EVALUATION OF NEW SOYBEAN VARIETIES FOR MARKET TRAITS AND ADAPTATION IN UGANDA

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EVALUATION OF NEW SOYBEAN VARIETIES FOR MARKET TRAITS AND ADAPTATION IN UGANDA

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BSc. Agric (Hons)

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A thesis submitted to the School of Agricultural Sciences in partial fulfillment of the requirements for the degree of Master of Science in Crop science of Makerere University, Kampala

2012

DECLARATION

This thesis is my original work and has not been presented for a degree in any other university.

Signed……………………………. **Date**……………………….

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This thesis has been submitted with our approval as the University supervisors

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DEDICATION

To all farmers who operate small farms under heterogeneous and unfavorable conditions and who have not yet tested the fruits of advances in Agricultural technologies

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ABSTRACT

This study was carried out to identify superior soybeans genotypes that are adapted to different farming environments in Uganda and most desired by farmers and processors through Participatory Crop Improvement approach. The field experiments were set up on-farm and on-station in the 2008 – 2009 cropping seasons. Researcher designed but farmer managed trials were set up in districts of Mayuge, Pallisa, Lira, Apac, Masindi, Hoima and Kamwenge, and run for three consecutive cropping seasons. Several univariate and multivariate methods were used to analyze qualitative (farmer and processor preference) and quantitative (yield) data. Preference scores of 82 farmers were recorded at pre and post harvest stages. Soybean genotype stability studies were conducted at five locations and analyzed with AMMI. Preference for new soybean genotypes varied from farmer to farmer however, genotypes DXTPYT06A8.11, DXTPROGENIES4.17-4, MAKSOY1N, DXTPYT06A7.10 and DXTBLP(SRB)12.4 were generally acceptable because of being early maturing. Data from on-farm trials also showed that 60% of the most farmer preferred new soybean genotypes were not the highest yielding genotypes. A case in point is genotypes DXTPROGENIES4.7, BSPS17B, BSPS48A and BSPS85 which were found to have yielded highest but were not selected because they were late maturing. Processors generally preferred genotypes DXTSPS4.19, NGDT8.10-10 and DXTPYT06A4.22 for their big seed size and clear/white hilum colour. Genotype DXTPROGENIES4.17-4 scored well for both farmers and processors and may thus be successfully grown and marketed. With AMMI analysis, genotypes BSPS48A, DXTPROGENIES4.7, DXTPYT06A8.3, NGDT8.10-10, DUIKER and DXTPROGENIES4.17-4 were identified as most stable across the five locations. Similarly, genotypes NAM11XGCBLP11.3, BSPS43, NAM11XGCBLP20.2 and BSPS48A were tolerant to soybean rust. Therefore involvement of end-users in the development of new soybean varieties helped in the identification of attributes valued by end-users but unknown to breeders.

CHAPTER ONE

INTRODUCTION

1.1 Origin of soybean and its distribution

Soybean (*Glycine max* [L] Merrill) is a legume that grows in tropical, subtropical and temperate climates (IITA, 2009). Soybean is thought to have been derived from *G. ussuriensis* Regel & Maack, a slender, prostrate, twining legume, which is found throughout eastern Asia (Cheng, 1963). *G. gracilis* Skvortzor is considered an intermediate semi-cultivated species between the wild *G. ussuriensis* and *G. max*. Soybean has 20 chromosomes pairs (2n = 40) and is a self-fertile species with less than 1% out-crossing. Soybean was domesticated in the 11th century BC around North-East of China and is believed to have been introduced to Africa in the 19th Century by Chinese traders along the East coast of Africa (IITA, 2009).

According to FAO, 2010 the world's leading soybean producing country is USA which produces about 34% of the world soybean. Brazil is the second with 26% of soybean produced while Argentina is third with 20 %. China produces 6%, India, 5%, Paraguay 3%, Canada 2% while the remaining countries account for 4% of soybean. In Africa, average soybean production is 1.46 million metric tons annually representing 0.6% of the world production. The three leading African countries in soybean production are South Africa (566,000 tons), Nigeria (393,860 tons) and Uganda (175,000 tons) (FAO, 2010).

1.2 Importance of soybeans

Soybean is a multipurpose crop used for human food, animal feed and industrial uses (Myaka *et al*., 2005). Soybean is a major source of protein and it contains significant amounts of all the essential amino acids for the human body. It has an average protein content of 40% and oil content of 20%, which is cholesterol-free (Anon, 2004; IITA, 2009) making it a good alternative to meat, poultry and sea food (Henkel, 2000; Foster, 2006). Soybean oil contains linolenic acid (omega-3 fatty acid), which has been shown to reduce the risk of heart disease (Sacks *et al*., 2006). The major unsaturated fatty acids in soybean oil are 7.5% linolenic acid (C-18:3); 54.0% linoleic acid (C-18:2); and 22% oleic acid (C-18:1), where the ratios indicate the number of carbon atoms and bonds respectively. Soybean also contains the saturated fatty acids (4% stearic acid and 10% palmitic acid) (Clemente and Cahoon, 2009).

Soybeans are the primary ingredient in many processed foods, including dairy product substitutes (e.g., margarine, soy ice cream, soy milk, soy yogurt, soy cheese and soy cream cheese, as well as crisco, soybean oil, tofu, veggie burgers, soy nut butter, soy crisps, etc.). These diverse soybean products have been utilized for several decades in both traditional and non-traditional soybean growing communities. Soybeans can also be used to make soybean infant formulas that are used by lactose-intolerant babies, who are allergic to cow milk proteins (Merritt and Jenks, 2004). Moreover, soybeans are also raw materials for industrial products including oils, soap, cosmetics, resins, plastics, inks, crayons, solvents, and clothing. Soybean oil is the primary source of bio-diesel (Radich, 2004). Consumption of soybean based foods may also reduce the risk of colon cancer, possibly due to the presence of sphingolipids (Symolon *et al*., 2004). Soybean also improves soil fertility by adding nitrogen from the atmosphere hence help in replenishing soil fertility (IITA, 2009).

1.3 Production constraints

Average soybean grain yield is still low (<1 t/ha) in Africa (FAO, 2010) mainly because the improved varieties of soybean have not reached many soybean growers (IITA, 2009). Several biotic, abiotic and social economic factors limit the attainment of optimum soybean yields in Africa. Pod shattering causes yield losses ranging from 57 – 175 kg ha^{-1} and 0 – 186 kg ha^{-1} in susceptible and intermediate susceptible soybean varieties respectively (Tukamuhabwa *et al*., 2002). Some farmers lack interest in soybean production because equipment for processing soybean is unavailable in many areas and many people do not know how to prepare the crop for home consumption (IITA, 2009).

Soybean production is also constrained by a number of biotic stresses soybean rust (*Phakopsora pachyrhizi*), bacterial pustule (*Xanthomonas campestris* pv. *glycines*), bacterial blight (*Pseudomonas amygdali* pv. *glycinea*), frog-eye leaf spot (*Cercospora sojina)* red leaf blotch (*Phoma glycinicola*) and soybean mosaic virus disease. It is not uncommon to see overlapping disease infections during soybean growth on many farmers' fields. The major insect pests affecting soybeans are; armyworm (*Pseudaletia unipuncta*), saltmarsh caterpillar (*Estigmene acrea*), soybean looper (*Pseudoplusia includens*), bean leaf beetle (*Cerotoma trifurcate*), blister beetles (*Epicauta funebris*, *Epicauta vittata*) and velvetbean caterpillar (*Anticarsia gemma*) (Catchot, 2010). By far, soybean rust (*Phakopsora pachyrhizi*) is the most stressing causing yield losses of up to 80% (Miles *et al*., 2003). Soybean production is also still low because improved varieties of soybean have not reached many soybean growers to increase production (IITA, 2009) and many still grow land races or obsolete varieties

1.4 Problem statement

Soybean is increasingly becoming an important crop in Uganda. For instance soybean harvested area in 2000 stood at 106,000 ha while in 2009, it stood at 150,000ha (FAO, 2010). However, there are relatively few improved soybean varieties under production in comparison with other crops and as such production of the crop is still low (IITA, 2009). Production and utilization of the crop has also been slow due to an array of cultural, technical and socioeconomic factors (Anon, 2004). Such challenges are partly attributed to insufficient attention to farmers' priorities during varietal development (Ashby and Sperling, 1995). The environment at research stations does not normally represent that in which many disadvantaged rural farming populations live and cultivate their crops. Also, the target traits of classical breeding (yield and to some extent pest resistance) are not always those of greatest importance to the impoverished small farmers (Cleveland and Soleri, 2002). So often, breeders working in isolation from farmers have sometimes been unaware of the multitude of preferences by farmers beyond yield, resistance to diseases and pests.

Crop earliness, ease of harvest, storage attributes, taste and cooking qualities are some of the key factors important to farmers, but often ignored by plant breeders. Because these traits are lacking and/ or deficient in many improved varieties, farmers have preferred their landraces owing to their superiority in these traits. This challenge therefore justifies the need for deliberate involvement of farmers and other end-users in variety selection and evaluation to ensure that the traits desired by them are not left out. In view of this, the purpose of this study was to identify superior soybean varieties that are adapted to different farming environments in Uganda and most desired by end-users.

1.5 Justification of the study

In Uganda several improved soybean cultivars have been developed with numerous desirable traits in an effort to boost production. As of this writing Duiker, Maksoy 1N and NAM1 varieties have been officially released and BSPS17B, BSPS34, BSPS42, BSPS43, BSPS48A, BSPS85, DXTBLP(SRB)12.4, DXTBLP(SRB)4.21 DXTPROGENIES1.3, DXTPROGENIES4.17-4, DXTPROGENIES4.7, DXTPYT06A2.14, DXTPYT06A4.22, DXTPYT06A7.10, DXTPYT06A8.11, DXTPYT06A8.12, DXTPYT06A8.3, DXTSPS4.19, NAMIIXGCBLP11.3, NAMIIXGCBLP20.2, NGDT8.10-10 unofficially released. Several instances have occurred where new improved varieties have been released, but not adopted by end-users primarily because they do not possess the desired attributes. There is thus a need to establish background information on these desired attributes. It is very important to assess whether the new genotypes are compatible with industry standards or requirements by other end-users. This therefore calls for involvement of end-users in selection of new soybean to assess their suitability before their official release.

Uganda’s plan for modernization of Agriculture advocates for a decentralized client-oriented and participatory formulated research characterized by technologies that are more relevant and responsive to the needs of farmers (Anon, 2001). Similar opinions were echoed by Comprehensive Africa Agriculture Development Programme (CAADP) and Forum for Agricultural Research in Africa (FARA) at a continental level in an effort to reduce hunger and extreme poverty (FARA, 2011). Therefore, involving end-users in evaluating new cultivars is a highly recommendable approach to research and improve chances of widespread technology adoption since specific needs of end-users will be targeted.

1.6 Study objectives

The main objective of this study is to determine superior soybean varieties that are adapted to different farming environments in Uganda and most desired by end-users.

1.7 Specific objectives

(i) Establish the traits in soybeans most desired by a cross-section of Ugandan farmers and other key end-users.

(ii) Determine the stability of soybean lines in different agro-ecological zones of Uganda

1.8 Hypothesis

(i) Value chain functionality requires certain crop traits that influence adoption of soybean lines.

(ii) Performance of newly developed soybean genotypes will be affected by different agro-ecological conditions.

CHAPTER TWO

LITERATURE REVIEW

2.1 Participatory crop improvement

Since the inception of formal plant breeding, it has made enormous contributions to global food security. Improved varieties have been developed and released increasing yield dramatically in favourable growing environments (Cleveland and Soleri, 2002). Performance of such improved varieties under less favourable conditions has however, been disappointing and many farmers operating small farms in heterogeneous and unfavourable regions have suffered from shortage of suitable new varieties (Stirling and Witcombe, 2004; Witcombe *et al*., 2005). These resource-constrained farmers have therefore benefited less from the efforts of plant breeders (Cleveland and Soleri, 2002).

In the late 1970s and early 1980s, scientists and development experts began realizing the problems of non-adoption or limited impact caused by top-down and linear development approaches of variety development. It was observed that environment in research stations did not represent farmer environment where developed technologies will be deployed. Also, the target traits of classical plant breeding (e.g. yield and pest resistance) were not those of greatest importance to impoverished small farmers (Cleveland and Soleri, 2002). As a response to these challenges, on-farm and farmer participatory plant breeding schemes were developed to increase selection efficiency and variety adoption (Cleveland and Soleri, 2002).

Participatory crop improvement is a systematic dialogue between farmers and scientists that aims at increasing the impact of agricultural research (Bellon, 2001). It involves farmers working with researchers in setting breeding goals, selecting parental lines, developing populations and their subsequent evaluation and selection (Thijssen *et al*., 2008). Participatory crop improvement is subdivided into two: one for work with stable genotypes, termed as Participatory Varietal Selection (PVS) and another referring exclusively to work with variable or segregating populations, termed as participatory plant breeding (PPB) (Witcombe *et al*., 1996). In PVS, farmers are given near-finished or finished products to test in their fields whereas PPB involves farmers selecting genotypes from segregating generations (Witcombe and Joshi, 1997). Farmers involved in these activities become co-researchers as they can help in setting overall goals, determine specific breeding priorities, screen germplasm entries in the pre-adaptive phases of research, make crosses, take charge of adaptive testing and lead the subsequent seed multiplication and diffusion process (Sperling and Ashby, 1999).

In participatory varietal selection, farmers evaluate all candidate varieties for the traits that are important to them and then trade the traits off against each other to come up with a variety suitable to their environmental and socioeconomic factors. For example, they may accept lower grain yields for earlier maturing because they want to have a second cropping (Witcombe *et al*., 2005). Participatory approaches have helped researchers to understand farmers' criteria for evaluating new varieties. These criteria have also helped the researchers to pick out germplasm with farmer-preferred traits and use them to develop new varieties. Moreover, participatory approaches ensure that farmers make choices that adequately meet their needs and enhances breeder's chances of producing varieties that will be widely adopted (Ashby, 1991).

Participatory research increases research efficiency since breeding priorities are normally oriented in ways that save time and money (Ashby and Lilja, 2004) and farmers' knowledge can be retained effectively from year to year (Grisley and Shamambo, 1993). The adoption bottlenecks caused by low levels of acceptability of new varieties to poor farmers are broken when farmers participate in variety testing and selection (Joshi *et al.*, 1995; Ashby and Lilja, 2004).

Results from participatory plant breeding programs are scanty and generally more recent than those for participatory varietal selection. Witcombe and Joshi (1997) attributed it to the high costs involved when farmers participate at an earlier breeding stage when a large number of genotypes are still segregating. However, since divergent genotypes are developed for different environmental and diverse end-users' needs, participatory plant breeding is a good scheme for increasing varietal diversity both at local and regional levels (Brush, 2000; Stirling and Witcombe, 2004). With PPB, varietal improvement has been extended to traditional landraces that would otherwise be lost from the production system (Sthapit *et al*., 2001) by addition of a few major genes conditioning traits of interest (Brown and Young, 2000). Examples where PPB has been carried out with success include sweetpotato breeding in Uganda (Gibson *et al*., 2008), maize breeding in India (Witcombe *et al*., 2003), selection of chilling tolerant rice from F5 bulk families in Nepal, cassava and beans in Latin America and barley in Syria (Witcombe *et al*., 2005).

There are quite many examples of success cases of participatory varietal selection in breeding. In East Africa, improved bean varieties are probably the best-known example of the successful application of PVS which has enhanced bean crop improvement in several countries including Uganda, Rwanda, Tanzania, and Malawi (Weltzien *et al*. 2003). Improved bean varieties released in the 1990's by Uganda National Agricultural Research Organization (NARO) including K132, K131 and NABE2 are classic examples of PVS success. In a survey conducted in 2003/2004 by NARO, the results showed that new varieties developed through participatory varietal selection had contributed about 41% of total bean output with K132 contributing 36% of total bean output (CIAT, 2008). In collaborative research between the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and Rajasthan Agricultural University, farmer participatory research was used to identify pearl millet cultivars suitable for Rajasthan (Weltzien *et al*., 1995).

Nkongolo *et al*. (2008) conducted participatory varietal selection in Malawi and noted that the introduction of a participatory approach to breeding allowed sorghum landraces that had out-performed breeder developed lines on more than one criterion to be selected. Farmers were interested in taste, seed colour, time to maturity and seed size. Surprisingly, yield was not among the key factors for selection though good yielding varieties for food security were preferred provided they had the other traits. In Namibia, when farmer evaluation of pearl millet in on-station trials was used, the farmers selected a cultivar that was subsequently released and became popular (Witcombe and Joshi 1997). It is on this premise that participatory selection of soybean genotypes was used in this study with the hope that this would lead to the selection of genotypes with attributes desired by end-users.

2.2 Soybean traits and breeding objectives

Based on heritability, crop traits have been classified by plant breeders as having low (5-10%), medium (10-30%) or high (>30%) heritability (Dabholkar, 1992). The highly heritable traits include plant height, resistance to some diseases, days to maturity, seed size, and seed colour. Grain crude protein and resistance to lodging are of medium heritability, while grain and forage yield are of low heritability (Rubaihayo, 1996). Highly heritable traits are easy to distinguish visually and are therefore easy to improve through selection in a breeding program. The main breeding objectives for soybeans include: pest and disease resistance, pod clearance, days to maturity, resistance to lodging, seed yield, pod/ pubescence colour, nodulation and resistance to pod shattering.

Breeding for resistance or tolerance to local pests and diseases is a practical and economical way of controlling soybean diseases (Herbek and Bitzer, 2009), enables crops to realize their yield potential and can lead to reduced use of agrochemical. Although no varieties have been identified to have complete resistance to diseases, there are varieties that have lower infection rates and produce higher yields than others under the same level of disease pressure (Staton and Thelen, 2009). Such varieties are potential candidates for release. Disease resistance and or tolerance has been bred into soybeans for *Phytophthora* root rot, soybean cyst nematode and some leaf diseases (Helsel and Minor, 1993) using classical breeding methods. This testifies the contribution of plant breeding towards increasing or stabilizing crop yields.

Soybean genotypes can be categorized as promiscuous or non-promiscuous with respect to their response to indigenous bradyrhizobia. Promiscuous genotypes form functional nodules without artificial inoculation whereas non-promiscuous genotypes need to be inoculated with compatible rhizobia inoculants to facilitate formation of functional nodules (Gwata *et al*., 2004). According to Gwata *et al*. (2004) development of promiscuous varieties is one of the best alternative for obtaining optimal yields for resource poor farmers who cannot afford artificial inoculums.

Soybean varieties have different plant types. They range from highly branching types to thin line types that produce a single main stem (Klein *et al*., 2004). Soybeans exhibit indeterminate, semi-determinate or determinate in growth habits (McWilliams *et al*., 2004). Determinate varieties complete their vegetative growth prior to flowering. The main stem ends in a large terminal cluster. Indeterminate varieties on the other hand, continue to increase in height for several weeks after they begin to flower and height frequently doubles after the first flowers appear (Helsel and Minor, 1993). Many of the varieties are determinate and cease vegetative growth when the main stem terminates in a cluster of mature pods (McWilliams *et al*., 2004). Semi-determinate varieties are characterized by addition of a small amount of vegetative growth after the onset of flowering and podding. Semi-determinate types have a long, seed-filling period with low seed filling rates compared with determinate types (Egli and Leggett, 1973). This may be due to overlapping vegetative and reproductive stages in the indeterminate types and the separation of these stages in semi-determinate types. Taller varieties are generally more susceptible to lodging and should not be grown in lodging- prone environments with high levels of moisture and fertility.

A variety must be able to remain erect throughout the growing season and to produce maximum yields. Lodging ratings give an indication of standability of a plant. Yield has been observed to decrease by 15-30% if lodging occurs during or before the pod and seed-filling period (Herbek and Bitzer, 2009). Standability varies among varieties and environments (Helsel and Minor, 1993; Staton and Thelen, 2009). Although lodging is largely genetically controlled, other factors such as high plant population, high soil moisture and high soil fertility can stimulate vegetative growth and increase plant height leading to lodging (Klein *et al*., 2004). It is for these reasons that lodging has been, and continues to be a major breeding objective of many soybean breeding programmes.

The number of days a variety takes to mature is an important aspect in breeding soybean varieties. The range of maturity groups adapted to an area should be selected (Staton and Thelen, 2009) and bred for in cases where day lengths differ significantly. Soybeans are photoperiod sensitive (McWilliams *et al*., 2004; Herbek and Bitzer, 2009), with the key to initiation of flowering being the length of darkness (Herbek and Bitzer, 2009). An early variety is sensitive to a shorter night and therefore requires fewer hours of darkness to initiate flowering than a later variety. A late variety requires longer hours of darkness to initiate flowering which allows a longer period of vegetative growth and maturing later in the season (Herbek and Bitzer, 2009). When varieties are grown where they are not adapted, maturity may be delayed or they may mature faster than normal. Helsel and Minor (2003) reported that when a variety is too early or too late at a location, it will be limited in potential performance.

2.3 Soybean market preferred traits

Soybean seeds occur in various sizes, and in many seed coat colors, including black, brown, blue, yellow, green and mottled. Varieties differ in hilum colour and can be yellow, imperfect yellow, grey, buff, brown, black or imperfect black. Yellow hilum/ clear hilum soybeans with large seed size and thin but strong seed coat that is free from cracking and discoloration are preferred (Gandi, 2009). Soybeans contain three lipoxynase isozymes that play a role in the development of beany off-flavor in food containing soy-protein that is unpleasant to some consumers. The off-flavor is caused by oxidation of polyunsaturated fatty acids (Wilson, 1996).The poor stability and off-flavors of soybean oil and protein products can be reduced by eliminating lipoxygenases from soybean seed (Reinprecht et al., 2011). Some varieties that are lipoxygenase free have been developed and are referred to as “triple null” soybeans. These are highly preferred and normally used for edible soy-products such as soymilk and tofu.

Soybean varieties in which linolenic acid content has been reduced from 8 to 1% have been developed. This trait makes it possible to reduce or eliminate the need for chemical hydrogenation, a process that is used to achieve the stability and shelf life necessary for some food applications (Fehr, 2007). The process of chemical hydrogenation has been associated with production of unhealthy trans fatty acids that can clog arteries. Some new soybean varieties that produce less saturated fat than traditional soybean oil have also been developed. These are preferred because less saturated fat results in healthier oil that is used for salads dressing and other food products

2.4 Soybean diseases

Plant diseases cause a significant crop loss with a total annual worldwide crop loss estimated at $220 billion (Agrios, 2005). Healthy plants develop and function to the maximum of their genetic potential. However, when plants are adversely affected by a disease-causing agent or environmental factors that interfere with their normal development and functioning, plants are considered to be diseased. Therefore for disease to occur there must be the right mix of environmental conditions, a host that is susceptible and a pathogen capable of inciting disease. If any one of these is not present, disease will not occur. Therefore evaluation of new soybean genotypes for diseases will help in the identification of genotypes that are tolerant and can be used to increase yield with less use of agrochemicals.

2.4.1 Soybean Rust

Soybean rust is the most destructive foliar disease of soybeans and can cause yield losses of up to 60 to 80% (Bonde *et al.*, 2006; Twizeyimana *et al*., 2008). Soybean rust is caused by two fungal species *Phakopsora pachyrhizi* and *Phakopsora meibomiae*. The former is more aggressive and the economically important species in soybean growing (Bond *et al*., 2006). Field trials conducted in Uganda showed that all commercial cultivars namely Nam 1, Nam 2 and Namsoy 3 heavily succumb to the disease with yield losses in commercial varieties ranging between 26.9- 36.3% (Kawuki *et al.*, 2003). Yield losses result from premature defoliation, decreased number of filled pods, seeds per plant, 100 seed weight and seed quality (Bromfield, 1984). The rapid spread together with the large number of host species that *Phakopsora pachyrhizi* infects increases it chances of survival (Hartman *et al*., 2005). In addition to soybeans, the pathogen infects *Desmodium canadense, Centrosema virginianum, Calopogonium caeruleum, Astragalus canadensis, Indigofera miniata, Lablab purpureus, Lathyrus sylvestris, Cologania lemmonii* and

Crotalaria incana (Slaminko, 2008). These hosts could explain the increasing spread of soybean rust in Africa.

2.4.2 Red leaf blotch

Red leaf blotch (RLB) of soybeans caused by *Phoma glycinicola*, can cause yield losses of up to 50% in endemic areas (Hartman *et al*., 1987). RLB has been detected in Cameroon, Ethiopia, Malawi, Nigeria, Democratic Republic of Congo, Zambia, Zimbabwe, Rwanda and Uganda (Hartman *et al*., 2009).

The pathogen causing RLB has undergone numerous name changes, from *Pyrenochaeta glycines* (Stewart, 1957) to *Dactuliophora glycines* (Leakey, 1964) to *Dactuliochaeata glycines* (Hartman and Sinclair, 1988) and most recently, the fungus was classified as a *Phoma* species and re-named *Phoma glycinicola* (Boerema *et al*., 2004). The fungus is unique among the *Phoma* species because it produces well-defined, melonized sclerotia that on their own can be infectious, or can produce pycnidia on their surface, which then produce infectious conidia (Hartman and Sinclair, 1988).

Bacterial pustule (*Xanthomonas axonopodia pv. glycines*) is another common soybean disease in the tropics (IITA, 2009). It causes premature defoliation and reduced seed size and quantity. Bacterial pustule survives between seasons in crop residue and is spread by water droplets splashing from the ground to the plant. In addition, the disease can be spread during cultivation while the foliage is wet and the bacterium will enter the plant through natural openings and wounds (Giesler, 2009). Although yield loss data associated with soybean bacterial pustule in Uganda are Scanty, yield loss evaluations conducted by Shukla (1994) at different levels of bacterial pustule revealed that the disease can cause yield loss of up to 53% and a reduction in 100 seed weight of up to 16%. Frog-eye leaf spot (*Cercospora sojina* K. Hara) is another common disease of soybean in most soybean-growing countries of the world (Mian *et al*., 2008). It causes yield loss of up to 60% (Dashiell and Akem, 1991) mainly due to reduction in photosynthetic leaf area by necrotic lesions and/or premature defoliation resulting in reduced seed weight. Soybean mosaic virus disease is the most prevalent and destructive viral disease in many soybean growing areas and causes yield loss and seed deterioration. Yield losses due to soybean mosaic virus disease generally range from 8 to 35 %, however losses as high as 94 % have been reported (Giesler, 2009).

2.5 Soybean varietal selection and evaluation

The ultimate goal of selection is to increase genetic gain and/or shift the population mean. Yield, resistance or tolerance to pests and diseases, standability and maturity are attributes normally considered when selecting the best adapted varieties (Staton and Thelen, 2009). Rouse (2007) described variety selection as prediction of lines which will do best in the future as opposed to identifying which lines did best over the past year. For this purpose, many desired attributes and the effects of the environment are therefore considered in the selection process.

Yield is the most important characteristic to look for in potentially successful varieties (Helsel and Minor, 1993; Staton and Thelen, 2009). However, is determined by many underlying genetic and environmental characteristics together with their interactions (Elings, 1999). Genotypes which perform well in different environments are preferred over varieties which only respond well in an environment which favors that genotype (Klein *et al*., 2004). Since the relative performance of different varieties can vary from year to year depending on weather and management, Rouse (2007) recommended that yield trial data should be used to make variety selections only if it includes regional yield averages.

Varieties could be desired and maintained for other reasons than yield or yield related characteristics. The main feature of traditional varieties in comparison with modern varieties is their better compatibility with local farming systems and social economic structures which reflects in specific characteristics (Elings, 1999). Other criteria such as double cropping, crop use, varietal purity, shattering resistance, seed cost and seed quality have been considered in variety selection (Helsel and Minor, 1993). A combination of all varietal characteristics will determine the overall suitability of a genotype (Elings, 1999), and a research approach that brings out these other attributes should be adopted.

2.5.1 Progeny handling through the different stages

Soybean breeding involves creating of variability that is achieved mainly by crossing parents with desired traits intended to be transferred to off-springs. Parental selection is therefore one of the most important decisions affecting gene frequencies and genetic variability of populations. Progenies of these crosses segregate in the course of successive generations of selfing forming new genotypes. After hybridization of the selected parents follows procedures for identifying progenies that posses desirable traits which include: pedigree selection, bulk breeding and single seed descent methods (Poehlman and Sleper, 1995). Pedigree method is used when the traits of interest in the breeding program are easy to identify, highly heritable and can be selected in early generation while single seed descent method is suitable for traits with low heritability (Fehr, 1987). Bulk breeding on the other hand which is Suitable for crops planted in thick spacing e.g. millet requires large populations to give chance to plants to be selected. Single seed descent is the most preferred and efficient breeding method for yield improvement of soybean (Boerma, 1975).

2.5.2 On-station and on-farm evaluation plots

The main emphasis of on-farm trials is on farmers' assessment of genotypes. It involves individual farmers' observations and discussions during cross visits. On-farm testing was conducted using mother -baby trial approach which was pioneered by Snapp *et al*., (1999). The mother trial is an on-farm trial in which a set of new lines or introduced varieties is compared with local checks using farmers' crop management practices. Mother trial contains all varieties in test laid out, planted and harvested under supervision of researchers (Paris et al., 2011). Groups of farmers are invited to visit the trial and farmers' opinions through visual rating are collected and used in selection decision through a technique called preference analysis (Paris et al., 2011). On-station evaluation plots on the other hand are conducted on public agricultural research institutions that are representative of soil type and environmental factors (Kassam, 1981). On-station trials reflect the prevailing cropping systems practiced and/or best farming practices. Varieties are compared in trial plots handled in such a way that the factors affecting yield and other characteristics are as nearly the same for all varieties at each location as is possible. For this reason, old varieties and new varieties are grown in replicated plots at each location.

2.6 Significance of environment on soybean performance

Ideally, plant breeder would prefer identifying and/or selecting varieties that are adapted to a wide range of target environments. Therefore understanding and predicting of crop response to environment is very important. An ideal variety should have a high mean yield combined with a low degree of fluctuation when grown over diverse environments. Genotype – environment interaction (GEI) in varieties is the differential response of genotypes to changing environmental conditions (Elings, 1999). Biotic and abiotic factors are responsible for GEI and yield instability in crops. A genotype showing a consistent performance in all environments does not necessarily respond to improved growing conditions with increased yield. Agronomists, therefore would prefer an ‘agronomic’ or ‘dynamic’ concept of stability in which it is not required that the genotypic response to environmental conditions be equal for all genotypes (Becker and Leon, 1988). Analyzing of GEI for varieties helps to reduce errors of recommending unsuitable varieties to particular regions in plant breeding process since promising varieties in one environment may not necessarily provide advantages in other environments (Tarakanovas and Ruzgas, 2006). In the presence of GEI, yield is less predictable and cannot be interpreted based on genotype and environmental means alone (Ebdon and Gauch, 2002).

Two frequently used statistical analyses have been the additive main effect and multiplicative interaction (AMMI) model and the Genotype main effects and Genotype x environment interaction effects (GGE) model (Gauch, 2006). AMMI model is a hybrid involving both additive and multiplicative components of two way data structure. The model separates the additive variance from multiplicative variance and then applies principal component analysis (PCA) to the interaction portion to a new set of coordinate axes that explains in more detail the interaction pattern and the estimation accomplished using the least squares principle. The Genotype main effects and Genotype x Environment Interaction effects (GGE) analysis helps determine whether the target cropping region is homogeneous or should be divided into different mega-environments

(Samonte *et al*., 2005; Dardanelli *et al*., 2006). It also helps evaluate test environments that effectively identify superior genotypes within a mega-environment (Blanche and Myers, 2006). Yan and Kang (2003) called a group of locations that consistently share the same best genotype(s) as a mega-environment.

According to Gauch (1992), the AMMI analysis is superior for visualizing data. It captures a large portion of the GxE sum of squares, clearly separating main and interaction effects that present agricultural researchers with different kinds of opportunities. The model thus provides an agronomically meaningful interpretation of data. Crop productivity can therefore be maximized by planting varieties which were selected specifically for the target environment. Virk *et al*., (1995) underscore the need testing new genotypes in areas congruent with the area of cultivation for agricultural performance of new genotypes to be predicted. Data collected also help to establish entries which are superior to existing ones, measure the stability of performance across sites and to establish the area of adaptation in which the cultivar will be recommended for cultivation. It is on this premise that the new soybean genotypes were test in different agro-ecological zones in Uganda.

CHAPTER THREE

DETERMINATION OF END-USERS' NEEDS IN THE SOYBEAN VALUE CHAIN

3.1 Introduction

Soybean breeding is an undertaking that requires careful planning in selection of parents to ensure that the progeny contain the traits desired by end-users. Proper testing should detect any major faults and establish the level of superiority or improvement over current varieties. In addition to showing superior performance, there must be a demand for a new variety that is compatible with industry standards or which creates a new market. The more traits a breeder must consider the more time it takes to achieve maximum improvement and the lower the rate of genetic progress. Trading traits off against each other is therefore involved at every step of the breeding process and researchers must decide which traits need the most attention in the area where the new variety will be grown.

Making plant breeding more market- oriented can help solve diverse problems that have been encountered in the past. Since the process from production to consumption involves various stakeholders, each contributing to value addition to the final product, soybeans and final products are owned by various actors who are linked by trade and services. It is therefore important to understand the pressing needs of the various stakeholders within the whole soybean value chain. Conventional plant breeding for many years has failed to meet needs of many farmers in marginal land because the target traits for classical breeding have not been those of greatest importance to rural farmers (Witcombe *et al*., 2005). Involving end-users in research ensures faster adoption by ensuring that research builds on farmers' knowledge of local environmental constraints, plant genetic resources, their own capabilities and consumer preferences (Ashby and Liljah, 2004). The varieties developed with end-users through participatory approaches are more likely to meet farmers' particular needs for specific environments. Moreover, involving end-users can help to identify farmer acceptable varieties and overcome the constraints that cause them to grow old or obsolete varieties (Witcombe *et al.*, 2005). It is on this premise that a study was conducted to establish the desirable traits in soybeans most desired by a cross-section of Ugandan farmers and other end-users.

3.2 Materials and methods

3.2.1 On-farm, farmer managed trials

Twenty one new soybean lines from the Advanced Yield Trial (AYT) were selected from a collection of breeding materials available with the soybean breeding programme (Table 1). To this list, three local checks (DUIKER, MAKSOY 1N and NAM1) were added. The assembled genotypes were planted on farmers' fields in the districts of Mayuge (Kigandaro), Pallisa (Jami), Lira (Adekokwok), Apac (Bala), Masindi (Pakanyi Labongo), Hoima (Bulindi) and Kamwenge (Businge). Farmers' crop management practices were followed. The trials were planted for three seasons, beginning with 2008B, 2009A and lastly 2009B (A and B being the first and second seasons respectively).

In each district, two farmer's fields were selected and both farmers were given all the new soybean lines at a meeting in which the objectives and procedures of the trial were explained. The farmers were chosen on the basis of their willingness and possession of enough land on which to conduct the trials. The host farmers worked jointly with 5 – 10 other participating farmers to manage the field trials. A new field was used each season at each station. The experiment was laid out in a randomized complete block design (RCBD) with two replicates. A spacing of 60 cm between and 5 cm within rows was used with three rows for each soybean line. Farmers conducting the trials and other interested neighboring farmers first listed the most important selection criteria. In addition, farmers also assessed the performance on soybean trials between flowering and maturity (Appendix 3) and seed characteristics after harvest by voting for five best soybean genotypes and five least preferred genotypes. Farmers "voted" for varieties they would like to grow on their own fields and for those they dislike, by putting a ballot into the envelopes that were placed in front of each plot. Votes were counted for each genotype and the whole group was requested to visit the genotypes that received most votes and explain the positive attributes of those genotypes. Comments on the least preferred genotypes were also collected. . At each site, a preference index was calculated according to Rasabandit *et al*., (2006) for each variety by expressing the number of positive votes cast minus the negative votes cast divided by the total number of positive and negative votes cast by the farmers. ANOVA on preference index was done for each region, with preference scores at each site for the different seasons considered replicates.

Table 1: Description of elite soybean genotypes evaluated for adoption attributes

Genotype	Genotype code	Source
BSPS17B	G1	Uganda
BSPS34	G2	Uganda
BSPS42	G3	Uganda
BSPS43	G4	Uganda
BSPS48A	G5	Uganda
BSPS85	G6	Uganda
DUIKER***	G7	Zimbabwe
DXTBLP(SRB)12.4	G8	Uganda
DXTBLP(SRB)4.21	G9	Uganda
DXTPROGENIES1.3	G10	Uganda
DXTPROGENIES4.17-4	G11	Uganda
DXTPROGENIES4.7	G12	Uganda
DXTPYT06A2.14	G13	Uganda
DXTPYT06A4.22	G14	Uganda
DXTPYT06A7.10	G15	Uganda
DXTPYT06A8.11	G16	Uganda
DXTPYT06A8.12	G17	Uganda
DXTPYT06A8.3	G18	Uganda
DXTSPS4.19	G19	Uganda
MAKSOY1N***	G20	Nigeria
NAM1***	G21	Colombia
NAMIIXGCBLP11.3	G22	Uganda
NAMIIXGCBLP20.2	G23	Uganda
NGDT8.10-10	G24	Uganda

*** Local check

3.2.2 Soybean traits desired by processors

The 24 test soybean genotypes (Table 1) were presented to five soybean factories in Kampala for evaluation of traits desired by processors. Soybean is a crop best utilized after processing and processors greatly influence the market for soybeans. The processors involved included animal feed formulators and producers of soybean based foods for human consumption. These processors were East African Basic Foods Limited, SESACO, Kayebe Sauce Packers, Maganjo Grain Millers and Formula Feeds. At all the five factories, information was obtained from the production manager and four members of staff involved in purchase and sorting of soybeans. This was done using an open ended questionnaire.

SESACO, Kayebe Sauce Packers and East African Basic Foods Limited are largely involved in production of soybean based foods for human consumption which include: soya cup, soya millet, soya nuts, brown butter, soya sauce, soya milk, soya cookies, soya posho, instant soya porridge, soya “Kaawa”, Health booster, and tofu. Maganjo Grain Millers make both human food and animal feeds, while Formula feeds make only animal feeds. Products made by Maganjo Grain Millers include soy meal, soy maize, soy flour, soy drink, soy dog food and bread.

An evaluation system using three levels of appreciation for each character as described by Elings (1999) was adopted. In this system, a variety that was considered good was awarded 5 points, fair (3 points) and poor (1 point). A genotype with 5 points is one which is fully acceptable by all the processors involved in the selection.

3.3 Results

3.3.1 Criteria for soybean evaluation by farmers

Farmers suggested positive and negative criteria believed to be important for evaluation of soybean genotypes (Table 2). A total of 82 farmers evaluated the new soybean genotypes; 36 farmers were from western region, 30 farmers from eastern region and 16 farmers from northern region (Appendix 2). Twelve field and four seed attributes were mentioned to identify the best soybean genotypes. The field attributes included: many pods on the plant, medium plant height, early maturing, big pods, strong stems, good pod spreading, low foliage at harvest and resistance to lodging, drought and diseases. The positive seed attributes that were preferred by farmers were: big seed size, attractive seed coat colour, high yielding and high market value. For rejecting the soybean genotypes, farmers mentioned eleven field and seven seed attributes.

Table 2: Criteria suggested by farmers for evaluating soybean genotypes

Positive attribute	**Negative attribute**
<u>Field attributes:</u>	<u>Field attributes:</u>
Many pods	Low pod load
Medium plant height	Hairy stems, branches and pods
Early maturing	Small pods
Big pods	Late maturing
Lodging resistant	Susceptibility to pests and diseases
Tolerant to drought	Yellow leaves
Resistant to diseases	Poor pod filling
Low foliage at harvest	Leaves that persist up to harvest
Uniform maturity at harvest	Short plants
Tolerant to low soil fertility	Susceptibility to lodging
Strong stem	Pod shattering
Good pod spreading (pods that appear even at the branch apices)	
<u>Seed attributes:</u>	<u>Seed attributes:</u>
Big seed size	Dull-coloured seeds
Attractive seed coat colour (cream seed coat)	Black hilum
High yielding	Small seed size
High market value	Un-uniform seeds
	Purple pigment
	Many immature seeds

The field attributes included low pod load, hairy stems and pods, small pods, late maturing, susceptibility to pests and diseases, yellow leaves, poor pod filing, leaves that persist up to planting, short plants susceptibility to lodging and pod shattering. The seed attributes that were not preferred included: dull-coloured seeds, black hilum, small seeds, un-uniform seeds, seeds with purple pigment and many immature seeds after harvest (Table 2).

3.3.2 Soybean genotype preference by farmers in three different regions of Uganda

The preference scores for twenty one new soybean genotypes compared with three local checks for the regions in which they were tested are shown in table 3. The results show that preference scores varied from genotype to genotype. Genotypes which got higher preference scores were more acceptable than those which got low preference scores. In Northern Uganda, genotypes DXTPROGENIES4.17-4 and BSPS85 were the most preferred with preference scores of 0.076 and 0.050 respectively. Genotypes NAMIIXGCBLP11.3 and BSPS43 with preference scores of -0.090 and -0.045 respectively were the least preferred. MAKSOY1N and BSPS43 with preference scores of 0.065 and 0.050 respectively were the most preferred genotypes in the Eastern Uganda while Genotypes NAMIIXGCBLP11.3 and BSPS17B with preference scores of -0.050 and -0.033 respectively were the least preferred. In Western Uganda, genotypes DXTPYT06A8.11 and DXTPYT06A4.22 with preference scores of 0.036 and 0.033 were the most preferred while genotypes NAMIIXGCBLP11.3 and BSPS34 with preference scores of -0.067 and -0.046 respectively were the least preferred.

Genotype DXTPYT06A8.11 with a combined preference scores of 0.029 for the three regions was more acceptable than all the local checks MAKSOY IN, NAM1 and DUIKER which had preference scores of 0.026, 0 and 0.014, respectively. Genotypes MAKSOYIN, DXTPYT06A7.10, DXTPROGENIES4.17-4 were the second and third most preferred genotypes for the three regions with combined preference scores of 0.026 and 0.025 respectively (Table 3). The least preferred genotypes by farmers across the three regions were NAMIIXGCBLP11.3, BSPS17B, NAMIIXGCBLP20.2, BSPS48A and NGDT8.10-10 with preference scores of -0.068, -0.027, -0.021, -0.018 and -0.010 respectively.

Table 3: Soybean genotype maturity group and their farmer's preference scores in three different regions of Uganda

		Preference Scores			
GENOTYPE	Maturity[1]	North	East	West	Combined
BSPS17B	Late	-0.021	-0.033	-0.027	-0.027 [e]
BSPS34	Late	0.017	0.033	-0.046	-0.005
BSPS42	Medium	0.021	0.033	-0.012	0.010
BSPS43	Late	-0.045	0.050	-0.013	-0.004
BSPS48A	Medium	-0.005	-0.033	-0.018	-0.018
BSPS85	Medium	0.050	0.017	-0.014	0.013
DUIKER	Late	0.016	0.015	0.013	0.014
DXTBLP(SRB)12.4	Medium	0.024	0.011	0.034	0.024
DXTBLP(SRB)4.21	Medium	0.006	-0.027	-0.004	-0.008
DXTPROGENIES1.3	Medium	-0.023	0.011	0.001	-0.003
DXTPROGENIES4.17-4	Early	0.076	-0.027	0.025	0.025[c]
DXTPROGENIES4.7	Late	-0.023	0.017	0.003	-0.001
DXTPYT06A2.14	Late	0.016	-0.013	-0.002	0.000
DXTPYT06A4.22	Medium	0.004	0.000	0.033	0.016
DXTPYT06A7.10	Medium	0.022	0.033	0.020	0.025[c]
DXTPYT06A8.11	Early	0.032	0.017	0.036	0.029[a]
DXTPYT06A8.12	Late	0.029	0.013	0.021	0.021
DXTPYT06A8.3	Medium	-0.018	-0.017	0.002	-0.009
DXTSPS4.19	Late	-0.025	0.004	-0.003	-0.007
MAKSOY1N	Early	-0.025	0.065	0.034	0.026[b]
NAM1	Medium	0.025	-0.027	0.002	0.000
NAMIIXGCBLP11.3	Late	-0.090	-0.050	-0.067	-0.068[d]
NAMIIXGCBLP20.2	Medium	-0.040	-0.004	-0.019	-0.021
NGDT8.10-10	Medium	-0.022	-0.021	0.004	-0.010
LSD		0.017	0.035	0.016	0.019

[1] Maturity: Early (<90 days), medium (91 -100 days), late (> 100 days), [a] -Most preferred, [b]-2nd most preferred, [c]-3rd most preferred, [d]-least preferred, [e]-2nd least preferred.

3.3.3. The least preferred genotypes by farmers

The soybean genotypes least preferred by farmers, their preference scores and their respective negative criteria are shown in Table 4. Five out of twelve genotypes that were least preferred by farmers were late maturing (<100 days) and these were NAMIIXGCBLP11.3, BSPS17B, BSPS34, BSPS43 and DXTPROGENIES4.7.

Table 4: Least farmer-preferred varieties, their preference scores and respective negative attribute

Genotype	Preference score	Negative attribute
NAMIIXGCBLP11.3	-0.068	Late maturing, Some pods empty, Hairy plants Many immature seeds, Black hilum, Low yielding.
BSPS17B	-0.027	Late maturing, Susceptible to leaf rollers,
NAMIIXGCBLP20.2	-0.021	Hairy stem and pods Black hilum, Low yielding
BSPS48A	-0.018	Hairy pods, Many immature seeds, Seeds with purple pigment
NGDT8.10-10	-0.01	Many immature seeds Seeds have a purple pigment
DXTPYT06A8.3	-0.009	Highly vegetative but with few pods, Some empty pods, Yellow leaves, Seeds whitish, Susceptible to drought
DXTBLP(SRB)4.21	-0.008	Some pods empty, Low yielding
DXTSPS4.19	-0.007	Many leaves at harvest, few pods, Many dead seeds
BSPS34	-0.005	Late maturing, low yielding, Many immature seeds, Seeds have a purple pigment
BSPS43	-0.004	Late maturing, hairy Seeds not uniform
DXTPROGENIES1.3	-0.003	Few pods, low yielding, many dead grains
DXTPROGENIES4.7	-0.001	Late maturing, Seeds with purple pigment

Five genotypes, BSPS34, NAMIIXGCBLP11.3, NAMIIXGCBLP20.2, DXTBLP(SRB)4.21, and DXTPROGENIES1.3 were not liked because they were low yielding. Genotypes BSPS48A, NAMIIXGCBLP20.2 and BSPS43 were also not liked because of hair they possessed on their pods and stems.

3.3.4 Soybean genotypes yield performance on farmers' fields

Soybean genotype yield performance in Western and Northern regions for three seasons (2008B, 2009A & 2009B) and Eastern region for two seasons (2008B and 2009A) are shown in the table below. Yield for 2009B in Eastern Uganda was not considered due to the fact that some farmers harvested early and mixed up different genotypes. The highest mean yield (1220 kg ha^{-1}) across all genotypes was observed in Western Uganda in 2009A while the lowest mean yield (484 kg ha^{-1}) was observed in Northern Uganda in 2009B. In Western region, BSPS43 (1389 kg ha^{-1}), BSPS48A (1917 kg ha^{-1}) and BSPS17B (867 kg ha^{-1}) yielded highest in 2008B, 2009A and 2009B respectively.

In Northern region, three genotypes DXTPROGENIES4.17-4, DXTPROGENIES4.7 and DXTPROGENIES4.7 each with mean yield of 1167 kg ha^{-1} yielded highest in 2008B. Genotypes BSPS17B and DXTPROGENIES1.3 each with mean yield of 1417 kg ha^{-1} yielded highest in 2009A while DXTPROGENIES4.17-4 (768 kg ha^{-1}) yielded highest in 2009B. Genotype BSPS17B yielded highest in Eastern region on both 2008B and 2009A with mean yield of 1476 kg ha^{-1} and 1550 kg ha^{-1}.Across all regions, the highest yielding genotypes were DXTPROGENIES4.7 (1208 kg ha^{-1}) and BSPS17B (1194 kg ha^{-1}) while the least yielding genotypes were DUIKER (697 kg ha^{-1}) and BSPS34 (823 kg ha^{-1}).

Table 5: Soybean genotypes yield performance (Kg ha^{-1}) on farmers' fields

	Locations								
	West			North			East		
Genotype	2008B	2009A	2009B	2008B	2009A	2009B	2008B	2009A	Mean across
BSPS17B	1278	1208	867	1083	1417	482	1467	1750	1194
BSPS34	972	917	621	722	958	286	967	1146	823
BSPS42	1056	1333	608	833	1250	586	917	1083	958
BSPS43	1389	1458	715	1056	1208	430	650	708	951
BSPS48A	1694	1917	738	972	1208	443	917	1021	1114
BSPS85	1250	1500	762	1111	1333	586	1133	1333	1126
DUIKER	583	375	702	583	875	456	917	1083	697
DXTBLP(SRB)12.4	1278	1458	754	778	1167	521	1050	1250	1032
DXTBLP(SRB)4.21	1139	1042	717	750	1125	508	1217	1375	984
DXTPROGENIES1.3	1028	1208	806	1111	1417	508	900	979	995
DXTPROGENIES4.17-4	667	583	658	1167	1375	768	950	1104	909
DXTPROGENIES4.7	1278	1667	733	1167	1333	586	1317	1583	1208
DXTPYT06A2.14	1222	1375	794	583	625	182	1250	1500	941
DXTPYT06A4.22	889	1125	794	1000	1208	456	1167	1375	1001
DXTPYT06A7.10	889	958	427	1000	1250	651	933	1083	899
DXTPYT06A8.11	1278	1500	742	722	958	508	867	1021	950
DXTPYT06A8.12	1111	1208	696	889	1083	573	1050	1250	983
DXTPYT06A8.3	917	1000	702	1167	1375	443	950	1083	955
DXTSPS4.19	1250	1417	698	806	958	234	1017	1187	946
MAKSOY1N	1333	1583	706	972	1208	599	1183	1312	1112
NAM1	667	708	860	1028	1292	586	983	1167	911
NAMIIXGCBLP11.3	1028	1208	558	778	1167	443	783	917	860
NAMIIXGCBLP20.2	833	1000	626	833	875	469	1117	1333	886
NGDT8.10-10	1306	1542	819	667	1000	326	983	1104	968
Mean	1097	1220	713	907	1153	484	1028	1198	975
LSD	538.9	627.7	240.4	640.6	1025.3	445.6	658.6	830.7	196

3.3.5 Genotype preference by processors

The data collected from five soybean processors in Uganda (SESACO, East Africa Basic Foods Limited, Maganjo Grain Millers, Kayebe Sauce Packers and Formula Feeds who evaluated soybean genotyes show that processors for animal feeds can use any available soybean varieties but Sesaco, East Africa Basic Foods Limited and Maganjo preferred soybean varieties with big seed size, yellow or cream colour of testa, and yellow or white hilum. On the other hand too large or too small grains and black hilum were not desired. Processors identified that varieties with sharp flavor/aroma and those whose seed coat don’t peel off during processing are lacking on market. Genotypes DXTPYT06A4.22, DXTSPS4.19 and NGDT8.10-10 were preferred by all the five soybean processors (Table 6) each with a maximum average score of 5.

Genotypes BSPS85, DUIKER, DXTBLP(SRB)12.4, DXTBLP(SRB)4.21, DXTPROGENIES1.3 and DXTPROGENIES4.17-4 were also equally good with a mean score of 4.6. Most of these genotypes were large seeded with a yellow or white hilum. DXTPYT06A7.10 is a large seeded genotype but was not liked by some processors because the seeds looked dirty and were not visually pleasant to them. It suffices to note that three of the five processors (East Africa Basic Foods, Sesaco and Maganjo Grain Millers) were willing to compromise on other attributes but not black hilum because it leaves black particles in the processed product which are not pleasing to consumers. The processors’ preference for large seeded genotypes was because they are easy to sort. They strive to use large seeded genotypes and resort to small seeded genotypes when there is scarcity of large seeded ones. A local check NAM1 was the least preferred by all the processors with an average score of 1.8. Genotypes MAKSOY 1N, NAMIIXGCBLP11.3 and NAMIIXGCBLP20.2 had mean scores below three which represented a fair genotype to all the processors.

Table 6: Genotype preference by processors and their mean acceptability scores

	Processors					
Genotype	**Sesaco**	**EBFL**	**Maganjo**	**Kayebe**	**F.F**	**Mean**
BSPS17B	5	1	3	5	5	3.8
BSPS34	5	1	1	5	5	3.4
BSPS42	5	1	3	5	5	3.8
BSPS43	5	5	3	5	5	4.6
BSPS48A	1	5	3	5	5	3.8
BSPS85	5	5	3	5	5	4.6
DUIKER	5	5	3	5	5	4.6
DXTBLP(SRB)12.4	5	5	3	5	5	4.6
DXTBLP(SRB)4.21	5	5	3	5	5	4.6
DXTPROGENIES1.3	5	5	3	5	5	4.6
DXTPROGENIES4.17-4	5	5	3	5	5	4.6
DXTPROGENIES4.7	5	1	3	5	5	3.8
DXTPYT06A2.14	5	1	3	5	5	3.8
DXTPYT06A4.22	5	5	5	5	5	5.0
DXTPYT06A7.10	3	3	3	5	5	3.8
DXTPYT06A8.11	1	1	3	5	5	3.0
DXTPYT06A8.12	5	1	3	5	5	3.8
DXTPYT06A8.3	5	1	1	5	5	3.4
DXTSPS4.19	5	5	5	5	5	5.0
MAKSOY1N	5	1	1	1	5	2.6
NAM1	1	1	1	1	5	1.8
NAMIIXGCBLP11.3	1	1	1	5	5	2.6
NAMIIXGCBLP20.2	1	1	1	5	5	2.6
NGDT8.10-10	5	5	5	5	5	5.0
Mean	4.08	2.92	2.75	4.67	5	3.88
LSD	-	-	-	-	-	1.49

Good =5, Fair =3, Poor = 1, EBFL = East Africa Basic Foods Limited, F.F = Formula Feeds

3.4 Discussion

The purpose of genotype evaluation is to determine the most suitable genotype (s) for cultivation, consumption, trade or any other purpose. Farmers' selection criteria of new genotypes largely depend on the importance of the crop in the farming system and their uses (Abebe *et al.*, 2005).

This study presents results from farmer assessment of 21 new soybean genotypes. Three local checks were included for comparison purposes. Results showed that genotype preference and acceptability differed greatly between different regions. Soybean attributes that were considered most important by farmers when selecting the best genotypes included early maturity, disease tolerance, high yielding, big seed size and attractive seed-coat colour (cream). Early maturity (<90days) was the most important field characteristic considered because early maturing varieties escape drought which normally appears towards the end of the growing season. It also allows farmers to have more planting seasons in a year. Poehlman and Sleper (1995) have also reported that early maturing genotypes may escape damage from heat, drought, insects, diseases or permit early removal of a crop so that the following crop may be planted.

Three genotypes DXTPROGENIES4.17-4 (909 kg ha^{-1}), DXTPYT06A7.11 (950 kg ha^{-1}) and MAKSOY1N (1112 kg ha^{-1}) out the five new genotypes that were selected as the best by the farmers (Table 4) were found to be early maturing but not the highest yielding genotypes. Similarly, genotypes BSPS17B (1194 kg ha^{-1}), BSPS48A (1114 kg ha^{-1}), BSPS85 (1126 kg ha^{-1}) and DXTPROGENIES4.7 (1208 kg ha^{-1}) were the highest yielding genotypes but among the least preferred by farmers because they were not early maturing. These results are in harmony with earlier findings by Witcombe *et al*. (2005) who found out that farmers may trade lower grain yields for other attributes such as earlier maturity and marketability. These results further confirm the need for early maturing soybeans. The least preferred genotype (NAMIIXGCBLP11.3) in addition to being late maturing had seeds with black hila (Table 4). In Uganda, soybean consumption at household level is still low. Most of it is grown for sell (Anon, 2004). Attractive seed coat colour/ clear hilum ensures easy marketing of soybean, it is therefore not surprising that it is a key selection criteria of acceptable soybean genotypes by farmers in all regions of Uganda.

Involvement of processors in selection of new varieties is a new practice in Uganda. However information gathered from them has shown that they can take on distinct roles in the soybean improvement. Processors' desired attributes were largely defined by the intended use of the final product. Processors of animal products for example, Formula Feeds, tend to use any variety that is available, while those of human products tend to be very selective. Soybean genotypes characterized by intermediate seed size, yellow colour and clear (yellow/white) hilum were preferred by all processors. Similar observations were made earlier by Sullivan (2003), who found out that soybean buyers were more interested in large seeded varieties with a clear hilum. Results show that DXTSPS4.19, NGDT8.10-10 and DXTPYT06A4.22 were excellent genotypes for processors with a maximum average acceptability score of 5.

Small seeded varieties MAKSOY 1N and NAM1 both local checks were among the least preferred genotypes by processors indicating that it is possible to meet their needs using the new genotypes. It was disappointing but not surprising that the most preferred genotypes by processors (DXTSPS4.19, NGDT8.10-10 and DXTPYT06A4.22) were among the least preferred by farmers. Processors and farmers value different attributes depending on their goals. Unfortunately, no single variety was noted to posses all the attributes valued by both farmers and processors. Hence, soybean breeding efforts should be oriented towards assembling new soybean genotypes that have a combination of traits desired by both end users for successful adoption of varieties. For now, genotype DXTPROGENIES4.17-4 though not among the best yielders, may be more successfully grown and marketed because it scores relatively well for both farmers and processors. Such a genotype may need to be promoted. Alternatively, this genotype can be used as a parental line for a breeding scheme that targets both farmer/processor traits.

CHAPTER FOUR

EVALUATION OF ELITE SOYBEAN GENOTYPES FOR ADAPTABILITY TO DIFFERENT AGROECOLOGICAL ZONES IN UGANDA

4.1 Introduction

A major objective of most soybean breeding programmes is to develop varieties with high productivity and having properties most liked by end-users. Development of a superior variety involves the combination of desirable traits from the parental germplasm through hybridization. Desirable traits in soybean may include high seed yield, resistance to diseases and insects, better agronomic and improved nutritional traits. The most difficult task is the identification of individuals that are genetically superior and can pass over these traits to their progeny. The genotype by environment interaction complicates the varietal development process.

Selecting for yield is more difficult as it is extremely affected by environmental factors. Staton and Thelen (2009) recommended that yield performance over locations, across several years should be considered when evaluating a variety. Selecting for disease resistance is also important because diseases account mostly for the low yields observed in soybean production areas. Although no varieties with complete resistance to diseases have been identified, there are some varieties that have lower infection rates and produce higher yields than others under the same level of disease pressure. Upright plants are more desirable because they make harvesting easier and reduce yield losses. Standability may however vary among environments. Since a variety's success in spreading across an area depends on its adaptability, the objectives of this experiment were therefore; to determine adaptation of these soybean lines over different agro-ecologies in Uganda and assess the most prevalent biotic factors affecting soybean production in different farming environments in Uganda.

4.2 Materials and methods

The study was conducted at public research institutions that are located in different agro-ecological regions of Uganda, namely Namulonge in central Uganda, Nakabango and Iki-

iki, in Eastern Uganda, Ngetta, in Northern Uganda and Bulindi in mid - western Uganda. The respective altitude, latitude and longitude positions of these stations are: Namulonge (0^o32'N/32^o37'E, 1150 m.a.s.l), Nakabango (0^o29'N/33°14'E, 1210 m.a.s.l), Bulindi (1°28'N/31°28'E, 1136 m.a.s.l) and Ngetta (2°17'N/32°56'E, 1182 m.a.s.l). Twenty one new soybean genotypes and three local checks (Table 1) were used for this study. The trials were conducted during the second rainy season of 2008B (September-December) and were repeated during the first (March-June) and second (September – December) rain seasons of 2009. These seasons are subsequently referred to as 2008B, 2009A and 2009B, respectively, in this write-up. Twenty one new soybean elite lines and three local checks were planted and evaluated. At each research station the genotypes were grown for three seasons under rain-fed conditions. The trial was arranged in a randomized complete block design with three replications. Each soybean line was planted in three rows with a spacing of 60cm between and 5cm within rows. NAM1 which is well know as being highly susceptible to soybean rust was planted along the borders to act as source of inoculum. The trials were kept weed free by constant weeding and no agrochemicals were used on the trials to control pests.

4.2.1 Data collection

The trials were assessed for resistance to soybean rust a major soybean disease in Uganda that causes yield losses of up to 80% and attacks all commercial cultivars. A scale of 1-5 adopted from Miles *et al*., (2006) was used for all the diseases where 1= no visible lesion, 2= few scattered lesions present, 3=moderate number of lesions on at least part of the leaf, 4= abundant number of lesions on at least part of leaf, and 5= prolific lesion development on most of the leaf. Lodging was rated on a scale of 1 to 5, with 1 being the most resistant or upright and 5 indicating that the soybeans are completely prostrate (Helsel and Minor, 1993). At maturity, the trials were harvested separately, threshed and yield per plot determined and consequently corrected to 12% moisture content before determining yield per hectare. Disease data were collected for two seasons (2009A and 2009B) while yield data was collected for three seasons.

4.2.2 Data analysis

Analysis of variance was performed initially for each environment to determine performance of the genotypes in different environments. A combined analysis over locations and seasons was conducted to determine performance of different genotypes across seasons and locations and establish genotype x environment interactions of grain yield and response to biotic constraints. Yield data were further subjected to Additive Main effects and Multiplicative Interaction (AMMI) analysis for identification of stable soybean genotypes. All this analysis was done using GenStat 13th Edition (Payne *et al*. 2010).

4.3. RESULTS

4.3.1 Genotype reaction to soybean rust

The results of rust severities on soybean genotypes at the five locations during seasons 2009A and 2009B are presented in Table 7**.** With exception of Namulonge and Ngetta in the first season (2009A) rust severities were significantly different (p<0.001) among genotypes with Nakabango showing the highest rust severity (mean severity of 3). The highest soybean rust severity was recorded on a local check DUIKER whereas the least rust severities were observed in BSPS43, BSPS48A and NAMIIXGCBLP20.2

In the second rains of 2009, rust scores for all locations were significant (p<0.001) with highest rust severity observed at Namulonge (mean severity of 3.6) and the lowest was at Iki Iki (mean rust severity of 2.2). Highest rust severities were recorded on local checks DUIKER and NAM 1. The new genotypes DXTPROGENIES 4.17-4, DXTPYT06A7.10, DXTPROGENIES 4.7 and DXTPYT06A8.12 showed mean rust scores above 3. The lowest scores were observed in genotypes NAM11XGCBLP11.3, BSPS43 and NAM11XGCBLP20.2. Over the two cropping seasons, mean rust scores of 2009A were generally lower than those of 2009B. The local checks DUIKER and NAM 1 showed the highest rust severities.

Table 7: Mean soybean rust scores of 24 soybean genotypes evaluated at five locations during 2009A and 2009B seasons

Genotype	**2009A**					**2009B**			**Mean across**
	Bul	**Nak**	**Iki**	**Bul**	**Nak**	**Nam**	**Nge**	**Iki**	
BSPS17B	2.5	2.7	2.0	2.3	2.3	3.5	3.0	2.2	2.4
BSPS34	2.8	3.2	2.0	2.7	2.8	4.0	2.8	2.0	2.5
BSPS42	1.8	2.5	1.8	2.5	2.2	3.5	2.8	2.2	2.1
BSPS43	1.5	1.2	1.7	1.3	1.8	2.0	1.3	1.7	1.5
BSPS48A	1.2	1.8	1.5	1.5	2.3	1.7	2.0	1.7	1.6
BSPS85	2.7	2.7	1.8	2.3	2.7	3.7	2.5	2.2	2.3
DUIKER	4.3	4.3	4.0	4.2	4.5	4.7	3.7	3.7	3.7
DXTBLP(SRB)12.4	2.7	2.5	2.0	2.5	2.7	3.3	2.8	2.3	2.4
DXTBLP(SRB)4.21	1.8	2.7	2.3	2.8	3.3	3.7	2.8	1.8	2.4
DXTPROGENIES1.3	2.3	2.3	2.5	2.3	2.7	3.3	2.5	1.7	2.2
DXTPROGENIES4.17-4	1.8	3.3	2.5	3.7	3.0	4.5	2.8	2.3	2.7
DXTPROGENIES4.7	2.5	3.0	2	2.8	2.5	4.3	3.3	2.5	2.5
DXTPYT06A2.14	3.0	2.7	2.2	2.5	3.0	3.8	3.2	2.5	2.6
DXTPYT06A4.22	3.3	2.7	2.2	2.8	2.7	4.2	3.0	2.2	2.5
DXTPYT06A7.10	3.5	3.2	2.7	2.8	3.3	4	2.7	2.7	2.7
DXTPYT06A8.11	2.8	2.5	2.0	2.5	3.0	3.8	2.8	2.7	2.5
DXTPYT06A8.12	3.3	3.2	2.0	3.0	3.0	4.2	3.0	2.2	2.7
DXTPYT06A8.3	2.8	1.3	1.8	1.8	2.7	3.7	3.2	2.2	2.2
DXTSPS4.19	2.5	2.2	2.3	2.3	2.8	4.2	2.7	2.3	2.4
MAKSOY1N	3.0	1.5	1.3	2.3	2.2	3.3	2.3	2.0	2
NAM1	3.2	4.3	3.5	3.2	3.3	4.8	3.2	2.7	3.2
NAMIIXGCBLP11.3	1.8	1.8	1.3	1.0	1.2	2.2	1.0	1.2	1.4
NAMIIXGCBLP20.2	1.8	1.3	1.2	1.0	1.2	2.7	1.3	1.8	1.5
NGDT8.10-10	3.2	2.3	2.5	2.5	2.8	4.0	2.7	2.0	2.5
Mean	2.6	3	2	2.5	2.7	3.6	2.6	2.2	2.3
CV%	22	21	26	17	14	13	14	16	37
LSD	0.9	0.9	0.9	0.7	0.6	0.7	0.6	0.6	0.4
Sed	0.5	0.4	0.4	0.3	0.3	0.4	0.3	0.3	0.2

1= no visible lesion, 2= few scattered lesions present, 3=moderate number of lesions on at least part of the leaf, 4= abundant number of lesions on at least part of leaf, and 5= prolific lesion development on most of the leaf

Nam = Namulonge, Nak = Nakabango, Bul = Bulindi, Iki = Iki Iki

Sed = Standard error of the difference, CV = Coefficient of variation, LSD = Least significant difference

4.3.2 Lodging

Lodging results of soybean genotypes at the five locations during two seasons are presented in Table 8. With exception of Ngetta in the first season (2009A) lodging mean scores were significantly different ($p<0.005$) among genotypes with Iki Iki having genotypes showing the highest lodging tendencies (mean lodging score of 2.2). The lowest lodging scores were observed at Namulonge (mean lodging score of 1.3) in the first season of 2009. Overall, the lowest lodging scores were recorded on local checks (DUIKER, MAKSOY 1N) whereas the highest lodging scores were observed in new genotypes NAMIIXGCBLP20.2 and DXTBLP(SRB)4.2. During the second rains of 2009, lodging scores were significant ($p<0.001$) only at Nakabango and Namulonge. Over the two cropping seasons, lodging scores of 2009A were generally higher than those of 2009B. The local checks DUIKER, MAKSOY 1N and NAM 1 showed the lowest lodging scores. The new soybean genotypes BSPS43, DXTBLP(SRB)4.21, DXTPROGENIES1.3 showed fairly high lodging tendencies

Table 8: Mean lodging scores of 24 soybean genotypes evaluated at five locations during 2009A and 2009B seasons

Genotype	2009A						2009B						Mean across
	Bul	**Nak**	**Nam**	**Nge**	**Iki**	**Mean**	**Bul**	**Nak**	**Nam**	**Nge**	**Iki**	**Mean**	
BSPS17B	1.3	1.0	1.0	1.7	2.7	1.5	1.0	2.0	1.5	1.0	1.0	1.3	1.4
BSPS34	1.0	1.0	1.0	1.2	2.7	1.4	1.0	2.2	1.5	1.0	1.2	1.4	1.4
BSPS42	1.0	1.0	1.0	1.3	1.5	1.2	1.0	1.0	1.0	1.0	1.0	1.0	1.1
BSPS43	2.7	1.2	1.2	1.5	2.7	1.8	1.2	3.5	3.8	1.0	1.0	2.1	2.0
BSPS48A	2.2	1.5	1.3	1.3	1.8	1.6	1.2	2.3	1.2	1.0	1.0	1.3	1.5
BSPS85	1.0	1.2	1.0	2.0	3.0	1.6	1.0	2.5	1.2	1.0	1.0	1.3	1.5
DUIKER	1.0	1.0	1.2	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
DXTBLP(SRB)12.4	2.0	1.0	1.0	1.0	1.7	1.3	1.0	1.5	1.2	1.0	1.0	1.1	1.2
DXTBLP(SRB)4.21	2.0	1.8	2.7	1.7	3.3	2.3	1.2	3.3	1.8	1.2	1.3	1.8	2.0
DXTPROGENIES1.3	2.5	1.7	1.7	1.0	4.0	2.2	1.3	3.0	3.2	1.0	1.3	2.0	2.1
DXTPROGENIES4.17-4	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.2	1.0	1.0	1.0	1.0	1.0
DXTPROGENIES4.7	1.0	1.2	1.0	1.2	2.5	1.4	1.0	1.8	2.2	1.0	1.0	1.4	1.4
DXTPYT06A2.14	1.0	1.0	1.3	1.0	1.8	1.2	1.0	1.3	1.0	1.0	1.0	1.1	1.2
DXTPYT06A4.22	2.5	1.5	1.2	1.0	2.3	1.7	1.0	2.7	3.0	1.0	1.2	1.8	1.7
DXTPYT06A7.10	1.5	1.0	1.0	1.0	1.3	1.2	1.0	1.3	1.0	1.0	1.0	1.1	1.1
DXTPYT06A8.11	3.5	1.5	1.2	1.3	2.8	2.1	1.0	2.2	3.0	1.0	1.0	1.6	1.9
DXTPYT06A8.3	1.0	1.5	1.7	1.2	3.3	1.7	1.2	3.0	3.0	1.0	1.0	1.8	1.8
DXTSPS4.19	1.5	1.3	1.3	2.2	2.3	1.7	1.0	2.2	1.5	1.0	1.2	1.4	1.6
MAKSOY1N	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
NAM1	1.0	1.0	1.0	1.2	1.0	1.0	1.0	1.2	1.0	1.0	1.0	1.0	1.0
NAMIIXGCBLP11.3	1.8	1.3	2.3	1.3	2.2	1.8	1.0	2.5	2.0	1.0	1.0	1.5	1.7
NAMIIXGCBLP20.2	1.8	3.5	2.0	1.5	3.0	2.4	1.0	2.3	1.5	1.0	1.0	1.4	1.9
NGDT8.10-10	1.7	1.0	1.8	1.2	2.3	1.6	1.0	3.0	2.0	1.0	1.2	1.6	1.6
Mean	1.6	1.3	1.3	1.3	2.2	1.6	1.0	2.1	1.7	1.0	1.1	1.4	1.5
CV%	47	34.	26	42	38	51	16	29	42	5.9	17	52	52
LSD	1.2	0.7	0.6	0.9	1.4	0.6	0.3	1	1.2	0.1	0.3	0.5	0.4
Sed	0.6	0.4	0.3	0.4	0.7	0.3	0.1	0.5	0.6	0	0.1	0.3	0.2

Lodging scored on scale of 1-5, 1 = upright and 5= completely prostrate on ground; Bul = Bulindi, Nak = Nakabango, Nam = Namulonge, Nge = Ngetta, Iki = Iki Iki

4.4 Seed yield

The results of analysis of variance for grain yield indicate that all the main effects (genotype, season and location) and the two-way interactions (genotype x season; genotype x location; season x location) were significant (Table 9). Location accounted for 56% of total variation whereas season accounted for only 5.7% of total variation.

Table 9: ANOVA for grain yield of soybean genotypes grown at 5 locations during the 2008B, 2009A and 2009B season

Source	Df	Sum of squares	Mean square
Genotype	23	7886964	342911***
Season	2	23347026	11673513***
Location	4	227001527	56750382***
Genotype x Season	46	4957264	107767**
Genotype x Location	92	13796821	149965***
Season x Location	8	69730060	8716257***
Genotype x Season x Location	184	13758424	74774^{ns}
Residual	718	46636507	64953
Total	1079	407549973	

*** Significant at 0.1% level of significance, ** significant at 5% level of significance.

The analysis of variance using AMMI indicated highly significant (p<0.001) sum of squares due to genotypes, environment and genotype x environment interaction (Table 10). Both IPCA 1 and IPCA 2 were significant (p<0.001). The AMMI analysis of variance captured 27.5% of the interaction sum of squares with the first IPCA and 18.4% of the interaction sum of squares with the second IPCA. The partitioning of the interaction sum of squares was effective, with the mean square (MS) of the first IPCA axis 4.2 times that of the residual MS and the second IPCA axis MS 2.9 times that of the residual MS.

Table 10: The analysis of variance for AMMI of the 24 soybean cultivars tested over 15 environments in Uganda during 2008B, 2009A and 2009B seasons

Source	Df	Sum of squares	Mean of squares
Total	1079	407549973	377711
Treatments	359	360478085	1004117***
Genotypes	23	7886964	342911***
Environments	14	320078612	22862758***
Blocks	30	10648835	354961***
Interactions	322	32512509	100971***
IPCA1	36	8946885	248525***
IPCA2	34	5986239	176066***
IPCA3	32	4408014	137750***
Residuals	220	13171370	59870^{ns}
Error	690	36423053	52787

[1] *** significant at 0.001 level of significance

The results for 2008B (Appendix 1) showed that Nakabango (1776 kg ha^{-1}) produced the highest mean yield followed by Bulindi (1299 kg ha^{-1}). The lowest yield was observed at Ngetta (316 kg ha^{-1}). Results for 2009A and 2009B seasons revealed a similar trend of highest and least yielding environments. Namulonge was the second highest yielding environment after Nakabango in 2009B. Across locations, high yielding genotypes were BSPS48A, NGDT8.10-10, DXTPROGENIES4.17-4, DXTPYT06A8.3 and DXTPYT06A7.10 with 1276 kg ha $^{-1}$, 1204 kg ha^{-1}, 1200 kg ha $^{-1}$, 1109 kg ha^{-1} and 1100 kg ha^{-1}, while the least yielding genotypes were DXTPYT06A4.22, DXTPYT06A2.14, BSPS34 and local check DUIKER.

Combined yield results of the 24 soybean genotypes for 3 seasons across the 5 locations showed that Nakabango was the highest yielding environment with mean grain yield of 1834 kg ha^{-1} while Ngetta was the least yielding environment with mean grain yield of 465 kg ha^{-1} (Table 11). The least yields observed at Bulindi, Namulonge, Nakabango and

Iki Iki were higher than the highest yield observed at Ngetta. Across location and season, BSPS48A produced the highest grain yield (1409 kg ha^{-1}) whereas a commercial variety NAM 1 produced the lowest grain yield (1044 kg ha^{-1}). BSPS48A was the highest yielder (2216 kg ha^{-1}) in the highest yielding environment (Nakabango). BSPS48A yielded only 574 kg ha^{-1} in the least yielding environment (Ngetta). Only BSPS48A yielded highest in more than one location (Nakabango and Bulindi) but was out yielded by BSPS85 (623 kg ha^{-1}), BSPS43 (1593 kg ha^{-1}) and NGDT8.10-10 (1185 kg ha^{-1}) in Ngetta, Namulonge and Iki Iki, respectively.

At Bulindi the highest seed yielders were BSPS48A (1744 kg ha^{-1}), DXTPYT06A7.10 (1605 kg ha^{-1}), DUIKER (1512 kg ha^{-1}), DXTBLP(SRB)4.21 (1509 kg ha^{-1}) and DXTBLP(SRB)12.4 (1479 kg ha^{-1}), the highest yielders in Iki Iki were NGDT8.10-10 (1185 kg ha^{-1}), DXTPROGENIES4.7 (1161 kg ha^{-1}), DXTPROGENIES1.3 (1074 kg ha^{-1}), BSPS48A (1056 kg ha^{-1}) and BSPS43 (1025 kg ha^{-1}) (Table 11). At Nakabango, the highest seed yielders were BSPS48A (2216 kg ha^{-1}), NGDT8.10-10 (2093 kg ha^{-1}), DXTPROGENIES4.17-4 (2068 kg ha^{-1}), DXTPROGENIES4.7 (2062 kg ha^{-1}) and DXTPYT06A8.3 (2037 kg ha^{-1}). The results from Namulonge showed that BSPS43 (1593 kg ha^{-1}), DXTPROGENIES1.3 (1481 kg ha^{-1}), BSPS48A (1457 kg ha^{-1}), DXTPROGENIES4.7 (1426 kg ha^{-1}) and DXTPYT06A8.11 (1420 kg ha^{-1}) were the highest yielders. In Ngetta the highest yielders were BSPS85 (623 kg ha^{-1}), BSPS48A (574 kg ha^{-1}), DXTPYT06A8.3 (543 kg ha^{-1}), NAMIIXGCBLP11.3 (537 kg ha^{-1}) and DXTBLP(SRB)12.4 (518 kg ha^{-1}).

Table 11: Mean grain yield (kg ha^{-1}) of 24 soybean genotypes grown at 5 locations during the 2008B, 2009A and 2009B seasons

Genotype	Location					
	Bul	Iki	Nak	Nam	Nge	Mean
BSPS17B	1185	877	1945	1173	506	1137.1
BSPS34	1173	963	1605	1327	438	1101.3
BSPS42	1374	753	1710	1278	506	1124.1
BSPS43	1306	1025	1833	1593	364	1224.1
BSPS48A	1744	1056	2216	1457	574	1409.3
BSPS85	1238	1012	1901	1346	623	1224.1
DUIKER	1512	963	1364	1315	395	1109.9
DXTBLP(SRB)12.4	1479	957	1901	1420	518	1254.9
DXTBLP(SRB)4.21	1509	963	1772	1352	457	1210.5
DXTPROGENIES1.3	1241	1074	1796	1481	389	1196.3
DXTPROGENIES4.17-4	1327	852	2068	1408	482	1227.1
DXTPROGENIES4.7	1316	1161	2062	1426	512	1295.3
DXTPYT06A2.14	1407	809	1481	1148	377	1044.4
DXTPYT06A4.22	1281	907	1691	1272	370	1104.3
DXTPYT06A7.10	1605	753	1741	1333	457	1177.8
DXTPYT06A8.11	1441	870	1895	1420	457	1216.7
DXTPYT06A8.12	1398	914	2000	1296	401	1201.8
DXTPYT06A8.3	1441	945	2037	1407	543	1274.7
DXTSPS4.19	1404	963	1994	1321	370	1210.5
MAKSOY1N	1306	735	1716	1247	512	1103.1
NAM1	1438	926	1519	858	482	1044.4
NAMIIXGCBLP11.3	1077	957	2019	1290	537	1175.9
NAMIIXGCBLP20.2	1182	926	1654	1210	414	1077.1
NGDT8.10-10	1426	1185	2093	1253	469	1285.0
Grand mean	1367.1	939.3	1833.8	1317.9	464.8	1184.6
Sed	135.7	199.7	215.1	248.3	106.8	120.05
CV%	21.1	45.1	24.9	40	48.8	21.5

Bul= Bulindi, Iki = Iki iki, Nak = Nakabango, Nam = Namulonge

Sed = Standard error of the difference

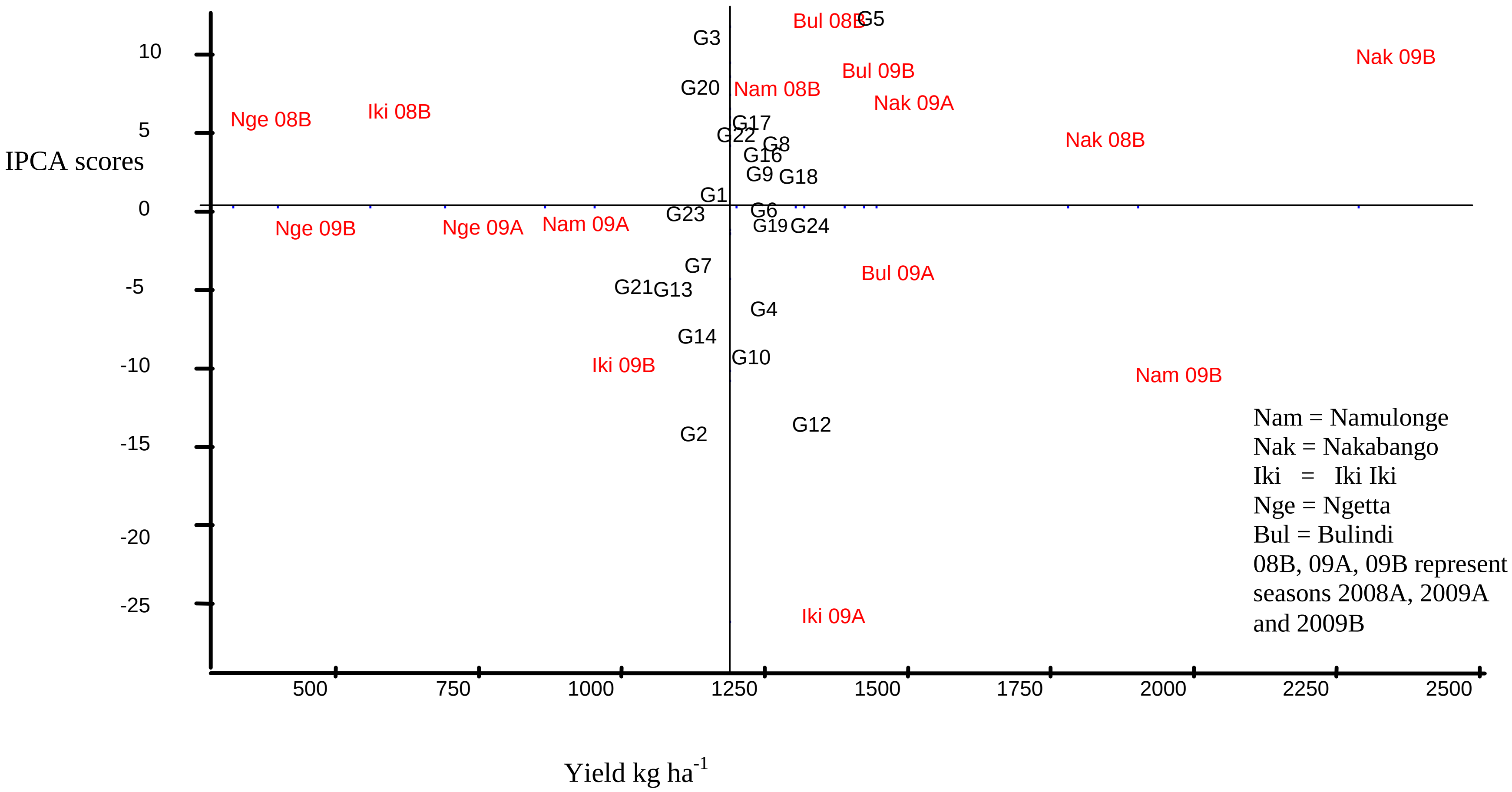
CV = Coefficient of variation

AMMI 2 explained 95% of the treatment sum of squares while the residual contained only 3.7%. The treatment and block sum of squares combined made up 91.1% of the total sum of squares with 36.1% of total degree of freedom. Error term's sum of squares made only 8.9% of the total sum of squares while containing 64.0% of the total degrees of freedom. These results indicate that AMMI model fits the data well and justified the use of AMMI 2.

The biplot was generated using genotypic and environmental scores of the first two IPCAs (Figure 1). The biplot showed that environments Namulonge (2009A), Ngetta (2009A) and Ngetta (2009B) had Environmental IPCAs close to zero. The environments were scattered without any grouping among them and the majority of the genotypes were clustered around the plot origin. Genotypes BSPS34 (G2) and DXTPROGENIES4.7 (G12) had the highest eigen vector scores while genotypes BSPS17B (G1), BSPS85 (G6), NAMIIXGCBPL20.2 (G23), NGDT8.10-10 (G24) and DXTSPS4.19 (G19) had the lowest eigen vector scores (GIPCA2) (Table 13). BSPS48A (G5) was the highest yielding with a relatively low interaction.

Genotypes BSPS34 (G2), DXTPYT06A4.22 (G14), DUIKER (G7), MAKSOY 1N (G20) and BSPS42 (G3) were positioned along the same ordinate axis and therefore differed only in the interaction effect and not in the main effect while DXTBLP(SRB)4.21 (G9) and DXTPYT06A8.12 (G18) showed little G x E interaction on IPCA 1 and were grouped together along the abscissa, although they differed in main effect.

Figure 1: AMMI2 biplot of 24 genotypes and 15 environments for soybean grain yield using genotypic and environmental scores



Nam = Namulonge
Nak = Nakabango
Iki = Iki Iki
Nge = Ngetta
Bul = Bulindi
08B, 09A, 09B represent seasons 2008A, 2009A and 2009B

Table 12: Summary of the genotypic IPCA scores for the 24 soybean genotypes grown at 5 locations during the 2008B, 2009A and 2009B seasons

Genotype	**Genotype code**	**Mean**	**GIPCA1**	**GIPCA2**
BSPS17B	G1	1137	9.70199	0.40026
BSPS34	G2	1101	0.50492	-14.8448
BSPS42	G3	1124	-6.80718	10.43303
BSPS43	G4	1224	9.07674	-6.90532
BSPS48A	G5	1409	4.44324	11.52664
BSPS85	G6	1224	3.17494	-0.53977
DIUKER	G7	1110	-24.3139	-4.12355
DXTBLP(SRB)12.4	G8	1246	-0.76588	3.6483
DXTBLP(SRB)4.21	G9	1218	-4.29997	1.70792
DXTPROGENIES1.3	G10	1191	3.29866	-9.94946
DXTPROGENIES4.17-4	G11	1228	7.10247	12.83951
DXTPROGENIES4.7	G12	1298	10.98272	-14.2239
DXTPYT06A2.14	G13	1058	-8.19812	-5.5947
DXTPYT06A4.22	G14	1098	-1.98147	-8.6067
DXTPYT06A7.10	G15	1183	-7.25016	12.80702
DXTPYT06A8.11	G16	1212	-2.66562	2.92733
DXTPYT06A8.12	G17	1197	5.26127	4.28954
DXTPYT06A8.3	G18	1275	6.80549	1.58828
DXTSPS4.19	G19	1211	3.66717	-1.00656
MAKSOY1N	G20	1103	-5.25526	7.23911
NAM1	G21	1044	-16.3225	-5.43788
NAMIIXGCBLP11.3	G22	1166	12.93656	4.22662
NAMIIXGCBLP20.2	G23	1077	-0.50921	-0.82183
NGDT8.10-10	G24	1295	1.4131	-1.57906

The best four genotype recommendations based on estimated yield are shown for each environment (Table 13). Genotype BSPS48A (G5) was the first recommendation in 11 out of 15 times third in 2 out of 15 times and fourth in one out of 15 times. This genotype was in the top four recommendations 14 out of 60 times. No other genotype matched the performance of BSPS48A.

Table 13: Summary of the mean yields of soybean genotypes, Environmental IPCA scores and first four AMMI2 selections for the 15 environments for 2008B, 2009A and 2009B seasons

Environment	Mean	Environmental IPCA score		First four AMMI2 selections			
		EIPCA1	EIPCA2	1	2	3	4
Bul 08B	1299	-22.32458	11.51803	G7	G15	G5	G3
Bul 09A	1418	-15.3659	-4.56029	G7	G21	G5	G24
Bul 09B	1384	0.2084	8.31752	G5	G11	G18	G15
Iki 08B	556	-3.64686	5.72105	G5	G15	G24	G11
Iki 09A	1314	6.1463	-26.44447	G12	G2	G10	G4
Iki 09B	948	-4.09775	-10.44091	G12	G24	G10	G5
Nak 08B	1776	12.61094	3.92783	G5	G12	G11	G18
Nak 09A	1441	6.18749	6.28521	G5	G11	G18	G24
Nak 09B	2284	24.3546	9.2111	G5	G23	G11	G18
Nam 08B	1195	4.82524	7.14918	G5	G11	G18	G24
Nam 09A	860	-2.97575	-1.42748	G5	G24	G12	G18
Nam 09B	1898	4.8915	-11.08309	G12	G4	G22	G10
Nge 08B	316	1.48274	5.22921	G5	G11	G18	G24
Nge 09A	686	-6.45781	-1.67208	G5	G24	G7	G12
Nge 09B	393	-5.83856	-1.73081	G5	G24	G7	G12
Dominant type				G5	-	G18	G24

4.5 Discussion

Use of resistant varieties is the most cost effective means of managing soybean diseases (Koenning and Dunphy, 2000). Equally important, is the need to identify stable genotypes. This study evaluated 24 soybean genotypes during the first and second seasons of 2009 for tolerance to soybean rust. These genotypes were also subjected to a GXE yield study.

Field observations showed that soybean rust was the major soybean disease in all soybean growing areas. Twizeyima *et al.* (2008) also reported that soybean rust is the most important and destructive foliar disease of soybeans. The results of rust severities showed that mean rust scores of 2009A were generally higher than those of 2009B. This may have resulted from the high amounts of rainfall that were received in the second season (Appendix 4). Soybean rust is known to be influenced by environmental factors notably rainfall, temperature, leaf wetness and relative humidity. The amount of rainfall received during a growing season greatly influences soybean rust development (DelPonte *et al*., 2006). According to DelPonte *et al*. (2006), rainfall is a good source of leaf wetness, which enhances rust infection and sporulation. Soybean genotypes that showed very low rust scores (<2) over the two seasons included NAM11XGCBLP11.3, BSPS43, NAM11XGCBLP20.2 and BSPS48A. These genotypes must be possessing specific genes that make them highly resistant to soybean rust. They have potential of providing resistance to susceptible genotypes through hybridization.

The analysis of variance of seed yield of soybean genotypes (Table 9) indicated significant differences among genotypes and environments, justifying genotype and environment interaction analysis. The genotype and environment main effects were highly significant ($p < 0.001$). This indicated the diversity of genotypes and heterogeneity of environments that were used for the study. ANOVA in Table 9 identified this interaction, however with AMMI analysis, it was possible to quantify the interaction and identify the sources of interaction (Table 10). The AMMI with only two IPCA axes was the best predictive model and had 70 degrees of freedom. The most accurate model for AMMI can be predicted by using the first two IPCAs (Kaya *et al*., 2002).

The biplot indicated that environments were scattered without any grouping among them. This showed that the test environments also showed season to season variation in mean yield of genotypes and were evenly distributed in all four quadrants. This suggested that two or more seasons of testing are better than a single season. Genotypes with IPCA scores near zero had little interaction across locations whereas genotypes with large IPCA scores were highly interactive (Carbonell *et al*., 2004). Conversely, locations or seasons with IPCA scores near zero had little genotype interaction and low genotype discrimination. The difference exhibited by genotypes over interaction and mean effect might have been due to differential adaptability of the genotypes to different environments. Genotypes BSPS17B (G1), BSPS85 (G6), NAMIIXGCBPL20.2 (G23), NGDT8.10-10 (G24) and DXTSPS4.19 (G19) had IPCA scores nearest zero and were the most stable across the environments studied. Among these stable genotypes BSPS85 (G6), DXTSPS4.19 (G19) and NGDT8.10-10 (G24) exhibited above average grain yield (1185 kg ha^{-1}), indicating that these genotypes were adapted to different agro ecological zones of Uganda.

Nakabango showed the highest overall yield across genotypes during the three growing seasons. This may be attributed to the high soil fertility and high amounts of rainfall that were received during the growing seasons. The station however showed relative stability in terms of G x E interaction in only 2009A while 2008B and 2009B were highly unstable. Ngetta experienced stormy weather with hailstones during the growing seasons. This resulted in low yields in this location over the three seasons. Bulindi showed yields higher than the grand mean during the three growing seasons. This could be attributed to high rainfall that was received during the growing season.

It was observed that all the new genotypes out-yielded the local checks. Among the local checks, only MAKSOY1N out yielded the new genotypes. Even then, it out-yielded only three genotypes. With AMMI2 (Table 13), it is possible to identify cultivars that are adapted to a narrow range of environments as well as a wider range of environments. Only genotypes BSPS48A (G5), DXTPROGENIES4.7 (G12), DXTPYT06A8.3 (G18), NGDT8.10-10 (G24), DUIKER (G7) and DXTPROGENIES4.17-4 (G11) were relatively stable during the three seasons making them suitable genotypes for release.

CHAPTER FIVE

GENERAL DISCUSSION AND CONCLUSION

Plant breeding has undoubtedly led to crop improvement over the last decades leading to creation of prolific varieties. However, small-scale farmers who routinely operate under heterogeneous and unfavorable growing conditions haven't benefited a lot from these advances in genetic improvement. Such farmers have maintained old varieties/ landraces that are often low yielding and susceptible to pests and diseases, an issue that has challenged scientists who have been working to create varieties with desirable attributes. Conventional breeding failures have led to the development of new concepts that are farmer oriented, with considerations of diverse socioeconomic conditions and environmental considerations.

This study was designed to respond to some of these challenges, and involved two objectives. First was to establish soybean traits most desired by a cross-section of Ugandan farmers and processors. Farmers and processors were thus involved in the evaluation of new soybean genotypes. This was due to the realization that end-users can take on distinct roles at various points in the crop improvement cycle. One of the great strengths of participatory crop improvement is that it is both an extension and a research method. Varieties tested using participatory approaches can rapidly spread from farmer to farmer as well as exposing farmers to novel cultivars. Participatory approaches therefore link research and extension to form an integral part of a coherent innovation system that develop and sustain their competitive edge (Ashby and Lilja, 2004).

Participation allows scientists and farmers to learn from each other. Scientists have a broad knowledge of available genetic resources and appropriate breeding methods while farmers contribute local knowledge and test varieties under local environments. The whole process speeds up the process of varietal adoption and increases the varietal biodiversity in farmers' fields (Stirling and Witcombe, 2004).

Attributes that were considered important by farmers when selecting the best soybean genotypes included early maturity, disease tolerance, high yielding, big seed size and attractive seed coat colour. Early maturity was the most important field characteristic considered because early maturing varieties escape drought and can be marketed early. A case in point is genotypes DXTPROGENIES4.7, BSPS17B, BSPS48A and BSPS85 which were found to have yielded highest but were not selected because they were not early maturing. It is therefore important that soybean breeding programmes initiate a breeding scheme for early maturity.

Results from on-farm trials showed that 60% of the most farmer preferred new genotypes were found not to be the highest yielding genotypes. This shows that farmers may choose lower yielding genotypes with other preferred attributes. Scientists should therefore always consider the farmers' contribution in the development of new varieties. The promising varieties were grown on a large scale by some farmers in subsequent seasons, confirming earlier reports by String and Witcombe (2004) that involving farmers can speed up varietal adoption and dissemination. The best preferred genotypes were DXTPYT06A8.11, DXTPROGENIES4.17-4, MAKSOY1N, DXTPYT06A7.10 and DXTBLP(SRB)12.4. Genotype DXTPYT06A8.11 was better than MAKSOY1N (local check) in terms of farmer preference showing that it the potential of meeting farmers' needs. Selection of varieties by farmers and researchers is a process. Since farmers compared the entire soybean genotypes together in their fields (mother trial), there is need for farmers to compare few (two to five) best genotypes they selected (baby trial) in order to come up with the best genotype among the selected new genotypes.

Processors of soy-based animal and human products in Kampala were also allowed to assess the new soybean genotypes. Results from assessment of processors' needs showed that their desired attributes varied depending on the intended use of the processed product. Processors of animal feeds for example Formula Feeds tend to use any soybean variety that is available while those of human products tend to be very selective. Generally traits desired by processors included big seed size, yellow or cream colour of testa, and yellow or white hilum. Processors of human products were willing to compromise on other attributes but not on black hilum. The genotypes which were considered excellent by processors included; DXTSPS4.19, NGDT8.10-10 and DXTPYT06A4.22. Local checks NAM1 and MAKSOY1N were among the least preferred genotypes indicating that it is possible to meet the processors' needs using available new genotypes. This also implies that more varieties within those evaluated in this study could be made use of if we identified farmers willing to grow varieties for a specific purpose. For example, the high yielding and black hilum genotypes could be promoted and grown for animal feed processing. Processors identified other desired attributes lacking in the current commercial varieties. These included sharp flavour/aroma and varieties whose seed-coat doesn’t peel off during processing. These constitute a breeding objective.

Results from on-station experiments showed that soybean rust was the major soybean disease in all farming environments in Uganda. Earlier studies by Miles *et al*. (2003) established that soybean rust is the most important foliar disease in soybean production globally. Mean rust scores during 2009A were generally higher than those of 2009B and genotypes NAM11XGCBLP11.3, BSPS43, NAM11XGCBLP20.2 and BSPS48A showed very low rust scores (<2) over the two seasons included, suggesting that they could be harbouring soybean rust resistance genes. Dissection of the genetic architecture of these resistance genes would be desirable for future soybean rust breeding both in Uganda and the region.

AMMI analysis indicated that genotypes BSPS17B (G1), BSPS85 (G6), NAMIIXGCBPL20.2 (G23), NGDT8.10-10 (G24) and DXTSPS4.19 (G19) were the most stable across environments. Among these stable genotypes BSPS85 (G6), DXTSPS4.19 (G19) and NGDT8.10-10 (G24) exhibited above average grain yield and thus suggesting that these genotypes were adapted to different agro ecological zones of Uganda. Nakabango showed the highest overall yield which could be attributed to the high soil fertility and high amounts of rainfall that were experienced at the location during the growing seasons. Genotype BSPS48A yielded highest during the three seasons making it a suitable genotype for release. The other genotypes that were relatively stable during the three seasons included DXTPROGENIES4.7, DXTPYT06A8.3 and NGDT8.10-10.

In conclusion, soybean production and its value addition involve a wide range of stakeholders linked by trade and services, each playing a crucial role in the soybean value chain. Development of new soybean varieties therefore requires careful planning in selection of parental lines to ensure that systematic genetic gain is achieved. Involvement of end-users in the development of new soybean genotypes helped in the identification of attributes valued by end-users but unknown to breeders. This finding further justifies the need for participatory crop improvement. Stability study helped in the identification of new soybean genotypes stable across environments and tolerant to soybean rust. No single genotype can supply all the attributes valued by stakeholders in the soybean value chain. Hence, the breeding efforts should aim at supplying a range of varieties that can enable farmers and other end-users to have a choice.

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Appendix 1: Summary of the environmental mean yields, genotypic IPCA scores and environmental IPCA scores for the 24 soybean genotypes grown at 5 locations during the 2008B, 2009A and 2009B seasons

Genotype code	Bul 08B	Nak 08B	Nam 08B	Nge 08B	Iki 08B	Bul 09A	Nak 09A	Nam 09A	Nge 09A	Iki 09A	Bul 09B	Nak 09B	Nam 09B	Nge 09B	Iki 09B	G mean	GIPCA1	GIPCA2
G1	852	1815	1259	333	463	1315	1593	796	852	1500	1389	2426	1463	333	667	1137	9.70199	0.40026
G2	1093	1648	1000	185	407	1333	1000	833	611	1574	1093	2167	2148	518	907	1101	0.50492	-14.8448
G3	1491	1648	1463	407	407	1407	1315	852	685	926	1222	2167	1519	426	926	1124	-6.80718	10.43303
G4	991	1908	1426	352	630	1481	1130	944	426	1426	1444	2463	2407	315	1018	1224	9.07674	-6.90532
G5	1620	2130	1278	518	833	1574	1759	1019	593	1315	2037	2759	2074	611	1019	1409	4.44324	11.52664
G6	1139	1815	1259	481	593	1204	1630	944	870	1352	1370	2259	1833	519	1093	1224	3.17494	-0.53977
G7	1704	1185	1037	148	648	1648	1370	889	593	1037	1185	1537	2019	444	1204	1110	-24.3139	-4.12355
G8	1417	1741	1241	370	611	1463	1556	1111	741	1370	1556	2407	1778	444	889	1246	-0.76588	3.6483
G9	1528	1630	1315	204	630	1481	1352	963	741	1370	1519	2333	1889	426	889	1218	-4.29997	1.70792
G10	1000	1778	1241	278	593	1426	1463	926	611	1444	1296	2148	2204	278	1185	1191	3.29866	-9.94946
G11	1296	2019	1371	407	907	1315	1667	722	722	963	1370	2519	2148	315	685	1228	7.10247	12.83951
G12	1148	1833	1129	222	481	1374	1704	907	815	1963	1426	2648	2278	500	1037	1298	10.98272	-14.2239
G13	1167	1629	1167	148	204	1537	1130	815	630	1370	1519	1778	1574	352	852	1058	-8.19812	-5.5947
G14	1102	1611	907	185	407	1407	1444	852	722	1407	1333	2000	1981	204	907	1098	-1.98147	-8.6067
G15	1574	1815	1204	278	630	1500	1296	815	722	815	1741	2185	1981	370	815	1183	-7.25016	12.80702
G16	1435	1833	1222	278	593	1500	1574	981	722	1204	1389	2204	2056	370	815	1212	-2.66562	2.92733
G17	1213	1741	1278	333	444	1500	1593	870	611	1241	1481	2593	1741	259	1056	1197	5.26127	4.28954
G18	1417	1982	1370	389	389	1278	1593	852	685	1519	1630	2537	2000	556	926	1275	6.80549	1.58828
G19	1343	1870	1093	259	463	1519	1611	870	537	1352	1352	2500	2000	315	1074	1211	3.66717	-1.00656
G20	1546	1463	1019	315	519	1222	1370	963	759	1056	1148	2315	1759	463	630	1103	-5.25526	7.23911
G21	1407	1685	741	241	592	1796	1130	463	852	1389	1111	1741	1370	352	796	1044	-16.3225	-5.43788
G22	898	2000	1333	537	685	1185	1500	722	630	1148	1148	2556	1815	296	1037	1166	12.93656	4.22662
G23	1194	1555	1074	352	685	1111	1333	778	667	1333	1241	2074	1778	222	759	1077	-0.50921	-0.82183
G24	1593	2296	1259	352	518	1463	1481	759	667	1463	1222	2500	1739	537	1574	1295	1.4131	-1.57906
E Mean	1299	1776	1195	316	556	1418	1441	860	686	1314	1384	2284	1898	393	948	1185		
EIPCA1	-22.3	12.61	4.83	1.484	-3.66	-15.4	6.188	-2.97	-6.5	6.15	0.21	24.35	4.89	-5.84	-4.1			
EIPCA2	11.51	3.922	7.14	5.241	5.718	-4.57	6.292	-1.43	-1.7	-26	8.32	9.221	-11.1	-1.73	-10			

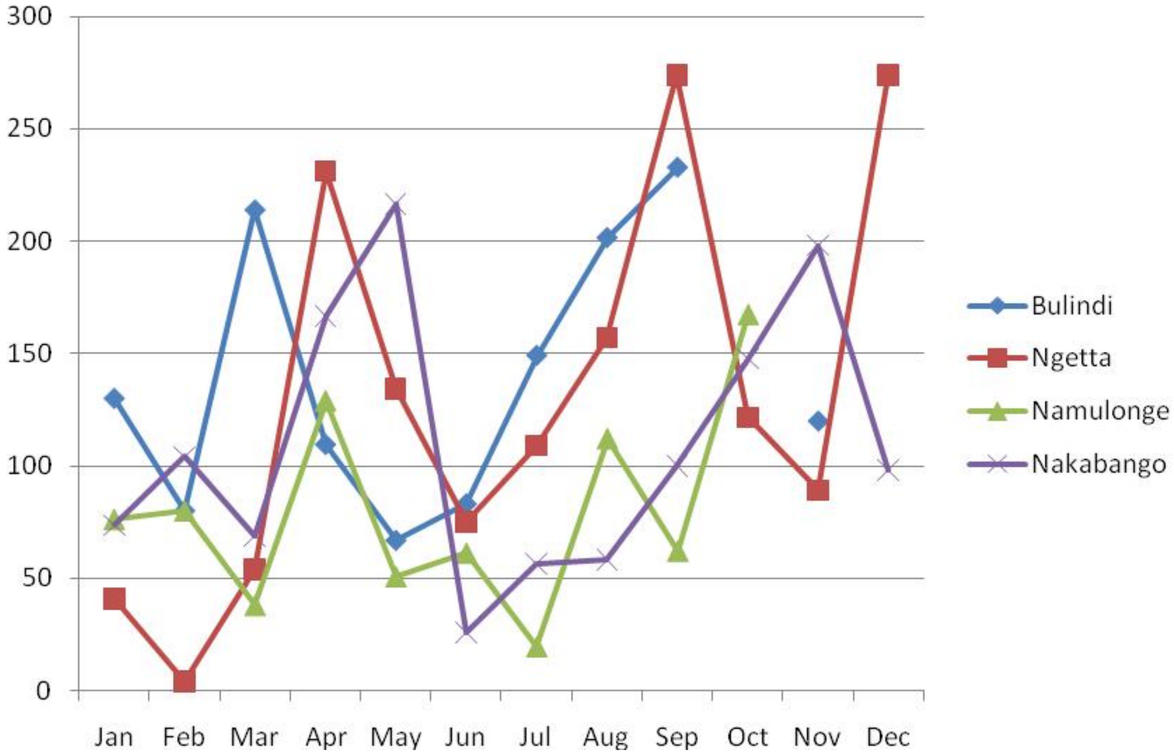
Appendix 2: Computed preference scores for 24 soybean genotypes grown in different districts of Uganda

	2009A							2009B						
Genotye	Lira	Apac	Jami	May	Mas	Hoima	Kam	Lira	Apac	Jami	May	Mas	Hoima	Kam
BSPS17B	-0.025	-0.020	-0.025	-0.033	-0.017	-0.025	-0.025	-0.020	-0.020	-0.050	-0.025	-0.075	0.000	-0.020
BSPS34	0.013	0.020	0.025	0.033	-0.050	-0.050	-0.075	0.017	0.017	0.050	0.025	0.000	-0.050	-0.050
BSPS42	0.013	0.020	0.025	0.033	0.000	0.000	0.000	0.033	0.017	0.050	0.025	-0.025	-0.025	-0.020
BSPS43	-0.050	-0.050	0.050	0.050	-0.017	-0.013	-0.025	-0.050	-0.030	0.050	0.050	-0.025	0.000	0.000
BSPS48A	-0.025	-0.010	-0.025	-0.033	-0.017	-0.025	-0.010	0.017	0.000	-0.050	-0.025	-0.025	0.000	-0.030
BSPS85	0.038	0.060	0.025	0.017	0.000	-0.013	0.000	0.067	0.033	0.000	0.025	-0.025	-0.025	-0.020
DUIKER	0.025	0.020	0.000	0.033	0.033	0.013	0.000	0.000	0.017	0.000	0.025	0.000	0.000	0.033
DXTBLP(SRB)12.4	0.025	0.020	0.025	0.017	0.017	0.038	0.038	0.017	0.033	0.000	0.000	0.050	0.025	0.033
DXTBLP(SRB)4.21	0.013	0.010	-0.050	-0.033	0.000	0.000	0.000	0.000	0.000	0.000	-0.025	0.000	-0.025	0.000
DXTPROGENIES1.3	-0.013	-0.020	0.000	0.017	0.000	0.000	-0.010	-0.030	-0.030	0.000	0.025	0.000	0.000	0.017
DXTPROGENIES4.17-4	0.088	0.080	-0.050	-0.033	0.017	0.025	0.025	0.067	0.067	0.000	-0.025	0.025	0.025	0.033
DXTPROGENIES4.7	-0.013	-0.010	0.025	0.017	0.000	0.000	0.000	-0.020	-0.050	0.000	0.025	0.000	0.000	0.017
DXTPYT06A2.14	0.025	0.020	-0.025	0.000	0.000	0.013	0.000	0.000	0.017	0.000	-0.025	0.000	-0.025	0.000
DXTPYT06A4.22	0.000	0.000	0.000	0.000	0.033	0.025	0.050	0.017	0.000	0.000	0.000	0.025	0.050	0.017
DXTPYT06A7.10	0.025	0.030	0.025	0.033	0.017	0.038	0.025	0.017	0.017	0.050	0.025	0.025	0.000	0.017
DXTPYT06A8.11	0.025	0.020	0.025	0.017	0.017	0.050	0.038	0.033	0.050	0.000	0.025	0.050	0.025	0.033
DXTPYT06A8.12	0.050	0.030	0.025	0.000	0.017	0.013	0.013	0.017	0.017	0.000	0.025	0.025	0.025	0.033
DXTPYT06A8.3	-0.013	-0.020	-0.025	-0.017	0.000	-0.013	0.000	-0.020	-0.020	0.000	-0.025	0.000	0.025	0.000
DXTSPS4.19	0.000	-0.030	0.000	0.017	0.000	0.000	0.000	-0.050	-0.020	0.000	0.000	0.000	0.000	-0.020
MAKSOY1N	-0.038	-0.040	0.075	0.083	0.050	0.013	0.050	0.000	-0.020	0.050	0.050	0.025	0.050	0.017
NAM1	0.013	0.020	0.000	-0.007	0.000	0.013	0.000	0.033	0.033	-0.050	-0.050	0.000	0.000	0.000
NAMIIXGCBLP11.3	-0.088	-0.090	-0.100	-0.100	-0.067	-0.088	-0.090	-0.100	-0.080	0.100	-0.100	-0.025	-0.050	-0.080
NAMIIXGCBLP20.2	-0.050	-0.030	0.000	-0.017	-0.033	-0.025	-0.010	-0.030	-0.050	0.000	0.000	0.000	-0.025	-0.020
NGDT8.10-10	-0.038	-0.030	-0.025	-0.033	0.000	0.013	0.013	-0.020	0.000	0.000	-0.025	0.000	0.000	0.000

May = Mayuge, Mas = Masindi, Kam = Kamwenge

Appendix 3: Farmers in the process of selecting desired soybean genotypes at their fields

Appendix 4: Monthly rainfall totals for research stations in (mm) for 2009



Data source: Uganda Department of Meteorology, Entebbe

Appendix 5: Questionnaire to ascertain soybean traits desired by processors in Uganda

1. Name of the company

………………………………………………………………………………………

……………………………………………………………………………………….

2. What range of soybean products do you process?

………………………………………………………………………………………

………………………………………………………………………………………

……………………………………………………………………………………

3.i) What is the source of the soybeans used?

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……………………………………………………………………………………..

ii) Which soybean varieties do you use? If known

………………………………………………………………………………………

………………………………………………………………………………………

………………………………………………………………………………………

4i) which soybean attributes are you interested in for each product?

Desired attributes

…………………………………………………………………………………………

…………………………………………………………………………………………

…………………………………………………………………………………………

Undesired attributes

…………………………………………………………………………………………

…………………………………………………………………………………………

………………………………………………………………………………………..

ii) Of the attributes mentioned above, what do you consider to be the most important for each soy product?

Desired	

5. Which desired soybean attributes are lacking in the available varieties?

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....

6. Among the 22 new soybean varieties (to be displayed), which ones meet your preferences?

Desired	**Undesired**

7. Do you have any other comment on soybean varieties?

…………………………………………………………………………………………………

…………………………………………………………..