (Tables 20 and 21). Pooled analysis of variance for the 25 genotypes common to both seasons indicated a highly significant (P<0.001) effect in both season and genotype by season (GxE) interaction. There was no pooled significant genotype effect with respect to viral disease severity index (Table 22). Season 2009A registered a higher disease severity index (mean 41.8%) than season 2009B (mean 27.8%). A similar trend was observed when genotypes were partitioned with respect to their places of origin.

All genotypes were more severely infected in 2009A; however, local types exhibited a relatively higher mean severity index (47.9%) than exotic types (38.3%). A similar trend was observed in 2009B with local types exhibiting a higher severity index (34.9%) than exotic types (24.8%). Local genotypes 2 and 4 were below the overall mean in both seasons 2009A (41.8%) and 2009B (27.8%). Genotypes 2, 5, and 10 were the most severely infected by viral diseases in 2009A while genotypes 5 and 6 were the most severely infected in 2009B (Tables 20 and 21). Local genotypes 4 and 10 consistently registered low severity indices in both seasons. On the other hand, exotic genotypes in 2009A were significantly more severely infected (mean 38.3%) than in 2009B (mean 24.8 %). Of the exotic genotypes in 2009A, four had their severity index scores above the overall mean with genotypes 17 (75%) and 1 (79.8%) having the highest scores. In 2009B, the infected genotypes were 14 (43.1%) and 26 (53.8%) while, genotypes 17 and 12 were the least infected with severity index of 4.8% and 7.9%, respectively. Mean severity indices for all the exotic genotypes in 2009B were below the overall mean (Table 21).

5.6.1.2.2 *Cercospora* leaf spot

Cercospora leaf spot severity indices were highly significantly (P<0.001) different among genotypes in both seasons 2009A and 2009B (Tables 20 and 21). Season 2009A had lower average severity indices (38.9%) than 2009B (58.8%). Pooled analysis of variance for the 25

genotypes common to both seasons indicated a highly significant season ($P<0.01$) and GxE ($P<0.001$) *Cersospora* severity index interaction effect. However, it did not vary significantly with genotype (Table 22). Local genotypes in 2009A registered a lower *Cercospora* leaf spot severity index (mean 34.1%) than in season 2009B (41.9%). Local genotypes 6 (67.5%) and 7 (68.4%) were the most severely infected in 2009A while genotypes 8 (61.6%) and 7 (71.3%) were the most severely infected in 2009B (Tables 20 and 21). Local genotypes 4 and 5 consistently registered low severity indices in both seasons.

Likewise, exotic genotypes in 2009A were significantly less severely infected with mean severity index at 41.7% than in 2009B (64.6%). Of the exotic genotypes in 2009A, seven genotypes had their severity index scores above the overall mean (38.9%) with genotypes 17 (75%) and 1 (79.8%) having the highest. In 2009B, the severely infected genotypes were 29, 32, 33, 27, 14, 28, 34, 16 (range 86.9%-99.1%) with genotypes 34 and 16 topping the list. Genotypes 25 and 17 were the least severely infected (severity index 19.1% and 23.1%, respectively) (Table 21). Some genotypes that scored high indices in season 2009A such as 15 and 17 scored low indices in 2009B. Similarly, some genotypes such as 14 and 16 that scored low indices in 2009A scored high indices in 2009B. Exotic genotypes 1 and 18 consistently registered high severity indices.

5.6.1.2.3 Anthracnose

Anthracnose was the second least severe disease observed in both seasons of 2009A and 2009B. Highly significant differences ($P<0.001$) were observed in both seasons with respect to anthracnose severity index (Tables 20 and 21). Plants in 2009A were generally more severely infected than those in 2009B with overall means being 23.9% and 16.6%, respectively. However, in both seasons exotic genotypes were consistently more infected than the local genotypes. When averaged, the means of local and exotic genotypes in 2009A were 21.5% and 25.2%, respectively. Similarly, anthracnose mean severity indices for local and exotic genotype in 2009B were 11.2% and 18.5%, respectively. In 2009A, local genotypes 6 (53.0%) and 7 (85.1%) had higher severity indices while in 2009B, genotypes 6 (40.5%) and 8 (50.5%) registered higher

anthracnose severity indices. Exotic genotypes 20, 17, 15 and 25 had higher severity indices (range 65.4%-93.8%) while in 2009B; genotypes 32 and 34 scored high severity index (48.2% and 69.1%, respectively).

Analysis of variance for genotypes common to both seasons showed a highly significant GxE ($P<0.001$) interaction effect with anthracnose severity indices. The index did not vary significantly with season and genotype (Table 22). Local genotypes 2, 3, 4, 5, 9, 10 and exotic genotypes 1, 11, 12, 18, 21 consistently scored low indices in both seasons while local genotype 6 and exotic genotype 19 consistently got severely infected in both seasons.

5.6.1.2.4 *Phytophthora* blight

Of all diseases whose severity indices were calculated, *Phytophthora* blight was the least severe in both seasons 2009A and 2009B (Tables 20 and 21). Genotypes differed highly significantly ($P=0.002$) in season 2009A and did not differ significantly in 2009B with respect to *Phytophthora* blight disease severity (Tables 20 and 21). Local genotypes in 2009B were more severely infected than those in 2009A with mean severity indices of 17.0% and 9.1%, respectively. On the other hand, the exotic genotypes in 2009A had a high but insignificant mean severity index (10.3%) compared with that of 2009B (8.5%). However, season 2009B generally had more severely infected genotypes compared to those in season 2009A with their overall means at 10.7 % and 9.8 %, respectively.

In 2009A, three local genotypes had severity indices above the overall mean with 8 and 2 being the most severely infected in that order while in 2009B, 78.8% of the local genotypes, had their severity indices above the overall mean (8.5%) with genotype 2 significantly being the most severely infected (53.6%) followed by 4 (25.4%). Four exotic genotypes in 2009A had their severity index means above the overall mean (8.5%) with genotype 20 being the most severely infected (44.2%) followed by genotype 17 (36.6%). Although the ANOVA failed to detect significant differences among genotypes in 2009B, genotypes 13 and 20 were the most severely infected with severity indices 32% and 21.4%, respectively with most exotic genotypes (55.2%)

scoring below the average mean (Table 21). For 25 genotypes common to both seasons, analysis of variance showed no significant genotype x season interaction effect with *Phytophthora* blight severity indices. However, the index varied significantly ($P<0.05$) with season and genotype (Table 22). Local genotypes 5, 6 and exotic genotypes 12, 14, 18 and 11 consistently registered low severity indices in both seasons while local genotypes 2, 3 and exotic genotypes 20 and 15 consistently got severely infected in both seasons.

5.6.1.3 Disease reaction rating

Grouping of genotypes on the basis of their reaction to individual field diseases facilitated the identification of resistant and susceptible genotypes in season 2009A and 2009B (Table 23). In 2009A, based on the wilt disease incidence rating, 16 accessions including both the AVRDC check accessions 11, 12 and the local commercial check accession 3 were rated highly resistant (0% wilting), 6 accessions were rated resistant (1-10% wilting), 2 moderately resistant (11-20% wilting) and 1 moderately susceptible (21-30% wilting) (Table 23). Fourteen genotypes were highly resistant, 13 resistant, and 8 moderately resistant in 2009B (Table 23). None of the genotypes were highly resistant to viral disease in both seasons 2009A and 2009B based on the severity index (SI) resistance rating (Table 23). Ten genotypes were moderately susceptible (21-40% SI), 14 were susceptible (41-60% SI) while, 1 local genotype (10) was highly susceptible (> 60% SI) in 2009A. In 2009B, 4 genotypes were resistant (<10% SI), 9 were moderately resistant, 13 were moderately susceptible (21-40% SI), 9 were susceptible (41-60% SI) and none was highly susceptible (> 60% SI) (Table 23).

Based on the *Cercospora* leaf spot disease severity index scores in 2009A, 2 genotypes including one AVRDC check genotype 12 were resistant (<10% SI), 3 moderately resistant (10-20% SI), 11 moderately susceptible (21-40% SI), 4 susceptible (0% SI), and 5 highly susceptible (> 60% SI). In 2009B, none of the genotypes were resistant. One genotype was highly resistant (0% SI), 2 moderately resistant (10-20% SI), 10 were moderately susceptible (21-40% SI), 4 were susceptible (41-60 % SI), and 18 highly susceptible (> 60% SI) (Table 23).

Table 23. Field disease reactions of 25 hot pepper genotypes evaluated at Namulonge, Uganda during season of 2009A and 2009B[a]

Genotype No.	2009A WIINC[b] (%)	DR	2009B WIINC (%)	DR	2009A Anthrac SI[c] (%)	DR	2009B Anthrac[d] SI (%)	DR	2009A CLS[e] SI (%)	DR
1	0	HR	0	HR	0	HR	0	HR	79.8	HS
2	0	HR	8.6	R	1.5	R	6.7	R	26.5	MS
3 Control 1	0	HR	0	HR	8.5	R	2.9	R	30.7	MS
4	0	HR	0	HR	0	HR	0	HR	15.9	MR
5	14.6	MR	0	HR	8.8	R	0	HR	21.9	MS
6	7.1	R	0	HR	53	S	50.5	S	68.4	HS
7	7.1	R	0	HR	85.1	HS	0	HR	67.5	HS
8	0	HR	3.6	R	17.9	MR	40.5	S	28.2	MS
9	0	HR	0	HR	2.9	R	0	HR	39	MS
10	0	HR	0	HR	15.4	MR	0	HR	8.6	R
11 Control 2	0	HR	0	HR	7.9	R	12.2	MR	17.5	MR
12 Control 3	0	HR	0	HR	0	HR	11.4	MR	6.7	R
13	0	HR	12.2	MR	35.3	MS	15.8	MR	33.3	MS
14	0	HR	3.6	R	0	HR	34.6	MS	11.7	MR
15	3.6	R	3.8	R	84.2	HS	18.7	MR	60.2	HS
16	0	HR	7.7	R	10	MR	38.1	MS	35	MS
17	11.1	MR	0	HR	79.3	HS	0	HR	75	HS
18	0	HR	3.6	R	0	HR	11.8	MR	58.9	S
19	4.5	R	13.6	MR	25.3	MS	38.1	MS	36.6	MS
20	4.5	R	18.7	MR	65.4	HS	29.7	MS	55	S
21	0	HR	14.9	MR	2.1	R	3.3	R	34.5	MS
22	0	HR	11.5	MR	0	HR	33.6	MS	33	MS
23	5.6	R	11.3	MR	0	HR	30.8	MS	57.3	S
24	21.7	MS	14.8	MR	0	HS	26.7	MS	25.5	MS
25	0	HR	0	HR	93.8	HS	18	MR	46.9	S
26			3.6	R			20	MR		
27			0	HR			3.1	R		
28			7.7	R			3.1	R		
29			3.6	R			2.9	R		
30			3.8	R			0	HR		
31			7.1	R			6.5	R		
32			7.7	R			48.2	S		
33			0	HR			0	HR		
34			14.9	MR			69.1	HS		
35			3.8	R			4.2	R		

[a]Original untransformed data
[b]Wilt Incidence; (%); DR = Disease reaction: Modified Bayoumi and El-Bramawy, 2007 (Appendix 10)
[c]Disease Severity Index (%); Disease reaction: Modified Galanhe *et al*, 2004 (Appendix 10)
[d]Anthrac = Anthracnose; [e]CLS = *Cercospora leaf* spot.

Table 23 continued

Genotype No.	2009B CLS[e] SI[e] (%)	DR	2009A VI[f] SI (%)	DR	2009B VI SI (%)	DR	2009A PH[g] SI (%)	DR	2009B PH SI (%)	DR
1	61.5	HS	42.5	S	18.6	MR	32.1	MS	14.6	MR
2	56	S	54.1	S	37.3	MS	39.8	MS	53.6	S
3 Control 1	29.5	MS	27	MS	27.2	MS	14.1	MR	12.7	MR
4	28.4	MS	51.2	S	12.1	MR	0	HR	25.3	MS
5	11.1	MR	54.2	S	48.6	S	0	HR	0	HR
6	38.9	MS	51.2	S	52.7	S	0	HR	0	HR
7	71.3	HS	48.6	S	45	S	0	HR	20	MR
8	61.6	HS	53.5	S	26.7	MS	20	MR	10.8	MR
9	21.4	MS	28.8	MS	40.1	S	0	HR	16.1	MR
10	59.1	S	62.9	HS	24.7	MS	7.7	R	14.3	MR
11 Control 2	42.3	S	52.1	S	41.7	S	7.9	R	5.8	R
12 Control 3	31	MS	22	MS	7.9	R	0	HR	0	HR
13	40.2	S	51.7	S	20	MR	5	R	32	MS
14	96.6	HS	23	MS	43.1	S	0	HR	0	HR
15	38.2	MS	45.4	S	40.3	S	18.4	MR	16.6	MR
16	99.1	HS	44.6	S	17	MR	17.8	MR	7.1	R
17	23.1	MS	23.1	MS	4.8	R	36.6	MS	0	HR
18	78.6	HS	39	MS	27.7	MS	0	HR	0	HR
19	72.7	HS	43.2	S	29.9	MS	1.4	R	18.8	MR
20	74.4	HS	37.7	MS	26.3	MS	44.2	S	21.4	MS
21	33.6	MS	55.1	S	28.7	MS	0	HR	19.6	MR
22	36.4	MS	22	MS	17.7	MR	0	HR	10.8	MR
23	71.4	HS	46.4	S	12.5	MR	1.4	R	7.1	R
24	75.6	HS	31.7	MS	40.9	S	0	HR	10.7	MR
25	19.1	MR	33	MS	30.6	MS	0	HR	7.1	R
26	67.5	HS			53.8	S			0	HR
27	95.7	HS			18.5	MR			3.6	R
28	97.2	HS			36	MS			4.2	R
29	86.9	HS			15.8	MR			3.6	R
30	49.6	S			9.6	R			3.8	R
31	36.7	MS			11.3	MR			11	MR
32	89.5	HS			38.1	MS			0	HR
33	92.3	HS			24.5	MS			0	HR
34	99	HS			21.4	MS			8.3	R
35	72.2	HS			8.7	R			14.6	MR

[e]Disease Severity Index (%); Disease reaction: Modified Galanhe *et al*, 2004 (Appendix 10)
[e]CLS = *Cercospora leaf* spot; [f]VI = Viral disease, [g]PH = *Phytophthora* blight.

The *Phytophthora* blight severity index rating in 2009A categorised 10 genotypes as highly resistant including the AVRDC control 12 and 5 local genotypes, (0% SI), 5 genotypes namely 10, 11, 13, 19 and 23 were resistant (<10% SI), 4 genotypes (Local check 3, 15, 16 and 8) moderately resistant (10-20% SI) and 3 moderately susceptible (21-40% SI) (Table 23). Similarly, in 2009B, 9 genotypes were highly resistant (0% SI), 9 genotype were resistant (<10%

SI), 13 moderately resistant (10-20% SI), 3 were moderately susceptible (21-40% SI), 1 was susceptible (41-60 % SI) and none was highly susceptible (> 60% % SI) (Table 23).

In 2009A, the results indicated that 28% of the genotypes including 5 local and 2 exotic genotypes were highly resistant (0% SI) for anthracnose (Table 23). While 24% of the genotypes were resistant (<10% SI) including the local commercial check 3, 12% exhibited moderate resistance (10-20% SI) including the 2 AVRDC checks 11 and 12; 8% were moderately susceptible (21-40% SI); 4% were susceptible (41-60% SI) and 24 % were categorised as highly susceptible (>60% SI). In 2009B, 26% of the genotypes were categorised as highly resistant (0% SI), 23% as resistant (<10% SI), 20% moderately resistant (10-20% SI), 20% moderately susceptible (21-40% SI), 9% susceptible (41-60% SI) while only 1 genotype 34 (3%) was rated as highly susceptible (>60% SI) (Table 23).

5.6.2 Trait correlation analysis

5.6.2.1 Relationship between yield and disease parameters in seasons 2009A and 2009B

In both season 2009A (Table 24) and 2009B (Table 25), the correlation between disease incidences and disease severity indices respectively indicated high, positive and significant correlations between *Colletotrichum* incidence and severity index (r = 0.971***, 0.821***), *Cercospora* leaf spot incidence and severity index (r = 0.736***, 0.626***), *Phytophthora* blight incidence and severity index (r = 0.946***, 0.985***) except for viral disease where its incidence did not significantly correlate with its severity index in season 2009A (r = 0.273, 0.852***). In season 2009A, the diseases that correlated positively were: *Colletotrichum* incidence and *Cercospora* leaf spot severity index (r=0.523*), *Colletotrichum* severity index and *Cercospora* leaf spot severity index (r=0.552*) and wilt incidence with virus incidence (r=0.409**). Similarly, in 2009B diseases that positively correlated with others were; wilt incidence with *Colletotrichum* severity index (r=0.501**), wilt incidence with *Colletotrichum* incidence (r=0.471**).

Table 24. Correlation coefficients between disease and yield traits in chilli pepper for season 2009A evaluation trial at Namulonge, Uganda

TRAIT	COINC	COSI	LSINC	LSSI	PHINC	PHSI	TFRY (t/ha)	TMFRY (t/ha)	VIINC	VSI	WINC
COINC	1.000										
COSI	0.971***	1.000									
LSINC	0.364	0.352	1.000								
LSSI	0.523**	0.552**	0.736***	1.000							
PHINC	0.351	0.384	0.210	0.387	1.000						
PHSI	0.210	0.233	0.176	0.334	0.946***	1.000					
TFRY (t/ha)	-0.615***	-0.562**	-0.336	-0.258	-0.273	-0.258	1.000				
TMFRY (t/ha)	-0.503**	-0.481*	-0.382	-0.338	-0.358	-0.338	0.819***	1.000			
VIINC	-0.028	-0.097	-0.083	-0.178	-0.180	-0.181	-0.035	0.070	1.000		
VSI	0.075	-0.016	0.043	-0.060	0.000	0.024	0.013	-0.035	0.273	1.000	
WINC	0.207	0.187	0.144	0.183	0.013	-0.053	-0.310	-0.206	0.409*	-0.062	1.000

*significant ($P < 0.05$) ** highly significant ($P < 0.01$); *** highly significant ($P < 0.001$); the rest non-significant

COINC= *Colletotrichum* incidence; COSI= *Colletotrichum* severity index; LSINC= *Cercospora* leaf spot incidence; LSSI = *Cercospora* leaf spot severity index; PHINC = *Phytophthora* incidence; PHSI= *Phytophthora* severity index; TFRY= Total fruit yield; TMFRY = Total marketable fruit yield; VIINC = Virus incidence; VSI= Virus severity index; WINC= Wilt incidence.

Table 25. Correlation coefficients between disease and yield traits in chilli pepper for season 2009B evaluation trial at Namulonge, Uganda

COINC	1.000										
COSI	0.821***	1.000									
LSINC	0.345*	0.261	1.000								
LSSI	0.223	0.352*	0.626***	1.000							
PHINC	-0.104	-0.159	-0.175	-0.173	1.000						
PHSI	-0.106	-0.151	-0.170	-0.179	0.985***	1.000					
TFY (t/ha)	0.113	0.173	-0.639***	-0.327	0.101	0.095	1.000				
TMFY (t/ha)	0.081	0.047	-0.196	-0.016	-0.121	-0.151	0.629***	1.000			
VINC	0.215	0.322	-0.063	0.183	0.061	0.075	0.178	-0.061	1.000		
VSI	0.166	0.258	-0.234	0.040	-0.018	-0.024	0.358*	0.195	0.852***	1.000	
WIINC	0.471**	0.501**	0.237	0.302	0.301	0.332*	-0.088	-0.213	0.256	-0.030	1.000
TRAIT	**COINC**	**COSI**	**LSINC**	**LSSI**	**PHINC**	**PHSI**	**TFY (t/ha)**	**TMFY (t/ha)**	**VINC**	**VISI**	**WIINC**

*significant ($P < 0.05$) ** highly significant ($P < 0.01$); *** highly significant ($P < 0.001$); the rest non-significant

COINC= *Colletotrichum* incidence; COSI= *Colletotrichum* severity index; LSINC= *Cercospora* leaf spot incidence; LSSI = *Cercospora* leaf spot severity index; PHINC = *Phytophthora* incidence; PHSI= *Phytophthora* severity index; TFRY= Total fruit yield; TMFRY = Total marketable fruit yield; VIINC = Virus incidence; VSI= Virus severity index; WINC= Wilt incidence.

In season 2009A (Table 24), except for viral disease, all diseases were negatively correlated with both total fruit yield (t/ha) and total marketable fruit yield but the correlation was only significant with both *Colletotrichum* incidence (r=-0.615**) and *Colletotrichum* severity index (r=-0.562**) for total fruit yield and both *Colletotrichum* incidence (r=-0.503**) and *Colletotrichum* severity index (r=-0.481**) for total marketable fruit yield respectively. Viral disease incidence negatively correlated with total fruit yield and positively with total marketable fruit yield non-significantly. The reverse was true for viral disease severity index. However, in season 2009B the pattern of correlation of diseases with yield was different (Table 25). The viral disease severity index significantly and negatively correlated (r=-0.358*) with total fruit yield. *Cercospora* leaf spot incidence significantly and negatively correlated with total fruit yield (r=-0.630***).

5.6.2.2 Disease trait stability analysis

Correlation coeffients across seasons for disease traits in this study are presented (Table 26). The correlations between 2009A and 2009B values were highly significant for the viral disease severity index (r= 0.5086; P=0.009) and significant for *Phytophthora* blight severity index (r=0.416; P=0.039). The rest of the parameters had insignificant correlations. The viral disease severity index was the most stable, while viral disease incidence was the least stable (r = -0.034) followed by *Cercospora* leafspot severity index (r=-0.138).

5.6.3 Diagnosis of field diseases

5.6.3.1 Serological detection of viruses

All the 75 samples tested positive for viruses with at least one antiserum although some samples yielded negative results for certain viruses (Table 27; Appendix 13). *Potato Virus* Y (PVY) (100%), ChiVMV and CMV (97.3%) were the most frequently detected viruses, while AMV (49.3%), TSWV (38.7%) and TMV (30.7%) were the least frequently detected viruses. All

identified viruses occurred in mixtures of more than two viruses among all selected 23 genotypes (Table 27). The highest frequency of viruses in mixed infections among symptomatic samples were obtained from genotypes 17 (78%), 8 (78%), 35 (78%), 4 (78%) while for symptomless samples, they were obtained in descending order from genotypes 34 (100%), 27 and 1 (89%), (89%) 23, 29 and 4 (78%) (Table 27). Genotypes 5, 9, 17, 18, 27, 30, 35, and 34 had all viruses in mixed infections (Table 28).

Table 26. Correlation coefficients of mean scored diseases between seasons 2009A and 2009B for the 25 pepper genotypes common to both seasons at Namulonge, Uganda

Trait	Correlation coefficient	F-probability
Anthracnose incidence [a]	0.077	0.716
Anthracnose severity index [a]	0.125	0.550
Cercospora leafspot incidence	0.113	0.591
Cercospora leafspot severity index	-0.138	0.511
Phytophthora blight incidence	0.312	0.129
Phytophthora blight severity index	0.416	0.039
Virus incidence	-0.034	0.873
Virus severity index	0.509	0.009
Wilt incidence	0.0737	0.726

[a]Disease assessed based on stem lesions and foliar symptoms.
Traits with high significant correlations across seasons were considered most stable

5.6.3.2 Fungal and bacterial diseases

Ralstonia solanacearum (Fig. 10B) was detected in 2 out of 7 samples tested, one from young plants and the other from older plants. In both samples, the pathogen was isolated from both stem and root extracts. *Fusarium oxysporum* (Fig. 10D) was detected in 4 out of 7 samples tested from both root and stem segments, while one sample had no pathogen detected. *Verticilium dahlia, Phytophthora capsis* and nematodes were not detected in any of the samples tested. The causal pathogen for bacterial spot, *Xanthomonas campestris* pv. *vesicatoria* (Fig. 10C) was detected in all five tested leaf samples drawn from each of the four selected genotypes. This pathogen was not detected in all the five leaf samples from control genotype (27) infected with *Cercospora*

Table 27. Viruses detected and their mixed infections on hot pepper genotypes from 2009B field trial at Namulonge, Uganda

			Virus serological detection by ACP-, TAS- and DAS-ELISA									
			ACP-ELISA	DAS-ELISA				TAS-ELISA	DAS-ELISA			
Genotype	Nature of sample	Samples tested	General potyvirus	PVY	ChiVMV	PVMV	PepMoV	TSWV	TMV	AMV	CMV	No. of Virus combination
1	Symptomatic	5	2	5	5	1	2	0	0	0	5	20 (44)[a]
	Symptomless	1	1	1	1	1	0	1	1	1	1	8 (89)
2	Symptomatic	4	4	4	3	0	3	1	0	0	4	19 (53)
3	Symptomatic	4	2	4	4	3	4	2	0	2	4	25 (69)
4	symptomless	1	0	1	1	1	0	1	1	1	1	7 (78)
	symptomatic	1	0	1	1	1	1	0	1	1	1	7 (78)
5	Symptomatic	5	3	5	5	5	1	4	4	3	5	35 (78)
8	Symptomless	2	2	2	2	2	0	2	0	2	2	14 (78)
9	Symptomatic	5	4	5	5	3	4	3	2	2	5	33 (73)
12	Symptomatic	1	1	1	1	1	1	1	1	0	1	8 (89)
13	Symptomatic	5	5	5	5	2	1	1	0	1	5	25 (56)
17	Symptomatic	2	1	2	2	2	1	2	1	1	2	14 (78)
18	Symptomatic	5	4	5	5	2	3	3	2	2	5	31 (69)
27	Symptomless	2	1	2	2	2	1	2	2	2	2	16 (89)
28	Symptomatic	5	5	5	5	2	1	0	1	0	5	24 (53)
29	Symptomatic	4	4	4	4	2	4	0	0	0	4	22 (61)
	Symptomless	1	1	1	1	1	0	1	0	1	1	7 (78)
30	Symptomatic	5	4	5	5	3	4	2	2	2	4	31 (69)
32	Symptomatic	5	5	5	5	2	2	0	1	1	5	26 (58)
33	Symptomatic	5	3	5	5	3	3	0	0	1	4	24 (53)
	Symptomless	1	1	1	1	1	0	1	0	1	1	7 (78)
34	Symptomless	1	1	1	1	1	1	1	1	1	1	9 (100)
35	Symptomatic	5	3	5	4	2	3	1	1	2	5	26 (58)
Total		75	57	75	73	43	40	29	21	27	73	
% samples positive			76.0	100	97.3	57.3	53.3	38.7	30.7	49.3	97.3	

[a]Figure in parenthesis is the proportion (%) of viral mixed infections in a genotype. PVY= *Potato virus Y*, ChiVMV= *Chilli veinal mottle virus*, PVMV= *Pepper veinal mottle virus*, PepMoV= *Pepper mottle virus*, TSWV= *Tomato spotted wilt virus*, TMV= *Tobacco mosaic virus*, AMV= *Alfalfa mosaic virus*, CMV= *Cucumber mosaic virus*

Table 28. Virus combinations in mixed infections found in hot pepper sampled genotypes during 2009B evaluation trial at Namulonge, Uganda

Genotype	Nature of sample	Virus combinations	Missing viruses
1	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, CMV	TSWV, TMV, AMV
1	Symptomless	General potyvirus, PVY, ChiVMV, PVMV, TSWV, TMV, AMV, CMV	PepMoV
2	Symptomatic	General potyvirus, PVY, ChiVMV, PepMoV, TSWV, CMV	PVMV, TMV, AMV
3	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, AMV, CMV	TMV
4	symptomless	PVY, ChiVMV, PVMV, TSWV, TMV, AMV, CMV	General potyvirus, PepMoV
4	symptomatic	PVY, ChiVMV, PVMV, PepMoV, TMV, AMV, CMV	General potyvirus, PepMoV
5	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, TMV, AMV, CMV	0
8	Symptomless	General potyvirus, PVY, ChiVMV, PVMV, TSWV, AMV, CMV	PepMoV, TMV
9	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, TMV, AMV, CMV	0
12	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, TMV, CMV	AMV
13	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, AMV, CMV	TMV
17	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, TMV, AMV, CMV	0
18	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, TMV, AMV, CMV	0
27	Symptomless	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, TMV, AMV, CMV	0
28	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TMV, CMV	TSWV, AMV
29	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, CMV	TSWV, TMV, AMV
29	Symptomless	General potyvirus, PVY, ChiVMV, PVMV, TSWV, AMV, CMV	PepMoV, TMV
30	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, TMV, AMV, CMV	0
32	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TMV, AMV, CMV	TSWV
33	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, AMV, CMV	TSWV, TMV
33	Symptomless	General potyvirus, PVY, ChiVMV, PVMV, TSWV, AMV, CMV	PepMoV, TMV
34	Symptomless	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, TMV, AMV, CMV	0
35	Symptomatic	General potyvirus, PVY, ChiVMV, PVMV, PepMoV, TSWV, TMV, AMV, CMV	0

PVY= *Potato virus Y*, ChiVMV= *Chilli veinal mottle virus*, PVMV= *Pepper veinal mottle virus*, PepMoV= *Pepper mottle virus*, TSWV= *Tomato spotted wilt virus*, TMV= *Tobacco mosaic virus*, AMV= *Alfalfa mosaic virus*, CMV= *Cucumber mosaic virus*

capsis. With anthracnose, the causal pathogen, *Colletotrichum spp.* (Fig. 10A) was isolated from all the three segments of each of the seven samples tested.

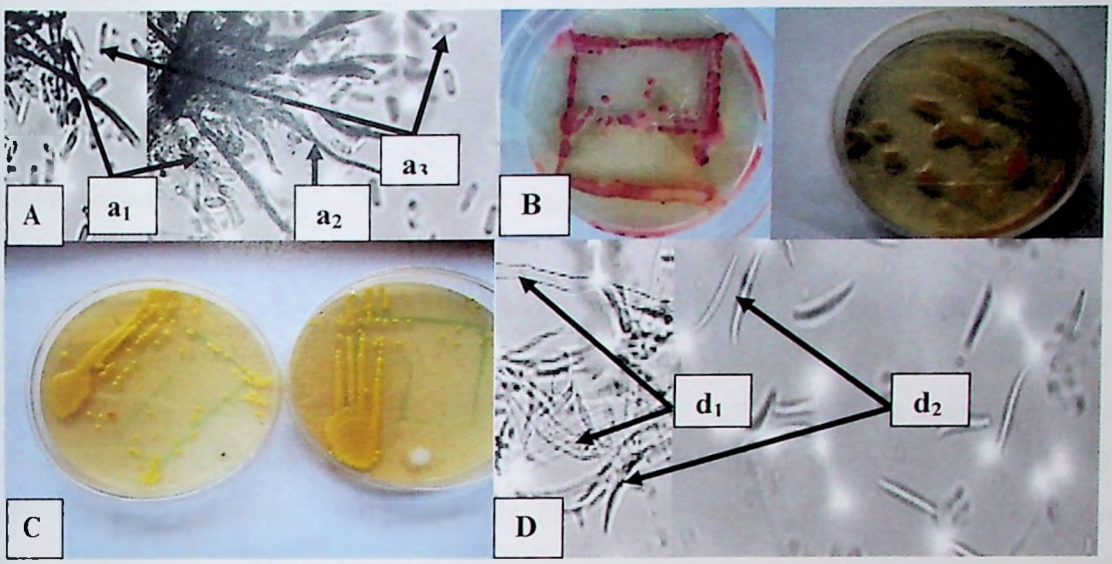

Figure 10. Isolated pathogens causing fungal and bacterial diseases in hot pepper field trial at Namulonge during 2009A and 2009B evaluation trials: A) *Colletotrichum spp.* pathogen isolated from infected field pepper plant observed under light microscopy at magnification 400X: a_1) dark spines borne from acervuli among the conidiophores, a_2) single celled oblong conidia typical of *Colletotrichum spp.* produced from conidiophores, a_3) conidiophores; B) Pinkish mucoidal colonies of *Ralstonia solanacearum* isolated from wilted pepper plants growing on Kelman's tetrazolium chloride medium in the laboratory; C) Colonies of *Xanthomonas campestris* pv. *vesicatoria* (Bacterial spot) isolated from pepper plants cultured on growing on YDC media in the laboratory; D) *Fusarium* spp. pathogen isolated from infected wilted pepper plant and observed under light microscopy at magnification 400X: d_1) Simple conidiophores that produce conidia, d_2) Several celled conidia bent at the ends (typical of *Fusarium oxysporum* f.sp. *capsici*).

5.7 Discussion and conclusion

Biotic factors have been identified for their significant contribution towards reduction inproductivity of hot pepper in Uganda. These factors include diseases caused by bacteria, fungi and viruses (ADC/IDEA, 2001; UEBP; 2005a; Tusiime *et al.*, 2010; Buyinza & Mugagga, 2010). High yielding genotypes with multiple disease resistance would present a relatively cheap and effective means of managing these diseases, especially among small scale farmers (Hanson *et al.*, 2007). The aim of this study was to identify potential sources of resistance to fungal, bacterial and viral diseases that infect hot pepper in Uganda.

Various diseases were observed to infect hot peppers in the field during both growing seasons of 2009A and 2009B, including viral diseases, wilts, *Phytophthora* blight, *Cercospora* leaf spot, anthracnose and bacterial spot. Bacterial spot was not scored in both seasons because it had unfamiliar symptoms compared to the symptoms described in the AVRDC field disease compendium (Black *et al.*, 1991), however, its presence was confirmed in the 2009B evaluation. Highly significant differences among genotypes for anthracnose and wilt disease incidences were observed in both 2009A and 2009B. Genotypes exhibited differential reactions to *Cercospora* leaf spot, *Phytophthora* blight and viral disease incidences and *Cercospora* leaf spot and *Phytophthora* blight severity indices in different seasons probably due to the effects of GxE interaction. Results indicated differential performance of genotypes with respect to disease incidences, with 2009A favoring the occurrence of viral and *Phytophthora* blight diseases while 2009B favored the occurrence of anthracnose, *Cercospora* leaf spot and wilt diseases. Severity indices were higher in 2009A than 2009B for viral and anthracnose diseases while *Cercospora* leaf spot and *Phytophthora* blight severity indices were higher in 2009B than 2009A. The environmental conditions presented by these seasons were as such favourable for the diseases that proliferated. Season 2009B in particular recorded high levels of precipitation and relative humidity, which favoured the development of bacterial (wilt) and fungal diseases such as anthracnose, *Cercospora* leaf spot and *Phytophthora* blight (Agrios, 2005). The enhanced incidence and severity of viral diseases in 2009A under dry weather conditions may be attributed to availability of a favorable conducive atmosphere for the growth and proliferation of insect

pests such as aphids, thrips, whiteflies that vector viral diseases (Agrios, 2005). On the whole, however, the inconsistency observed in expression of some diseases across seasons highlighted the need for a directed approach in breeding to target seasons.

Pooled analysis of variance showed no significant influence of season and genotypes on all disease incidences except viral incidence that highly differed across seasons. However, all disease incidences were highly influenced by (GxE) interaction. Similarly, absence of significant genetic variability among genotypes for all disease severity indices was observed except *Phytophthora blight* severity index when pooled across seasons. On the other hand, environments differed significantly from each other for all disease severity indices except anthracnose severity index. The effect of G x E interaction was also highly significant for all disease severity indices except *P. blight* severity index. When pooled across seasons, all the 25 genotypes evaluated performed similarly for all disease incidences and severity indices although season had a differential effect on viral disease incidence and the anthracnose severity index. The effect of GxE interaction however, indicates genotypic performance varied with change in environment for disease incidences and severity indices apart from *Phytophthora* blight severity index. The differential response of genotypes to field diseases under different seasons has been observed in cowpea (Adipala *et al.*, 2001) and Chilli pepper (Galanihe *et al.*, 2004).

Local genotypes performed better than exotic genotypes for wilt, *Cercospora* leaf spot, and *Phytophthora* blight diseases as shown by their consistently lower incidences and severities in both seasons implying that these genotypes could be used as sources of resistance against these diseases. Exotic genotypes, however, could be used as sources of resistance for viral diseases since they recorded lower incidences and severity indices for these diseases. The inconsistent occurrence of anthracnose in both seasons may be attributed to the influence of GxE interactions, therefore, this disease could not be used for assessing disease resistance under the experimental conditions.

Methods used in assessing disease reactions on genotypes are useful in predicting yield loss through correlation analysis. Except for viral disease, all diseases negatively correlated with both

total fruit yield (t/ha) and total marketable fruit yield in 2009A implying that they contributed to the loss of both total and marketable fruit yields. However, anthracnose caused by *Colletotrichum spp* contributed more to this loss since only its incidence and severity index highly significantly correlated negatively with total and marketable fruit yields. The disease has been found to cause up to 80% marketable yield loss in Thailand (Poonpolgul & Kumphai, 2007). On the other hand, in 2009B, only the viral disease severity index and *Cercospora* leaf spot incidence significantly correlated negatively with total fruit yield implying that viral severity and *Cercospora* leaf spot incidence contributed more to total fruit yield loss. This also suggests that resistance to these diseases may be enhanced by genotypes with higher total and marketable fruit yields. Disease incidence on Chilli (AVRDC, 2007), cassava mosaic disease incidence, bacterial blight severity with yield and cassava bacterial blight incidence and severity with storage root number in cassava (Fokunang *et al.*, 2000) and severity of maize streak virus with yield in maize (Pratt *et al.*, 1994).

In this study, variability in the influence of disease incidence and severity on total and marketable fruit yields was observed in 2009A and 2009B as shown for example, by the low and high negative correlations for *Cercospora* leaf spot incidence with total (r=-0.336, -0.639***) and marketable (r=-0.382, -0.196) fruit yields, *Cercospora* leaf spot severity index with total marketable fruit yields (r=-0.338, -0.016), low positive and high positive correlation for viral disease severity index with total fruit yield (r= 0.013, 0.358*) and low and high negative correlation for wilt incidence with total fruit yield (r=-0.310, -0.088). This is attributed to the effect of GxE interactions, which influence epidemiology of field diseases (Fokunang *et al.*, 2000). The lack of negative correlation of disease assessment methods in both 2009A and 2009B with fruit yield yield complicates interpretation since it would imply that increase in disease incidence and severity increased the total fruit and marketable fruit yields they respectively correlated with positively. This was demonstrated for virus incidence with total marketable fruit yield, virus severity index with total fruit yield in 2009A and *Colletotrichum* incidence and severity index with total fruit and marketable fruit yield, *Phytophthora* blight incidence and severity with total fruit yield, virus incidence with total fruit yield, viral disease severity index with total and marketable fruit yield in 2009B. This however, could probably indicate that the

conditions that favored the occurrence and expression of these diseases also favored total and marketable fruit yields. This phenomenon has also been observed by Fokunang *et al.* (2000) on positive correlation (r=0.21) of cassava anthracnose disease severity with storage root yield.

High significant and positive correlation (P<0.001) of disease incidences with their respective disease severity indices except for viral disease indicated that more precision was allowed during assessment (González-Pérez *et al.*, 2011). This further suggests that the incidence of anthracnose, *Cercospora* leaf spot and *Phytophthora* blight diseases can predict their severity. Because disease incidence data is easily obtained and severity scoring with visual inspection tends to be subjective due to the variations or errors of visual acuity (Scott & Rosenkranz, 1981; González-Pérez *et al.*, 2011), future assessment of these diseases could be based on disease incidence.

However, some genotypes had high disease incidences but low severities and vice versa. For example in combined season analysis (data not shown) the local genotype 4 had the incidence for *Cercospora* leaf spot was 75.2% and severity index was 44.9% while incidence for the AVRDC genotype 22 was 97.7% and severity index of 34.7%. This indicated that for such genotypes, none of the assessment methods was consistent and thus both methods were equally good and could be used in evaluation for resistance to this disease. The same can be said of viral diseases that lacked consistent incidence and severity index among some genotypes for pooled analysis across seasons (data not shown) such as in the AVRDC genotype 8 whose viral incidence was 81.5 % and severity index 40.1% and genotype 25 that had a virus incidence of 95.8% and a severity index of 31.8%. This finding is further supported by the lack of consistent significant positive correlation of incidence and severity in the two evaluation seasons probably due to the effect of GxE interaction. Such discrepancies were reported by Pratt *et al.* (1994) with viral disease caused by the *Maize streak virus*.

Correlation to identify stable disease assessment methods for individual disease traits among genotypes common to both 2009A and 2009B indicated insignificant correlation for majority disease traits except *Phytophthora* blight severity index ($r = 0.416$, $P = 0.039$) and viral disease severity index ($r = 0.509$, $P = 0.0094$). This indicates that for most disease traits, both assessment

methods were not stable except for the viral disease severity index that was most stable followed by *Phytophthora* blight severity index. This might have been due to the differences in environmental factors that influenced the disease occurrence (inoculum levels) in the different seasons. Therefore, for these two diseases, the severity index is the most efficient assessment method and for the rest, both methods are equally important.

The significant correlation observed between *Colletotrichum* incidence, severity index and *Cercospora* leaf spot severity index (r=0.523*, 0.552*, respectively), wilt incidence with viral disease incidence (r=0.409**) among genotypes in 2009A and between wilt incidence and severity index, (r=0.471**, r=0.501**, respectively) in 2009B, suggest possible synergistic relationship of the involved causal pathogens (Fokunang *et al.*, 2000). This implies that in a breeding program, selection for resistance to either disease could result in resistance to the other disease (Fokunang *et al.*, 2000). Studies on controlled inoculation of the causal pathogens among pepper genotypes would confirm this synergy, which if present would still be dependent on environmental conditions. A disease synergistic relationship was observed on Cassava clones inoculated with cassava bacterial blight and cassava anthracnose disease pathogens in nurseries and screen house trials (Muyolo, 1984) cited in Fokunang *et al.*, 2000).

When disease reactions were assigned to genotypes on the basis of incidence (wilt disease) and severity indices (other diseases), reactions were differential. No genotype was found to be resistant to all evaluated field diseases although some were resistant to one or more diseases. One such case is the AVRDC control genotype 12 that was resistant to all diseases and moderately resistant to viral disease. The majority of the genotypes were susceptible to all the diseases apart from the wilts and *Phytophthora* blight that were not as significant, when ranked. It is not clearly known whether the evaluated genotypes were resistant to these two diseases or, if it was due to disease escape because of low level of inocula. The high resistance reactions against these diseases could thus, be due to genetic differences among genotypes, environmental conditions and composition in the pathogen population responsible for the different diseases (Adipala *et al.*, 2001). Disease resistance evaluation in uncontrolled inoculation field experiments can be constrained by environmental differences that cause disease escape due to unpredictable

occurrence, severity, and non uniformity of epiphytotics (Fokunang *et al.*, 2000; Agrios, 2005). Artificial inoculation would, therefore, be a more reliable avenue for confirming field resistance to wilt and *Phytophthora* blight diseases.

Laboratory diagnostic analyses identified the causative organisms of diseases whose symptoms could not be easily associated with wilts, anthracnose and bacterial spot. The antisera used in this study detected the species and genus targeted. Similarly, the wilt disease with no visible signs characteristic of *Phytophthora capsici*, was found to be caused by two pathogens: *Fusarium oxysporium* f.sp. *capsici* that causes *Fusarium* wilt and *Ralstonia solanacearum* that causes bacterial wilt. Other pathogens identified that often caused confusing visual symptoms in the field were *Colletotrichum spp* on stems and *Xanthomonas campestris* pv. *vescatoria* on leaves. Anthracnose disease caused by *Colletotrichum spp* was observed on both fruits and foliar parts as reported by Cerkauskas (2004) although it is the foliar disease symptoms that were scored in disease assessment while the fruit infections were treated as fruit rots that caused non-marketability of fruits. While the disease was linked to *Colletotrichum*, the exact species that infects hot pepper in Uganda could not be identified and should be confirmed by future studies. Bacterial spot caused by *Xanthomonas campestris* pv. *vesicatoria* was identified from severely infected plants that gave no yield although Hansen (2000) and Mohamed & Shymaa (2008) only recorded reduced yield and loss of quality of harvested fruit under severe defoliation.

Wilt disease in pepper fields is known to be caused by various pathogens including *Verticillium dahliae*, *Phytophthora capsici*, *Fusarium oxysporum* f.sp. *capsici*, *Ralstonia solanacearum* and nematodes (AVRDC, 1989; Black *et al.*, 1991; Sanogo & Carpenter, 2007). In this study, the disease was linked to *P. capsici, F. oxysporum* f.sp. *capsici*, and *R. solanacearum*. Wilt caused by *Phytophthora capsici* was easily identified from field symptoms (Black *et al.*, 1991; Sanogo & Carpenter, 2009) and was thus scored independently. The causal pathogen has been reported to infect peppers worldwide (Thabuis *et al.*, 2003) causing up to 100% yield reduction in severe infections (Sun *et al.*, 2002). The wilt disease with no visible signs, characteristic of *Phytophthora capsici*, was found to be caused by *F. oxysporium* f.sp. *capsici* and *R.*

solanacearum, which did not occur in mixed infection, probably due to antagonism between the two pathogens that has been reported (Zecevic *et al.*, 2010).

The detection of all viruses tested in the samples agrees with earlier studies that confirmed their presence in Uganda (Ssekyewa, 2006; Dafala, 2008; Nono-Womdim, 2008) and also recorded high levels of mixed infections on tomato (Ssekyewa, 2006). Viral mixed infections have been reported in various crops including hot peppers (Alegbejo, 1999; Hiskias *et al.*, 1999; Rodríguez *et al.*, 2004) and could possibly contribute towards disease synergy (Palukaitis & Kaplan, 1997; Wang *et al.*, 2002). These mixed infections imply that during viral resistance breeding, selection for a specific virus cannot rely on symptom expression and thus, needs molecular detection techniques for that specific virus. Potyviruses were the major genus of viruses detected because the kits used were purposively selected, although it is known that potyviruses are the most important group that infect hot pepper and other vegetable crops (Black *et al.*, 1991; Green & Kim, 1991; Hiskias *et al.*, 1999; Nono-Womdim, 2008). Failure of the general Potyvirus antiserum to detect infection where specific kits detected Potyvirus species probably indicated infection with non-target species, especially considering the monoclonal nature of antibodies used to develop the kits that would enhance specificity at the expense of wide detection within the genus (Naidu & Hughes, 2009).

The high incidences of PVY (100%), ChiVMV and CMV (93.3%) compared with other viruses from the sampled genotypes indicate susceptibility to these viruses. On the other hand the low frequency of detection for AMV (49.3%), TSWV (38.7%) and TMV (30.7%) in sampled genotypes implies that they may be of less importance in the region. Alternatively, resistance to these viruses may have been emphasized in the development of genotypes evaluated in this study. Interestingly, latent infection was recorded in serological tests that detected presence of viruses in symptomless samples, a phenomenon Marame *et al.* (2010) linked to partial resistance also termed symptomless tolerance. Nevertheless it is significant that the viruses that recorded low frequency on hot pepper in Uganda have been reported to be prevalent in regions that experience Mediterranean climate (Kostova *et al.*, 2003). Worldwide, hot pepper is known to be infected with more than 35 viruses (Green & Kim, 1991), most of which were outside the scope

of analysis used in this study. Notably, leaf curl symptoms that are associated with members of the geminiviridae were observed in the field but not analysed. Future diagnoses should, thus, target a wider range of viruses and probably characterize viruses that occur in mixed infections.

In conclusion, the majority of the genotypes evaluated in this study performed poorly in response to *Cercospora* and viral diseases. Genotypes that performed best for wilt disease included: 1 (CA-PPCHI-08-1), 3 (CA-UGCE 09-3), 4 (CA-UGKI 09-1), 9 (CA-UGKI 09-6), 10 (CA-UGKA 09-4), 11 (PP0437-7506), 12 (PP97-7195-1), 25 (PP0337-7546), 8 (CA-UGKA 09-3), 14 (PP0237-7508), 18 (PP9852-149). Genotypes with the best response to infection with *Phytophthora* blight were: 5 (CA-UGKI 09-5), 6 (CA-UGKI 09-4), 12 (PP97-7195-1), 14 (PP0237-7508), 18 (PP9852-149), 25 (PP0337-7546). For anthracnose, the best performers were: 1 (CA-PPCHI-08-1), 4 (CA-UGKI 09-1), 9 (CA-UGKI 09-6), 21 (PP0337-7562), 2 (CA-EASC-09-1), 5 (CA-UGKI 09-5), 3 (CA-UGCE 09-3), 12 (PP97-7195-1), 18 (PP9852-149), 10 (CA-UGKA 09-4). In the case of *Cercospora* leaf spot, the genotypes that exhibited good performance included: 5 (CA-UGKI 09-5), 12 (PP97-7195-1), 4 (CA-UGKI 09-1) and for viral disease the best performing genotypes were: 17 (PP0337-7545), 12 (PP97-7195-1), 22 (PP0537-7504). Local genotypes 3 (CA-UGCE 09-3) and 5 (CA-UGKI 09-5); and exotic genotypes 14 (PP0237-7508), 18 (PP9852-149), 22 (PP0537-7504), 25 (PP0337-7546), 11 (PP0437-7506), and 12 (PP97-7195-1) consistently scored better in all disease traits across seasons as well as the exotic genotypes 27 (PBC 535), 28 (PP9852-110), 29 (PP9852-173), 30 (PP9955-15), 31 (PP0007-2247), 32 (PP0042-17), 33 (PP0237-7502), 35 (PP0537-7558) evaluated only in season 2009B. However, these genotypes require further evaluation for a second season to confirm their performance.

Genotypes that scored well for disease resistance yielded poorer. Only exotic genotypes 1 (CA-PPCHI-08-1), 12 (PP97-7195-1) and 25 (PP0337-7546) that were high-yielding in both seasons scored well for at least two diseases while exotic genotypes 33 (PP0237-7502), 27 (PBC 535), 31 (PP0007-2247), 35 (PP0537-7558), 29 (PP9852-173), 30 (PP9955-15) evaluated in season 2009B only recorded high yields and scored well in more than 2 diseases. Such genotypes are recommended for possible release to farmers as well for breeding for disease resistance.

Genotypes 33 (PP0237-7502), 32 (PP0042-17), 27 (PBC 535), 26 (PBC 375), 31 (PP0007-2247), 35 (PP0537-7558), 29 (PP9852-173) and 30 (PP9955-15) had high yields and good attributes for the traits evaluated. Breeding for hot pepper disease resistance in Uganda should target viral diseases, *Cercospora* leaf spot and anthracnose, which were the most important diseases infecting pepper. Multi-locational trials should also be considered in order to cater for the diversity of pathotypes that may occur in other agro-ecological zones of Uganda where hot pepper is grown. Where funding is limited, controlled pathogenicity tests could target selection of priority materials. Since fruit yield in pepper is influenced by several parameters as found in chapters 4 and 5 above, it was eminent to study the genetics for yield and the associated traits through combining ability analysis. This study would provide information on the nature of gene action in studied traits in hot pepper for future *Capsicum* improvement in Uganda and was dealt within chapter 6.

CHAPTER SIX

HETEROSIS, COMBINING ABILITY AND NATURE OF GENE ACTION FOR IMPROVED DISEASE RESISTANCE AND FRUIT YIELD IN HOT PEPPER

6.1 Introduction

The hot pepper sub-sector in Uganda is characterized by poor quality and low production due to lack of improved cultivars for disease resistance, fruit yield and associated traits (UEBP, 2005a; Douglas, 2008; Buyinza & Mugagga, 2010; Tusiime *et al.*, 2010). Successful breeding involves developing genotypes that are genetically superior to those in production (Lynch & Walsh, 1998) through combination of desired traits into target genotypes to generate hybrids with a wide genetic base and that are capable of expressing heterosis under local conditions. Selection and improvement of these traits in hot pepper requires knowledge on the magnitude of useful genetic variances present in cultivars, in terms of combining ability and heterosis (Marame *et al.*, 2008). Partitioning of such variances into its genetic components facilitates the understanding of the nature of gene action controlling such desired qualitative and quantitative traits (Marame *et al.*, 2008).

Thus, prior to initiation of hot pepper improvement programme in Uganda, the knowledge of combining ability of parents and crosses and the gene effects involved in the inheritance of various traits is a prerequisite. It provides a guideline for selecting elite parents or combiners which may later be hybridized either to exploit heterosis or to accumulate fixable genes through selection (Ahmed *et al.*, 2003). In addition, such knowledge helps in choosing appropriate breeding methods for crop improvement (Ahmed *et al.*, 2003; Chowdhary *et al.*, 2007; Marame *et al.*, 2008). Combining ability can be general (GCA) or specific (SCA), with GCA being a measure of additive gene action, while SCA is due to non-additive (dominant or epistatic) gene action (Pace *et al.*, 1998; Chowdhary *et al.*, 2007). Genetic studies of this nature have been examined using the diallel analysis techniques developed by Griffing (1956) and have proved useful in providing precise information about types of gene action involved in the expression of

traits and in predicting the performance of progenies in latter segregating generations (Marame *et al.*, 2008). However, this information about heterosis, GCA and SCA for important traits in hot pepper has not been exploited in Uganda. This study aimed at generating such information so as to identify good parent combiners in hybridization for improved disease resistance, yield and its components through a diallel mating design.

6.2 Materials and Methods

6.2.1 Study area

Crossing and establishment of seedlings were done at the National Agricultural Research Laboratories (NARL) in Kawanda. Field evaluation was done at the National Crops Resources Research Institute (NaCRRI) in Namulonge. The geographical characteristics of these two locations are described in sections 3.2.1 and 4.2.1, respectively.

6.2.2 Genotypes and mating design

Eight varieties were selected based on their contrasting growth (early, intermediate and late-maturing) and fruit characteristics such as size (small, intermediate and big) and mature fruit colour (orange and red) as observed during 2009A field performance evaluation and screen house characterization (Table 29). Fruit length and width values were averages of 10 fruits picked randomly from 4 plants while plant height and width were averages of 4-6 plants per genotype. The 8 parents were crossed in a full-diallel cross in a screen house from August 2009-April 2010. Due to mite infestation on the crossing block, only 15 out of the expected 56 crosses succeeded to maturity. Of the 15 crosses, there was only one cross for parent 8 (8x29) and none for parent 32. One reciprocal pair (29x31, 31x29) from the cross of parents 29 and 31 was present. The cross for parent 8 and one reciprocal cross (29x31) were removed from the diallel, leaving only 6 parents whose remaining 13 crosses were analyzed as for a 6 parent half-diallel analysis (Table 30). With only 2 missing crosses, each parent had at least 4 of the 5 possible crosses present, and parent 29, had all the five possible crosses.

6.2.3 Procedures for hybridization and generation of F_1 hybrids

Controlled hybridization was performed. Hand emasculation was done a day before the flowers opened. Pollen grains were collected from male parents between 7am and 10 am using eppendoff tubes and the pollination done immediately by rubbing pollen grains on the stigma of the receptive flower. The pollinated flowers were then covered with a white cloth bag made from fine-net for 2 days to avoid any cross pollination from mechanical influence during watering and spraying. At full physiological maturity, when fruits acquired their expected maturity colour (red or orange), the F_1 ripe fruits were picked and cured for 2-3 days. Seed were then extracted and propagated to raise progeny of the F_1 hybrids (Geleta *et al.*, 2004; Shankarappa *et al.*, 2008).

6.2.4 Evaluation of parentals and hybrids

Seedlings were raised in the screen house at NARL from April-May 2010 in 5-litre plastic buckets using a field soil-sand-cow dung mixture (in the ratio 3:1:1) that had been steam-sterilized. Seedlings were sprayed with fungicides and insecticides twice a week to protect them against disease and insect attack as described in section 3.2.3. Six-week old seedlings were transplanted into fine seedbeds at NaCRRI and evaluated from May-October, 2010. A 5x4 alpha lattice design was adopted, with two replications, each of which contained 5 incomplete blocks with 4 plots. Each replicate thus, had 20 experimental plots to accommodate the 19 entries that comprised of 6 parents and 13 crosses. Variety 8 was included to fill the vacant experimental plot. The experimental plots were made up of raised beds, 1m x 3.6m in size, with one row of plants at a spacing of 0.6m x 0.45m between and within rows, respectively. Beans were planted in guard rows to avoid border effects. Fertilizer application and other management practices were effected as described in section 4.2.5.

Table 29. Some attributes of hot pepper genotypes selected for diallel analysis at Namulonge, Uganda in April-October 2010

			Plant character			Fruit character			
No.	Genotype Name	Type	Height (cm)	Width (cm)	Mature colour	Length (cm)	Width (cm)	Position	Shape
8	PP9955-15	Exotic	40	34	Red	13.4	2.5	Pendant	Elongate
18	PP0337-7562	Exotic	57	34	Red	11.0	1.7	Pendant	Elongate
25	PP0537-7504	Exotic	57	40	Red	7.9	1.6	Intermediate	Elongate
28	PP9852-115	Exotic	59	48	Red	12.4	1.4	Erect	Elongate
29	CA-UGKI 09-6	Local	54	27	Orange	3.1	1.7	Erect	Triangular
31	CA-UGCE 09-3	Local	71	48	Red	4.5	0.8	Erect	Elongate
32	CA-UGKA 09-3	Local	65	39	Red	9.8	1.2	Pendant	Elongate
35	CA-UGKI 09-4	Local	74	42	Orange	3.4	1.1	Pendant	Triangular

Table 30. Diallel of F1 progeny and selfed hot pepper parents evaluated for 13 agronomic and 4 disease traits at Namulonge, Uganda from May-October 2010

		♀					
	Parental genotypes[d]	**18**	**25**	**28**	**29**	**31**	**35**
	18	**18**					
♂	**25**	25x18	**25[c]**				
	28	M[a]	28x25	**28**			
	29	29x18	29x25	29x28	**29**		
	31	31x18	31x25[b]	31x28	31x29	**31**	
	35	35x18	35x25	35x28	35x29	M[a]	**35**

[a]Missing crosses

[b]This cross was susceptible to most diseases and gave no yield. It was scored for diseases and not quantitative traits.

[c]Bold figures are selfed parents

[d]Genotypes 18, 25 and 28 are from AVRDC; 29, 31 and 35 are local genotypes.

6.2.5 Data collection and analyses

Data were taken on 13 agronomic traits: days to flowering, days to fruit maturity, plant height (cm), plant width (cm), fruit length (cm), fruit width (cm), pedicel length (cm), number of seeds per fruit, stem height at first bifurcation (cm), stem diameter (cm), primary branch numbers, secondary branch numbers, and number of fruits per plant. Observations were also made on incidences of four diseases that occurred, including bacterial spot, *Cercospora* leaf spot, viral disease and wilt. Heterosis (mid- and high-parent), general combining ability (GCA) and specific combining ability (SCA) were calculated for all observed quantitative and disease parameters.

Data were summarized in the Excel program (Microsoft Office, 2007) and exported into the GenStat statistical computer package (12^{th} edition, version 2; VSN International Ltd, 2010) for further analysis. In this program, the F-test procedure was used to generate the ANOVA that examined variations among entries. Where the ANOVA showed significant differences, means were separated using Fisher's Least Significant Difference (LSD) test. General and specific combining abilities were also analysed according to the Griffing (1956) fixed effect model I method II (with parents and one set of crosses excluding reciprocals) to estimate SCA and GCA effects for the hybrids and parents, respectively as: $Y_{ijk} = \mu + G_i + G_j + S_{ij} + E_{ijk:}$ where: μ = general means effect; Yij is the mean (performance) of the cross between i^{th} female parent and j^{th} male parent over; G_i is the general combining ability (GCA) effect of the i^{th} female parent; G_j is the general combining ability (GCA) effect of the j^{th} male parent; S_{ij} is the specific combining ability (SCA) effect of the cross between i^{th} female genotype and j^{th} male genotype and E_{ij} is the experimental error effect. The GCA effects were estimated using the weighted parental means in order to adjust for missing crosses.

Heterosis of the hybrids over parents (mid and high) was estimated according to Saira *et al.* (2001) as follows: Mid-parent heterosis (MPH) (%) = [(F1-MP)/MP] x 100; High-parent heterosis (HPH) (%) = [(F1-HP)/HP] x 100; where, F1 = Performance of F1 hybrid, MP = Performance of mid parent = (P1+P2)/2, HP = High performing parent in the desirable direction.

Where the ANOVA revealed significance differences among the hybrids and parents for measured traits, Hayman (1954a) analysis was used to separate the genetic components and their ratios, after testing the validity of the assumption regarding adequacy of the additive-dominance model (Singh & Chaudhary, 1977; Sharma, 1998). The missing data values for each trait, three for quantitative traits and two for disease traits, were estimated from the GCAs calculated from Griffing analysis of their parents and the general mean for the trait in order to best fit in Hayman analysis (P. Gibson, former Professor of Plant Breeding, Genetics and Biometry, University of Southern Illinois; *personal communication*, 2010) as: $IJ = (\bar{U} + g_i + g_j) \pm z$; where IJ = cross of parent I and J, $\bar{U}$ = grand mean, gi = general combining ability of parent I, gj = general combining ability of parent J, Z is a factor added and/or subtracted from estimated crosses of replications 1 or 2 respectively depending on the number of significant figures to allow for some variation.

Relative importance of additive and non-additive gene effects was estimated from Baker's ratio, (Baker, 1978) as: $X = [2\sigma^2gca/(2\sigma^2gca+\sigma^2sca)]$. The coefficient of genetic determination in the narrow sense (CGD-ns), which is the fixed parent equivalent of heritability in the narrow sense and the coefficient of genetic determination in the broad sense (CGD-bs), were estimated as follows (Falconer, 1963; Adefris & Heiko, 2005; P. Gibson, 2010, *personal communication*):

$$\text{CGD-ns: } [2\sigma^2gca/(2\sigma^2gca+\sigma^2sca+\sigma^2e)]*100 \approx h^2;$$
$$\text{CGD-bs: } [(2\sigma^2gca+\sigma^2sca)/(2\sigma^2gca+\sigma^2sca+\sigma^2e)]* 100 \approx H,$$

where σ^2gca = Variance component of GCA, σ^2sca = Variance component of SCA and σ^2e = Error variance, h^2 = Narrow sense heritability, H = Broad sense heritability.

6.3 Results

6.3.1 Performance of F_1 hybrids and parental lines for agronomic and disease traits

6.3.1.1 Growth and yield traits

Analysis of variance showed significant differences among genotypes for all agronomic traits except fruit width and stem height (Appendix 14). Variability for parents and their F_1 hybrids indicated that the overall performance of hybrids was better than that of the parents in number of fruits per plant, number of seeds per fruit, primary branch numbers, secondary branch numbers and stem diameter (Table 31). Similarly, hybrids flowered and matured earlier, and grew vigorously taller and wider than the parents. However, not all hybrids were better than parents in these traits. For example a trait such as the number of fruits per plant where hybrids had the highest net difference (close to 2x) among others, parents 25, 29, 31 and 35 performed better than 4 hybrids (25x18, 31x18, 35x18 and 35x28) in this trait.

On the other hand, parents generally performed better than hybrids in fruit and pedicel lengths. However, five and six hybrids performed better than the majority of parents for fruit length and pedicel length, respectively. Nevertheless, hybrids 25x18, 31x29 and 35x28 performed poorer than four parents 25, 35, 31 and 29. Parent 18 performed worst in number of fruits per plant compared to all hybrids. Of all the hybrids, 29x28 was exceptional with the highest number of fruits per plant (58) and most traits above the average (Table 31).

6.3.1.2 Disease incidence

Disease traits varied highly significantly ($P<0.01$) among the genotypes except in the case of wilt incidence (Appendix 15). Mean incidences of all scored diseases traits were lower for parents than those of hybrids (Table 32). However, hybrids 31x29, 28x25, 31x28 registered lower incidence of viral disease, compared with 29, 35, 18 and 25. For *Cercospora* leaf spot, only hybrid 35x25 registered the lowest incidence relative to all the parents apart from parent 35 that

Table 31. Mean performance for 11 growth and yield characters measured from 12 crosses and 6 parents evaluated in one season at Namulonge, Uganda from May-October 2010

	PARAMETERS										
	Fruit			Branch numbers		Stem	Maturity days		Plant dimensions		
Genotype	FL	NF/P*	NS/F	PBN	SBN	STD	DFL	DFM	PL	PLHT	PLWD
18	11.0h	5a	74de	6.3abc	13.8b	0.5a	64.3f	97.7abc	4.4g	38.2c-f	30.4ab
25	6.7de	26bc	64bc	9.4e-h	18.8def	0.7bcd	50.0a-d	104.3cde	2.7abc	32.2a-d	32.9abc
28	11.6h	12ab	81ef	4.9a	10.3a	0.7a-d	49.0abc	97.5abc	2.5a	28.2ab	31.6abc
29	1.9a	17abc	60b	8.5def	17.5cd	0.8b-e	86.8g	129.9f	2.4a	32.6a-d	31.4abc
31	4.6b	21bc	37a	9.5e-h	18.4de	0.7abc	49.4abc	102.4bcd	2.7a-d	24.9a	22.9a
35	2.5a	31.c	63bc	9.4e-h	22.1fg	1.0e	60.3ef	130f	2.5a	42.1ef	44.4de
25x18	9.1g	12b	60b	8.9efg	18.4de	0.7bcd	54.5b-e	111.1de	3.0c-f	32.7a-d	32.2abc
28x25	7.9f	25bc	73de	9.2e-h	18.2de	0.8b-e	45.9ab	90.6a	2.4a	35.0b-e	36.8b-e
29x18	5.6cd	22bc	114g	7.9cde	18.1de	0.8b-e	55.4cde	111.8de	3.0c-f	39.6def	39.2b-e
29x25	5.2bc	46d	112g	7.0bcd	19.5def	0.7a-d	49.2abc	104.1cde	2.9b-f	43.1ef	45.7de
29x28	7.1ef	58d	79ef	10.5ghi	20.1def	0.9de	52.3a-e	106.4cde	2.6ab	37.6c-f	39.8b-e
31x18	7.7ef	19abc	70cd	6.9bcd	14.5bc	0.6ab	46.2ab	92.1ab	3.1def	29.8abc	29.8ab
31x28	7.6ef	11ab	81ef	6.1ab	11.3ab	0.7a-d	55.5cde	110.6de	2.5a	37.9c-f	41.9cde
31x29	4.3b	55d	78ef	11.5i	20.3def	0.9cde	55.8c-f	102.1bcd	3.3f	39.6def	47.3e
35x18	4.2b	20bc	61b	9.9f-i	21.03fg	0.9de	51.9a-e	102.9cd	2.6ab	36.5b-f	40.6b-e
35x25	4.5b	57d	77def	9.4e-h	19.7def	0.8b-e	58.4def	114e	3.2ef	40.2def	46.3de
35x28	4.9bc	14ab	83f	9.1e-h	19.4def	0.8b-e	52.3a-e	110.2de	2.8a-e	37.9c-f	36.2bcd
35x29	2.5a	55d	85f	10.7hi	24.0g	1.0e	45.1a	107.1cde	2.6ab	44.7f	47.5e
Mean parents	6.77	17.71	62.71	8.13	17.04	0.73	59.19	110.41	2.89	32.99	32.26
Mean hybrids	5.59	34.73	84.00	8.93	18.74	0.81	51.64	104.72	2.82	38.35	41.01
Fpr (Genotypes)	<.001	<.001	<.001	<.001	<.001	0.014	<.001	<.001	<.001	0.014	0.005
LSD0.05	1.07	15.36	7.96	1.70	3.45	0.19	8.73	10.30	0.41	9.124	10.985
CV (%)	8.4	25.9	5.0	9.4	9.0	11.6	7.6	4.6	6.9	11.9	13.8

Means followed by the same letter along the same column are not statistically significant at $P < 0.05$

FL=Fruit length, FW =Fruit width, PL=Pedicel length, NS/F=Number of seeds/fruit, PBN=Primary branch numbers, SBN=Secondary branch numbers, STHT=Stem height, STD=Stem diameter, NF/P=Number of fruit/plant, DFL= Days to flowering, DFM= Days to fruit maturity, PLHT= Plant height, PLWD= Plant width

*number includes all observed immature fruits/plant at third harvest.

scored higher incidences than all the hybrids except hybrid 31x25 for this trait. Hybrids 25x18, 28x25, 29x25, 29x28, 31x25, 31x29, 35x18, 35x25, 35x29 exhibited lower incidences than the four parents for wilt disease, while hybrid 29x18 scored higher incidence with respect to this trait compared to all evaluated genotypes.

Assigning resistance rating to genotypes, only parent 31 was moderately resistant to viruses, while hybrids were all highly susceptible to virus disease apart from 28x25 that was rated susceptible. All genotypes were highly susceptible to *Cercospora* leaf spot. For bacterial spot, the exotic parents 18, 25, 28 and local parents 29 and 31 were resistant as well as hybrids 28 x 25, 29 x 25, 29, 28, 31 x 29, 35 x 28 (Table 32).

6.3.2 Heterotic performance for measured traits

6.3.2.1 Heterosis for disease resistance

Estimates of heterosis varied from trait to trait (Table 33). None of the overall means of mid-parent and high-parent heterosis was in the negative desirable direction for all disease traits. Except for wilt incidence, all mean values for hybrids were higher than those for parents (Table 33). Generally, hybrids expressed better MPH than HPH for all the disease traits.

The mid-parent heterosis for virus incidence was negative for two hybrids (28x25, 35x29). Similarly, its high-parent heterosis was negative for two hybrids (29x18, 35x29). One hybrid (35x25) registered neither mid nor high-parent heterosis. The maximum negative (-32.4%) and positive mid-parent (heterosis 92.3%) were observed in hybrids 28x25 and 31x18, respectively. Hybrids 29x25 (-11%) and 31x25 (809.1%) registered maximum negative and positive high parent heterosis, respectively.

Mid-parent heterosis for *Cercospora* leaf spot was negative for two hybrids while only one hybrid (31x28) expressed negative high parent heterosis (-5.6%). Four hybrids for MPH and five hybrids for HPH showed no heterosis. The maximum negative (-5.6%) and positive mid-parent

Table 32. Mean disease incidence (%) and resistance reaction for three disease scores from 13 crosses and their 6 parents evaluated in one season at Namulonge, Uganda from May-October 2010

Genotype	Viral disease incidence	RN	*Cercospora* leafspot incidence	RN	[a]Bacterial spot incidence	RN
18	80.0cde	HS	100.0b	HS	1.0 (0.0)a[b]	R
25	100.0e	HS	100.0b	HS	1.0 (0.0)a	R
28	37.5ab	S	100.0b	HS	1.0 (0.0)a	R
29	100.0e	HS	90.0b	HS	1.0 (0.0)a	R
31	11.0a	MR	100.0b	HS	1.0 (0.0)a	R
35	100.0e	HS	58.5a	HS	8.2 (54.2)cd	HS
25x18	100.0e	HS	100.0b	HS	3.5 (12.5)ab	MR
28x25	46.5abc	S	100.0b	HS	1.0 (0.0)a	R
29x18	100.0e	HS	100.0b	HS	6.4 (30)bcd	MS
29x25	89.0de	HS	100.0b	HS	1.0 (0.0)a	R
29x28	90.0de	HS	90.0b	HS	1.0 (0.0)a	R
31x18	87.5de	HS	100.0b	HS	4.5 (25)abc	MS
31x25	100.0e	HS	100.0b	HS	10.7 (94.5)d	HS
31x28	75.0b-e	HS	94.4b	HS	3.5 (12.5)ab	MR
31x29	61.5bcd	HS	100.0b	HS	1.0 (0.0)a	R
35x18	100.0e	HS	100.0b	HS	5.4 (19.5)bc	MR
35x25	100.0e	HS	89.0b	HS	4.3 (22)abc	MS
35x28	100.0e	HS	100.0b	HS	1.0 (0.0)a	R
35x29	93.0de	HS	100.0b	HS	7.6 (43.7)bcd	S
Mean parents	71.42		91.42		2.20 (9.03)	
Mean hybrids	87.88		97.95		3.92 (19.98)	
Fpr (Genotypes)	0.002		0.002		0.002	
LSD0.05	37.74		14.41		4.358	
CV (%)	21.7		7.2		61.4 (90.6)	

[a]Square root transformed ($\sqrt{(x+1)}$)

[b]Mean separation based on transformed original values in parenthesis

RN = disease reaction

R = Resistance rating based on observed disease incidences in the field on the scale (Modified Bayoumi and Bramawy, 2007).

Table 33. Mid and high-parent heterosis (%) values for 4 disease incidence characters scored in 13 hybrids and six parents at Namulonge (2010)

	Mid parent heterosis				High parent heterosis			
Cross	Virus disease	*Cercospora* leaf spot	Wilt disease	Bacterial leaf spot[(a)]	Virus disease	*Cercospora* leaf spot	Wilt disease	Bacterial leaf spot [(a)]
25x18	11.1	0.0	20.9	267.4	25.0	0.0	510.1	267.4
28x25	-32.4	0.0	-0.9	0.0	24.0	0.0	400.0	0.0
29x18	11.1	5.3	16.6	456.8	25.0	11.1	23.0	456.8
29x25	29.5	5.3	-100.0	0.0	-11.0	11.1	-100.0	0.0
29x28	30.9	-5.3	-58.3	0.0	140.0	0.0	-56.0	0.0
31x18	92.3	0.0	101.8	409.9	695.5	0.0	918.2	409.9
31x25	80.2	0.0	401.0	877.2	809.1	0.0	401.0	877.2
31x28	35.1	-5.6	610.1	267.4	581.8	-5.6	610.1	267.4
31x29	10.8	5.3	-9.7	0.0	459.1	11.1	401.0	0.0
35x18	11.1	26.2	-65.0	7.5	25.0	70.9	-63.0	352.8
35x25	0.0	12.3	-12.3	13.8	0.0	52.1	300.0	379.6
35x28	45.5	26.2	-30.3	-76.3	166.7	70.9	-26.2	0.0
35x29	-7.0	34.7	-67.1	58.7	-7.0	70.1	-63.1	568.7
Mean heterosis	24.5	8.0	62.1	175.6	225.6	22.5	250.4	275.4
Mean value of parents	71.4	91.4	35.2	2.1	71.4	91.4	35.2	2.1
Mean value of crosses	87.9	98.0	29.4	4.6	87.9	98.0	29.4	4.6

[a]Data square root transformed (√(x+1).

(heterosis 34.7%) were observed in hybrids 31x28 and 35x29, respectively. Hybrids 35x18 and 35x28 exhibited maximum HPH (70.9%) followed by 35x29 (70.1%)

Mid-parent heterosis for wilt incidence was negative for eight hybrids. None of the hybrids exhibited zero mid-parent heterosis. Maximum negative MPH heterosis was expressed by 29x25 (-100%) followed by 35x29 (-67.1%) while maximum positive MPH was expressed by 31x28 (610.1%) followed by 31x25 (401.0%). High-parent heterosis (HPH) was negative for 5 hybrids with the maximum (-100%) being registered by hybrid 29x18 followed by 35x18 (-63.0 %). The maximum positive HPH was expressed by hybrid 31x18 (918.2 %) followed by 31x28 (610.1 %).

With bacterial spot, only one hybrid (35x28) exhibited negative MPH (-76.3%) with no negative HPH registered for this trait. Four hybrids and 5 hybrids expressed no MPH and HPH respectively. Hybrid 31x25 exhibited both maximum positive MPH and HPH of 877.2%.

6.3.2.2 Heterosis for growth and yield traits

Significant mid- and high-parent heteroses for agronomic traits were observed though they varied from trait to trait (Tables 34 and 35, respectively). For agronomic traits, negative heterosis is desirable for pedicel length, stem height, plant height, days to flowering and days to fruit maturity. In contrast, positive heterosis is desirable for fruit length, fruit width, primary branch numbers, stem diameter, secondary branch numbers, plant width, number of fruits per plant and number of seeds per fruit. For all measured traits, the mean MPH was in the desired direction except for fruit length (-2.3%), pedicel length (1.3%), stems height (17.9%), and plant height (14.9%) (Table 34) while only three out of the 13 measured agronomic traits had their HPH in the desired direction including: number of seeds per fruit (13.8%), number of fruits per plant (38.3%) and plant width (13.8%) (Table 35). Only one hybrid (35x25) registered no mid and high-parent heterosis for primary branch numbers.

The proportion of hybrids with negative to positive mid-parent heterosis (MPH) were 8:4 (fruit length), 4:8 (fruit width), 6:6 (pedicel length), 2:10 (number of seeds per fruit), 3:9 (primary

branch numbers), 3:9 (secondary branch numbers), 0:12 (stem height), 3:9 (stem diameter), 3:9 (number of fruits per plant), 10:2 (days to flowering), 10:2 (days to fruit maturity), 3:9 (plant height) and 1:11 (plant width). The maximum desirable MPH was observed in cross 31x29 (33.4%) for fruit length, 31x28 (44.5%) for fruit width, 35x18 (-23.9%) for pedicel length, 29x25 (81.7%) for number of seeds per fruit, 29x28 (57%) for primary branch numbers, 29x28 (44.7%) for secondary branch numbers, none for stem height, 29x28 (17.9%) for stem diameter, 29x28 (295.2%) for number of fruits per plant, 35x29 (-38.7%) for days to flowering, 35x29 (-17.6%) for days to fruit maturity, 35x18 (-9.1%) for plant height and 31x29 (74.2%) for plant width.

For HPH, the proportion of hybrids with negative to positive heterosis were 11:1 (fruit length), 10:2 (fruit width), 2:10 (pedicel length), 5:7 (number of seeds per fruit), 7:5 (primary branch numbers), 7:5 (secondary branch numbers), 0:12 (stem height), 9:3 (stem diameter), 6:6 (number of fruits per plant), 6:6 (days to flowering), 5:7 (days to fruit maturity), 1:11 (plant height) and 4:8 (plant width). The maximum desirable HPH was observed in cross (es) 35x29 (1%) for fruit length, 31x28 (13.5%) for fruit width, 28x25 (-4.6%) for pedicel length, 29x18 (53.9%) for number of seeds per fruit, 29x28 (23.5%) for primary branch numbers, 29x28 (14.8%) for secondary branch numbers, none for stem height, 29x28 (11.5%) for stem diameter, 29x28 (236.3%) for number of fruits per plant, 35x29 (-25.2%) for days to flowering, 35x29 (-17.5%) for days to fruit maturity, 35x18 (-4.4%) for plant height and 31x29 (50.9%) for plant width.

6.3.3 Specific and general combining abilities for measured trait

For all the traits studied, the mean square (MS) values of GCA were significant except for wilt disease (Table 36). Similarly, the MS for SCA were significant for majority of the studied traits except fruit width, plant height, and stem height, stem diameter and wilt disease. The MS for GCA were always higher than those of SCA except for bacterial spot. To understand the relative importance of the general and specific combining abilities for studied parameters, estimates of components of GCA and SCA that approximate their variances were calculated according to Baker's ratio since mean square values often give erroneous estimates (Baker, 1978). From this ratio, majority of the quantitative agronomic traits were far from unity except for secondary branch numbers (0.6), stem diameter (0.69), fruit length (0.85) and fruit width (0.91), stem

Table 34. Mid-parent heterosis (%) values for 13 quantitative characters measured in twelve hybrids and six parents at Namulonge, Uganda in 2010

Cross	AGRONOMIC PARAMETERS												
	Fruit				Branch numbers		Stem		Maturity days		Plant dimensions		
	FL (cm)	FW (cm)	NF/P	NS/F	PBN	SBN	STHT (cm)	STD (cm)	DFL (day)	DFM (day)	PL (cm)	PLHT (cm)	PLWD (cm)
25x18	2.5	-4.5	-22.9	-12.6	12.8	12.6	12.4	13.9	-4.7	10.0	-14.2	-7.1	1.6
28x25	-13.5	-5.1	31.6	1.2	28.9	25.3	22.8	11.5	-7.3	-10.2	-7.2	15.9	13.9
29x18	-12.7	-8.4	104.3	70.5	6.7	15.4	33.7	17.5	-26.7	-1.8	-11.2	11.9	27.1
29x25	21.0	-8.0	116.2	81.7	-21.8	7.4	22.1	-6.9	-28.1	-11.1	15.7	33.0	42.3
29x28	4.9	13.1	295.2	12.8	57.0	44.7	27.6	17.9	-23.0	-6.5	3.2	23.6	26.5
31x18	-0.9	2.7	43.8	25.9	-12.8	-10.0	6.8	4.7	-18.7	-7.9	-12.6	-5.6	11.8
31x28	-6.1	44.5	-31.7	37.9	-15.4	-21.5	2.2	2.3	12.8	10.6	-5.5	42.7	53.6
31x29	33.4	16	184.4	62.5	27.8	13.1	10.0	17.0	-18.0	-12.1	29.9	37.4	74.2
35x18	-37.6	16.7	13.9	-11.5	25.8	16.9	34.8	15.7	-16.7	-9.6	-23.9	-9.1	8.4
35x25	-2.6	2.2	100.4	22.2	0.0	-3.7	12.3	-6.4	5.9	-2.7	23.7	8.3	19.6
35x28	-29.7	8.7	-32.9	14.9	27.8	19.8	19.6	-3.4	-4.4	-3.1	11.4	7.8	-4.7
35x29	13.5	3.2	127.9	38.8	19.6	21.2	10.6	7.3	-38.7	-17.6	6.0	19.6	25.4
Mean heterosis	-2.3	6.8	77.5	28.7	13.0	11.8	17.9	7.6	-14.0	-5.2	1.3	14.9	25.0
Mean value of parents	6.4	1.3	18.7	62.9	8.0	16.8	16.3	0.7	60.0	110.3	2.9	33.1	32.3
Mean value of crosses	5.9	1.4	32.9	81	8.9	18.7	19.0	0.8	51.9	105.3	2.8	37.9	40.3

FL= Fruit length, FW= fruit width, PL=Pedicel length, NS/F=Number of seeds/fruit, PBN=Primary branch numbers, SBN=Secondary branch numbers, STHT=Stem height, STD=Stem diameter, NF/P=Number of fruit per plant, DFL=Days to flowering, DFM=Days to fruit maturity, PLHT=Plant height, PLWD=Plant width.

Table 35. High-parent heterosis (%) values for 13 quantitative characters measured in twelve hybrids and six parents evaluated at Namulonge, Uganda from May-October 2010

Cross	AGRONOMIC PARAMETERS												
	Fruit				Branch numbers		Stem		Maturity days		Plant dimensions		
	FL (cm)	FW (cm)	NF/P	NS/F	PBN	SBN	STHT (cm)	STD (cm)	DFL (day)	DFM (day)	PL (cm)	PLHT (cm)	PLWD (cm)
25x18	-17.7	-15.5	-54.3	-18.6	-5.6	-2.3	28.7	-2.0	8.9	13.7	13.8	1.5	-2.3
28x25	-31.8	-12.4	-3.7	-9.4	-2.1	-3.2	55.9	9.5	-6.3	-7.1	-4.6	24.2	11.7
29x18	-48.7	-9.6	31.0	53.9	-6.9	3.3	46.6	-2.1	-13.8	14.4	24.2	21.4	25.1
29x25	-22.0	-17.6	79.5	75.7	-25.5	3.7	27.0	-10.4	-1.6	-0.2	20.8	33.9	38.9
29x28	-38.8	9.3	236.3	-2.0	23.5	14.8	54.8	11.5	6.8	9.1	4.8	33.3	25.9
31x18	-29.9	-21.9	-11.8	-6.0	-27.4	-21.2	32.4	-6.0	-6.5	-5.7	14.7	19.4	-1.8
31x28	-34.5	13.5	-46.6	0.2	-36.0	-38.9	41.4	-0.8	13.3	13.4	-2.0	51.9	32.6
31x29	-5.2	-11.0	156.3	31.1	21.1	10.3	23.1	7.5	13.1	-0.3	36.9	58.4	50.9
35x18	-61.8	-1.1	-34.2	-18	5.3	-5.0	63.1	-10.3	-14.0	5.4	6.2	-4.4	-8.7
35x25	-33.3	-2.8	83.9	21.4	0.0	-10.9	17.9	-17.5	16.7	9.3	28.9	24.9	4.1
35x28	-57.3	-4.1	-53.5	2.4	-2.9	-12.3	61.1	-16.2	6.6	13.0	9.9	34.5	-18.4
35x29	1.0	-11.5	76.8	34.9	13.8	8.6	21.0	-2.1	-25.2	-17.5	6.1	37.1	6.9
Mean heterosis	-31.7	-7.1	38.3	13.8	-3.6	-4.4	39.4	-3.2	-0.2	4.0	13.3	28.0	13.8
Mean value of parents	6.4	1.3	18.7	62.9	8.0	16.8	16.3	0.7	60.0	110.3	2.9	33.1	32.3
Mean value of crosses	5.9	1.4	32.9	81.0	8.9	18.7	19.0	0.8	51.9	105.3	2.8	37.9	40.3

FL= Fruit length, FW= fruit width, PL=Pedicel length, NS/F=Number of seeds/fruit, PBN=Primary branch numbers, SBN=Secondary branch numbers, STHT=Stem height, STD=Stem diameter, NF/P=Number of fruit per plant, DFL=Days to flowering, DFM=Days to fruit maturity, PLHT=Plant height, PLWD=Plant width.

diameter (0.8), virus incidence (%) (0.59) and wilt disease (%) (0.57) (Table 36).

Narrow sense heritability estimates for agronomic traits were found to be low and inconsistent for the majority of parameters compared to broad sense heritability (Table 36). This inconsistency can be demonstrated for example, in traits such as days to flowering that had low h^2ns (24.4) compared to very high h^2bs (92.6) and secondary branch numbers had medium h^2ns (24.4) compared to very high h^2bs (92.6). Fruit width, stem diameter and stem height had consistently high narrow and broad sense heritabilities. This was the same trend for disease traits (Table 36). Inconsistency was shown in bacterial spot with very low h^2ns (16.1) but very high high h^2bs (85.7).

6.3.3.1 General combining abilities for measured traits

For all the studied traits, the parents exhibited significant and non-significant positive and negative GCA effects (Table 37). Parents 28, 31 and 25 significantly exhibited higher positive GCA effects for days to flowering respectively, with -3.28, -3.17 and -2.62. Only parent 29 showed the highly significant and positive GCA effect (6.36). With days to fruit maturity, significant negative GCA effects were shown by parents 28 (-5.45), and 31 (-2.85) while significant positive effects were displayed by parents 29 (5.41) and 35 (5.96). All parents significantly showed high GCA effects for fruit length (Table 37). Negative effects were contributed by parents 29 (-1.80), 31 (-1.05), 35 (-1.99) while parents 18, 25 and 28 contributed significantly positively with 1.91, 0.47 and 2.59 GCA effects, respectively. The high significant negative GCA effects for fruit width were displayed by parents 28 (-0.27) and 35 (-0.32). The high significant positive GCA effects were contributed by only parent 18 (0.79).

Parents 29 (9.16) and 35 (5.67) highly significantly showed positive GCA effects for number of fruit per plant whereas parents 18 (-12.44) and 28 (-7.29) significantly showed high negative GCA effects. For number of seeds per fruit, significant high negative GCA effects were shown by parents 31 (-13.57) and 35 (-3.13) while three parents showed significant positive GCA effects with parents 28 and 29 exhibiting the highest with 4.36 and 7.61 effects, respectively.

Table 36. Mean squares, components of variance and heritability for combining ability for disease and quantitative traits in hot pepper evaluated at Namulonge, Uganda from May-October 2010

Trait	gca MS	sca MS	Error MS	σ^2 gca	σ^2 sca	Baker's Ratio	CGD-ns (h^2ns)[a]	CGD-bs (h^2bs)[b]
Days to flowering	99.07***	87.40***	8.560	14.142	78.840	0.26	24.4	92.6
Days to fruit maturity	159.84***	92.69***	11.920	23.113	80.770	0.36	33.3	91.4
Fruit length (cm)	22.54***	1.41***	0.128	3.503	1.282	0.85	83.3	98.5
Fruit width (cm)	0.088*	0.024	0.026	0.010	0.002	0.91	41.1	44.9
Number of fruit per plant	467.4***	251.40***	26.490	68.892	224.910	0.38	35.4	93.2
Number of seeds per fruit	360.3***	314.70***	7.125	55.184	307.575	0.26	26.0	98.3
Primary branch numbers	4.40***	2.57***	0.325	0.636	2.245	0.36	33.1	91.5
Pedicel length	0.43**	0.15***	0.019	0.064	0.128	0.50	46.7	93.1
Plant height (cm)	44.28**	21.55	9.350	5.458	12.200	0.47	33.6	71.2
Plant width (cm)	56.03*	49.12**	13.555	6.637	35.565	0.27	21.3	78.3
Secondary branch numbers	26.96***	6.67*	1.336	4.004	5.334	0.60	54.6	90.9
Stem diameter	0.024**	0.01	0.004	0.003	0.003	0.69	48.4	69.8
Stem height	13.59*	4.18	3.397	1.592	0.782	0.80	43.2	53.9
Virus incidence (%)	1345.9***	399.70*	161.350	170.849	238.350	0.59	46.1	78.2
Cercospora leaf spot (%)	147.17**	78.28**	23.535	17.832	54.745	0.39	31.3	79.3
Wilt disease (%)	506.0	268.20	201.500	43.918	66.700	0.57	24.7	43.4
Bacterial spot (%)	549.3**	657.30***	111.950	63.079	545.350	0.18	16.1	85.7

gca = general combining ability, sca = specific combining ability, MS = mean square; *Significant at $P \leq 0.05$; ** highly significant at $P \leq 0.01$; *** highly significant at $P \leq 0.001$; the rest not significant.

[a]CGD-ns= Coefficient of genetic determination in the narrow sense which is analogous to heritability in the narrow sense (h^2ns)

[b]CGD-bs= Coefficient of genetic determination in the broad sense which is analogous to heritability in the broad sense (h^2bs).

The most significant negative GCA effects for primary and secondary branch numbers were contributed by parents 18 and 28 with their respective GCA effects of -0.87 and -1.23 for primary branch numbers and -1.31 and -3.23 for secondary branch numbers. Significant positive effects were demonstrated by parents 29 (0.56), 31 (0.53), and 35 (0.94) for primary branch numbers while for secondary branch numbers, significant positive effects were demonstrated by parents 29 (1.32) and 35 (2.73). For pedicel length, parent 18 highly significantly expressed positive GCA effects with 0.47 while three parents 28, 31 and 35 significantly showed negative GCA effects of -0.18,-0.11 and -0.10 respectively. Parent 35 exhibited high significant positive GCA effects for both plant height and width with GCA effects of 3.46 and 3.93, respectively while significant negative GCA effects were seen for plant height by parents 28 (-2.42) and 31 (-3.07) and by parent 18 (-2.74) for plant width. The highest significant positive GCA effects for stem diameter were shown by parents 29 (0.05) and 35 (0.09) while only parent 18 expressed significant negative GCA effects (-0.07). Two parents 31 and 35 showed significant positive GCA effects for stem height with 1.50 and 1.36, respectively whereas, only parent 28 had significant negative GCA effects (-2.56).

Significant positive GCA effects were shown by parent 25 (11.82) for virus incidence while parents 28 and 31 significantly exhibited negative GCA effects (-13.67) and (-19.90), respectively for this disease. With *Cercospora* leaf spot, only parent 18 significantly portrayed significant positive GCA effects (3.53) while it was parent 35 that significantly portrayed positive GCA effects (-8.81). For wilt disease significant GCA effects were shown by parent 18 (12.08) positively and 25 (-12.70) negatively. Similarly, only parent 28 exhibited significant negative GCA effects (-13.36) and parent 35 positive GCA effects (13.28) for bacterial spot.

6.3.3.2 Specific combining abilities for measured traits

Data on specific combining ability effects for quantitative traits were collected from only 12 crosses and disease traits from 13 crosses (Table 38). Significant negative SCA effects were shown by the crosses 35x29 (-15.8), 29x18 (-6.7), 29x25 (-8.8), 31x18 (-6.5) and significant positive SCA effects were shown by crosses 31x28 (6.1), 35x28 (6.7) for days to flowering. For

Table 37. Estimates of general combining ability effects of parental genotypes evaluated for disease, yield and contributing at Namulonge, Uganda from May-October 2010

	PARENT							
TRAIT	**18**	**25**	**28**	**29**	**31**	**35**	**Mean**	**SE**
Days to flowering	1.44	-2.62*	-3.28**	6.36***	-3.17**	-0.32	-0.27	1.02
Days to fruit maturity	-3.50**	-0.74	-5.45***	5.41***	-2.85*	5.73***	-0.23	1.20
Fruit length (cm)	1.91***	0.47***	2.59***	-1.80***	-1.05***	-1.99***	0.02	0.12
Fruit width (cm)	0.79***	-0.07	-0.27***	-0.05	-0.09	-0.32***	-0.00	0.06
Number of fruit per plant	-12.44***	3.29	-7.29***	9.16***	0.12	5.67**	-0.25	0.74
Number of seeds per fruit	2.34*	-1.12	4.36***	7.61***	-13.57***	-3.13**	-0.59	0.93
Primary branch numbers	-0.87***	0.07	-1.23***	0.56**	0.53*	0.94***	-0.00	0.20
Pedicel length (cm)	0.47***	-0.01	-0.18**	-0.07	-0.11*	-0.10*	-0.00	0.05
Plant height (cm)	0.22	-1.01	-2.42*	2.00	-3.07**	3.46**	-0.14	1.07
Plant width (cm)	-2.74*	-0.30	-2.07	2.39	-1.94	3.93**	-0.12	1.28
Secondary branch numbers	-1.31**	0.29	-3.23***	1.32**	-0.02	2.73***	-0.04	0.40
Stem diameter (cm)	-0.07**	-0.03	-0.03	0.05*	-0.02	0.09***	-0.00	0.02
Stem height (cm)	-0.94	0.37	-2.56***	0.45	1.50*	1.36*	0.03	0.64
Virus incidence (%)	5.89	11.82**	-13.67**	7.33	-19.90***	7.30	-0.20	4.31
Cercospora leaf spot (%)	3.53*	1.95	2.93	-0.58	1.06	-8.81***	-0.02	1.65
Wilt disease (%)	12.08*	-12.70*	5.12	2.37	-4.28	-3.01	-0.07	4.83
Bacterial spot (%)	-2.79	3.21	-13.36**	-4.30	7.44	13.28**	0.58	3.59

*Significant at $P \leq 0.05$; ** highly significant at $P \leq 0.01$; *** highly significant at $P \leq 0.00$; the rest not significant; SE= standard error = $(1/h)*(p-1)/ (p (p+2))*EMS$; h = proportion of total number of parental combinations (crosses) present with inclusion of parents; p= number of parents; EMS= Error mean square.

days to fruit maturity, significant positive SCA effects were shown by crosses 25x18 (10.8), 31x28 (11.3) while significant negative SCA effects were shown by crosses 28x25 (-9.7), 31x18 (-7.3), 31x29 (-7.3), 35x29 (-12.6.), 35x18 (-6.8). Concerning fruit length, significant negative SCA effects were exhibited by crosses 28x25 (-0.9), 29x18 (-0.7), 35x18 (-1.6) and 35x28 (-1.1) while, no cross showed significant positive SCA effects (Table 38).

Significant SCA effects for fruit width were only displayed by hybrid 31x28 (0.32), positively. The top performers for number of fruits per plant were hybrids 31x29 (17.6), 29x28 (26.9), 35x29 (11.5) and 35x25 (19.5) with significant positive SCA effects, while hybrid 35x28 (-12.7) with significant negative SCA effects was the poorest performer. Other hybrids with high negative SCA effects were 31x28 (-9.8) and 25x18 (-6.8). With number of seeds per fruit, crosses 29x18, 29x25, 31x18, 31x28, 31x29, 35x25, 35x28 and 35x29 were the best performers with significant positive SCA effects of 29.2, 30.1, 5.6, 13.8, 7.4, 7.6, 6.9, and 5.7, respectively, while crosses 25x18, 28x25, 29x28 and 35x18 performed poorly, with highly significant SCA effects of -15.0, -5.2, 8.6 and -11.9, respectively.

The significant positive SCA effects for primary branch numbers were found in crosses 28x25 (1.4), 29x28 (2.5), 31x29 (2.1) and 35x18 (1.3) while significant negative SCA effects were found in crosses 29x25 (-2.4) and 31x28 (-1.7). For secondary branch numbers, significant positive SCA effects were seen in crosses 29x28 (3.6) and 28x25 (2.4) whereas significant negative SCA effects were found in cross 31x28 (-3.3). For pedicel length, crosses 31x29, 35x25 and 35x28 highly significantly exhibited positive SCA effects with 0.6, 0.5 and 0.3, respectively, while 35x18 was the only hybrid with highly significant negative SCA (-0.6) effects. Only hybrid 31x28 exhibited high significant positive SCA effects for plant height (6.9) and none was significant negatively for this trait. However, crosses 26x18 (-2.4), 31x18 (-2.5) and 35x18 (-2.6) had high negative SCA effects. For plant width, no significant negative SCA effects were observed among hybrids but significant positive effects were observed in crosses 31x28 (8.7) and 31x29 (10.9). No significant positive and negative SCA effects were observed for both stem diameter and stem height (Table 38). But, hybrids 29x18 (2.3) and 35x18 (3.3) had high positive SCA effects for stem height.

Table 38. Estimates of specific combining ability effects of cross combinations for F_1 hot pepper generation grown at Namulonge, Uganda from May-October 2010

	CROSSES								
TRAIT	**25x18**	**28x25**	**29x18**	**29x25**	**29x28**	**31x18**	**31x28**	**31x29**	**SE**
Days to flowering	1.8	-2.7	-6.7*	-8.8**	-5.7*	-6.5*	6.9*	-2.1	2.59
Days to fruit maturity	10.8**	-9.7**	3.8	-6.2	-1.5	-7.3*	11.3**	-7.3*	3.06
Fruit length (cm)	0.5	-0.9*	-0.7*	0.5	0.5	0.2	-0.2	0.6	0.32
Fruit width (cm)	-0.02	-0.10	-0.13	-0.07	0.11	-0.05	0.32*	0.09	0.14
Number of fruit per plant	-6.8	0.2	-2.1	5.5	26.9***	4.1	-9.5	17.6**	4.56
Number of seeds per fruit	-15.0***	-5.2*	29.2***	30.1***	-8.7**	5.6*	13.8***	7.4**	2.37
Primary branch numbers	0.9	1.4**	-0.3	-2.4***	2.5***	-1.1	-1.7**	2.1***	0.51
Pedicel length (cm)	-0.3	-0.2	-0.2	0.2	0.0	-0.2	-0.2	0.6***	0.12
Plant height (cm)	-2.4	1.2	1.7	5.4	1.0	-2.5	6.9*	4.6	2.71
Plant width (cm)	-1.9	0.7	2.5	5.8	1.2	-1.4	8.7*	10.2**	3.26
Secondary branch numbers	1.3	2.4*	0.3	-0.6	3.6**	-1.3	-3.3**	1.5	1.03
Stem diameter (cm)	0.05	0.07	0.04	-0.09	0.08	-0.02	-0.02	0.08	0.06
Stem height (cm)	-0.2	1.6	2.3	1.6	1.6	-0.1	-0.5	0.5	1.63
Virus incidence (%)	0.0	-29.4*	4.5	-12. 5	14.0	19.2	26.3*	-8.2	11.26
Cercospora leaf spot (%)	-1.8	9.5*	0.7	2.3	-8.7	-0.9	-5.9	3.2	4.30
Wilt disease (%)	2.7	-6.0	15.6	-21.1	-16.9	16.8	6.8	-2.0	12.58
Bacterial spot (%)	-2.9	-14.9	22.1*	-13.9	2.7	5.4	3.5	-18.1	9.38

*Significant at $P \leq 0.05$; ** highly significant at $P \leq 0.01$; *** highly significant at $P \leq 0.00$; the rest not significant.

Table 38 continued

TRAIT	CROSSES					
	35x18	35x25	35x28	35x29	31X25	SE
Days to flowering	-3.7	6.9*	0.7	-15.8***	NT[a]	2.59
Days to fruit maturity	-6.8*	1.9	0.5	-12.6***	NT	3.06
Fruit length (cm)	-1.6***	0.3	-1.1**	0.5	NT	0.32
Fruit width (cm)	0.18	0.02	-0.02	0.00	NT	0.14
Number of fruit per plant	-0.6	19.5***	-12.7*	11.5*	NT	4.56
Number of seeds per fruit	-11.9***	7.6**	6.9**	5.7*	NT	2.37
Primary branch numbers	1.3*	-0.4	0.7	0.6	NT	0.51
Pedicel length	-0.6***	0.5***	0.3*	0.0	NT	0.12
Plant height (cm)	-2.6	1.3	0.1	3.0	NT	2.71
Plant width (cm)	1.8	4.3	-4.4	2.9	NT	3.26
Secondary branch numbers	1.8	-1.8	1.4	1 .8	NT	1.03
Stem diameter	0.1	-0.1	-0.1	0.0	NT	0.06
Stem height	3.3	0.4	1.0	-0.5	NT	1.63
Virus incidence (%)	4.5	-1.4	24.1*	-3.9	25.8*	11.26
Cercospora leaf spot (%)	8.9	-0.5	9.5*	13.0**	0.6	4.30
Wilt disease (%)	-23.9	6.3	-0.5	-14.3	13.1	12.58
Bacterial spot (%)	-5.9	-9.4	-14.9	19.8*	68.9***	9.38

*Significant at $P \leq 0.05$; ** highly significant at $P \leq 0.01$; *** highly significant at $P \leq 0.001$; the rest not significant; [a]NT = Data not taken.

Table 38 continued

TRAIT	SELFED PARENTS						
	18x18	25x25	28x28	29x29	31x31	35x35	SE
Days to flowering	7.5**	1.4	0.4	19.5***	0.8	5.9*	2.59
Days to fruit maturity	-0.3	1.6	-0.3	11.9***	1.6	8.5**	3.06
Fruit length (cm)	0.8*	-0.2	0.9**	-0.6	-0.3	1.0**	0.32
Fruit width (cm)	0.01	0.08	-0.16	0.00	-0.18	-0.09	0.14
Number of fruit per plant	2.7	-9.2	-2.4	-29.7***	-6.0	-8.8	4.56
Number of seeds per fruit	-3.9	-8.7**	-3.4	-31.8***	-13.4***	-4.2	2.37
Primary branch numbers	-0.4	0.2	-1.5**	-1.2*	0.3	-1.1*	0.51
Pedicel length (cm)	0.6***	-0.1	0.1	-0.3*	-0.1	-0.1	0.12
Plant height (cm)	2.9	-2.7	-4.5	-7.9**	-4.5	-0.8	2.71
Plant width (cm)	-0.5	-4.4	-3.1	-11.2**	-8.7*	-2.2	3.26
Secondary branch numbers	-1.0	-0.6	-2.0	-3.3**	1.6	-1.6	1.03
Stem diameter (cm)	-0.08	0.01	-0.04	-0.07	-0.02	0.00	0.06
Stem height (cm)	-2.7	-1.6	-1.8	-2.7	0.1	-2.1	1.63
Virus incidence (%)	-14.1	-5.9	-17.5	3.0	-31.5**	3.1	11.26
Cercospora leaf spot (%)	-3.4	-0.3	-2.2	-5.2	1.5	-20.2***	4.30
Wilt disease (%)	-5.6	-0.5	8.3	19.3	-17.4	19.3	12.58
Bacterial spot (%)	-9.4	-21.4*	11.8	-6.3	-29.8**	12.7	9.38

*Significant at $P \leq 0.05$; ** highly significant at $P \leq 0.01$; *** highly significant at $P \leq 0.00$; the rest not significant.
SE= standard error = $(p^2+p+2)/ (p+1) (p+2)$*EMS; p= number of parents; EMS= Error mean square.

Significant positive SCA effects were shown by hybrids 31x28 (26.3), 35x28 (24.1), 31x25 (25.8), for virus incidence while one cross 28x25 significantly exhibited negative SCA effects (-29.4). For *Cercospora* leaf spot, significant positive SCA effects were realized in crosses 28x25 (9.5), 35x28 (9.5), 35x29 (13.0) while no cross significantly registered negative SCA effects (Table 38). However, crosses 29x28 and 31x28 registered higher negative SCA of -8.7 and -5.9, respectively.With wilt disease, no significant SCA effects were seen among crosses. Nevertheless, crosses 29x18 (15.6), 31x18 (16.8), 31x25 (13.1) had high positive GCA effects while crosses 29x25 (-21.1), 29x28 (-16.9), 35x18 (-23.9), 35x29 (-14.3) had high negative GCA effects. Three crosses 29x18 (22.1), 35x29 (19.8) and 31x25 (68.9), expressed significant positive SCA effects for bacterial spot while none of the hybrids expressed significant negative SCA effects. However, hybrids 35x28 (-14.9), 28x25 (-14.9), 29x25 (-13.9), 31x29 (-18.1) expressed the highest negative SCA effects for this disease.

6.3.4 Estimates of genetic components for various traits

Among the genetic components of variability, the additive gene effect (D) was significant for all the traits, apart from number of fruit per plant and plant width (Table 39). The measure of dominance gene effect (H_1) was significant for only eight traits (days to flowering, days to fruit maturity, number of fruit per plant, number of seeds per fruit, primary branch numbers, plant height, plant width and secondary branch numbers). Similarly, the proportion of dominance due to positive and negative effect of genes (H_2) was significant for only six traits (days to fruit maturity, number of fruit per plant, number of seeds per fruit, primary branch numbers, plant height and plant width). The estimate of the relative proportion of the dominant and recessive alleles 'F' was positive for all measured traits except the number of fruit per plant and stem diameter.

Estimates of the dominance effects over all heterozygous loci (h^2) were only significant for three traits (days to flowering, number of seeds per fruit, and number of fruit per plant). The environmental factor (E) was significant for only six traits (number of fruit per plant, plant height, plant width, secondary branch numbers, stem diameter and *Cercospora* leaf spot).

Table 39. Estimates of genetic components of variability in hot pepper evaluated at Namulonge, Uganda from May-October 2010

TRAIT	GENETIC COMPONENT					
	D	H_1	H_2	F	h^2	E
Days to flowering	205.4** ± 42.4	289.5* ± 107.7	197.6 ± 96.2	276.3* ± 103.6	183.7* ± 64.7	17.1 ± 16.0
Days to fruit maturity	228.7** ± 36.9	239.6* ± 93.8	194.8* ± 83.8	198.4* ± 90.3	66.3 ± 56.4	23.8 ± 14.0
Fruit length (cm)	17.0** ± 2.8	3.1 ± 7.1	2.3 ± 6.3	3.5 ± 6.8	0.4 ± 4.3	0.3 ± 1.1
Number of fruit per plant	44.0 ± 58.6	779.2**± 148.7	589.3**± 132.8	-158.6 ± 143.1	481.1**± 89.4	53.0*± 22.1
Number of seeds per fruit	219.3* ± 81.8	1035.6**± 207.7	829.9**± 185.5	172.5 ± 199.9	654.2**±124.9	14.3 ± 30.9
Primary branch numbers	3.4** ± 0.8	9.7**± 2.1	8.7**± 1.9	1.5 ± 2.0	1.8 ± 1.3	0.7 ± 0.3
Pedicel length	0.5** ± 0.1	0.5 ± 0.3	0.4 ± 0.2	0.5* ± 0.3	-0.02 ± 0.2	0.04± 0.04
Plant height (cm)	28.4* ± 8.9	71.4* ± 22.5	44.7* ± 20.1	33.7* ± 21.7	38.4 ± 13.5	18.7**± 3.4
Plant width (cm)	28.0 ± 14.2	118.7* ± 37.6	89.4* ± 33.6	18.0 ± 36.2	41.2 ± 22.6	27.1**± 5.5
Secondary branch numbers	15.2** ± 3.0	17.3* ± 7.6	14.04 ± 6.8	1.1 ± 7.3	6.5 ± 4.6	2.7* ± 1.1
Stem diameter	0.02** ± 0.0	0.009± 0.0	0.01 ± 0.0	-0.0004± 0.0	0.003 ± 0.007	0.008**±0.002
Virus incidence	1371.4* ± 536.2	1831.7 ± 1361.1	625.1 ± 1215.9	1846.1 ± 1309.9	907.3± 818.4	322.7 ± 202.7
Cercospora leaf spot	252.0**± 39.1	253.5 ± 99.3	166.3 ± 88.7	293.9*± 95.6	118.8± 59.7	47.1* ± 14.8
Bacterial spot	299.1**± 61.6	379.0 ± 156.5	260.4 ± 139.8	356.7 ± 150.6	145.0± 94.1	0.008 ± 23.3

*Significant at $P < 0.05$; ** highly significant at $P < 0.01$; others not significant

D= additive gene effects

H_1= measure of dominance gene effects

H_2= measure of proportion of dominance due to positive and negative effect of genes

h^2= estimates of the dominance effects over all heterozygous loci

F= estimate of the relative proportion of the dominant and recessive alleles

E= environmental factor.

The ratios of different genetic components and heritability estimates are given in Table 40. The proportion of $(H_1/D)^{1/2}$, a measure of the degree of dominance was more than unity for most of the traits apart from fruit length, pedicel length and stem diameter. The ratio $H_2/4H_1$, a measure of the distribution of positive and negative alleles in the parents was not equal to the expected 0.25 for all the traits under study. The ratio KD/KR, an indicator of the proportion of dominant to recessive genes was more than unity in the expression of the traits apart from number of fruit per plant and stem diameter. The number of dominant genes and gene groups controlling the trait (h^2/H_2) was maximum for virus incidence (1.45) followed by days to flowering (0.93), while it was minimum in pedicel length (0.05).

Table 40. Ratios of genetic components of variance for various traits and heritability in chilli peppers evaluated at NaCRRI, 2010

TRAIT	RATIOS			
	$(H1/D)^{0.5}$	$H_2/4H_1$	KD/KR	h^2/H_2
Days to flowering	1.19	0.17	3.61	0.93
Days to fruit maturity	1.02	0.20	2.47	0.34
Fruit length (cm)	0.42	0.19	1.64	0.15
Number of fruit per plant	4.21	0.19	0.40	0.82
Number of seeds per fruit	2.17	0.20	1.44	0.79
Primary branch numbers	1.69	0.22	1.31	0.21
Pedicel length	0.99	0.17	2.98	0.05
Plant height (cm)	1.59	0.16	2.20	0.86
Plant width (cm)	2.06	0.19	1.37	0.46
Secondary branch numbers	1.07	0.20	1.07	0.46
Stem diameter	0.68	0.27	0.97	0.29
Virus incidence	1.16	0.09	3.79	1.45
Cercospora leaf spot	1.00	0.16	3.78	0.71
Bacterial spot	1.13	0.17	3.25	0.56

h^2/H_2 = number of dominant genes and gene groups controlling the trait

$H_2/4H_1$ = measure of the distribution of positive and negative alleles in the parents

$(H_1/D)^{1/2}$ = measure of the degree of dominance

KD/KR = indicator of the proportion of dominant to recessive genes

6.5 Discussion and conclusion

Heterotic breeding can be used to facilitate hot pepper improvement in order to enhance quality and productivity that are compromised by the lack of improved cultivars for disease resistance, fruit yield and associated traits. Hybridization of genetically diverse genotypes yields hybrids with various heterotic effects, from which selection for desirable traits among segregating populations in later generations would be made (Ramalho do Rêgo *et al.*, 2010). Knowledge on heterosis, combining ability and the nature of gene action controlling such desirable traits is vital to the identification of the magnitude of useful genetic variances present among genotypes and helps in selection and improvement of these traits (Chowdhary *et al.*, 2007; Marame *et al.*, 2008). This study was conducted to generate information on heterosis, general and specific combining abilities to identify good parent combiners in hybridization for improved disease resistance, yield and its components through a half diallel mating design with genetically-diverse parents selected from the season 2009A evaluation.

As expected from the diversity of genotypes, significant differences occurred among both the parentals and F_1s for most of the quantitative and disease traits as has been reported in sesame (Bayoumi & El-Bramawy, 2007) and wheat (El Attari *et al.*, 1996). Specifically, the variability in quantitative traits such as fruit length and numbers per plant, days to flowering, days to fruit maturity, plant height and width as well as response to viral disease, bacterial spot and *Cercospora* leaf spot was indicative of the high potential available for improvement of these traits.

Agricultural heterosis has been widely used globally to increase productivity in plants and animals (Hua *et al.*, 2003) since it was first observed nearly 100 years ago (Zamir, 2008). In this study, heterotic studies were carried out as a means to generate knowledge for improved chilli pepper productivity through heterotic breeding. Heterosis was generally observed in traits such as number of fruits per plant, primary and secondary branch numbers, stem diameter, number of fruits per plant, days to flowering and fruit maturity, plant height and width where overall mean of hybrids were better than for parents. When percent heterosis over both mid-parent (MPH) and better parents (HPH) for disease, yield and yield associated traits were calculated, the degree of

heterosis varied from cross to cross and from character to character. Varying heterotic effects for parameters have been reported elsewhere in pepper (Geleta & Labuschagne, 2004; Geleta *et al.*, 2004) and in another self-pollinated crop, Kenaf (Pace *et al.*, 1998). In both HPH and MPH, negative and positive heterosis was observed. The results indicate majority of the traits displayed desirable mean MPH heterosis compared to HPH.

Negative heterosis was desirable for disease incidence, days to flowering and fruit maturity and pedicel length. The mean positive MPH heterosis for fruit width, plant height, primary branch numbers, secondary branch numbers, number of seeds per fruit (NS/F), stem height, stem diameter, number of fruits per plant (NF/P) and plant width (PLWD) was desirable suggesting, the involvement of dominant genes in these traits (Saira *et al.*, 2001). Desirable HPH in traits implies over-dominance of genes, thus for traits such as number of fruits per plant (NF/P), plant width (PLWD), number of seeds per fruit (NS/F), days to flowering (DFL) and days to fruit maturity (DFM) that expressed both desirable MPH and HPH, both dominance and over-dominance of genes were indicated in their control. The lack of desired MPH and HPH for the other traits possibly indicates the occurrence of allelic interactions.

The analysis of variance for combining ability indicated significant differences among parents and crosses. For all the studied traits the parents exhibited significant and non-significant positive and negative GCA effects, implying that both desirable and non-desirable GCA effects were transferred by parents to the progeny. Negative GCA effects are considered desirable for traits such as days to flowering and fruit maturity, pedicel length, and disease incidence. In contrast, positive GCA effects are desirable for fruit width, fruit length, number of fruits per plant, number of seeds per fruit, primary branch numbers, plant height, plant width, secondary branch numbers, stem diameter and stem height.

None of the parents used in this study proved to exhibit good general combining ability for all the studied traits. However, parents that expressed significant desired GCA effects in traits were better general combiners for these traits in the F_1 progeny. For example, local parent 31 (GCA -19.90) was the best general combiner for virus resistance followed by local parent 28 (GCA -

13.67) while AVRDC parent 25 was the worst general combiner (GCA 11.82). Similarly, for DFM and plant height (PHT), the best general combiners were local parents 28 and 35 with GCA effects of -5.45 and 3.46, respectively while parent 35 and 31 were the poorest general combiners in DFM and PHT, respectively with 5.73 and -3.07 GCA effects. On the other hand, for the number of fruits per plant, parent 29 (GCA 9.16) was the best general combiner while parent 18 (GCA -12.44) was the worst general combiner.

From this study, parents with various GCA effects combined to produce crosses varying in SCA effects. For example, some parents with negative GCA effects combined to produce significant positive SCA such as 31x28 for days to fruit maturity, one parent with negative and the other with positive GCA effects produce a hybrid with significant negative SCA effects (29x25 for days to flowering), both parents having significant negative GCA effects produce a hybrid with significant negative SCA effects (31x18 for days to fruit maturity) and both parents having significant positive GCA effects produce a hybrid with significant negative SCA effects (31x28 for days to flowering and fruit maturity, 35x29 for days to fruit maturity) as previously reported by Pace *et al.* (1998). However, from this study, majority of the significant negative SCA effects came from parents with contrasting significant GCA effects as well as those with significant positive SCA effects.

Specific combining ability effects measure the usefulness of a particular cross combination in the exploitation of heterosis. In this study, desired significant SCA effects were observed among various studied traits. Traits of cross combinations with desirable negative SCA effects are days to flowering and fruit maturity, pedicel length, and disease incidence whereas positive SCA effects in crosses are desirable for fruit width, fruit length, number of fruit per plant, number of seeds per fruit, primary and secondary branch numbers, plant height, plant width, stem diameter and stem height. Consequently, crosses with desirable significant SCA effects are considered the best and can be exploited through heterotic breeding to generate better purer lines through transgressive segregation in later generations (Chowdhary *et al.*, 2007; Bayoumi & El-Bramawy, 2007).

The significance in general and specific combining abilities is an indication of both additive and non-additive gene action in the expression of traits. Baker's ratio indicated that most of the agronomic traits apart from fruit length, fruit width, secondary branch numbers, stem diameter and stem height were mainly controlled by non-additive gene effects since their Baker's ratio is far from unity (X<0.5) (Baker, 1978). Pedicel length seems to be controlled by both additive and non-additive gene actions in equal proportions because of their intermediate Baker's ratio (X=0.5). In contrast to the findings of Doshi (2003) and Ramalho do Rêgo *et al.* (2009) who found additive gene action to be prevalent in the expression of most quantitative traits in hot pepper, results from this study agree with other findings (Marame *et al.*, 2008; Reddy *et al.*, 2008). Additive gene action controlled the expression of virus and wilt disease incidences while non-additive gene action controlled the expression of *Cercospora* leaf spot and bacterial spot traits. Like the results of this study, several authors have indicated the relative importance of additive over non-additive gene effects in the expression of disease traits in various crops such as *Fusarium* head blight (scab) in wheat (Khorzoght *et al.*, 2010) and soybean rust disease in soybean (Kiryowa *et al.*, 2008).

The low narrow sense heritability in most of the agronomic traits and disease traits further confirms the importance of non-additive gene action in their control. High estimates of broad sense heritability (71.2-98.3) in most traits, the phenotypic expression was largely due to genotypic and not environmental effects. Rapid improvement of such traits can thus be made using standard selection procedures based on the phenotypes of parents such as mass selection (Mwanga *et al.*, 2002; Sharma *et al.*, 2010). However, since most of these traits are controlled by non-additive genes, such selection procedures should take care of variance due to non-additive gene effects (Mwanga *et al.*, 2002) by selection in later generations when desirable genes have been fully fixed.

In this study, inconsistency in narrow and broad sense heritability was observed in some traits such as days to flowering and number of seeds per fruit. Similar findings have been observed by Deb & Khaleque (2009) with quantitative traits in Chick pea and Ekvised *et al.* (2006) with

peanut agronomic traits and could be attributed to sampling error or environmental effects (Ekvised *et al.*, 2006; Deb & Khaleque, 2009).

The significant differences among genotypes for various traits in this study and the significance of additive-dominant model for these traits (Singh & Chaudhary, 1977; Dabholkar, 1992; Sharma, 1998) allowed further analysis of their genetic components. Estimates of these genetic components and the derived ratios for various measured traits indicated the presence of both additive and non-additive gene actions controlling expression of traits although additive gene action dominated. The significance of genetic components varied as for previous studies (Marame *et al.*, 2008; Schuelter *et al.*, 2010) and study this variation depended on the trait and parents.

The number of fruits per plant and plant width seemed to be controlled by non-additive gene action since their additive gene effects (D) values were non-significant. This implies that their selection should be deferred to later generations when desirable segregates become available. For the rest of the traits, selection in early generations is possible due to their significant additive gene effects. The number of fruits per plant and stem diameter are controlled by recessive alleles because their F estimate values were negative and the rest of the parameters whose F values are positive, are controlled by dominant alleles (Singh & Chaudhary, 1977; Dabholkar, 1992; Sharma, 1998). The significance of estimates of the dominance effects over all heterozygous loci (h^2) in days to flowering, number of seeds per fruit, and number of fruit per plant indicates the effect of heterozygous loci in the control of these traits. Non-significance of h^2 in the rest of the traits such as days to fruit maturity, fruit length and others indicate additive effects or partial dominance. The traits mostly affected by environmental factors were number of fruit per plant, plant height, plant width, secondary branch numbers, stem diameter and *Cercospora* leaf spot incidence due to their significant E estimate.

The greater than unity estimate for the measure of the degree of dominance in most traits signifies presence of over dominance gene effect (a component of non-additive gene effect) in their expression, while its less than unity estimate in fruit length, pedicel length and stem

diameter indicates partial or incomplete dominance in the expression of these traits. This further confirms the findings from Griffing (1956) analysis and Baker's ratio (X< 0.5) analysis for most traits that found non-additive gene effects more preponderant than the additive gene effects. However, this observation seems to disagree with the heterosis results since HPH was not realized for most traits. The possibility of this may be due to large variability found for dominance effect (H_1) for most traits using the Hayman model, calling for further investigation using other genetic models.

There was unequal distribution of positive and negative alleles among the parents judged from the ratio of the measure of the distribution of positive and negative alleles in the parents away from the expected value of 0.25 (Dabholkar, 1992; Singh & Chaudhary, 1977; Sharma, 1998). The ratio KD/KR indicated high proportions of recessive genes were critical in the expression of number of fruit per plant and stem diameter parameters since it was less than unity. For the rest of the parameters, this ratio has shown that they were controlled by a higher proportion of dominant genes since it was more than unity. Estimates of number of dominant genes and gene groups controlling the trait indicated that the number of blocks of dominant genes controlling traits was maximum for virus incidence (1.45) and minimum in pedicel length (0.05). In fact, the number of dominant groups of genes controlling virus incidence suggest that this trait was governed by a group of genes with dominant gene effects. For all the other studied traits whose values were less than unity, there is no valid interpretation on groups of genes exhibiting dominance in their control (El-Bramawy & Shaban, 2007).

In conclusion, differences in performance among hybrids and their parents allowed significant differences in heterotic, GCA and SCA effects among various studied traits. General combining ability effects were more predominant than SCA effects in viral and wilt disease incidences and in a few agronomic traits (fruit length and width, secondary branch numbers and stem height and width). Additive gene action was critical in these traits, selection for which can be effected in early generations while selection for traits such as days to flowering and fruit maturity, number of fruits per plant and number of seeds per fruit controlled by non-additive gene action should be deferred to later generations when desirable segregates become available during breeding. The

AVRDC genotype 28 and local genotype 35 demonstrated highly significant desirable GCA effects for most of the studied traits followed by local parents 29 and 31 and are thus considered good combiners. However, for wilt disease, only the AVRDC parent 25 emerged as a significant general combiner in reducing its incidence. Hybrid 31x29 was the best performer among all crosses for measured traits (with the best SCA) followed by hybrids 29x28 and 31x18. Hybrid 31x28 exhibited poor SCA effects for most of the traits and was thus the poorest cross. Hybrids 31x28 and 29x28 were also better performers for *Cercospora* leaf spot resistance while hybrid 28x25 was the best for virus resistance.

CHAPTER SEVEN

GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS

7.1 General discussion

The aim of this study was to contribute towards the improvement of hot pepper production in Uganda through: characterization of exotic and local genotypes, identification of genotypes with superior agronomic, yield and disease-resistance traits for combination in the development of improved cultivars. The study to determine diversity among hot pepper genotypes using qualitative and quantitative traits revealed a wide range of diversity, with qualitative traits such as nodal anthocyanin, stem pubescence type, stem pubescence density, pedicel position and stigma exertion exhibiting high diversity indices that could mostly be used to discriminate among genotypes. Similarly, quantitative traits were also highly significant in almost all measured traits among genotypes. These results strengthen our hypothesis that local and exotic genotypes differ in morphological traits and agree with previous studies on chilli (Manju & Sreelathakumary, 2002; Adetula & Olakojo, 2006). The Cluster analysis, however, revealed a high degree of relatedness among some genotypes probably because they were of the same species albeit from different geographical locations.

Very high variations due to genotype by season (environment) (GxE) interaction were also observed in all traits except number of seeds per fruit indicating that genotypic performance was not consistent due to seasonal changes. The differential response of genotypes for various growth, quality and yield traits when grown under different seasons has been observed elsewhere (AVRDC, 2004; Idowu-Agida *et al.*, 2010). Pooled analysis of variance showed no significant influence of season and genotypes on all disease incidences except for viral disease incidence that highly differed across seasons. However, all disease incidences and severities were highly influenced by genotype by season (GxE) interaction except for the *Phytophthora* blight severity index. This indicates that genotypic performance varied with change in environment for disease incidences and severity indices apart from *Phytophthora* blight severity index. The differential

sponse of genotypes to field diseases under different seasons has been observed in cowpea Adipala *et al.*, 2001) and Chilli pepper (Galanihe *et al.*, 2004). The traits where G x E interactions were not significant can be evaluated in one environment (Benardo, 2002). However, to provide reliable results for the majority of traits that displayed the role of G x E effects, genotypes need to be evaluated for many seasons or across a wide range of environments Bakhsh *et al.*, 2006; AVRDC, 2007; Balkaya & Karraağaç, 2009).

Evaluation results for growth, quality and yield traits indicated highly significant differences among genotypes in both 2009A and 2009B seasons except for the number of seeds per fruit in 2009A. Similar variations have been reported in *Capsicum annuum* genotypes evaluated in different environments (AVRDC-RCA, 2003; Qaryouti *et al.*, 2003; AVRDC, 2004; Akinci & Akinci, 2004; Sermenli & Mavi, 2010; Idowu-Agida, *et al.*, 2010). Most findings from this study agree with findings of these researchers but disagree on others. This may have been due to differences in genotypes used in the study and or environmental differences prevailing in the experimental areas. The differential seasonal variations in performance of majority traits suggest the need to identify suitable cropping seasons for better performance of most traits except number of seeds per fruits that can perform well across seasons. This may have resulted from variations in climatic variables in different seasons including, rainfall, evaporation, sunshine duration, temperature and relative humidity which affect the growth and yield of hot pepper (Omonijo & Afuye, 2009).

Exotic genotypes performed better in most traits than local genotypes in both seasons. Exotic genotypes flowered and matured earlier, exhibited longer and heavier fruits, and even produced higher total and marketable fruit yields than local genotypes. However, local genotypes grew taller with wider canopies and had more number of seeds per fruit than exotic genotypes. Therefore, the hypothesis that local and exotic genotypes differ in growth, quality and yield traits is accepted. Tall plants with wider canopies produce many primary and secondary branch numbers that bear many fruits (Seleshi, 2011). Tall plants have long stem height that prevents fruit contact with soil thereby preventing infection with fruit rots caused by fungal and bacterial soil pathogens (Rodríguez *et al.*, 2008). The higher number of seeds per fruit of local genotypes

exotic genotypes could be exploited for improved seed yield to especially benefit the seed industry.

Results from correlation studies indicated significant correlation between more traits in season 2009B than in 2009A. There were also changes in trait correlations between genotypes and seasons. This is demonstrated in traits whose correlation was either positive and negative or high positive and low positive and/or high negative and low negative in 2009A or 2009B and vice-versa. This observation is attributed to the effect of the environmental differences on genotypes. This finding confirms the ANOVA on GxE interaction and is supported by observations by other researchers in hot pepper elsewhere (Todorova *et al.*, 2003; Rodríguez *et al.*, 2008). Nevertheless, some traits exhibited consistent positive relationship among genotypes across seasons e.g. between total fruit yield, average fruit weight; total fruit yield, fruit length; fruit length; average fruit weight, fruit width, and plant height, plant width to mention but a few. This consistence implies that the relationship is stable and one trait can be used to predict and or determine the other. On the other hand, number of fruit per plant and average fruit weight, number of fruits per plant and fruit width consistently related with each other negatively in both seasons implying that, an increase in fruit size reduced number of fruits per plant. Similar negative relationships between average fruit weight, number of fruits per plant were reported by earlier studies (Kumar *et al.*, 2003; Nandadevi & Hosamani, 2003; Rodríguez *et al.*, 2008).

Five diseases were found important in the two season field evaluations, including: *Cercospora* leaf spot, viral disease, *Phytophthora* blight, wilt and anthracnose in order of importance. However, there was irregular but differential expression of significant differences in both seasons for *Cercospora* leaf spot, *Phytophthora* blight and viral disease incidences and *Cercospora* leaf spot and *Phytophthora* blight severity indices, all of which may be attributed to the effect of G x E interaction. Exceptions such as the occurrence of higher *Phytophthora* blight incidence and anthracnose severity index in 2009A than 2009B might have been due to G x E interaction or sampling error. The higher viral incidence and severity in 2009A than 2009B is attributed to dry weather conditions in 2009A that provided a more favorable atmosphere for the

growth and proliferation of insect pests such as aphids, thrips and whiteflies that vector viral diseases (Agrios, 2005).

Generally, the inconsistent occurrence and severity of some diseases suggest that breeding for their resistance should target specific seasons. The higher occurrence and expression of bacterial and fungal diseases (bacterial wilt, *Cercospora* leaf spot, anthracnose and *Phytophthora* blight) in 2009B than 2009A was attributed to high levels of precipitation that consequently provided conditions of high humidity to favor disease development (Agrios, 2005). The exceptions of higher *Phytophthora* blight incidence and Anthracnose severity index in 2009A than 2009B might have been due to GxE interaction.

In both seasons, local genotypes scored lower *Cercospora* incidence and severity indices, and anthracnose severity indices although these genotypes consistently scored poorly in both virus incidence and virus severity indices when compared with exotic genotypes. Other diseases where both local and exotic genotypes did not score consistently well include *Phytophthora* blight, anthracnose and wilt incidences where the role of seasonal and/or season x genotype interaction is suggested. The role of G x E interaction was found in all disease traits other than *Phytophthora* blight severity implying that disease scores were not stable across seasons. Local genotypes 3 and 5 and exotic genotypes 14, 18, 22, 25, 11, 12, and 3 consistently scored better in all disease traits across seasons as well as the exotic genotypes 27, 28, 29, 30, 31, 32, 33 and 35 evaluated only in season 2009B. However, these genotypes need to be evaluated for a second season to confirm their performance.

No genotype was found to be resistant to all observed field diseases but some were resistant to some or more diseases. Most genotypes were susceptible to all the diseases apart from the wilts and *Phytophthora* blight where high levels of field resistance were observed probably due to inherent resistance or low levels of inocula that may have resulted in disease escape. Disease resistance evaluation in uncontrolled inoculation field experiments can be constrained by environmental factor differences that cause disease escape due to unpredictable occurrence, severity, and non uniformity of epiphytotics (Fokunang *et al.*, 2000; Agrios, 2005). Artificial

inoculation would, therefore, be a more reliable avenue for confirming field resistance to wilt and *Phytophthora* blight.

Field inoculation would only be possible if the identity of causal pathogens were known. In this study several viral, bacterial and fungal diseases were observed to infect pepper in the field as reported by ADC/IDEA (2001) and UEBP (2005). Eight virus species were detected, including TSWV, ChiVMV, TMV, PVY, PepMoV, PVMV, AMV and CMV in agreement with earlier studies (Ssekyewa, 2006; Dafala, 2008; Nono-Womdim, 2008). The most common species were ChiVMV, PVY, PVMV and CMV; which should be targeted in breeding for resistance. Symptoms were not diagnostic of a particular virus and mixed infection of virus species was common and could possibly result in synergism, which has been reported elsewhere in pepper (Palukaitis & Kaplan, 1997; Wang *et al.*, 2002). Potyvirus and CMV infections were more common than viruses from other genera. Hiskias *et al.* (1999) reported similar findings on tomato and hot pepper in Ethiopia. Viruses belonging to the potyvirus genus are the most prevalent on vegetable crops (Black *et al.*, 1991; Green & Kim, 1991; Nono-Womdim, 2008). However, a comprehensive survey for pepper virus diseases country-wide is needed to verify the relative importance of potyviruses and *Cucumber mosaic virus* in Uganda since this study involved samples from on-station trials in central Uganda only.

The occurrence of wilt in the absence of diagnostic symptoms for *Phytophthora capsici*, was linked to *Fusarium oxysporum* f.sp. *capsici* that causes *Fusarium* wilt and *Ralstonia solanacearum* that causes bacterial wilt. The two pathogens did not occur together in samples tested probably due to antagonism confirmed to occur elsewhere *in vitro* (Zecevic *et al.*, 2010). Other identified pathogens that caused confounding symptoms in the field included *Colletotrichum spp* on stems and *Xanthomonas campestris* pv. *vesicatoria* on leaves. Anthracnose caused by *Colletotrichum spp* was observed on both fruits and foliar parts in agreement with Cerkauskas (2004) who reports occurrence of the disease on leaves, stems and both pre-and post-harvest fruits. Bacterial spot (*Xanthomonas campestris* pv. *vesicatoria*) was identified from diseased plants characterized by numerous dark water-soaked spots on leaves, extensive leaf defoliation, shoot die-back and stunted growth. Plants with early infection got

verely infected and gave no fruit yield at all. This agrees with reports by Hansen (2000) and Shamed & Shymaa (2008) where the pathogen causes reduced yield and loss of quality in harvested fruit under severe defoliation.

Correlation analysis between yield and disease assessment methods showed all diseases were negatively correlated with both total fruit yield (t/ha) and total marketable fruit yield in 2009A except for viral diseases implying that they contributed to the loss of both total and marketable fruit yields. Only the severity indices for viral disease and *Cercospora* leaf spot incidence significantly correlated negatively with total fruit yield implying that viral severity and *Cercospora* leaf spot incidence contributed more to total fruit yield loss. This also suggests that resistance to these diseases is associated with poor yielding genotypes. These results agree with those of previous researchers who reported negative correlation between disease traits and yield in various crops (Pratt *et al.*, 1994; Fokunang *et al.*, 2000; AVRDC, 2007). High significant and positive correlation ($P<0.001$) of for all diseases except for viral disease suggests that the incidence of anthracnose, *Cercospora* leaf spot and *Phytophthora* blight diseases can predict their severity. For these diseases, assessment based on disease incidence in future would be efficient because this data is easily obtained and severity scoring with visual inspection tends to be subjective due to the variations or errors of visual acuity (Scott & Rosenkranz, 1981; González-Pérez *et al.*, 2011).

Stability analysis indicated that average fruit weight, fruit length, fruit width, seed weight, 50% days to fruit maturity, plant width and number of seeds per fruit were the most stable traits. Unstable traits may be improved by using suitable cropping seasons and management practices. Likewise, stability assessment methods for individual diseases among genotypes indicated that for most diseases, incidence and severity assessments were not stable except for virus severity index followed by *Phytophthora* blight severity index. This might have been due to the differences in environmental factors that influenced disease occurrence in the different seasons. Therefore, for these two diseases, severity index is the most efficient assessment method and for the rest, both methods are equally important.

analysis of genetic control for agronomic traits among selected hot pepper genotypes icated significant mean squares among parents and crosses for most traits. This is an ication of both additive and non-additive gene action in the expression of traits. This supports hypothesis that hybridized pepper genotypes differ in combining ability, and hence gene ion for disease, fruit yield and associated traits. Non-additive gene action was, however, found dominant in the expression of most traits as reported by Reddy *et al.* (2008) and Marame *et* (2008). Virus and wilt disease incidences were controlled mainly by additive gene effects, nfirming expression of these disease traits as for other crops (Mwanga *et al.*, 2002; Bonos, 06; Kiryowa *et al.*, 2008; Khorzoght *et al.*, 2010).

r all the studied traits the parents exhibited significant and non-significant positive and gative GCA effects, implying that both desirable and non-desirable GCA effects were nsferred by parents to the progeny. None of the parents used in this study proved to exhibit od general combining ability for all the studied traits. However, parents that expressed nificant desired GCA effects in traits were better general combiners for these traits in the F_1 ogeny. Desired significant SCA effects were observed among various studied traits. onsequently, crosses with desirable significant SCA effects are considered the best and can be ploited through heterotic breeding to generate better purer lines through transgressive gregation in later generations (Chowdhary *et al.*, 2007; Bayoumi & El-Bramawy, 2007).

stimates of genetic heritable components and their derived ratios for most disease, growth and eld traits further implied that these traits were under the control of over-dominance gene tion, a component of non-additive gene action. This confirms the findings of Griffing (1956) d Baker's ratio analysis in this study that found non-additive gene effects more predominant an the additive gene effects for most traits. However, this observation seems to disagree with e heterosis results since HPH was not realized for most traits, probably due to large variability und for dominance effect for most traits using the Hayman model. Further investigation using ther genetic models will confirm this and or provide valuable information regarding these eritable components.

Conclusion

s study has provided considerable information, indicating that appreciable variability exists ng collected hot pepper germplasm for most of the traits studied. Good genotypes could be cted from this germplasm for introgressing superior traits into desirable but otherwise poor tivars in order to hot pepper enhance production in Uganda. Genetic analyses have indicated genetic variation among traits is controlled by both additive and non-additive gene actions h non-additive gene effect being more predominant. However, multi-location trials are ential across seasons to confirm and enrich the findings of this study.

3 Recommendations

e to limited time and resources, certain aspects of this study have left important questions for rther investigation.

1. Genotypes evaluated in this study should be evaluated over several seasons and environments to confirm their stability and value. This evaluation should integrate aspects previously not covered including evaluation of the population dynamics of important pests.
2. Morphological characterization done in this study should be enhanced with molecular or biochemical studies since quantitative traits are subject to environmental modification and interaction and thus may not accurately indicate the existing genetic diversity among genotypes
3. In order to complement the yield analysis done in this study, the genotypes evaluated in this study need to be assessed for pungency, flavour and aroma that are important attributes critical to export markets.
4. The genotypes that produced high yields with other good horticultural attributes across seasons including CA -UGCE 09-3, PP0537-7513, PP0337-7065, PP0337-7546, PP0007-2259, CA-PPCHI-08-1, PP97-7195-1, PP0337-7545, PP0537-7528, PP0537-7539, PP0007-2269, PP9848-4996, PP0337-7562 and PP0237-7508 should be made available to farmers.

5. Local genotypes CA -UGCE 09-3 and CA -UGKI 09-5 and exotic genotypes PP0237-7508, PP9852-149, PP0537-7504, PP0337-7546, PP0437-7506 and PP97-7195-1 that consistently scored well in all disease traits across seasons plus exotic genotypes PBC 535, PP9852-110, PP9852-173, PP9955-15, PP0007-2247, PP0042-17, PP0237-7502, PP0537-7558 evaluated only in season 2009B are recommended for use in the improvement of disease resistance in preferred cultivars.
6. The East African Seed Company local genotype CA-EASC-09-1, though with the poorest yield, was the earliest maturing variety among all exotic and local genotypes in both seasons is a prime source of genes for early yield improvement.
7. Good general combiners such as the local parents CA -UGCE 09-3 and CA -UGKI 09-6 should be considered for integrating resistance to viral diseases and enhanced yield (number of fruits per plant).
8. The important crosses such as CA-UGCE 09-3 x CA -UGKI 09-6, CA -UGKI 09-6 x PP9852-115 and CA-UGCE 09-3 x PP0337-7562 identified for various traits in this study should be exploited by breeders through heterotic breeding to generate pure lines through transgressive segregation in later generations.

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Appendix i. Export trends of Ugandan traditional and non traditional crops between 2004 and 2009

Crops	YEAR											
	2004		2005		2006		2007		2008		2009	
	Qnty[a] (Tons)	Value US$'000	Qnty (Tons)	Value US$'000	Qnty (Tons)	Value US$'000	Qnty (Tons)	Value Us$'000	Qnty (Tons)	Value US$'000	Qnty (Tons)	Value US$'000
Traditional Exports												
Coffee	159,983	124,237	142,513	172,942	126,887	189,830	164,540	265,853	200,640	403,179	181,324	280,209
Cotton	29,293	42,758	30,403	28,821	18,480	20,474	16,230	19,571	7,960	13,214	17,888	23,186
Tea	36,874	37,258	36,532	34,274	30,584	50,873	44,015	47,629	46,022	47,222	44,446	59,761
Tobacco	27,843	40,702	23,730	31,486	15,794	26,964	26,384	66,301	29,042	66,448	32,000	57,170
Non-Traditional Exports												
Maize	90,576	17,896	92,794	21,261	115,259	24,114	101,233	23,816	66,671	18,250	94,440	29,066
Beans & other Legumes	26,233	8,968	28,332	8,693	27,087	8,162	22,532	10,099	37,211	17,630	38,140	14,720
Sesame seeds	4,283	2,788	7,412	4,779	7,568	4,547	5,945	5,447	14,154	15,884	12,107	13,369
Soya beans	468	118	574	126	3,048	609	5,798	1,331	3,250	1,536	2,630	1,076
Pepper	394	368	817	594	218	189	194	256	304	580	320	617
Vanilla	71	6,120	234	6,135	195	4,808	422	6,262	191.5	3,039	253.7	4,908
Fruits	1,297	917	3,061	1,158	7,821	1,167	7,361	1,976	3,114	5,332	3,290	932
Groundnuts	1	1	22	23	63	8	101	148	30.1	28	66.2	69
Bananas	1,792	850	2,196	806	494	127	1,151	430	396	211	695	118

Source: Uganda Bureau of Statistics (UBOS), (2009, 2010); [a]Qnty = Quantity

endix 2. Morphological descriptors used in characterization of 37 genotypes in the en house at NARL in Uganda from 2009-2010

Vegetative descriptors (15: 9 qualitative; 6 quantitative)

(NA) Nodal anthocyanin (whole plant) at plant maturity: 1 = Green 3 = Light- purple 5 = Purple 7 = Dark-Purple

(SPT) Stem pubescence type: Recorded on mature plants, at two nodes below the shoot when first fruit turning red. 0 = Absent 3 = Short 5 = Intermediate 7 = Long.

(SPD) Stem pubescence density: Recorded on mature plants, excluding the first two nodes below the shoot: 0 = Glabrous 3 = Sparse 5 = Intermediate 7 = Dense

(PH) Plant height (cm): Recorded when 50% of the plants the first fruit has began to ripen: 1 = (< 25) 2 = (25-45) 3 = (46-65) 4 = (66-85) 5 = (>85)

(PGH) Plant growth habit: Observed when 50% of the plants bear ripe fruits 3 = Prostate 5 = Intermediate (compact) 7 = Erect 9 = Other (specify)

(PCW) Plant canopy width (cm) measured immediately after first harvest, at the widest point

(SL) Stem length (cm): Height to first bifurcation. Measured immediately after first harvest

(SD) Stem diameter (cm) measured in the middle part to first bifurcation (10 cm from ground), at mature stage

For descriptors 9-15: Recorded when in 50% of the plants the first fruit has begun to ripen. Average of 10 mature leaves (from the main branches of the plant)

(PBN) Primary branch numbers: Counted at plant maturity

0. **(SBN)** Secondary branch Numbers: Counted at plant maturity

1.. **(LS)** Leaf shape: 1 = Deltoid 2 = Ovate 3 = Lanceolate

2.. **(LM)** Lamina margin 1 = Entire 2 = undulate 3 = Ciliate

3. (LSF) Leaf surface 1 = smooth 2 = intermediate 3 Rough

4. **(LPT)** Leaf pubescence type: Observed on the youngest mature leaves when first fruit matures. 0 = Absent 3 = Short 5 = Intermediate 7 = Long

5. **(LP)** Leaf pupescence: Observed on the youngest mature leaves when first fruit matures : 0 = Glabrous 3 = Sparse 5 = Intermediate 7 = Dense

Inflorescence descriptors: Recorded on fully open flowers in the first fresh flowering (9: 6 qualitative; 3 quantitative)

(DFL) Days to flowering: Number of days from transplanting until 50% of plants have at least one open flower

(PP) Pedicel position: Recorded at anthesis. 3 = Pendant 5 = Intermediate 7 = Erect

(CC) Corolla colour 1 = White 2 = Light-yellow 3 = Yellow 4 - Yellow-green 5 = Purple with white base 6 = White with purple base 7 = White with purple margin 8 Purple 9 Other

(CL) Corolla length (cm): Average of 10 petals of dissected corolla

(AC) Anther colour: Observed immediately after blooming before anthesis: 1 = White 2 = Yellow 3 = Pale-blue 4 = Blue 5 = Purple 6 = Other (Specify)

(AL) Anther length (mm): Average anther length of ten representative flowers selected from different plants. Observed immediately at anthesis

(SE) Stigma exsertion in relation to anthers at full anthesis. Average of 10 stigmas from representative flowers selected from each plant per plot. 3 = Inserted 5 = Same level 7 = Exserted

(CM) Calyx margin 1 = Entire 2 = Intermediate 3 = Dentate 4 = Other (specify)

(CAC) Calyx annular constriction: At junction of calyx and pedicel. Observed at mature stage. 0 = Absent 1 = Present

Fruit descriptors: Recorded on mature fruits in the second harvest (19: 13 qualitative and 8 quantitative)

(DFR) Days to fruiting: Number of days from transplanting until 50% of the plants bear fruits of about 2 cm in length at the first and second bifurcation.

(DFM) Days to fruit maturity: Number of days from transplanting until 50% of the plants bear mature fruits at the first and second bifurcation.

(AS/S) Anthocyanin spots or stripes: Recorded just before the ripening stage. 0 Absent 1 Present

(IFC) Fruit colour at intermediate stage: Recorded on fruits just before the ripening stage. 1 White 2 Yellow 3 Green 4 Orange 5 Purple 6 Deep purple 7 Others

(IFCI) Intermediate fruit colour intensity: Recorded on fruits just before the ripening stage. 3 = Light 5 = Medium 7= Dense X= Mixture

(MFC) Fruit colour at mature stage: 1 White 2 Lemon-Yellow 3 Pale orange-Yellow 4 Orange-Yellow 5 Pale orange 6 Orange 7 Light red 8 Red 9 Dark red 10 Purple 11 Brown 12 Black 13 Others

(MFCI) Mature fruit colour intensity: Recorded on fruits at maturity. 3 = Light 5 = Medium 7= Dense X= Mixture

(FS) Fruit shape: 1 = Elongate 2 = Almost round 3 = Triangular 4 = Campanulate 5 = Blocky 6 = Others

(FL) Fruit length (cm): Average fruit length of 10 ripe fruits of the second harvest

(FW) Fruit width (cm): Measured at the widest point. Average fruit length of 10 ripe fruits of the second harvest

(FWT) Fruit weight (g). Average fruit weight of 10 ripe fruits of the second harvest

(FPL) Fruit Pedicel length (cm). Average length of 10 pedicels of the second harvest to one decimal place

(FWTH) Fruit wall thickness (mm): Average of 10 ripe fruits of the second harvest, measured at point of maximum width to one decimal Point

(FSP) Fruit shape at pedicel attachment: 1 = Acute 2 = Obtuse 3 = Truncate 4 = Cordate 5 = Lobate

(FN) Neck at base of fruit: 0 = Absent 1 = Present

(FSB) Fruit shape at blossom end: Average of 10 fruits: 1 = Pointed 2 = Blunt 3 = Sunken 4 = Sunken and Pointed 5 = Other (specify)

(FBA) Fruit blossom end appendage: 0 = Absent 1 = Present

(FXC) Fruit cross-sectional corrugation: Average of 10 fruits (1/3 from pedicel end). 3 = Slightly corrugated 5 = Intermediate 7 = Corrugated

(FS) Fruit surface: 1 = Sooth 3 = Semi-wrinkled 3 = Wrinkled

(NFP) Number of fruit per plant: Fruit harvests for the duration of the experiment 1= <20 2 = 20-50 3= >50

(NSF) Number of seeds per fruit: Averaged over 10 fruits per plot in a replication.

Seed descriptors (3: all quantitative)

(SD) Seed diameter (mm): The maximum diameter of 10 seeds to two decimal places

(SWT) 500-seed weight (g)

(FNS) Number of seeds per fruit: Average of at least 10 fruits selected from 10 random plants. 1= <20 2 = 20-50 3= >50

Appendix 3. Means for 20 quantitative characters of 37 *C. annuum* L. genotypes characterized under screen house conditions at NARL in Uganda during 2009-2010

Genotype No.[a]	DFL (days)	DFR (days)	DFM (days)	FL (cm)	FW (cm)	FPL (cm)	FWTH (cm)	300 SWT (g)	NSF (seeds)	NFP (fruits)
1	28	33	82	9.3	1.8	3.5	0.2	1.7	61	12
2	38	41	91	11.5	2.0	2.6	0.2	1.8	72	8
3	51	55	92	9.7	1.7	3.6	0.2	1.6	70	11
4	34	38	78	9.1	1.3	3.7	0.1	1.7	61	21
5	47	50	94	5.6	1.3	2.9	0.1	1.8	50	21
6	44	48	93	12.6	1.8	3.2	0.2	1.6	70	14
7	45	48	91	8.6	1.5	3.2	0.2	1.6	62	12
8	33	36	78	15.2	2.0	3.8	0.2	1.5	148	12
9	24	28	82	9.0	1.6	2.7	0.2	1.6	64	7
10	28	31	85	11.2	1.7	3.0	0.2	1.7	80	11
11	28	31	78	12.6	1.9	5.3	0.2	1.5	51	13
12	41	42	95	11.3	1.6	4.0	0.2	1.6	40	23
13	31	35	80	11.6	1.5	2.6	0.2	1.4	81	7
14	55	59	103	10.6	1.4	3.5	0.2	1.7	58	12
15	23	26	71	11.3	1.5	3.5	0.2	1.3	102	18
16	33	35	77	12.3	2.1	3.4	0.4	1.6	101	8
17	33	36	89	10.1	1.8	2.6	0.2	1.8	64	10
18	46	50	93	14.0	2.0	5.3	0.2	1.5	69	11
19	49	52	94	14.9	2.3	3.3	0.3	1.9	72	7
20	41	46	91	6.7	1.4	2.5	0.2	1.4	59	16
21	23	27	73	12.7	1.4	2.9	0.2	1.5	82	14
22	35	39	82	12.0	1.5	3.4	0.2	1.6	57	8
23	44	48	100	13.3	1.8	3.7	0.2	1.2	60	11
24	37	40	84	10.2	2.0	4.7	0.2	2.0	63	9
25	35	39	82	8.8	1.2	3.5	0.1	1.3	62	16
26	10	13	60	9.7	1.5	2.9	0.2	2.0	45	15
27	37	41	83	16.9	3.1	3.9	0.3	1.9	133	4
28	27	30	80	14.7	1.9	3.5	0.2	1.9	115	5
29	48	52	94	3.2	2.0	2.6	0.2	1.5	70	22
30	51	56	101	3.6	2.0	4.0	0.1	1.3	70	13
31	46	50	101	4.7	1.0	3.2	0.1	1.2	31	62
32	31	34	75	11.2	1.3	3.3	0.1	1.8	51	11
33	45	48	93	6.1	1.6	5.5	0.2	1.8	48	12
34	47	51	95	4.1	1.5	3.6	0.1	1.4	59	14
35	59	63	112	2.8	1.2	3.3	0.2	1.4	55	18
36	51	53	99	2.2	1.6	3.0	0.1	1.4	77	15
37	55	59	105	3.5	0.9	2.4	0.1	1.1	65	21

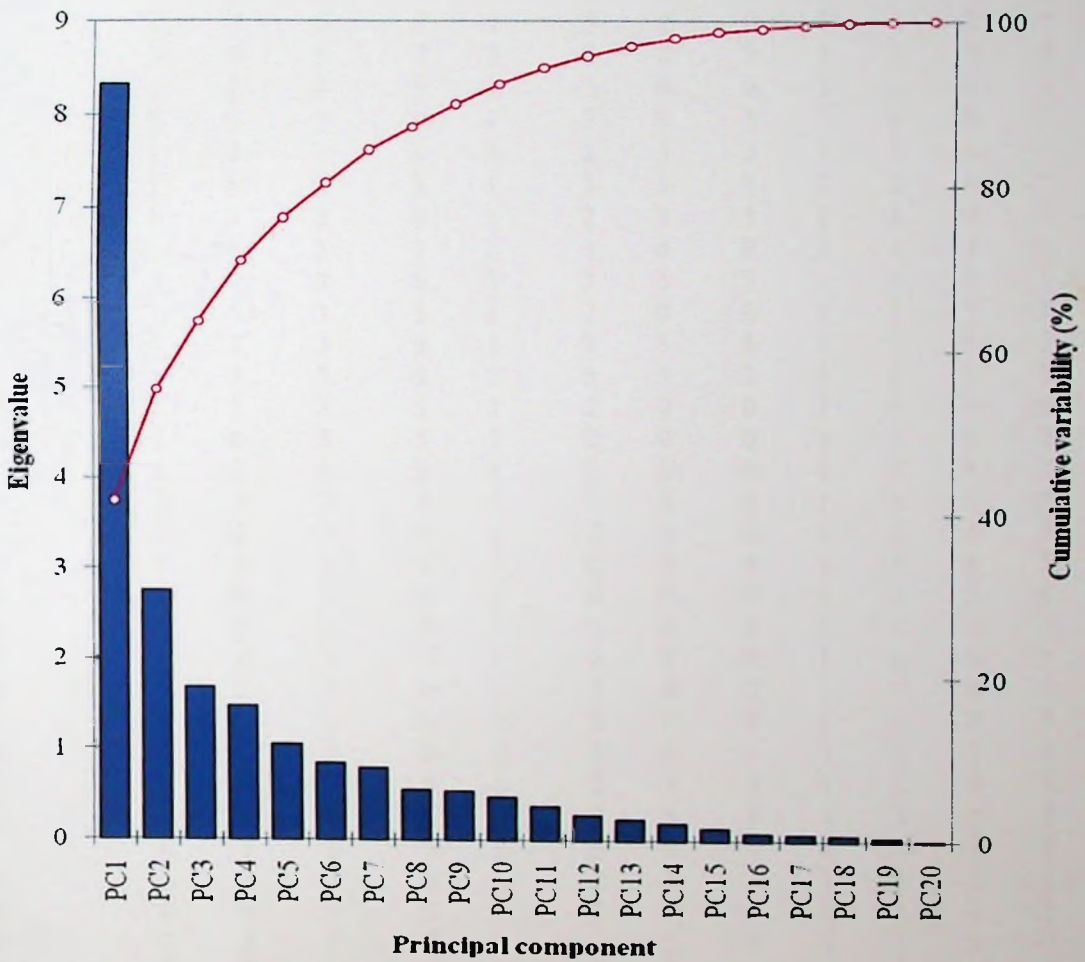
[a]Genotype numbers, see Table 1; Trait abbreviations and trait codes, see Appendix 2

Appendix 3 continued

Genotype No.[a]	SHT (cm)	SBN	PBN	PWD (cm)	PHT (cm)	SD (cm)	FRTWT (g)	CL (cm)	AL (cm)	STD (cm)
1	26.0	8	2	77.7	68.2	0.4	7.8	1.3	0.3	1.0
2	17.3	4	2	68.4	72.4	0.4	10.8	1.2	0.3	1.0
3	21.5	6	2	66.4	86.4	0.3	7.4	1.4	0.3	1.3
4	31.1	10	2	87.1	83.8	0.4	3.0	1.1	0.3	1.1
5	33.8	10	2	65.5	76.4	0.4	2.8	1.2	0.3	1.2
6	36.8	5	2	79.0	92.4	0.4	9.6	1.2	0.3	1.5
7	27.3	6	3	77.5	97.4	0.4	8.3	0.8	0.3	1.1
8	23.3	6	2	66.7	64.9	0.4	22.9	1.7	0.4	1.0
9	21.1	4	2	69.5	77.5	0.4	6.5	1.3	0.3	1.0
10	21.0	5	2	63.5	75.5	0.3	9.0	0.5	0.3	0.9
11	26.8	8	2	62.1	62.1	0.4	5.9	0.6	0.4	0.9
12	37.7	7	3	68.7	70.1	0.4	6.6	1.2	0.2	1.1
13	21.4	4	2	71.4	82.3	0.4	7.9	1.0	0.3	1.0
14	16.6	5	2	70.0	85.5	0.4	7.2	1.3	0.3	1.2
15	23.0	7	2	49.6	48.9	0.4	8.5	1.1	0.3	0.8
16	19.9	4	2	72.4	60.9	0.4	18.3	1.6	0.4	1.1
17	24.2	4	2	83.4	81.1	0.4	7.9	1.0	0.3	1.3
18	29.4	5	2	72.8	94.6	0.4	15.0	1.5	0.3	1.2
19	24.2	4	2	62.0	77.4	0.4	20.9	1.0	0.2	1.1
20	27.4	5	2	72.6	90.2	0.4	3.7	1.1	0.2	1.0
21	25.0	6	2	65.8	68.7	0.4	9.2	1.0	0.3	0.8
22	25.3	4	2	58.4	59.1	0.4	9.8	0.8	0.3	0.9
23	23.9	5	2	58.2	72.2	0.4	11.8	1.6	0.3	1.3
24	31.8	8	2	81.7	83.9	0.4	12.7	1.1	0.3	1.2
25	34.6	7	2	90.4	76.6	0.3	4.9	1.2	0.4	1.1
26	22.9	7	2	56.4	66.3	0.4	4.6	1.3	0.3	1.2
27	23.8	5	2	55.8	62.4	0.4	44.4	1.1	0.4	1.0
28	20.0	5	2	41.8	57.9	0.5	12.5	1.2	0.4	0.7
29	27.1	9	2	79.1	93.8	0.3	2.7	1.6	0.3	1.3
30	54.2	8	2	86.9	105.2	0.3	3.4	1.3	0.3	1.3
31	36.9	11	2	85.2	90.4	0.4	1.5	1.1	0.3	1.3
32	8.2	7	2	56.2	55.3	0.5	4.0	1.4	0.3	0.8
33	24.2	8	2	82.3	110.1	0.4	5.4	1.2	0.3	1.1
34	46.1	10	2	118.7	123.6	0.4	3.1	0.8	0.2	1.5
35	50.9	7	2	93.5	136.4	0.4	1.3	0.8	0.3	1.4
36	24.5	10	2	84.3	89.7	0.3	2.8	1.6	0.3	1.3
37	45.3	9	3	99.3	124.8	0.4	1.3	1.8	0.3	1.4

[a]Genotype numbers, see Table 1; Trait abbreviations and trait codes, see appendix 2

Appendix 4. A scree test of a plot of eigenvalues associated with each component showing breaks between the eigenvalues of one component and another



Appendix 5. Scores of 28 qualitative characters of 37 C. annuum L. genotypes characterized under screen house conditions at NARLin Uganda during 2009-2010

Genotype No.[a]	NA	SPT	SPD	PGH	LS	LSH	LP	LPT	LM	CC	AC	SE	PP	STC
31	1	3	3	5	1	3	3	3	1	1	4	7	7	1
9	1	3	3	5	1	3	3	3	1	1	3	7	3	1
17	1	3	3	5	1	3	0	0	1	1	4	5	3	1
6	1	7	5	7	1	3	0	0	1	1	3	7	3	1
30	5	3	3	7	3	3	3	3	1	1	5	7	3	1
33	3	3	3	5	1	2	0	0	1	1	4	7	3	1
29	3	7	7	5	1	3	5	5	1	1	5	7	7	1
5	1	3	3	5	1	2	3	3	1	1	4	7	7	1
2	1	5	3	3	1	3	3	3	1	1	4	7	3	1
13	1	3	3	3	1	2	3	3	1	1	4	7	3	1
18	1	0	3	7	2	3	0	0	1	1	4	5	3	1
28	5	0	3	5	3	3	3	3	1	1	5	5	7	1
1	1	3	3	5	1	2	0	0	1	1	3	7	3	1
23	3	3	3	5	1	2	3	3	1	1	5	7	3	1
12	1	3	3	5	3	3	3	3	1	1	5	5	3	1
8	1	3	3	5	1	2	0	0	1	1	5	5	3	5
26	1	0	3	5	1	2	0	0	1	1	4	7	3	1
15	1	3	3	5	1	3	0	0	1	1	4	7	3	1
32	1	3	3	5	2	2	0	0	1	1	5	7	3	1
19	1	0	3	5	1	2	0	0	1	1	4	7	3	1
7	1	3	3	5	3	2	0	0	1	1	4	7	3	5
16	1	0	3	3	1	3	0	0	1	1	5	5	3	1
35	1	7	7	7	1	3	5	5	1	1	4	7	3	1
21	1	0	3	7	1	3	0	0	1	1	5	7	3	1
34	1	3	3	5	1	3	0	0	1	1	4	7	3	1
3	1	3	3	5	1	2	0	0	1	1	4	7	3	1
20	1	5	5	5	2	3	0	0	1	1	5	7	3	1
27	1	0	3	5	1	2	3	3	1	1	4	7	3	1
22	1	3	3	5	1	2	3	3	1	1	5	7	3	1
4	1	3	3	5	2	3	0	0	1	1	4	7	7	1
24	5	7	5	5	3	2	3	3	1	1	5	3	3	1
11	1	0	3	5	1	2	5	5	1	1	4	7	3	1
10	1	3	3	5	1	2	5	5	1	1	3	7	3	1
25	1	7	7	5	1	3	3	3	1	1	5	7	7	1
14	1	3	3	5	1	3	3	3	1	1	4	7	3	1
36	3	5	5	5	1	3	5	5	1	1	4	7	3	1
37	1	7	7	5	1	3	5	5	1	1	4	7	3	1

[a]Genotype numbers, see Table 1; Trait abbreviations and trait codes, see Appendix 2

Appendix 5 continued

Genotype No.[a]	CM	CAC	AS/S	IFC	IFCI	MFC	MFCI	FS	FSP	FN	FSB	FBA	FXC	FS
31	3	0	0	3	7	5	5	1	2	0	1	0	0	1
9	3	1	0	3	3	5	7	1	2	0	1	0	0	1
17	2	1	0	3	7	5	7	1	2	0	1	0	0	1
6	2	1	0	3	5	5	7	1	2	0	1	0	0	3
30	1	0	0	3	7	5	7	3	2	0	2	0	0	1
33	3	1	0	3	5	5	5	1	2	0	1	0	0	5
29	1	1	1	3	7	3	5	3	3	0	1	0	0	1
5	3	0	0	3	5	5	5	1	2	0	1	0	0	5
2	2	1	0	3	5	5	5	1	2	0	1	0	0	3
13	2	1	0	3	7	5	7	1	2	0	1	0	0	3
18	3	0	1	3	3	5	5	1	1	0	1	0	0	3
28	2	1	0	3	7	5	7	1	2	0	1	0	0	5
1	3	1	0	3	5	5	7	1	2	0	1	0	0	3
23	3	0	0	3	5	5	5	1	1	0	1	0	0	5
12	3	1	0	3	7	5	7	1	1	0	1	0	0	1
8	3	1	0	3	3	5	5	1	2	0	1	0	0	5
26	3	0	0	3	5	5	7	1	2	0	1	0	0	5
15	3	0	0	3	3	5	7	1	1	0	1	0	0	5
32	3	0	0	3	7	5	7	1	2	0	1	0	0	5
19	1	1	0	3	5	5	5	1	2	0	1	0	0	3
7	2	0	0	3	5	5	5	1	2	0	1	0	0	1
16	2	1	0	3	5	5	5	1	2	0	1	0	0	1
35	2	1	0	3	3	3	5	3	2	0	1	0	0	1
21	2	0	0	3	7	5	5	1	2	0	1	0	0	5
34	1	1	0	3	7	5	7	1	2	0	2	0	0	1
3	1	1	0	3	5	5	7	1	2	0	1	0	0	1
20	2	1	0	3	5	5	7	1	2	0	1	0	0	1
27	3	1	0	3	5	5	5	1	3	0	1	0	0	1
22	2	0	0	3	5	5	5	1	2	0	1	0	0	3
4	2	0	0	3	7	5	7	1	1	0	1	0	0	5
24	1	0	0	3	7	5	7	1	2	0	1	0	0	1
11	3	1	0	3	5	5	7	1	1	0	1	0	0	5
10	3	0	0	3	3	5	5	1	2	0	1	0	0	3
25	1	0	0	3	3	5	5	1	1	0	1	0	0	5
14	2	0	0	3	5	5	5	1	1	0	1	0	0	5
36	1	1	1	3	5	5	5	3	3	0	1	0	0	5
37	2	0	1	3	5	5	5	1	1	0	1	0	0	5

[a]Genotype numbers, see Table 1; Trait abbreviations and trait codes, see Appendix 2

Appendix 6. Analysis of variance for 3 quantitative growth traits in twenty-five genotypes evaluated during season 2009A at Namulonge, Uganda

Characters	Source of Variation – df			Mean	SEM±
	Replication (R)-1	Genotypes (G)-24	Residual (RxG)-24		
	Mean squares				
Days to 50% fruit maturity	32.000*	208.042***	7.208	77.0	1.898
Plant height (cm)	0.110ns	91.820***	11.060	25.6	2.35
Plant width (cm)	132.130*	154.700***	29.240	31.6	3.82

[ns]non significant; ** highly significant ($P \leq 0.01$); *** highly significant ($P \leq 0.001$)

Appendix 7. Analysis of variance for 10 quantitative yield traits in twenty-five genotypes evaluated during season 2009A at Namulonge, Uganda

Characters	Source of Variation – df			Mean	SEM±
	Replication (R)-1	Genotypes (G)-24	Residual (RxG)-24		
	Mean squares				
200 seed weight (g)	0.000003ns	0.053***	0.007	0.9	0.06
Average fruit weight	0.520ns	22.072***	0.245	4.4	0.35
Fruit length (cm)	0.017ns	18.279***	0.319	7.7	0.39
Fruit seed yield (t/ha)	0.0017ns	0.221***	0.055	0.5	0.24
Fruit width (cm)	0.201***	0.226***	0.011	1.2	5.49
Number of fruit per plant	0.320ns	687.540***	63.410	38.0	5.63
Non marketable fruits (%)	1.092ns	9.234***	1.988	59.0	5.63
Number of seeds per fruit	4.500ns	343.800ns	361.100	81.0	13.44
Total fruit yield (t/ha)	1.092ns	9.234***	1.988	4.9	0.99
Total marketable fruit yield (t/ha)	0.039ns	4.273***	0.781	2.8	0.63

ns non significant; ** highly significant ($P \leq 0.01$); *** highly significant ($P \leq 0.001$).

Appendix 8. Analysis of variance for 4 growth quantitative traits in 35 genotypes evaluated during season 2009B[a] at Namulonge, Uganda

Characters	Source of Variation - df			Mean	SEM±
	Replication (R)-1	Genotypes (G)-25	Residual (RxG)-25		
		Mean squares			
Days to 50% flowering	0.57[ns]	380.48***	28.10	41.5	5.301
Days to 50% fruit maturity	0.000[ns]	284.37***	36.82	84.7	6.068
Plant height (cm)	0.92[ns]	127.83***	14.33	39.3	3.786
Plant width (cm)	2.79[ns]	179.09***	17.39	41.3	4.170

[a]Trial was conducted from September 28th, 2009 to May 11th 2010.
[ns]non significant (p>0.05); *** highly significant ($P \leq 0.001$).

Appendix 9. Analysis of variance for 10 yield quantitative traits in 35 genotypes evaluated during season 2009B[a] at Namulonge, Uganda

Characters	Source of Variation - df			Mean	SEM±
	Replication (R)-1	Genotypes (G)-34	Residual (RxG)-33		
	Mean squares				
200 seed weight (g)	0.000034^{ns}	0.026**	0.009	0.7	0.095
Average fruit weight	0.201^{ns}	24.104***	2.484	6.4	1.576
Fruit length (cm)	0.037^{ns}	26.467***	0.920	9.6	0.959
Fruit seed yield (t/ha)	0.050^{ns}	0.043**	0.018[b]	0.4	0.094
Fruit width (cm)	0.00024^{ns}	0.207***	0.021	1.4	0.146
Number of fruit per plant	280.00^{ns}	348.63***	95.850[b]	34.4	6.920
Non marketable fruits (%)	5.45^{ns}	397.65***	60.150	73.1	7.756
Number of seeds per fruit	51.43^{ns}	600.63***	91.190	81.5	6.750
Total fruit yield (t/ha)	32.777*	37.239***	6.513[b]	7.7	1.805
Total marketable fruit yield (t/ha)	0.024^{ns}	1.806**	0.772[b]	1.7	0.621

[a]Trial was conducted from September 28th, 2009 to May 11th 2010.
[b]df = 34 because one local variety (8) never gave any yield in replication 2 and thus was given 0 score for these parameters and was missing for the rest.
*Significant $P \leq 0.05$ ** highly significant ($P \leq 0.01$); *** highly significant ($P \leq 0.001$).
^{ns}non significant.

Appendix 10. Disease rating scales used in scoring observed diseases in field trials established during season 2009A, 2009B and evaluation of F_1s and their parents (2010) at Namulonge, Uganda

1. Cercospora leaf spot: No disease symptoms (0); 10% of the canopy showing disease symptoms (1); 10-25% of the canopy showing disease symptoms (3); 25-50% of the canopy showing disease symptoms (5); 50-75% of the canopy showing disease symptoms (7); >75% of the canopy showing disease symptoms (9) (Reference: Galanhe *et al.*, 2004).

2. Virus disease: health, asymptomatic plant (0); mild mosaic, mottle or chlorosis on leaves (1); moderate chlorosis, mottle or mosaic without significant leaf distortion (2); Score 1 or 2 plus leaf malformation(3); Severe chlorosis, mottle or mosaic plus stunting or dwarfing of the whole plant (4); Score 4 plus leaf drop, and dying (5) (Reference: Modified after Yayeh, 1994).

3. *Phytophthora* blight: Symptomlesss/healthy plant (0); Leaf yellowing and no stem necrosis (1); Leaf yellowing, small lesions on lower leaves/minor stem necrosis (2); Lesions on lower leaves and middle leaves; leaf drop and shallow stem necrosis (3); Lesions on most leaves, extensive leaf drop/deep stem lesions (4); Extensive leaf and stem necrosis/dead plant (5) (Reference: Modified AVRDC, 2004).

4. Anthracnose (*Colletotrichum* spp): Healthy (0); 1-5% of mature leaves with necrotic and chlorotic symptoms (1); 6–15% of mature leaves with necrotic and chlorotic symptoms (2); 16–50% of young shoots and stem with water soaked lesions and minor shoot die back (3); 51–95%water-soaked lesions with abundant mycelia growth and fructification, and extensive shoot dieback (4); Dead plant (5) (Reference: Siddiqui *et al.*, 2008).

5. Wilt disease: 0 % wilt infection (0); 1 – 10 % wilt infection (1); 11-20 % wilt infection (2); 21 - 30 % wilt infection (3); 31 - 50 % wilt infection (4); 51 - 100 % wilt infection (5) (Reference: Modified Bayoumi and El-Bramawy, 2007).

Appendix 11. Analysis of variance for 5 observed field diseases during season 2009A pepper evaluation at Namulonge, Uganda

Parameter	Source of Variation – df			Mean [a]	SEM±
	Replication (R)-1	Genotypes (G)-24	Residual (RxG)-24		
	Mean squares				
Anthracnose incidence (%)	0.025[ns]	21.867***	3.108	4.5 (31.1)	1.763
Anthracnose severity index (%)	0.930[ns]	19.865***	1.817	3.8(23.9)	1.348
Cercospora leaf spot incidence (%)	1.283[ns]	1.828*	0.910	9.4(88.4)	0.954
Cercospora leaf spot severity index (%)	2.500[ns]	6.192***	1.352	6.0(38.9)	1.163
P. blight incidence (%)	3.107[ns]	10.975***	1.917	2.9(13.7)	1.385
P. blight severity index (%)	11.466*	7.178**	2.044	2.5(9.8)	1.430
Virus incidence (%)	1.367[ns]	0.7012[ns]	0.577	9.6(93.0)	0.760
Virus severity index (%)	0.029[ns]	1.998*	0.906	6.4(41.8)	0.952
Wilt incidence (%)	1.737[ns]	2.345**	0.719	1.7(3.2)	0.848

[a]Square root transformed values, original values in parenthesis

[ns]not significant; * significant ($P < 0.05$); ** highly significant ($P < 0.01$); *** highly significant ($P < 0.001$)

Appendix 12. Analysis of variance for 5 observed field diseases during season 2009B pepper evaluation trial at Namulonge, Uganda

Parameter	Source of Variation – df			Mean[a]	SEM±
	Replication (R)-1	Genotypes (G)-34	Residual (RxG)-34		
		Mean squares			
Anthracnose incidence (%)	0.012^{ns}	16.933***	4.819	4.8 (32.2)	2.195
Anthracnose severity index (%)	3.896^{ns}	9.678***	1.817	3.5 (16.6)	1.348
Cercospora leaf spot incidence (%)	0.232^{ns}	0.824***	0.168	9.7 (93.1)	0.409
Cercospora leaf spot severity index (%)	6.947*	6.887***	1.142	7.5 (58.8)	1.069
P. blight incidence (%)	4.613^{ns}	5.484^{ns}	3.176	2.9 (11.6)	1.782
P. blight severity index (%)	2.769^{ns}	4.550^{ns}	3.221	2.8 (10.7)	1.795
Virus incidence (%)	0.019^{ns}	5.389***	0.942	8.5 (74.4)	0.971
Virus severity index (%)	1.172^{ns}	3.639***	0.564	5.2 (27.7)	0.751
Wilt incidence (%)	0.006^{ns}	2.539**	1.026	2.1 (5.1)	1.013

[a]Square root transformed values, original values in parenthesis

^{ns}not significant; * significant ($P \leq 0.05$); ** highly significant ($P \leq 0.01$); *** highly significant ($P \leq 0.001$)

Appendix 13. Absorbance values from the detection of 9 viruses by 3 types of Enzyme linked immunosorbent assay (ELISA) in several samples from 16 genotypes of pepper picked randomly from season 2009B evaluation trial at Namulonge, Uganda

		Virus Absorbance Values (405 nm)								
Genotype No.	Sample	GPV	TSWV	ChiVMV	TMV	PVY	PMoV	PVMV	AMV	CMV
18	S1[b]	2.39	1.04	2.52	0.44	2.53	2.48	1.49	0.87	2.48
18	S2	2.25	0.94	2.58	1.28	2.50	2.32	2.02	0.72	2.52
18	S3	2.19	1.12	2.66	1.28	2.63	1.50	2.17	0.93	2.60
18	S4	1.85	0.60	2.60	0.66	2.56	2.16	0.74	0.60	2.61
18	S5	2.42	0.52	2.37	0.93	2.48	1.40	0.65	0.50	2.05
2	S6	2.13	0.56	2.42	0.63	2.53	2.27	0.82	0.47	2.39
2	S7	2.04	0.83	1.95	0.76	2.56	2.43	1.06	0.74	1.80
2	S8	2.47	0.55	2.56	0.78	2.51	1.77	0.89	0.25	2.17
2	S9	2.41	0.85	2.53	0.75	2.58	2.52	1.18	0.41	2.68
30	S10	2.09	0.77	2.54	1.31	2.62	2.59	1.74	0.47	2.42
30	S11	2.38	0.90	2.39	0.45	2.42	2.40	1.78	0.94	2.40
30	S12	2.39	0.61	2.43	0.82	2.36	1.07	0.84	0.48	1.57
30	S13	2.28	0.84	2.51	1.30	2.52	2.09	2.03	0.85	2.60
30	S14	1.86	0.67	2.55	0.85	2.47	1.86	0.80	0.55	2.22
29	S15	2.48	0.80	2.65	1.09	2.53	2.22	1.94	0.71	2.41
29	S16	2.51	0.69	2.37	0.95	2.46	2.40	1.58	0.74	2.31
29	S17	2.24	0.52	2.41	1.02	2.52	2.30	2.03	0.75	2.40
29	S18	2.83	0.66	2.48	0.81	2.43	2.25	1.49	0.24	2.21
33	S19	2.01	0.76	2.40	0.56	2.41	1.22	0.69	0.47	1.67
33	S20	2.27	0.57	2.54	0.92	2.58	2.07	1.68	0.70	2.47
33	S21	2.52	0.80	2.52	0.58	2.46	2.08	1.78	0.87	2.50
33	S22	1.93	0.76	2.49	0.42	2.42	1.67	1.49	0.73	2.37
33	S23	2.26	0.81	2.41	0.43	2.45	2.38	1.70	0.27	2.56
1	S24	2.80	0.44	2.46	0.77	2.41	0.96	0.52	0.41	2.53
1	S25	2.41	0.59	2.45	0.63	2.46	1.20	0.73	0.43	2.51
1	S26	1.92	0.57	2.48	0.86	2.44	1.32	1.08	0.57	2.47
1	S27	2.02	0.62	1.97	0.56	2.44	2.22	1.14	0.60	2.18
1	S28	1.98	0.54	2.52	0.78	2.48	2.37	1.64	0.33	2.31
35	S29	2.35	0.54	1.59	0.59	2.33	1.05	1.01	0.57	2.05
35	S30	1.99	0.66	2.51	0.75	2.48	2.03	1.21	0.79	2.62
35	S31	2.10	0.63	2.50	0.96	2.51	1.56	1.46	0.68	2.44
35	S32	2.26	1.10	2.55	1.18	2.52	2.25	1.82	0.90	2.33
35	S33	1.99	0.74	2.54	0.53	2.53	1.92	1.91	0.35	2.48
3	S34	2.06	0.71	2.56	0.92	2.54	2.08	1.70	0.70	2.39
3	S35	2.00	0.94	2.43	0.81	2.53	2.37	1.80	0.85	2.40
3	S36	2.01	1.08	2.51	0.85	2.51	2.38	1.84	0.85	2.49
3	S37	2.09	0.49	2.49	0.46	2.54	2.20	0.74	0.50	2.50
9	S38	1.95	0.58	2.47	0.91	2.53	2.30	1.18	0.56	2.43
9	S39	2.13	0.64	2.50	0.73	2.54	1.19	1.00	0.23	2.18
9	S40	2.50	0.93	2.57	1.29	2.57	2.29	1.87	0.46	2.55
Control		**0.58**	**0.28**	**0.69**	**0.37**	**0.75**	**0.61**	**0.53**	**0.26**	**0.60**

[a]Genotype numbers, see Table 1; Sample considered positive when absorbance value is at least 3x average absorbance value of the control; [b]S = Symptomatic sample.

Appendix 13 continued

Genotype No.[a]	Sample	Virus Absorbance Values (405 nm)							
		GPV	TSWV	ChiVMV	TMV	PVY	PMoV	PVMV	AMV
9	S41[b]	2.33	1.02	2.55	1.30	2.49	2.44	1.85	1.02
9	S42	2.31	0.86	2.48	0.49	2.48	2.43	1.96	0.80
28	S43	1.94	0.45	2.74	0.42	2.56	1.52	1.36	0.61
28	S44	2.16	0.70	2.66	1.12	2.54	2.17	2.11	0.22
28	S45	2.20	0.52	2.49	0.75	2.34	0.8	0.82	0.5
28	S46	1.97	0.39	2.35	0.69	2.46	1.34	0.77	0.5
28	S47	2.21	0.74	2.42	1.00	2.41	1.26	1.83	0.77
32	S48	2.19	0.45	2.08	0.81	2.52	2.35	1.34	0.58
32	S49	2.29	0.60	2.49	1.07	2.56	1.83	1.96	0.8
32	S50	2.16	0.79	2.56	1.18	2.49	1.58	2.09	0.28
32	S51	2.80	0.56	2.56	0.81	2.51	1.56	0.78	0.54
32	S52	2.14	0.47	2.48	0.40	2.46	1.43	1.2	0.63
13	S53	2.85	0.71	2.51	0.94	2.53	1.36	1.3	0.84
13	S54	1.87	0.63	2.59	0.50	2.56	1.64	1.85	0.75
13	S55	2.16	0.72	2.47	0.91	2.52	2.51	1.52	0.64
13	S56	2.18	0.64	2.46	0.97	2.48	1.43	1.63	0.64
13	S57	1.84	0.87	2.40	0.98	2.39	1.01	1.06	0.5
5	S58	1.84	1.02	2.48	1.13	2.48	1.78	1.84	1.05
5	S59	1.58	1.3	2.57	1.25	2.58	1.49	2.15	0.91
5	S60	1.8	1.26	2.57	1.14	2.56	1.81	1.67	0.77
5	S61	1.57	0.72	2.58	0.98	2.55	1.42	1.86	0.56
5	S62	1.83	0.85	2.48	1.12	2.44	2.13	1.94	0.87
27	SL1[c]	1.57	0.93	2.17	1.12	2.28	1.6	1.63	0.79
27	SL2	1.75	0.9	2.48	1.14	2.46	1.86	1.84	0.89
12	S63	1.76	0.87	2.57	1.14	2.59	2.33	2.12	0.71
4	SL3	1.65	1.32	2.5	1.35	2.55	1.27	1.97	1.03
4	S64	1.72	0.67	2.28	1.23	2.32	2.16	2.01	0.94
8	SL4	2.62	1.13	2.32	0.96	2.33	1.33	1.92	0.87
8	SL5	2.41	1.25	2.53	0.99	2.52	1.26	2.22	0.85
17	S65	1.64	0.85	2.59	1.26	2.51	1.79	1.77	0.82
17	S66	1.77	1.18	2.54	1.1	2.5	2.2	2.02	0.77
1	SL6	1.81	1.21	2.46	1.19	2.5	1.03	1.76	0.79
33	SL7	2.08	1.02	2.45	0.81	2.38	1.42	2.05	0.92
29	SL8	1.97	0.84	2.41	0.91	2.45	1.49	2.06	0.99
34	SL9	2.26	1.67	2.47	1.17	2.52	2.23	2.32	0.98
Control	**0.58**	**0.28**	**0.69**	**0.37**	**0.75**	**0.61**	**0.53**	**0.26**	**0.60**

[a]Genotype numbers, see Table 1; Sample considered positive when absorbance value is at least 3x average absorbance value of the control. [a]S = Symptomatic sample; [b]SL= Symptomless sample

Appendix 14. Analysis of variance for 13 quantitative traits scored in 12 F_1 Progeny with their 6 parental lines during 1 season evaluation (May-October 2010) at Namulonge, Uganda

Characters	Source of Variation - df			Mean	SEM±
	Replication (R)-1	Genotypes (G)-17	Residual (RxG)-17		
	Mean squares				
Days to Flowering	143.430**	181.660***	17.110	54.58	2.93
Days to Fruit maturity	6.710^{ns}	224.880***	23.840	106.93	3.45
Fruit length (cm)	1.044^{ns}	15.250***	0.255	6.04	0.36
Fruit width (cm)	0.070^{ns}	0.086^{ns}	0.052	1.34	0.16
Number of fruit per plant	1.730^{ns}	629.870***	52.980	28.10	5.15
Number of seeds per fruit	44.020^{ns}	656.170***	14.250	74.94	2.67
Primary branch numbers	6.181**	6.215***	0.650	8.62	0.57
Pedicel length	0.004^{ns}	0.461***	0.038	2.84	0.14
Plant height (cm)	3.950^{ns}	56.470*	18.700	36.28	3.06
Plant width (cm)	5.220^{ns}	102.310**	27.110	37.61	3.68
Secondary branch numbers	48.225***	25.277***	2.672	18.07	1.16
Stem diameter	0.018^{ns}	0.025*	0.008	0.78	0.06
Stem height	6.596^{ns}	13.890^{ns}	6.794	18.12	1.84

^{ns} non significant; ** highly significant ($P \leq 0.01$); *** highly significant ($P \leq 0.001$).

Appendix 15. Analysis of variance for 4 disease data scored in 13 F1 Progeny with their 6 parental lines during 1 season evaluation (May-October 2010) at Namulonge, Uganda

Characters	Source of Variation – df			Mean	SEM±
	Replication (R) -1	Genotypes (G)-18	Residual (RxG) -18		
		Mean squares			
Virus incidence (%)	176.90^{ns}	1325.1**	322.70	82.7	12.7
Cercospora leafspot incidence (%)	0.98^{ns}	194.8**	47.07	95.9	4.85
Wilt incidence (%)	86.20^{ns}	668.5^{ns}	403.00	16.5	10.58
Wilt incidence (%)^{T}	0.064^{ns}	10.1^{ns}	6.10	3.4	1.47
Bacterial leafspot incidence (%)	3.60^{ns}	1254.6***	223.90	31.3	14.20
Bacterial leafspot incidence (%)[a]	1.38^{ns}	18.6**	4.30	5.9	1.75

[a]Square root transformed ($\sqrt{X + 1}$)

^{ns}non significant; ** highly significant ($P \leq 0.01$); *** highly significant ($P \leq 0.001$).

Appendix 16. Monthly weather data for the time hot pepper field trials were conducted at Namulonge, Uganda (2009 -2010)

	2009A[a]				2009B[b]			
Month	Rainfall (mm)	Min temp. °C	Max temp. °C	Mean temp. °C	Rainfall (mm)	Min temp. °C	Max temp. °C	Mean temp. °C
Jan	76.2	16.8	30.0	23.4	11.8	16.8	30.6	23.7
Feb	89.3	16.9	29.7	23.3	164.8	17.0	28.4	22.7
Mar	29.0	16.5	30.2	23.4	153.8	16.9	29.7	23.3
Apr	134.4	16.6	28.6	22.6	196.7	16.6	28.6	22.6
May	45.3	16.6	29.1	22.9	201.8	16.6	28.3	22.4
Jun	61.3	16.5	28.8	22.6	29.9	17.0	29.2	23.1
Jul	19.7	16.5	28.4	22.5	3.8	16.7	28.6	22.7
Aug	112.1	16.2	28.2	22.2	72.9	16.3	29.0	22.6
Sep	62.2	16.6	29.5	23.1	89.4	16.7	29.0	22.9
Oct	189.5	16.9	29.0	23.0	150.1	16.5	29.0	22.8
Nov	112.6	16.7	28.9	22.8	96.4	16.6	29.4	23.0
Dec	70.9	16.2	28.9	22.6	67.2	16.1	29.2	22.7

Source:Meteorological unit, National Crops Resources Research Institute, Namulonge
[a]Evaluated from June 22nd 2009 and terminated on November 26th, 2009.
[b]Evaluated December 1st, 2009 up to May 11th, 2010.