THESIS

GENETIC DIVERSITY IN THE SOUTHEAST ASIAN *SOLANUM*

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THESIS

GENETIC DIVERSITY IN THE SOUTHEAST ASIAN *SOLANUM*

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Patcharin Taridno 2008: Genetic Diversity in the Southeast Asian *Solanum*. Master of Science (Agriculture), Major Field: Horticulture, Department of Horticulture. Thesis Advisor: Associate Professor Sutevee Sukprakarn, Ph.D. 211 pages.

Eighty-nine accessions of *Solanum* spp. originally collected from Southeast Asia have been regenerated and characterized, using a standard set of IBPGR descriptors, at Genetic Resources and Seed Unit (GRSU), Asian Vegetable Research and Development Center (AVRDC), Shanhua, Tainan, Taiwan from October 2005 to May 2006. Eleven species were identified as follows: *Solanum melongena* L. (38 accessions), *S. aculeatissimum* (2 accessions), *S. aethiopicum* (1 accession), *S. ferox* (17 accessions), *S. indicum* (8 accessions), *S. mammosum* (1 accession), *S. sanitwongsei* (1 accession), *S. torvum* (11 accessions), *S. trilobatum* (3 accessions), *S. viarum* (1 accession) and *S. xanthocarpum* (6 accessions). The 69 accession of 89 accessions were grouped into ten clusters based on the quantitative traits and nine clusters based on qualitative traits. The quantitative traits however had more variation than qualitative traits and showed almost the same composition in each cluster. The variation among the eleven *Solanum* spp. can be also attributed to their inherent variation and geographic distribution.

The interspecific hybridization was also applied to determine the genetic relationships between cultivated *Solanum melongena* and other four species (*S. torvum*, *S. americanum*, *S. villosum* and *S. nigrum*). The crossiblility among the species was determined by percentage of fruit set and number of seeds per fruit. The results showed that *S. torvum* was more closely related to *S. melongena* than the other *Solanum* (*S. americanum*, *S. villosum* and *S. nigrum*). From the interspecific crossability among these three *Solanum*, the *S. americanum* is more closely related to *S. villosum* than *S. nigrum.* Furthermore, The pollen fertility of interpecific hybrids (F_1 hybrids) was lower than their parents. F_1 hybrids showed intermediate morphological charaterisitics and ploidy levels when compared to their parents.

Student’s signature   Thesis Advisor’s signature   ___ ___ ___

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LIST OF ABBREVIATIONS

cm	=	centimeter
°C	=	degree Celsius
DAP	=	day after pollination
DNA	=	deoxyribonucleic acid
DTT	=	dithriothreitol
g	=	gram
HCl	=	hidrochlorice acid
l	=	liter
M	=	molar
m	=	meter
µg	=	microgram
µl	=	microliter
µM	=	micromolar
µm	=	micrometer
mg	=	milligram
ml	=	mililiter
mm	=	milimeter
NaOH	=	sodium hydroxide
Na_2HPO_4	=	sodium phosphate dibasic
PBS	=	phosphate bi sodium
PI	=	propidium iodide
RAPD	=	randomly amplified polymorphic DNA

GENETIC DIVERSITY IN THE SOUTHEAST ASIAN *SOLANUM*

INTRODUCTION

Solanum is the largest and the most complex genus of the *Solanaceae* family. It is composed of more than 1,500 species (Esmonds and Chweya, 1997). The best known species and the most economically important in term of production volume is eggplant (*S. melongena*). It is domesticated in the Indo-Burmese region and cultivated nowadays all over the world (Daunay *et al*., 2000). Cultivation of *S. melongena* or wild relatives are covering a wide range of *Solanum* species (mainly subgenus *Leptostemonum*). The geographical origin of *Solanum* is mainly in Asia and Africa. Although *Solanum* species are grown everywhere, the main cultivation area is in the tropical and warm regions. Specifically, the centers of diversity are in South America, Australia and Africa, while relatively less diverse species are found in Europe and Asia (Esmonds and Chweya, 1997).

However, *S. melongena* is mainly cultivated in Asia (Daunay *et al*., 1995). In addition, more than 90 % of the world's *S. melongena* is produced in Asia like China, with 54 % of supply (12 million ton) followed by India (6 million ton) and Turkey (850,000 ton). In contrast, Thailand produces only 0.7 % of the world's *S. melongena* crop (FAO, 2006).

At present, the primitive cultivars of *S. melongena* are still in Asian countries, but not preferable by consumers especially in Indonesia, Philippines, Thailand and Malaysia, due to the used of high yielding varieties (Daunay *et al*., 1995). In 1977, *S. melongena* was added to the list of species having priority for genetic resources conservation (Daunay *et al*., 1995). Therefore, several prospecting expeditions, sponsored by International Board for Plant Genetic Resources (IBPGR), were conducted in Asia and Africa (Lester, 1986).

Asian Vegetable Research and Development Center (AVRDC) - The World Vegetable Center also maintains a *S. melongena* germplasm for crop improvement program and other research purposes. In 2006, there are 3,096 accessions, including 1,777 accessions of *S. melongena* and 1,319 accessions of other *Solanum* species. To date, a total of 870 accessions have been regenerated. AVRDC's collections of vegetable germplasm, as well as *S. melongena* collection, are conserved in the Genetic Resources and Seed Unit (GRSU) which houses as the genebank. GRSU is also responsible for the regeneration, characterization, evaluation and distribution of vegetable germplasm.

Moreover, many reports have been studied on the genetic diversity but information of wild species of *Solanum* spp. is still lacking and divergence is usually related to adaptation to different geographical areas or climates or different ecological habitats. In the process of adaptation, populations may become genetically distinct (Webb *et al*., 1988). The availability of information on the taxonomic status and the geographic origin of germplasm accessions is a vital prerequisite for both the conservation and effective utilization of plant genetic resources.

Therefore, morphological and genetic relationship is being employed in the genetic characterization of species. The use of morphological characteristics is considered as the most classical because it only uses the external characters of the individuals to determine genetic variability. These are also a powerful tool which could yield significant information enhancing the use of germplasm in crop improvement programs.

Interspecific hybridization can exhibit evolutionary path; the closely related species have high possibility of success in crossing. Additionally, the experiments on crossability of *S. melongena* with its wild relatives have been attempted and new approaches, such as somaclonal variation, somatic hybridization and genetic transformation, have been investigated for induction of genetic variability.

Therefore, the purpose of this study is to determine the genetic diversity of *Solanum* in Southeast Asia based on morphological characters and genetic relationship between *Solanum* and wild relatives using interspecific hybridizatio

OBJECTIVES

1. To characterize using a standard set of descriptors sample of *Solanum* accessions originating from Southeast Asia.

2. To determine the Southeast Asian *Solanum* from major groups based on morphological characters.

3. To determine the correlation between morphological traits and geographical origin of Southeast Asian *Solanum*.

4. To study the genetic relationships among cultivated *Solanum melongena* and other species using interspecific hybridization.

LITERATURE REVIEW

1. The genus *Solanum*

The family *Solanaceae* is composed of approximately 90 genera and between 2,000 and 3,000 species. The family is widely distributed throughout tropical and temperate regions of the world, with center of diversity occurring in Central and South America and Australia. Within this family, *Solanum* contributes the largest and most complex genus. It is composed of more than 1,500 species, many of which are also economically important throughout their cosmopolitan distribution. Examples of food plants in the *Solanaceae* are potato (*S. tuberosum*), aubergine or eggplant (*S. melongena*) and lulu or naranjilla (*S. psuedocapsicum*) and jasmine nightshade (*S. jasminoides* Paxt.) (Edmonds and Chewya, 1997).

At the beginning of the 20th century, amongst other studies, the *Solanaceae*, focusing on the genus *Solanum* (Daunay *et al*., 2001). *S. melongena* is one of the non-tuberous species of the family *Solanaceae*. It belongs to subfamily *Solanoideae*, the tribe *Solaneae*, the genus *Solanum* and the subgenus *Leptostemonum* (Dun.) Bitt., including more than 450 species distributed among 22 sections (D'Arcy, 1972; Whalen, 1984). There are also many other species, for example, *S. nigrum* and *S. nodiflorum* Jacq., which are at times cultivated or semi-cultivated in Africa and Asia (Daunay *et al*., 2000).

1.1 Morphological characters

Hasan and Jansen (1994) described the botanical characters of *Solanum* as follow: <u>Plant habit</u> annual or perennial herbs, erect or climbing, shrubs or rarely small trees. Plant unarmed or spiny, usually pubescent with simple, branched, glandular or stellate hairs. <u>Leaves</u> variable, usually alternate, exstipulate, petiolate, simple and entire, or lobed, pinnatisect or imparipinnate. <u>Inflorecence</u> a terminal, usually apparently lateral (by the growth of an axillary bud), often extra-axillary cyme, appearing racemose or subumbellate. <u>Flower</u> usually hermaphrodite; calyx campanulate, rotate or copular, mostly 5 lobed; corolla stellate, rotate or campanulate, mostly 5 lobed; stamens usually 5, inserted on the corolla throat; anthers often connivent, forming a cone around the style, often dehiscing by terminal pores or slits; ovary superior, locules usually 2 with many ovules; style simple; stigma small, capitate or bifid. Fruit a berry, usually globose, with persistent and sometimes enlarged calyx. Seeds few to many, orbicular or subreniform, compressed, often minutely pitted or reticulate. Epigeal germination, first true leaves usually entire.

1.2 Utilization

The leaves and stems of many species are often cooked or steamed and eaten as a vegetable. The unripe fruits are eaten in curries, whereas the ripe ones of some *Solanum* species are edible either cooked or raw. Caution must be taken when eating *Solanum*, as several species are poisonous. Example for *S. melongena*, the young and almost mature fruit is used as a vegetable. They may be roasted, fried, stuffed, cooked as curry, pickled or prepared in some other manner. In Thailand, Indonesia and Malaysia young fruit are also eaten raw (Sutarno *et al*., 1994).

Immature fruits of *S. torvum* are eaten raw or cooked as a vegetable or are used as an ingredient in curry sauce. In Indonesia *S. torvum* is considered as one of the best vegetable side-dishes with rice (Boonkerd *et al*., 1994). The mature, acidic fruit of *S. ferox* are used as a sour relish in India, Malaysia and Thailand. They are also used for curries and in Thailand, it is an ingredient of the well known sauce “Nam Prik”. In Indonesia the fruits are eaten raw or cooked with rice (Hasen and Jansen, 1994).

Many species of *Solanum* are used as medicine. *Solanum* is used to cure digestive and intestinal problems, including stomach-ache, diarrhea, piles and dysentery and for various skin problems such as sores, boils, cuts, wound and bruises. Many species are also employed to treat fever and malaria, headache and rheumatism. Some considered being stimulants whereas others have sedative properties. Furthermore, *Solanum* is frequently used for various diseases of the respiratory tract, such as coughs, sore throat, bronchitis and asthma. Finally, many species are applied to treat urinary problems. Also, *Solanum* shows insecticidal and fungicidal properties. (Blomqvist and Ban, 1999).

However, *S. melongena* is widely used in traditional medicine. In Malaysia the ashes of the fruit are prescribed for use in a dry hot poultice on haemorrhoids and the pounded root applied inside the nostrils against ulceration. In India the *S. melongena* is used in medicines to cure diabetes, asthma, cholera, bronchitis and dysuria. The fresh or dry leaf and fruit are said to reduce blood cholesterol level. In New Guinea, the juice from the roots is used to cure otitis and toothache (Sutarno *et al*., 1994).

Furthermore, solanine is a glycoalkaloid poison found in species of the nightshade family including tomato, potatoes, all peppers (except black pepper) and eggplant. It can be occur naturally in the any part of the plant including the leaves, fruit, and tubers. It is very toxic even in small quantities. Solanine has fungicidal and pesticidal properties, and it is one of the plant's natural defences. Solanine has been used as a commercial pesticide but never on a large scale. Solanine has sedative and anticonvulsant properties and has been used as a treatment of bronchial asthma, as well as for cough and cold medicines (Singh and Rai, 2005).

Moreover, *Solanum* steroidal alkaloids are useful industry as steroid precursors. Solasodine is a nitrogen analogue of diosgenin, a compound often used as raw material for the production of medicinal steroids. The synthetic steroids have three main applications in medicine: as anti-inflammatory corticosteroids, as contraceptive sex steroids and anabolic steroids (Blomqvist and Ban, 1999).

2. Genetic diversity

Genetic diversity is essential to the survival of a species and essential in the creation of new varieties (Engle, 2001). Genetic diversity research is needed because of its emphasis on broadening the gene pools in a collection with representative samples of related wild species (Islam, 1992).

Moreover, genetic diversity has an important role in plant breeding programs. The loss of genetic diversity, in part due to the conventional breeding programs associated with modern agricultural practices, has been dramatic in many cultivated species (Wilkes, 1983). In consequence, the narrow genetic base of the elite germplasm has increased the potential vulnerability to pests and abiotic stress. Therefore, the wild relatives and even alien species are needed to broaden the genetic bases of breeding program through interspecific hybridization (Stoskopf, 1993). Therefore, plant breeders can succeed their breeding programs by relying on the diversity or variation in plant populations. A comprehensive understanding of the amount and pattern of genetic variation that exists within and between the available cultivated and wild accessions is important for enhancing genetic potential because the diverse germplasm may include traits needed for effective improvement of the crop (Seehalak, 2005). Moreover, plant diversity study also reveals the relationship among plants in a population which guides the researcher to understand their evolution, indicates the centers of origin (Xu-xiao *et al*., 2003).

Germplasm collections are assembled and maintained primarily because of their potential use in crop improvement in the present and in the future. Additionally, the collection aims to provide a broad genetic base from which plant breeders can obtain desirable genotypes. Therefore, for the materials in the genebank to be of interest to the breeder, characterization and evaluation data should be available (Engle, 1992).

Characterization and evaluation are required to identify the desirable germplasm for utilization as well as to avoid duplication in management efforts (Engle, 1992). The role of characterization and evaluation in the utilization of genetic resources is recognized and need to be more clearly understood. The curator's responsibilities are maintained and characterize a collection, to assemble the information resulting from all parts of the process and to transmit it to the data banks (Islam, 1992). Moreover, evaluation is the essential link between conservation and use. For a better utilization, evaluation must be related to the breeder or consumer needs. Usually these are characters related to high yield, resistance to pests and diseases, adaptation to different environments and improved quality (Engle. 1992).

S. melongena has a wide range in its morphological characters (color, shape and size), physiological attributes and biochemical features. *S. melongena* exhibits partial resistance to most its pest and pathogens but often at rather low levels (Daunay *et al*., 1991). Sources of resistance to diseases and environmental stresses exist within member of the *Solanaceae* related to *S. melongena*. Resistance to bacterial wilt (*Ralstonia solanacearum*) has been identified in some varieties of *S. melongena*, *S. sisymbrifolium* Lam. and *S. torvum* (Daunay *et al*., 1991). However, the resistance to bacterial wilt has become insufficient in hot panting season or poorly drained fields (Ano *et al*., 1991). Resistance to *Phomopsi*s blight and fruit borer (*Leucinodes orbonalis*) has also been reported in *S. sisymbrifolium* Lam. and *S. khasianum* Clarke. Lastly *S. aethiopicum* has some interesting traits of resistance to the shoot and fruit borer, bacterial and *Fusarium* wilts (Daunay *et al*., 1991).

As far as environmental stress is concerned, the traits of resistance against frost damage have been found in *S. grandiflorum* Ruiz&Pavon, *S. mammosum* L. and *S. viarum* Dun. (Baksh and Iqbal, 1979). Moreover, *S. linnaeanum* Heeper&Jaeger and *S. macrocarpon* L. are tolerant to salinity and drought, respectively (Daunay *et al*., 1991).

Moreover, many reports have been studied on genetic diversity but its still lack of information of wild species of *Solanum* and divergence is usually related to adaptation to differing geographical areas or climates or to differing ecological habitats. In the process of becoming adapted, populations may become genetically distinct (Webb *et al*., 1988). The availability of information on the taxonomic status and the geographic origin of genebank accessions is a vital prerequisite for both the conservation and effective utilization of plant genetic resources. The taxonomists have also considered particular characters of taxonomic significance. The vast amount of available literature has, however, led to approximately 1,500 *Solanum* species with more than 3,000 binomial names (Daunay and Lester, 1988).

Therefore, germplasm characterization is essential provide valuable information for breeding programs. The information on the level of diversity for important agronomic traits of *S. melongena* is limited. Knowledge on genetic diversity and relationships among the *S. melongena* germplasm may play significant role in breeding programs to improve fruit quality and resistance to biotic and abiotic stresses of *S. melongena*. Inter-specific hybridization is possible among *Solanum* spp. This may accelerate diversity and increase gene pool for breeding programs. Diversity within germplasm is critical for *S. melongena* breeding programs.

3. Geographic distribution of diversity

Genetic diversity is not distributed uniformity throughout the range of environments in which a taxon is grown. Current evidence suggests that geographic distribution accounts for most of the observed variation in wild plant species. In crop geographic distribution patterns reflect both the specific selection pressures prevailing in a particular environment as well as crop history (Hawtin *et al*., 1997).

The most widely studied distribution patterns are for diseases resistance genes. Resistance is most commonly found in regions where diseases pressures are strongest and that coincide with centers of crop diversity (Dinoor, 1975). Common locally distributed alleles are most likely to include those of adaptive significance which confer an advantage for a population which possesses them and are necessary for survival in a particular environment (Allard, 1992). While some genes of this type may be easy to recognize as those conferring resistance to particular diseases or environmental stresses, the precise value of others may be less easy to determine. The evidence suggests that it may cases specific adaptation to particular environments is the result of the action of multiple genes and that individual effects of minor genes and interactions among them, together determine environmental fitness (Allard, 1992).

From an understanding of distribution patterns of genetic diversity, breeders can simplify their search for useful traits. Passport data providing information on collection sites can provide a useful entry point to large germplasm collections.

Knowledge of the spatial pattern of distribution of the crop or species, coupled with information on the geographic location of environments which have particular features of interest, can be used to identify those regions in which the desired adaptive trait is most likely to occur. Targeted collecting in such regions maximizes the probability of finding useful genetic diversity. Geographic Information System (GIS) provide a particularly variables (Guarino, 1995). They are proving to be of increasing value of germplasm specialists and breeders as ever more data sets are assembled and as the GIS techniques themselves become more sophisticated (Hawtin *et al*., 1997).

Origin and distribution can also influence the distribution of adaptative traits. *Solanum tuberosum* species are good plant models for study the assosication of genetics and geographical distribution and exhibit different genetic characteristics that have strong effect on the organization of diversity (Loveless and Hamrick, 1984). For example, *Solanum tuberosum* growing in Chiloe Island is considered to be a derivative of *S. andigena*, which is adapted to the Andean Highlands. The Chiloe potatoes have become adapted to the long-day conditions in the island and are an origin of present day modern potato cultivars in Europe and North America (Hawtin *et al*., 1997).

Moreover, significant associations have been found between altitude and frost killing temperature in *S. acaule* Bitter as well as altitude and resistance to potato leafhopper and glycoalkaloid content in *S. chacoense* Bitter (Hijmans *et al*., 2003). del Rio and Bamberg (2004) reported that the RAPD markers could be used to associate the genetic variation with proximity of *S. verrucosum* accessions to other Mexican wild potato species.

However, the main problem encounter in applying morphological criteria in *Solanum* spp. classification arises from the considerable variability in morphological features within different environmental conditions. Diversification through ecological acclimation, adaptation and stabilization of diverse morpho- and ecotypes, as well as changes caused by mutation and possibly also genome transfers (Hawtin *et al*., 1997). Nearly all populations of *Solanum* spp. from different geographical locations differ to some degree from each other and these deviations may stabilize in long-term cultures (Hawtin *et al*., 1997). This process indicates that new forms continually develop and are stabilized under new constant conditions. Diversification within the *Solanum* spp. is a continuing process in which new types develop from continually modified *Solanum* genotypes under different environmental conditions at different geographical locations (Hawtin *et al*., 1997).

With respect to the identification and classification of genebank accessions, markers promise to be very effective tools for achieving these purposes. Dehmer and Hammer (2004), indicated by the information on provenance in geographically, separated subclusters in *S. americanum* and partially in *S. villosum*, clues on the currently unknown origin of accessions from the genebank seem feasible by AFLP data.

Therefore, the availability of information on the taxonomic status and the geographic origin of genebank accessions is a vital prerequisite for both the conservation and effective utilization of plant genetic resources, yet it is often lacking for *Solanum* (Spooner *et al*. 1992; Waycott and Ford 1994).

4. Interspecific hybridization

Interspecific hybridization plays an important role for transferring the desirable traits from one species to another, increasing genetic variation, producing new alloploid species, clarifying the taxonomic relationship by testing several interspecific combinations, investigating natural selection and speciation process, being a prominent tool for theoretical and empirical studies in evolutionary biology, and recently being used to construct genetic linkage map (Briggs and Knowles, 1967).

Harton and de Wet (1971) provided a useful practical approach to classify crop species and their wild relatives using the concepts of primary, secondary and tertiary genepools. The primary genepool comprise those species which cross freely with the crop; the secondary are those species which difficult crossing with the crop and giving few fertile seeds and the tertiary genepool includes those species which can only be crossed using artificial techniques such as embryo rescue. The increasing ability to make inter-specific crosses and to move genes among very different biological taxa using genetic engineering allows plants breeders to extend their search for adaptive characters to entirely unrelated species which may not even be part of the plant kingdom (Hawtin *et al*. 1997).

The main breeding objectives have been improved fruit quality, adaptation to different environmental conditions and resistance to several pests and diseases. The genetic basis of *S. melongena* is narrow and so the explorable variability in *S. melongena* germpalsm is insufficient. Despite the fact that the related species constitute a potentially large reservoir of useful genes they have rarely been used for breeding purpose (Daunay *et al.*, 1999).

The reason for the poor utilization of wild relatives for *S. melongena* improvement is due to many potential species for crossing programs, which contribute towards taxonomic uncertainties within the genus *Solanum* (Daunay *et al*., 1999). In addition, although it is expected that several species are crossable with *S. melongena* (Daunay *et al*., 1991), crossability with many wild species remains to be assessed. Desirable traits have been identified in several wild species of the subgenus *Leptostemonum* of family *Solanaceae*. For examples, *S. indicum*, *S. integrifolium* and *S. incanum* have resistance to *Fusarium* wilt (Kashyap *et al*., 2003), *S. caripense*, *S. periscum*, *S. scabrum*, *S. sisymbrifolium* and *S. torvum* have resistance to *Verticillium* wilt (Kashyap *et al*., 2003; Gousset *et al*., 2005), *S. integrifolium* and *S. torvum* have resistance to baterial wilt (Kashyap *et al*., 2003; Gousset *et al*., 2005), *S. gilo*, *S. integrifolium* and *S. macrocarpon* have resistance to fruit rot (Kashyap *et al*., 2003), *S. xanthocarpum*, *S. khasianum*, *S. integrifolium* and *S. sisymbrifolium* have resistance to fruit and shoot borers (Kashyap *et al*., 2003), *S. sisymbrifolium*, *S. torvum, S. aethiopicum* and *S. warscewiczii* have resistance to root-knot nematodes (Kashyap *et al*., 2003) and *S. macrocarpon*, *S. integrifolium*, *S. mammosum*, *S. pseudocapsicum* and *S. sisymbrifolium* have resistance to spider mite (Kashyap *et al*., 2003).

Interspecific hybrids between wild and cultivated of *S. melongena* species have been successful in only a few cases. Such as *S. melongena* x *S. aethipoicum* (Daunay *et al*., 1993), *S. melongena* x *S. indicum* (Rao and Kumar, 1980; Rao and Rao, 1984; Patel, 2001), *S. melongena* x *S. sodomeum* (Tudor and Tomescu, 1995), *S. melongena* x *S. macrocarpon* (Schaff *et al*., 1982), *S. melongena* x *S. insanum* (Rao and Rao, 1984), *S. melongena* x *S. gilo* (Kashyap *et al*., 2003) and *S. melongena* x *S. integrifolium* (Rao and Baksh, 1979).

Moreover, embryo rescue was successfully used to recover hybrids of *S. melongena* with *S. khasianum* (Sharma *et al*., 1980), *S. sisymbrifolium* (Sharma *et al*., 1984; Blestsos *et al*., 1998) and *S. torvum* (Daunay *et al*., 1991; Blestsos *et al*., 1998) but these hybrids were sterile. Fertility was reported in hybrids of *S. melongena* with *S. macrocarpon* (Gowda *et al*., 1990) and *S. torvum* (Daunay *et al*., 1991) when diploid hybrids (2x) were brought to the amphiploid status (4x) by colchicines treatment. However, the successful in interspecific crosses have been obtained with only few wild species. In such attempted, the hybrids have been developed through embryo rescue. In addition, such hybrids have either been sterile or have had very low pollen fertility. This may be due to pre- and post- pollination effects (Kashyap *et al*., 2003).

Nevertheless, interspecific crosses between *S. melongena* and other *Solanum* species, bearing interesting agronomical traits, have sometimes been limited by sexual barriers (Collonnier *et al*., 2001). Crossability between *S. melongena* and species of other genera or distant subgenera such as subgenus *Archaesolanum*, subgenus *Potatoe* or subgenus *Solanum* is very low (Daunay *et al*., 1991). This may result from lack of genetic information in one partner about the other, due to evolutionary divergence; this is known as incongruity (Franklin *et al*., 1995).

However, plant regeneration from protoplast has been achieved in both cultivated and wild species of *S. melongena*. The protoplast culture and somatic hybridization would be useful in overcoming the pre- and post- fertilization breeding barriers encountered during conventional breeding. Further, protoplast cultures are excellent means for understanding cytological and ultrastructural changes during cell growth and differentiation, behavioural patterns of plastids and mitochondria (Fournier *et al*., 1995). For cultures *S. melongena*, protoplasts isolated from mesophyll cell grew best usig both cytokinin and auxin (Sihachakr and Ducreux, 1987). However, protoplast isolated from petioles and stems showed better regenerating compared to cells isolated from lamina (Sihachakr and Ducreux, 1987).

Moreover, the somatic hybridization experiments via protoplast fusion have been performed to facilitate the introduction of agronomically important traits from wild relatives into cultivated *S. melongena*. These characters were mainly resistance against diseases and parasites and particularly resistance to bacterial and fungal wilts, nematodes, mites and fruit borers (Sihachakr *et al*., 1994).

Therefore, to overcome the difficulty of interspecific hybridization, somatic hybridization is considered to be an alternative technique for producing the interspecific hybrids since a number of somatic hybrids have previously been produced between *S. melongena* and wild *Solanum* such as *S. sisymbrifolium* (Gleddie *et al*., 1986), *S. khasianum* (Sihachakr *et al.,* 1988), *S. torvum* (Guri and Sink, 1988a; Sihachakr *et al.,* 1989; Jarl *et al*., 1999), *S. nigrum* (Guri and Sink, 1988b), *S. aethiopicum* (Daunay *et al*., 1993; Collonier *et al*., 2001), *S. sanitwongsei* (Asao *et al*., 1994), *S. marginatum* (Borgato *et al*., 2007). Likewise, the somatic hybrid between *S. integrifolium* and *S. sanitwongsei* (Iwamoto *et al*., 2007). Althrough these hybrids have desirable characters, the sterility of most of them has hindered further use of this material in *S. melongena* breeding programs. It is nevertheless known that the somatic fusion between *S. melongena* and the closely related *S. aethiopicum* produces highly fertile hybrids (Daunay *et al*., 1993), suggesting that besides the regeneration capacity of hybrid cells, the phylogenetic distance between two parental species must be taken into account. Fertile hybrids were obtained from *S. melongena* and *S. torvum* when fragmentation by irradiation of the donor genome preceded protoplast fusion to limit the incompatibility reactionof genomes, as well as to reduce the introduction of unwanted characters of the wild species into domesticated gene pool (Jarl *et al*., 1999).

Moreover, lines of *S. melongena* showed a variable ability to cross with a given wild species, and successful crosses may depend on one-way incompatibility (Rao, 1979). The partial sterility of interspecific hybrids of *S. melongna* with other *Solanum* species may be linked to self-incompatilbility problems brought by the wild parent, and not by the *S. melongena* being self-compatible (Daunay *et al*., 1991). Self -incompatibility in the family *Solanaceae* is gametophytic and mainly controlled by muti-allelic S-locus (Franklin *et al*., 1995).

Therefore, understanding the germplasm diversity presented in *Solanum* species may bring valuable information for *S. melongena* breeding programs and determine diversity and relationships among *S. melongena* and its wild relatives.

MATERIALS AND METHODS

1. Investigation of major groups and their association with geographical origin of Southeast Asian *Solanum* based on morphological characteristics

1.1 Characterization and determination of major groups of *Solanum* accessions originating from Southeast Asia using a standard set of descriptors

The 94 accessions of *Solanum* spp. were obtained from the Genetic Resource and Seed Unit (GRSU), Asian Vegetable Research and Development Center (AVRDC) - The World Vegetable Center, Tainan, Taiwan. These germplasm were originally collected from six Southeast Asian countries including Cambodia, Laos, Malaysia, Myanmar, Thailand and Vietnam (Table 1). The seeds of those accessions were sown in seedling trays inside the greenhouse. Sixteen seedlings per accession were transplanted to the field under the net cages at 30 days after sowing. The characterization data were based on seedling, vegetative part, inflorescence, fruit and seed, following the IBPGR descriptors (IBPGR, 1990) modified by AVRDC (Appendix A). Species identification is based upon the work of Backer and Bakhuizen (1965) and Blomqvist and Ban (1999).

1.2 Association of morphological traits and geographical origin of Southeast Asian *Solanum*

The characterization data of 89 accessions of *Solanum* spp. (Appendix Table A2) originally collected from Southeast Asia were used for cluster analysis. Morphological characterization of the accessions was based on a standard set of descriptors developed by the IBPGR and modified by AVRDC. This record sheet was composed of 61 descriptors with 36 nominal (qualitative) and 25 ratio scale (quantitative) traits. Data analysis was divided into two steps, preliminary analysis and cluster analysis. The preliminary analysis based on ratio scale (quantitative) traits using SAS Software Release 6.03 (SAS, 1999). The cluster analysis was further divided into individual analyses based on the ratio scale (quantitative) and nominal (qualitative) traits. The cluster analysis and dendrogram of ratio scale traits were carried out using the UPGMA method TREE program of SAS version 6.03 computer software (SAS, 1999), while nominal traits, cluster analysis and dendrogram construction were done using R program version 2.6.1 (Hornik, 2007).

1.2.1 Preliminary analysis

The selected 89 accessions which were used in the morphological analysis possess primarily uniform and complete characterization data (Appendix Table A2 and A3). The morphological characterization of 89 accessions covered the seedling, vegetative part, inflorescence, fruit and seed traits. Descriptor without the needed actual measurement removed and in effect, could allow the accommodation of more accessions. Moreover, those that have identical character state codes for all the accessions were not included at all. This was necessary because these state codes have little discriminating power and as a consequence, accessions could not be distinguished from each other (Rumbaoa, 1981). Further, Sneath and Sokal (1963) reasoned that their presence was obvious in a small study. If they were standardized, they will be automatically disqualified since their standard deviation is zero and computations performed on the standardized character state codes would require division by zero.

I. Selection of accessions and descriptors

The deficient characterization data accessions were disqualified from the study. The verified characterization database file, descriptors without the required actual measurements were removed therefore more accessions were accommodated. Those descriptors that have identical character state codes for all the accessions were not included at all (Sneath and Sokal, 1963; Rumbaoa, 1981).

II. Identification of species outliers

Basic statistic (e.g. mean, variance and standard deviation), stem-and-leaf and probability and boxplots for each ratio scale traits were constructed using the PROC UNIVARIATE of the SAS software. From boxplots obtained, outliers were recognized as an asterisk (*) and/or zero (0) which are found beyond the traits of outer fence. Accessions recognized as outliers can be optionally removed from the data set.

III. Selection of less correlated traits

Unreduced data set, quantitative morphological traits were selected for stratification of accessions. This selection process using PROC CORR statement, the Pearson correlation coefficients were calculated between ratio scale traits. Based on the correlation coefficients, groups of highly correlated traits were formed using PROC VARCLUS command and setting the statistic *propor* (total proportion of variance explained by the clusters) to 95 %. From each set of highly correlated traits, the trait that was normally distributed was selected (Cababasay, 1996). For traits that had the same p-value for the test of normality, the ones considered easier to be measured and had less probability in committing error were used. The selected ratio scale traits correspond to the less correlated traits were considered in the cluster analysis.

1.2.2 Cluster analysis

I. Ratio scale traits

Based on the selected ratio scale traits, a separate cluster analysis was done using the PROC CLUSTER statement (method = average with *std* option). The PROC TREE statement was performed to construct the dendrogram showing the groups of highly similar accessions.

Plots of the clustering statistics (pseudo *F*, cubic clustering criterion and pseudo t^2) against the member of cluster were obtained using the PROC PLOT statement. A consensus among these statistics (local peaks of pseudo *F* and t^2 and local dips of cubic clustering criterion) was used to determine the number of clusters to be considered in the analysis. The process that involves the use of these statistics in determining the right number of cluster is considered to as "stopping point". The good stopping points referred to are the local peaks of pseudo *F* and pseudo t^2 and the local dips of cubic clustering criterion (Callantes, 2003). Using PROC PLOT statement, the plots of these statistics against the number of cluster were obtained (Figure 3 to 5).

II. Nominal traits

The qualitative data listed in Appendix Table A3 was analyzed by R program version 2.6.1 (Hornik, 2007). The cluster analysis was done the interaction mode of the software (method = average). The dendrogram showing the stratified accessions of *Solanum* spp. based on selected nominal traits was then generated using the tree plot of the graphics window.

Table 1 Ninety four accessions of *Solanum* spp. conserved at GRSU, AVRDC- The World Vegetable Center, Tainan, Taiwan.

Temporary No.	Species	Country of origin
TS00175	*S. melongena*	Thailand
TS00176	*S. melongena*	Thailand
TS00177	*S. melongena*	Thailand
TS00178	*S. melongena*	Thailand
TS00179	*S. melongena*	Thailand
TS00417	*S. aculeatissimum*	Thailand
TS00418	*S. aculeatissimum*	Thailand
TS00422	*S. aculeatissimum*	Thailand
TS00426	*S. stramonifolium*	Thailand
TS00455	*S. parkinsonii*	Thailand
TS00456	*S. parkinsonii*	Thailand
TS00473	*S. parkinsonii*	Thailand
TS00483	*S. aculeatissimum*	Thailand
TS00487	*S. aculeatissimum*	Thailand
TS00491	*S. indicum*	Thailand
TS00513	*S. torvum*	Thailand
TS00540	*S. torvum*	Thailand
TS00541	*S. stramonifolium*	Thailand
TS00549	*S. linociera*	Thailand
TS00550	*S. linociera*	Thailand
TS00551	*S. linociera*	Thailand
TS00552	*S. linociera*	Thailand
TS00553	*S. stramonifolium*	Thailand
TS00554	*S. torvum*	Thailand
TS00555	*S. linociera*	Thailand
TS00563	*S. stramonifolium*	Thailand
TS01321	*S. ferox*	Myanmar
TS01322	*S. melongena*	Myanmar
TS01447	*S. anguivi*	Thailand
TS01947	*S. indicum*	Thailand
TS01979	*S. stramonifolium*	Thailand
TS01994	*S. linociera*	Thailand
TS02062	*S. stramonifolium*	Thailand

Table 1 (Continued)

Temporary No.	Species	Country of origin
TS02216	*S. parkinsonii*	Thailand
TS02217	*S. parkinsonii*	Thailand
TS02218	*S. parkinsonii*	Thailand
TS02245	*S. melongena*	Vietnam
TS02246	*S. melongena*	Vietnam
TS02247	*S. melongena*	Vietnam
TS02268	*S. undatum*	Vietnam
TS02271	*S. melongena*	Vietnam
TS02273	*S. melongena*	Vietnam
TS02435	*S. ferox*	Thailand
TS02440	*S. seaforthianum*	Thailand
TS02441	*S. seaforthianum*	Thailand
TS02445	*S. trilobatum*	Thailand
TS02491	*S. trilobatum*	Thailand
TS02495	*S. trilobatum*	Thailand
TS02728	*S. torvum*	Thailand
TS02731	*S. torvum*	Thailand
TS02739	*S. trilobatum*	Thailand
TS02812	*S. melongena*	Laos
TS02813	*S. torvum*	Laos
TS02815	*S. torvum*	Laos
TS02816	*S. melongena*	Laos
TS02818	*S. melongena*	Laos
TS02821	*S. melongena*	Laos
TS02822	*S. melongena*	Laos
TS02843	*S. torvum*	Laos
TS02862	*S. torvum*	Laos
TS02877	*S. torvum*	Laos
TS02894	*S. mammosum*	Malaysia
TS02901	*S. ferox*	Malaysia
TS02902	*S. ferox*	Malaysia
TS02903	*S. ferox*	Malaysia
TS02906	*S. indicum*	Malaysia
TS02937	*S. torvum*	Malaysia

Table 1 (Continued)

Temporary No.	Species	Country of origin
TS02938	*S. torvum*	Malaysia
TS02939	*S. torvum*	Malaysia
TS02940	*S. torvum*	Malaysia
TS02941	*S. torvum*	Malaysia
TS02945	*S. xanthocarpum*	Malaysia
TS02946	*S. xanthocarpum*	Malaysia
TS02950	*S. macrocarpon*	Cambodia
TS02955	*S. torvum*	Cambodia
TS02965	*S. sisymbrifolium*	Laos
TS02967	*S. ferox*	Laos
TS02971	*S. ferox*	Laos
TS02973	*S. torvum*	Laos
TS02976	*S. sisymbrifolium*	Laos
TS02978	*S. ferox*	Laos
TS02989	*S. ferox*	Laos
TS02990	*S. sisymbrifolium*	Laos
TS02992	*S. sisymbrifolium*	Laos
TS03005	*S. sisymbrifolium*	Laos
TS03009	*S. ferox*	Laos
TS03012	*S. ferox*	Laos
TS03018	*S. sisymbrifolium*	Laos
TS03020	*S. ferox*	Laos
TS03029	*S. aethiopicum*	Laos
TS03049	*S. melongena*	Cambodia
TS03050	*S. melongena*	Cambodia
TS03051	*S. melongena*	Cambodia
TS03052	*S. melongena*	Cambodia
TS03053	*S. melongena*	Cambodia

2. Genetic relationships of *Solanum* spp. using interspecific hybridization

Five collections of *Solanum* species at GRSU, AVRDC (Table 2) comprised of four accessions of *S. melongena* (S00022, S00388, S00625 and S00809), one accession each of *S. torvum* (S00429) and *S. nigrum* (TS02930), four accessions of *S. americanum* (S00269, S00859, S00861 and S00865) and three accessions of *S. villosum* were sown in seedling trays in the greenhouse. Seedlings were transplanted into black plastic pots (42 cm in diameter and 30 cm heigh) after 30 days after sowing (5 pots for each accession).

Young flower buds of female parents were emasculated and bagged in a glassine bag, two days before anthesis at flowering stage to prevent self-pollination. Pollens were collected and stored at 4-5 °C. Hand-pollination was done when the stigma was receptive, then re-bagged and labeled. The pollination was done for 2 days after being emasculated and the crosses were made during 8.00-11.00 A.M. The intra- and interspecific crosses pollinations were made in 169 crossing combinations:

1. *S. melongena* x *S. melongena*
2. *S. melongena* x *S. torvum*
3. *S. melongena* x *S. americanum*
4. *S. melongena* x *S. villosum*
5. *S. melongena* x *S. nigrum*
6. *S. torvum* x *S. torvum*
7. *S. torvum* x *S. americanum*
8. *S. torvum* x *S. villosum*
9. *S. torvum* x *S. nigrum*
10. *S. americanum* x *S. americanum*
11. *S. americanum* x *S. villosum*
12. *S. americanum* x *S. nigrum*
13. *S. villosum* x *S. villosum*
14. *S. nigrum* x *S. nigrum* and their reciprocal crossing.

Table 2 Five species with 13 accessions of *Solanum* used for interspecific hybridization.

Species	Accession number	Country of origin
S. melongena	S00022	India
	S00388	South Africa
	S00625	South Africa
	S00809	Bangladesh
S. torvum	S00429	Thailand
S. americanum	S00269	Philippines
	S00859	Tanzania
	S00861	Japan
	S00865	Vietnam
S. villosum	S00854	Tanzania
	S00860	Japan
	TS02600	Kenya
S. nigrum	TS02930	Malaysia

The degree of crossabilility among the species was determined by percentage of fruit set and number of seed per fruit. The confirmation of interpecific hybrids were verified by determining pollen fertility, ploidy level and morphological characters.

2.1 Pollen fertility

The parents and F_1 hybrids were tested for pollen fertility status by using 2 % iron acetocarmine staining method. Flower buds, flowers or inflorescences of those species were collected between 8.00-10.00 A.M. Using dissecting forceps and a needle, anthers of various species were opened to allow extraction and subsequent transfer of pollen dust on to a slide in a drop of 2 % iron acetocarmine stain. Mature anthers were crushed and pollen grains were mixed thoroughly with the 2 % iron acetocarmine stain. Cover slips were gently placed on to different slides for each species. The slides were then observed under a light microscope. For each slide, 500 pollen grains from randomly selected fields were observed under at 100 X magnification. Three replicates per plant from each species were investigated.

To determine pollen fertility, darkly stained pollen grains were recorded as fertile and viable, and unstained or very lightly stained ones were considered as sterile or non-viable. Pollen fertility was calculated by dividing the number of viable pollen grains by the total number of grains counted in the field of view. Pollen viability was expressed as pollen fertility percentage in each plant species.

2.2 Ploidy determination

The parents and F_1 hybrids were evaluated using flow cytometry. The samples were prepared for using the protocol of Arumunganathan and Erale (1991). The young leaves from each cross were collected from the field. Approximately 400 mg of leaf tissue was used in each sample. The leaves were placed in a polystyrene petri dish containing 1.4 ml of PBS buffer (2.04 g Na_2HPO_4, 0.5944 g sodium phosphate, 16.36 g NaCl dissolved in 2 L, pH of the buffer was adjusted to 7.2 with HCl or NaOH). The leaves were cut into fine strips with a razor blade. The samples were filtered through a 167 µm nylon mesh into 50 ml falcon tube. A solution of 200 ml PI [6 mg Propidium iodide dissolved in 6 ml of distilled water and take 6 ml of solution PI mixed with 24 ml of DTT solution (40 mg DTT dissolved in 40 ml PBS buffer and 2.4 ml triton X100 dissolved in 40 ml of DTT solution)] was added. The samples were then stirred, incubated at room temperature for 15 min and then kept in ice until analyses were done on a FACS Calibur flow cytometer.

Approximately 10,000 nuclei were counted for each sample. Ploidy levels of gynogenic plants were assigned based on the DNA content of their nuclei in relation to the standards.

2.3 Morphological characters

The hybridity of the plants produced was confirmed by comparing the morphological characters with those of the parental species following the IBPGR descriptors (IBPGR, 1990) modified by AVRDC in Appendix A.

PLACE AND DURATION

The experiments were conducted at the Genetic Resources and Seed Unit (GRSU), Asian Vegetable Research and Development Center (AVRDC) - The World Vegetable Center in Shanhua, Tainan, Taiwan from May 2005 to May 2006.

RESULTS AND DISCUSSION

In this study, the experiments were divided into 2 parts which consisted of the study on morphological characters of *Solanum* in Southeast Asia and genetic relationships of *Solanum* spp. using interspecific hybridization.

1. Investigation of major groups and associated with geographical origin of Southeast Asian *Solanum* based on morphological characteristics

1.1 Characterization and determination of major groups of *Solanum* accessions originating from Southeast Asia using a standard set of descriptors

One hundred and two accessions of *Solanum* spp. had been registered at AVRDC. The 89 of 102 accessions have been regenerated and characterized using the IBPGR descriptors (IBPGR, 1990) modified by AVRDC (Appendix A). They were identified into 11 species (Table 3) as follows: 38 accessions of *Solanum melongena* (Appendix Figure A1), 2 accessions of *S. aculeatissimum* (Appendix Figure A2), 1 accession of *S. aethiopicum* (Appendix Figure A3), 17 accessions of *S. ferox* (Appendix Figure A4), 8 accessions of *S. indicum* (Appendix Figure A5), 1 accession of *S. mammosum* (Appendix Figure A6), 1 accession of *S. sanitwongsei* (Appendix Figure A7), 11 accessions of *S. torvum* (Appendix Figure A8), 3 accessions of *S. trilobatum* (Appendix Figure A9), 1 accession of *S. viarum* (Appendix Figure A10) and 6 accessions of *S. xanthocarpum* (Appendix Figure A11).

Within the accessions studied *S. melongena* is the majority due to its popularity as vegetable in most Asian Countries; the rest belongs to the species consumed in a limited region such as *S. ferox* (19.10 %) and S. *torvum* (12.36 %), and a group of species which is not consumed as vegetable. The latter group includes *S. aculeatissimum* (2.25 %), *S. indicum* (8.99 %), *S. sanitwongsei* (1.12 %), *S. trilobatum* (3.37 %), *S. viarum* (1.12 %) and *S. xanthocarpum* (6.74 %).

On other hand, *S. aethiopicum* and *S. mammosum,* collected in Laos and Malaysia, respectively. This account for the 1.10 % of the total accessions stratified. It was very uncommon in Southeast Asia. *S. aethiopicum* is domesticated throughout a large part of Africa for its edible fruits and leaves. Its distribution range is in Central Africa from Ivory Coast to Kenya and Tanzania (Furini and Wunder, 2004). Moreover, *S. aethiopicum*, TS03029, was easily spotted among the genotypes analyzed because of the white stelliform corolla and orange or scarlet fruit (Appendix Figure A3). *S. mammosum* has native distribution range in North America (Mexico) and South America (from Barbados to Brazil). This specie was easily recognized because of its bright orange fruit and nipple shaped (Furini and Wunder, 2004).

The 89 accessions considered in this study were grown in the field under the net cages. Plants were maintained until seed set and were observed for their morphological traits. Considering the descriptor of *S. melongena* such as growth habit, leaf shape, presence or absence of spines, flower and fruit color and shape and comparison among accessions, we conclude that 43 accessions were misidentified (Table 4).

The accessions of TS00418, TS0422-A, TS00483 and TS00487 collected in Thailand were originally classified as *S. aculeatissimum*. According to their identical morphology, they belong to *S. xanthocarpum.* The high similarity among these accessions made it difficult to understand whether the same species or if different species, these accessions were so closely related to make it impossible to distinguish them on the basis of morphological features. The careful consideration of the corolla color helped them to distinguish between white with green base of corolla for *S. aculeatissimum* and purple corolla for *S. xanthocarpum* (Backer and Brink, 1965).

This result indicated that morphological considerations were important for the reassignment of names to accessions but also the molecular evidence were important to confirmation of the new classification and can be use for establishment of a genetic distance between accessions or species also the distinction among domesticated and wild forms of *S. melongena* (Daunay *et al*., 1991).

Furthermore, TS02950 collected in Cambodia was received as *S. macrocarpon*, which native in Africa such as Ivory Coast, Guinea, Mali and Nigeria. This specie was domesticated with edible fruit and leaf, cultivated throughout a large part of Africa (Furini and Wunder, 2004). Based on morphology, TS02950 was identified as *S. xanthocarpum.* A distinct phenotype was observed for the accession of *S. xanthocarpum.* They had purple corolla and stellate hairy on both surface. Fruit seated onenlarged calyx, yellow when mature. Stem was aculeate. Leaves were incircumference ovate-oblong, with unequal, broadly rounded-truncate base, acutish to obtuse, deeply pinnatifid with irregularly dentate, acutish to obtuse segments, young with epually by branched stellate hairs on both surfaces.

The morphological characterization of TS00455, TS00456, TS00473, TS02216, TS02217 and TS02218, collected in Thailand, received as *S. parkinsonii*, TS00549, TS00551, TS00552, TS00555 and TS01994, collected in Thailand, received as *S. linociera* and TS02440, TS02441-A and TS02441-B received as *S. seaforthianum* (Brazilian nightshade), collected in Thailand. TS02496 collected in Malaysia was received as *S. xanthocarpum*. TS02268 collected in Vietnam was received as *S. undatum,* which is reported to be synonym for *S. melongena* (Sutarno *et al.*, 1994). All of these accessions were candidated to be included into *S. melongena* (*S. melongena* complex) bases on morphology. The groups of accessions included in this complex were very distinct from all others, in fact, although the morphological investigations indicated a wide diversity in vegetative floral and fruit characters, their overall morphology allowed them to be clustered into the *S. melongena* aggregate. It is an erect, branching, very polymorphous, perennial herb, grown as an annual and 1 to 2 m high. All parts cover with a grey tomentum, sometimes they are somewhat spiny, older plants might become woody. Leaves alternate, simple, petiole up to 10 cm long, leaf-blade ovate to ovate-oblong, densely stellate hairy, base rounded or cordately, often unequal, margin sinuate lobed, apex acute or obtuse. Flower varied from flowers borne singly or in clusters with white, lavender or purple stelliform corolla. The observations for fruit form were ovoid, oblongoid, obovoid or subglobose to globose. Fruit color variable, smooth, shiny, white, green, yellow, purple, black or mixed colored. While based on several traits, all these accessions clearly belonged to

S. melongena complex. In some lines, it was possible, nevertheless, to recognized distinct characters of wild species (frequent presence of spines, small flowers and berries).

Furthermore, the accessions of TS02815 and TS02496 collected in Laos and Malaysia, respectively, were received as *S. torvum*. Also TS01321 collected in Myanmar was received as *S. ferox*. These accessions were identified as *S. melongena*. In this case, it is possible that seed collectors confused and misidentified.

Moreover, the five accessions of TS00426, TS00541, TS00563, TS01979 and TS02062, all collected in Thailand, as *S. stramonifolium* but were identified as *S. ferox*. Siemonsma and Jansen (1994) reported that *S. ferox* has a synonym for *S. stramonifolium*. *S. stramonifolium* has also been used as the correct name for *S. ferox*. *S. stramonifolium*, however, their were different species occurring in South America. A simple observation of these plants indicated that their phenotypes were very distinguishable. Their ovary and berry with many long white stellate hairs, inflorescence lateral, sessile or subsessile, 4-10 flowered, pedicels densely stellate-hairy, calyx pale and densely stellately pubescent, corolla white or purple, as long as or shorter than calyx and outside stellate-hairly. Fruits globose, yellow when ripe and densely pubescent with long white stellate hairs. Stem stellately hairy, Leaves broadly ovate, with truncate or slightly cordate, often unequal base, shallowly pinnatilobed, aculeate on the nerves on both sides and stellately hairy on both surfaces.

The accession TS00553 was received as *S. linociera* collected in Thailand. While, TS02976 collected in Laos was received as *S. sisymbrifolium* but both accessions were identified as *S. ferox*. The morphology of *S. ferox* is distinct from all other accessions and is easily recognized because of it's covered with stellate throughout of plants especially ovary and berry with many long white stellate hairs. Fruit globose and yellow when mature (Backer and Brink, 1965). In contrast, *S. sisymbrifolium* is native of South America, from Argentina to Brazil (Furini and Wunder, 2004), which have been reported to be synonym for *S. aculeatissimum* (Harden, 1992). Vegetatively, they are similar to accessions of *S. ferox* but with fruits distinct from those species. Fruit globose-obovoid and red when mature (Webb *et al*., 1988).

The accessions of TS02965, TS02990, TS02992, TS03005 and TS03018, were collected in Laos. These accessions were received as *S. sisymbrifolium.* While TS02967 collected in Laos was received as *S. ferox.* These accessions were identified as *S.* indicum. It is a small spineless shrub up to 1.5 m high. Stem is densely stellate. Leaves sinuate to entire, grey and densely stellate beneath. Corolla is white or purple. Young fruit is green and turning yellow and becoming orange.

From the *S. trilobatum* accessions, based on morphology, TS02491 and TS02495, both accessions collected in Thailand, were identified as *S. sanitwongsei* and *S. inducum*, respectively. *S. sanitwongsei* distributes in Thailand and is cultivated in Philippines (Blomqvist and Ban, 1999). It is a small, stellately hairy shrub to 1 m high, leaves oblong-ovate, base cordate to cuneate, apex obtuse, inflorescence an extra-axillary, short raceme on a short peduncle, corolla stellate and purple, ovary glabrous except for the apex, fruit subglobose, glabrous orange when mature.

The accessions of TS01947 and TS02906 collected in Thailand and Malaysia, respectively; both were received as *S. indicum* but were identified as *S. trilobatum* and *S. torvum* respectively. *S. trilobatum* have been reported to distribute in India, Vietnam, Thailand and Peninsular Malaysia (Blomqvist and Ban, 1999). Plant nearly glabrous, thorny herb, slightly woody at base, leaves broadly elliptical to broadly ovate, sinuate-lobed, base rounded to slightly cordate , apex rounded. Inflorecence was extra-axillary, composed of a few flowered cyme or 6-10 flowered raceme, calyx campanulate, glabrous, not enlarged in fruit. Corolla is stellate and blue. Fruit red when maturity. In contrast, *S. torvum*, originates from the Antilles, but is now a pantropical weed. Occasionally it is also cultivated, especially in South, Southeast and East Asia (Boonkerd *et al*., 1994). It is a spreading or scrambling slender shrub, up to 3 m high, pubescent with stellate hairs. Prickles scattered on stem, branches and leaves, especially in young branches, slightly hooked. Leaves alternate, solitary or in pairs, leaf blade ovate, coarsely, sinuously lobed, base unequal, somewhat sagittate to auriculate. Inflorescence a compact, branched, 50-100 flowered corymb, at first terminal, later become lateral and markedly supra-axillary. Flower hermaphrodite, upper ones may be male, corolla stellate, white, lanceolate, inserted on corolla. Fruit globular berry, glabrous and dirty brown or black when ripe.

Moreover, five accessions can be divided in two accessions (Table 3) such as TS00179 collected in Thailand both were identified as *S. melongena* but TS00179-A had a green hypocotyls, white corolla and uniform distribution fruit color when unripe and yellow orange fruit at maturity. TS00179-B had purple hypocotyls, light violet corolla, mottled distribution when unripe and deep yellow at maturity.

Accession TS00422 collected in Thailand, received as *S. aculeatissimum* can divided into two accessions, TS00422-A identified as *S. xanthocarpum* because this accession had light purple corolla, petiole color is green-violet, leaf blade angle was obtuse and few prickles on fruit stalk. In contrast, TS00422-B identified as *S. aculeatissimum* because this accession has a white corolla, green petiole, leaf blade angle was intermediate and intermediate of Fruit stalk prickles.

The accession of TS01447 collected in Thailand, received as *S. anguivi* which is recognized wild progenitor of *S. aethiopicum* (Lester, 1986), can be divided into 2 accessions by using seed color when sowing seed. TS01447-A had brown seed, while TS001447-B had yellow seed. Moreover, these accessions were identified as *S. viarum* and *S. indicum*, respectively. TS01447-A, *S. viarum*, have been reported as a native of Brazil to Northeastern Argentina (Furini and Wunder, 2004). This plant was characterized by many celled, simple, mostly glandular hairs. Stems and branches terete, densely and evenly pubescent with many-celled, simple hairs, armed with recurved prickles and sometimes with needlelike prickles. Leaves unequal paired, petiole stout, armed with erect, flat straight prickles. Leaf blade broadly ovate with prickles and coarse, many-celled, glandular simple hairs on both surfaces, these mixed with sparse, sessile, stellate hairs abaxially, base truncate, lobes blunt at apex. Inflorescence is extra-axillary, subfasciculate, hairy and sometimes prickly abaxially. Corolla is white or green, calyx campanulate and pubescent as on calyx. Berry pale yellow and globose. While, TS001447-B, *S. indicum*, has the characteristic white stelliform corolla and orange-yellow fruit.

TS02441 collected in Thailand and TS02773 collected in Vietnam, each is separated into 2 accessions based on corolla color. TS02441-A was greenish violet petiole. Leaf tip obtuse and dark green leaf. Corolla is purple. Seed is grey-yellow. While TS02441-B has green petiole. Leaf tip approximately 75° and green leaf. Corolla is white. Seed is brownish yellow. In case of TS02773, TS0273-A has light violet corolla, greenish violet petiole. Leaf tip is obtuse and dark green leaf and green fruit at commercial ripeness. TS0273-B has white corolla, green petiole. Leaf tip approximately 75° and green leaf and milky white fruit at commercial ripeness. This work clearly shows that the mixed seed of different species in an accession is common in seed gene bank. These also indicate that the work on maintaining and characterization is important for germplasm works and more clear information about the morphological characters of each species is needed.

Table 3 Identification of 89 accessions of *Solanum* spp.

Species	Accession
Solanum melongena	TS00175 TS00176 TS00177 TS00178 TS00179-A TS00179-B TS00455 TS00456 TS00473 TS00549 TS00551 TS00552 TS00555 TS01321 TS01322 TS01474-A TS01474-B TS01994 TS02216 TS02217 TS02218 TS02245 TS02246 TS02247 TS02268 TS02273-A TS02273-B TS02440 TS02441-A TS02441-B TS02812 TS02815 TS02816 TS02821 TS02822 TS02939 TS02946 TS03049 TS03052 TS03053
Solanum aculeatissimum	TS00417 TS00422-B
Solanum aethiopicum	TS03029
Solanum ferox	TS00426 TS00541 TS00553 TS00563 TS01979 TS02062 TS02435 TS02901 TS02902 TS02903 TS02971 TS02976 TS02978 TS02989 TS03009 TS03012 TS03020
Solanum indicum	TS01447-B TS02495 TS02965 TS02967 TS02990 TS02992 TS03005 TS03018
Solanum mammosum	TS02894
Solanum sanitwongsei	TS02491
Solanum torvum	TS02728 TS02731 TS02813 TS02862 TS02877 TS02906 TS02937 TS02938 TS02940 TS02955 TS02973
Solanum trilobatum	TS01947 TS02445 TS02739
Solanum viarum	TS01447-A
Solanum xanthocarpum	TS00418 TS00422-A TS00483 TS00487 TS02945 TS02950

Table 4 Identification of 43 accessions of *Solanum* spp.

Accession No.	Species (previous)	Species (reidentified)	Country of origin
TS00418	*S. aculeatissimum*	*S. xanthocarpum*	Thailand
TS00422-A	*S. aculeatissimum*	*S. xanthocarpum*	Thailand
TS00426	*S. stramonifolium*	*S. ferox*	Thailand
TS00455	*S. parkinsonii*	*S. melongena*	Thailand
TS00456	*S. parkinsonii*	*S. melongena*	Thailand
TS00473	*S. parkinsonii*	*S. melongena*	Thailand
TS00483	*S. aculeatissimum*	*S. xanthocarpum*	Thailand
TS00487	*S. aculeatissimum*	*S. xanthocarpum*	Thailand
TS00541	*S. stramonifolium*	*S. ferox*	Thailand
TS00549	*S. linociera*	*S. melongena*	Thailand
TS00551	*S. linociera*	*S. melongena*	Thailand
TS00552	*S. linociera*	*S. melongena*	Thailand
TS00553	*S. linociera*	*S. ferox*	Thailand
TS00555	*S. linociera*	*S. melongena*	Thailand
TS00563	*S. stramonifolium*	*S. ferox*	Thailand
TS01321	*S. ferox*	*S. melongena*	Myanmar
TS01447-A	*S. anguivi*	*S. viarum*	Thailand
TS01447-B	*S. anguivi*	*S. indicum*	Thailand
TS01947	*S. indicum*	*S. trilobatum*	Thailand
TS01979	*S. stramonifolium*	*S. ferox*	Thailand
TS01994	*S. linociera*	*S. melongena*	Thailand
TS02062	*S. stramonifolium*	*S. ferox*	Thailand
TS02216	*S. parkinsonii*	*S. melongena*	Thailand
TS02217	*S. parkinsonii*	*S. melongena*	Thailand
TS02218	*S. parkinsonii*	*S. melongena*	Thailand
TS02268	*S. undatum*	*S. melongena*	Vietnam
TS02440	*S. seaforthianum*	*S. melongena*	Thailand

Table 4 (Continued)

Accession No.	Species (previous)	Species (reidentified)	Country of origin
TS02441-A	*S. seaforthianum*	*S. melongena*	Thailand
TS02441-B	*S. seaforthianum*	*S. melongena*	Thailand
TS02491	*S. trilobatum*	*S. sanitwongsei*	Thailand
TS02495	*S. trilobatum*	*S. indicum*	Thailand
TS02815	*S. torvum*	*S. melongena*	Laos
TS02906	*S. indicum*	*S. torvum*	Malaysia
TS02939	*S. torvum*	*S. melongena*	Malaysia
TS02946	*S. xanthocarpum*	*S. melongena*	Malaysia
TS02950	*S. macrocapon*	*S. xanthocarpum*	Cambodia
TS02965	*S. sisymbrifolium*	*S. indicum*	Laos
TS02967	*S. ferox*	*S. indicum*	Laos
TS02976	*S. sisymbrifolium*	*S. ferox*	Laos
TS02990	*S. sisymbrifolium*	*S. indicum*	Laos
TS02992	*S. sisymbrifolium*	*S. indicum*	Laos
TS03005	*S. sisymbrifolium*	*S. indicum*	Laos
TS03018	*S. sisymbrifolium*	*S. indicum*	Laos

Table 5 Re-identification of 5 accessions of *Solanum* spp.

Original accession	New designated accession	Species (previous)	Species (reidentified)	Country of origin
TS00179	TS00179-A	*S. melongena*	*S. melongena*	Thailand
	TS00179-B	*S. melongena*	*S. melongena*	Thailand
TS00422	TS00422-A	*S. aculeatissimum*	*S. xanthocarpum*	Thailand
	TS00422-B	*S. aculeatissimum*	*S. aculeatissimum*	Thailand
TS01447	TS01447-A	*S. anguivi*	*S. viarum*	Thailand
	TS01447-B	*S. anguivi*	*S. indicum*	Thailand
TS02441	TS02441-A	*S. seaforthianum*	*S. melongena*	Thailand
	TS02441-B	*S. seaforthianum*	*S. melongena*	Thailand
TS02273	TS02273-A	*S. melongena*	*S. melongena*	Vietnam
	TS02273-B	*S. melongena*	*S. melongena*	Vietnam

However, of theses 102 accessions, 9 accessions (TS00513, TS00540 TS00550, TS00554, TS02818, TS02843, TS02941, TS03050 and TS03051) were not germinated (Appendix Table A4). The seeds of these accessions might be harvested at immature stage. Moreover, the 2 accessions are misidentified as *Solanum*. TS00491 is identified as *Lycopersicon* sp. and TS02271 is identified as *Capsicum* sp. in Appendix Table A3.

Therefore, it indicated that the characterization and identification using the morphological characteristics are important process for germplasm work. Especially, after collecting from different places it is necessary to characterize and re-identify to present confusion and misunderstanding.

In addition, *Solanum* is mainly propagated by seed. Germplasm collections were assembled and maintained primarily then regenerated and characterized, this process was important to get a good seed quality. Hence, the harvest stage of seeds is prime important for *Solanum* spp. materials in the genebank. Engle (1993) reported that seed maturity of *S. melongena* is attained at 55-77 DAA. Likewise Hayati (2005) reported the fruit of *S. ferox* and *S. torvum* should be harvested at more than 65 DAA when the fruits turned orange (*S. ferox*) or greenish yellow (*S. torvum*). On the other hand, *S. melongena* and *S. trilobatum* fruits should be harvested from 55-65 DAA when the fruit turned yellow or yellow orange for *S. melongena* and red for *S. trilobatum*. It was assumed that at these stages, they were at physiological maturity and ripening (harvest mature) stages.

1.2 Determination on morphological traits of Southeast Asian *Solanum* can be uses to associate with geographical origin

1.2.1 Preliminary analysis

A. Selection of accessions and descriptors

Both quantitative (ratio) and qualitative (nominal) characters were used to describe the accessions. Out of the 61 descriptors in Appendix A, 25 are ratio scale traits. On the other hand, those are non-ration traits in the characterization sheet were referred to as nominal or qualitative traits. Of the 36 nominal traits, only 11 traits were used to cluster-analyze the 89 accessions of *Solanum* spp. Appendix Table A4 gives the list of these characters.

B. Identification of species outliers

The descriptive statistic of the 19 ratio scale traits computed prior to the identification of species outliers within the *Solanum* spp. data set were noted (Table 6). These values are used to properly describe the various features of the data set. On the other hand, the use of boxplot for outlier recognition is much easier and more practical to use.

The species outliers refer to the accessions with values which are either too large or too small relative to given accessions on any of the traits. They exhibit unusual values that are not ordinarily exhibited by the majority of the given accessions, hence, considered to have rare values (Cababasay, 1996). In the boxplots, they are generally highlighted with in an asterisk (*) and/or zero (0) which are found beyond the tails of outer fences (Gardiner, 1997).

From the sample of the PROC UNIVARIATE (species outlier) output for germination period descriptor (Figure 1), the boxplot indicates that 12 accession (13.5 %); TS02906, TS02245, TS03049, TS03052, TS03053, TS02728, TS02813, TS02862, TS02877, TS02937, TS02940 and TS02955 were the possible outlier. This was because they have asterisk and zero mark outside the fence which means they have extreme values not normally exhibited by the 77 accessions. The identified outliers (Table 6) show wide range of variation since these outliers were taken from six countries in Southeast Asia. For instance, the TS02813 and TS02877 accessions of Laos were a *Solanum torvum*. Accessions regarded as an outlier in 6 traits. Of the same species, TS02728 accession from Thailand and TS02955 accession from Cambodia had extreme values for germination period, plant height, plant breadth, number of flowers per inflorescence and number of fruit per infructescence. This indicated that the species had been taken from different parts of Southeast Asia.

However, plant breadth was the higest among the population for outlier (20.2 %) and follows by fruit length (18.0 %). This indicated that both characters have higher variation than other characters. In contrast the characters of 100 seeds weight (1.1 %) and Fruit stalk length (1.1 %) were small in the oulier populations.This result shows that both characters have less variation among 89 accessions belonging to *Solanum* spp. and both characters should be considered in the cluster analysis.

In addition, if they were dropped, the 89 accessions used will be reduced to 33 accessions, which is 37.08 % of total number of accessions considered. Hence, the outliers identified from the given set of accessions were suspected to their own group isolated from normal non-outliers. Except the accessions of *S. melongena* were eliminate from normal non-outliers. Therefore, the 69 accessions were considered in the cluster analysis.

Table 6 Species outliers identified for each ratio scale trait.

Traits	Outlier (s)	Probability
Germination period (day)	13, 14, 17, 21	12 accs. (13.5 %)
Plant height (cm)	191.5, 204.5, 210.0, 212.5, 235.0, 237.5, 245.0, 247.5, 250.0, 251.5, 272.5	14 accs. (15.7 %)
Plant breadth (cm)	41.0, 42.0, 48.0, 49.0, , 51.0, 54.0, 56.5, 125.5, 126.5, 132.5, 135.0, 136.5, 185.0, 193.5, 201.0, 215.0, 242.5, 244.5, 310.0	18 accs. (20.2 %)
Plant branching	17.5, 18, 19	4 accs. (4.5 %)
Number of flowers per inflorescence (flower)	57.5, 63, 64, 71, 73.5, 82.5, 89, 94, 97, 103, 290	11 accs. (12.4 %)
Fruit length (cm)	6.1, 6.6, 7.0, 7.1, 8.6, 9.2, 9.3, 9.9, 10.9, 14.8, 16.5, 22.5, 24.6, 32.0, 32.5	16 accs. (18.0 %)
Fruit breadth (cm)	8.0, 8.9, 9.5, 9.7, 10.2, 10.3, 30.4	7 accs. (7.9 %)
Fruit stalk length (mm)	65.4	1 accs. (1.1 %)
Fruit stalk thickness (mm)	12.3, 12.5, 14.6, 14.9	4 accs. (4.5 %)
Fruit calyx length	39.4, 47.4	2 accs. (2.2 %)
Number of fruits per infructescence (fruit)	4.0, 4.5, 5.5, 6.5, 7.0, 8.0, 9.0	9 accs. (10.1 %)
100 seeds weight (g)	0.96	1 accs. (1.1 %)

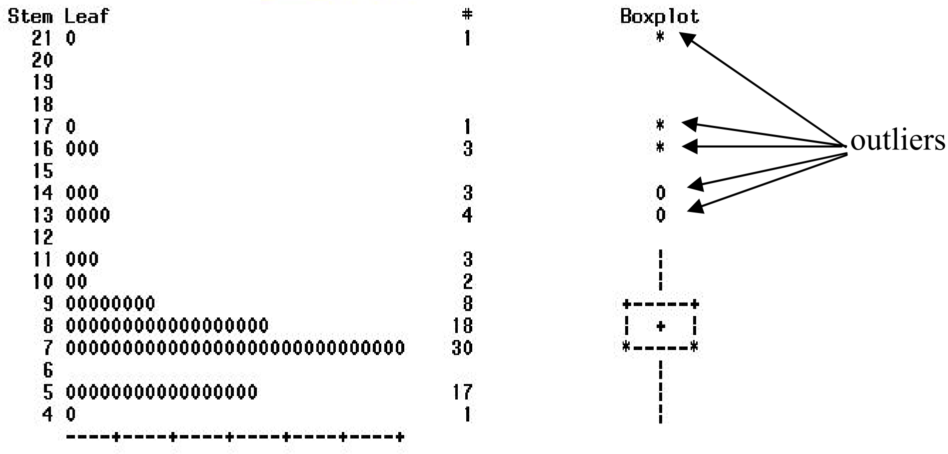

Figure 1 Selected items from PROC UNIVARIATE output for germination period with the analysis of the *Solanum* spp. dataset.

C. Selection of less correlated traits

Not all of the 25 ratio scale traits were considered in the cluster analysis of 89 accessions. Traits described to be highly correlated are regarded as surrogates of each other and any representation of two highly correlated can be considered redundant (Collantes, 2003; Laban, 2003). Hence, these traits are required to be examined using the PROC CORR and PROC VARCLUS to determine the traits considered to be highly correlated.

Using PROC CORR statement, the Pearson correlation coefficients were calculated between 19 traits. Table 7 displays the upper triangular of the correlation matrix for such traits. From the given correlation matrix, groups of highly correlated traits were formed using VARCLUS procedure and setting the proportion of variation explained by the cluster 95 %. This type of procedure utilizes oblique multiple-group component analysis to generate both hierarchical and disjoint clustering of variables (SAS, 1999). The PROC VARCLUS corresponding dendrogram (Figure 3). At 95 % *propor*, the following traits were immediately considered in cluster analysis:

1) Plant breadth
2) Plant branching
3) Number of flowers per inflorescence
4) Number of fruits per infructescence
5) Germination period
6) Fruit stalk length
7) Fruit length
8) Fruit breadth
9) Cotyledon leaf length/width ratio
10) Seed weight

However, the remaining four sets of traits (Table 8) considered to be highly correlated were further examined. For each set, the trait that is normally distributed was chosen to represent that set. To illustrate this selection process, the set containing petiole length, leaf blade length and leaf blade width was considered. Using the Shrapiro-Wilk test for normality from the PROC UNIVARIATE output (Appendix Figure B7, B8 and B9), the *p*-values of these traits were 0.0618, 0.0074 and 0.0001, respectively. Such set exhibited normal distribution. However, the leaf blade width was more normal distribution compared to leaf blade length and petiole length, therefore, leaf blade width was chosen to present that set. In case of plant height and flowering time set of traits, both p-values were equal to 0.0001. The flowering time was chosen to present that set because plant height exhibited non-normal distribution but flowering time was normal distribution. For cotyledon leaf length and cotyledon leaf width set of traits, both traits were more normal distribution. The cotyledon leaf width was chosen over cotyledon leaf length because the measurement of the former was considered to be easier and p-value (0.0005) was almost to 0.0001 (Manigbas, 2005).

Table 7 Correlation coefficients scale calculated between 19 ratio scale traits of 89 accessions, belonging to *Solanum* spp.

Traits	Germination period	Cotyledon leaf length	Cotyledon leaf width	Cotyledon leaf length/width ratio	Plant height	Plant breadth	Plant branching	Petiole length	Leaf blade length	Leaf blade width
Germination period	1.00	-0.58	-0.68	0.01	0.58	0.58	0.52	0.46	0.51	0.53
Cotyledon leaf length		1.00	0.85	0.53	-0.44	-0.38	-0.45	-0.62	-0.59	-0.72
Cotyledon leaf width			1.00	0.01	-0.67	-0.54	-0.59	-0.62	-0.55	-0.69
Cotyledon leaf length/width ratio				1.00	0.24	0.16	0.09	-0.23	-0.28	-0.30
Plant height					1.00	0.73	0.65	0.43	0.44	0.52
Plant breadth						1.00	0.67	0.44	0.51	0.52
Plant branching							1.00	0.42	0.47	0.51
Petiole length								1.00	0.79	0.86
Leaf blade length									1.00	0.93
Leaf blade width										1.00
No. of flowers per inflorescence										
Flowering time										
Fruit length										
Fruit breadth										
Fruit stalk length										
Fruit stalk thickness										
Fruit calyx length										
No. of fruit per infructescence										
100 seeds weight										

Table 7 (Continued)

Traits	No. of flowers per inflorescence	Flowering time	Fruit length	Fruit breadth	Fruit stalk length	Fruit stalk thickness	Fruit calyx length	No. of fruit per infructescence	100 seeds weight
Germination period	0.41	0.66	0.14	0.04	-0.19	-0.19	-0.28	0.47	-0.39
Cotyledon leaf length	-0.39	-0.73	0.29	0.33	0.47	0.52	0.55	-0.37	0.75
Cotyledon leaf width	-0.55	-0.84	0.22	0.36	0.48	0.55	0.62	-0.55	0.63
Cotyledon leaf length/width ratio	0.16	-0.05	0.16	0.05	0.18	0.14	0.05	0.24	0.41
Plant height	0.67	0.85	-0.28	0.33	-0.30	-0.41	-0.50	0.73	-0.44
Plant breadth	0.61	0.70	-0.22	-0.24	-0.25	-0.27	-0.36	0.63	-0.40
Plant branching	0.64	0.66	-0.18	-0.18	-0.27	-0.28	-0.40	0.57	-0.52
Petiole length	0.44	0.63	-0.02	-0.21	-0.48	-0.26	-0.31	0.23	-0.39
Leaf blade length	0.50	0.67	-0.01	-0.18	-0.37	-0.13	-0.13	0.29	-0.46
Leaf blade width	0.53	0.79	-0.14	-0.27	-0.55	-0.32	-0.35	0.36	-0.54
No. of flowers per inflorescence	1.00	0.65	-0.19	-0.24	-0.23	-0.26	-0.33	0.70	-0.43
Flowering time		1.00	-0.28	-0.37	-0.52	-0.51	-0.57	0.67	-0.64
Fruit length			1.00	0.59	0.38	0.57	0.61	-0.26	0.42
Fruit breadth				1.00	0.27	0.52	0.49	-0.33	0.26
Fruit stalk length					1.00	0.47	0.57	-0.25	0.32
Fruit stalk thickness						1.00	0.89	-0.36	0.53
Fruit calyx length							1.00	-0.45	0.55
No. of fruit per infructescence								1.00	-0.39
100 seeds weight									1.00

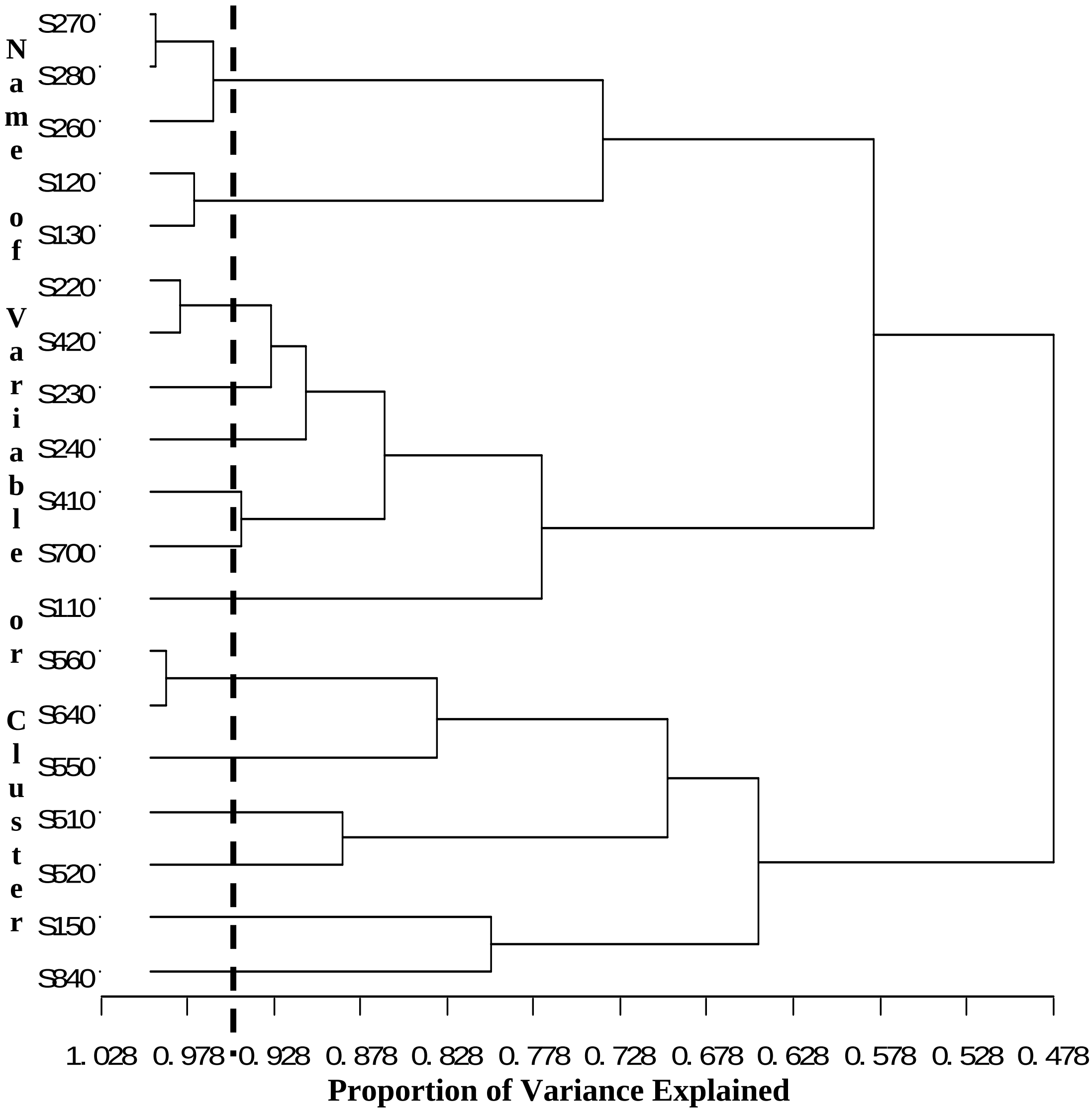

Figure 2 Dendrogram corresponding to the PROC VARCLUS output on the accessions of *Solanum* spp.

S110 = Germination period, S120 = Cotyledonous leaf length, S130 = Cotyledonous leaf width, S150 = Cotyledon length/width ratio, S220 = Plant height, S230 = Plant breadth, S240 = Plant branching, S260 = Petiole length, S270 = Leaf blade length, S280 = Leaf blade width, S410 = No. of flowers per inflorescence, S420 = Flowering time, S510 = Fruit length, S520 = Fruit breadth, S550 = Fruit stalk length, S560 = Fruit stalk thichness, S640 = Fruit calyx length, S700 = No. of fruits per infructescence, S840 = 100 seeds weigth

Table 8 The Shaprio-Wilk test of normality values for the highly correlated traits among the accessions of *Solanum* spp.

Correlated traits	p-value (Pr < W)	Selected trait	Remarks
Cotyledon leaf length (mm)	0.0021	Cotyledon leaf width	easier to measure and less prone to errors
Cotyledon leaf width (mm)	0.0005		
Leaf blade length (cm)	0.0074		
Leaf blade width (cm)	0.0001	Leaf blade width	more normally distributed
Petiole length (mm)	0.0618		
Plant height (cm)	0.0001	Flowering time	more normally distributed
Flowering time (day)	0.0001		
Fruit stalk thickness (mm)	0.0001	Fruit stalk thickness	more normally distributed
Fruit calyx length	0.0001		

1.2.2 Cluster analysis

I. Ratio scale traits (quantitative traits)

The 69 accessions belonging to *Solanum* spp. was analysed based on the 13 traits selected using the PROC CLUSTER statement. This procedure searched throughout the data for accessions that were similar enough to be considered as part of a common cluster (Cababasay, 1996).

Using the standardized data, the Unweighted Pair Group of Matheretic Average (UPGMA) was chosen to stratify the 69 accessions. This could be attributed to the fact that average linkage method (UPGMA) can be used with any resemblance coefficients compared with Ward's method. Moreover, the similarity between pairs of clusters can be determined in a manner less extreme compare with single or complete linkage (Romesburg, 1984). This was done by taking the average distance between all pairwise combinations of observations one in each cluster (SAS, 1999). This method was also recommended by Cababasay (1991) due to its best over-all performance.

The PROC CLUSTER statement provided useful statistics (pseudo *F*, pseudo t^2 and cubic clustering criteria) that can estimate the number of clusters that will be formed out of a given data. They refer to the values that are measures of fit for the analysis of each specified number of clusters (Callantes, 2003). These statistics were given using the PSEUDO and CCC options, respectively, which are one of the options used to control the printing of the cluster history (SAS, 1999).

With pseudo *F* statistic, Figure 3 reveals that the possible numbers of clusters used to stratify the 69 accessions of *Solanum* spp. were 2 and 10. With the pseudo t^2 statistic, however, Figure 4 shows that the accessions could be grouped in to 1 and 6 clusters. Figure 5, on the other hand, gave an estimate of 7 clusters using the cubic clustering criterion. In this case, there was no consensus that could be found among these criteria.

Collantes (2003) emphasized that the biggest cluster should not be too large and that there should not be too many small clusters. Following this, the use of 1 to 7 clusters as indicated by these criteria would stratify the majority of the accessions into one large cluster and 10 clusters would be left. Conversely, the use of 10 clusters would separate the majority of the accessions into relatively few clusters. Hence, the 69 accessions of *Solanum* spp. were stratified into 10 clusters.

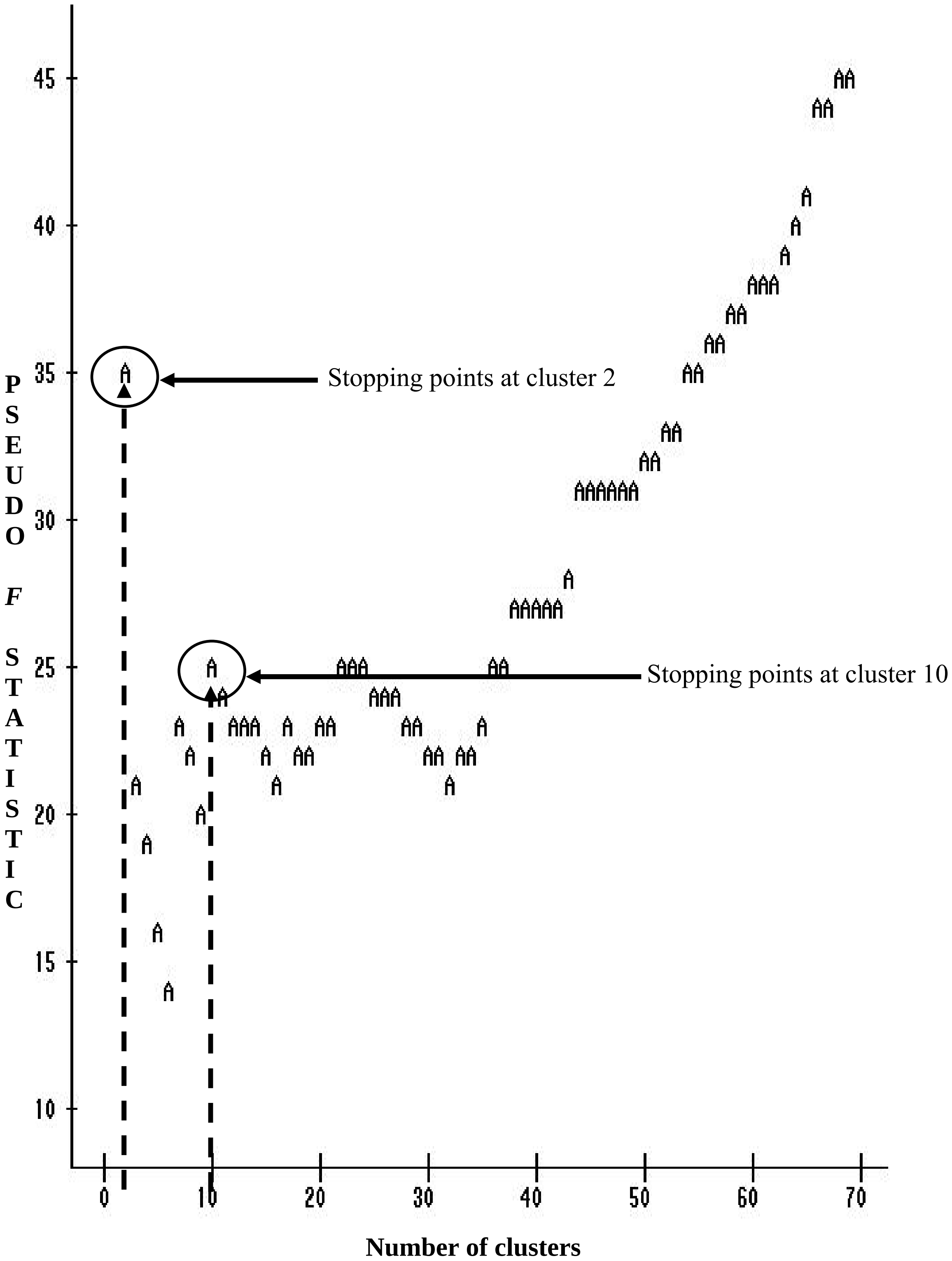

Figure 3 Plot of Pseudo *F* the clustered accessions of *Solanum* spp.

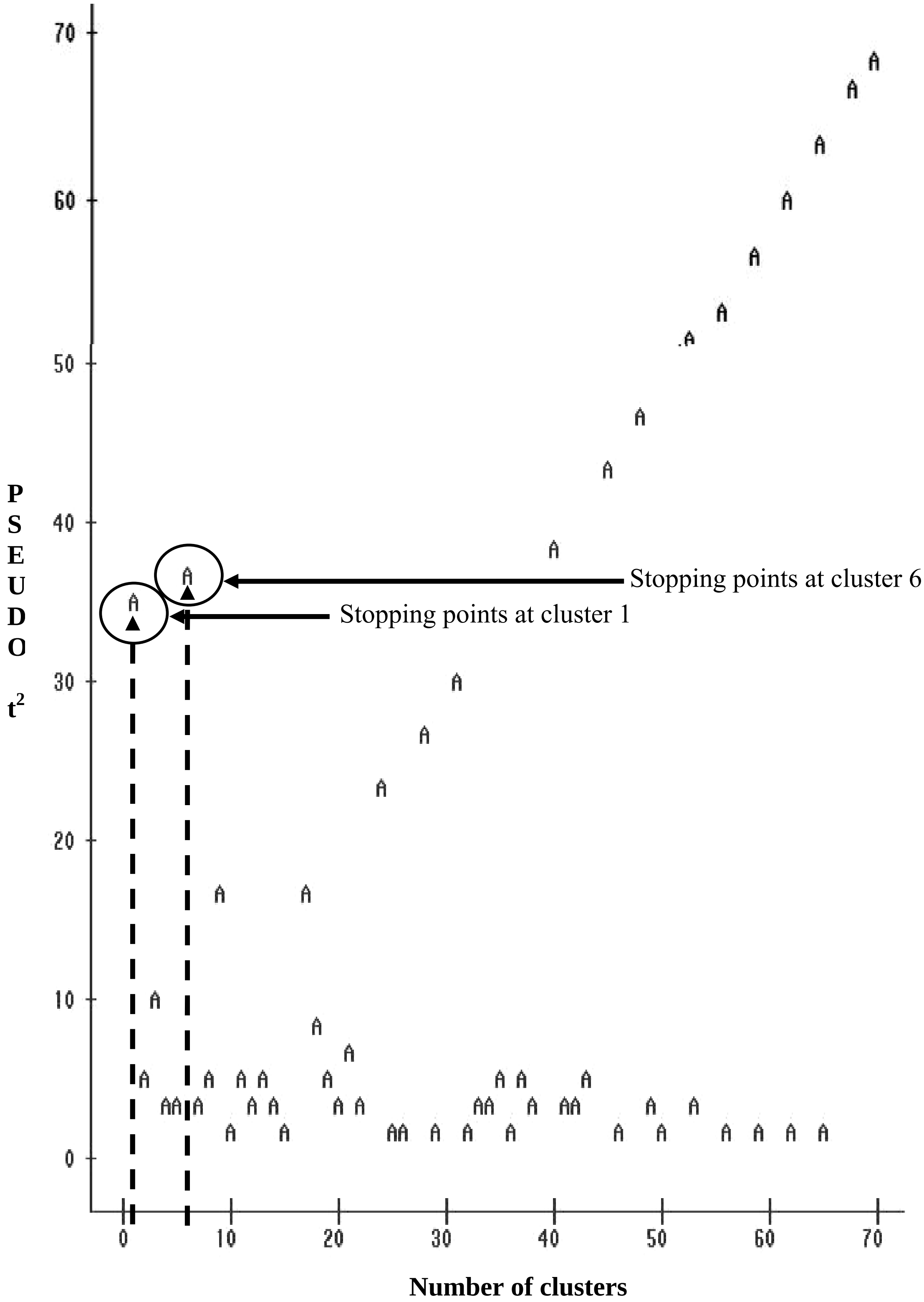

Figure 4 Plot of pseudo t^2 the clustered accessions of *Solanum* spp.

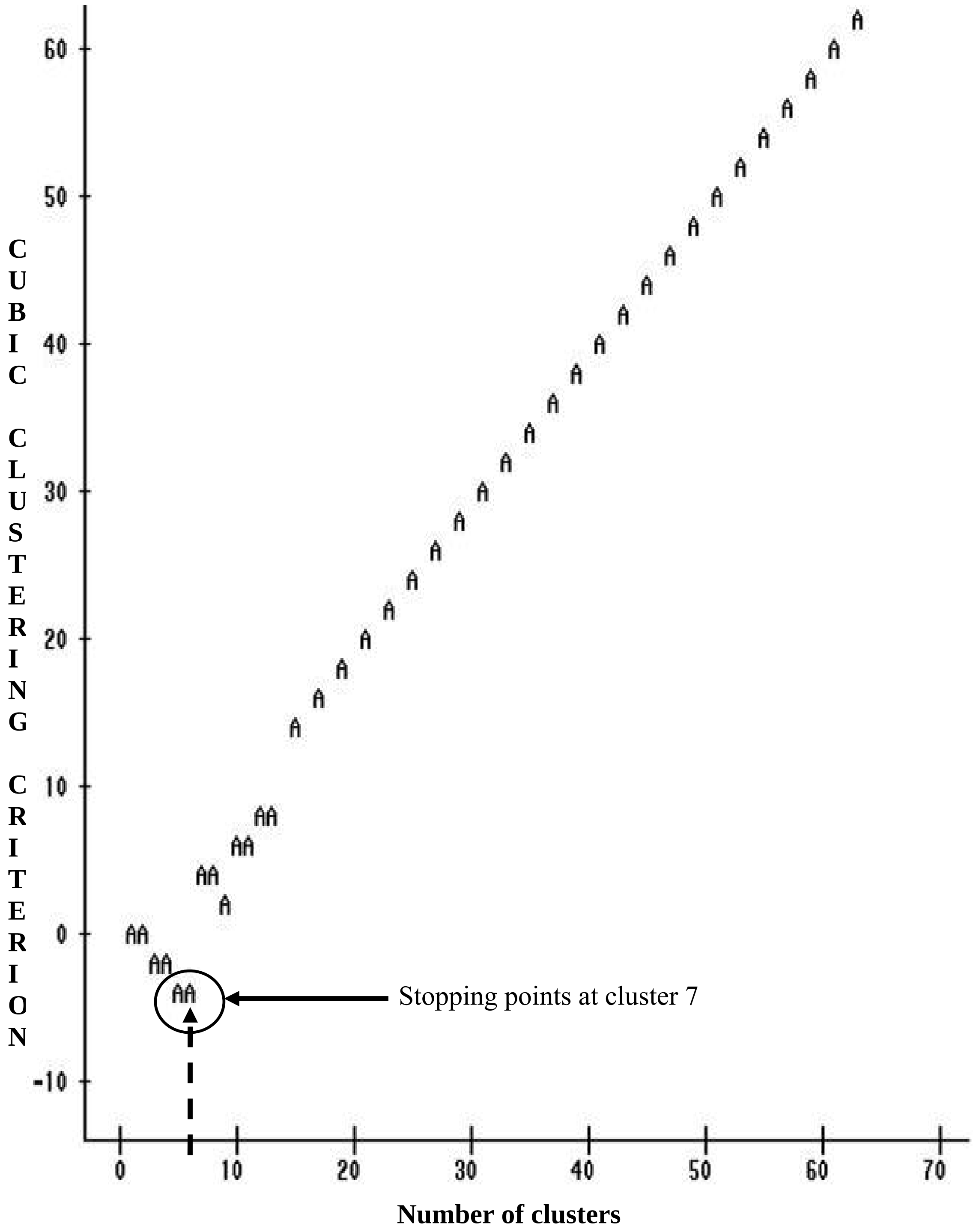

Figure 5 Plot of cubic clustering criterion in the clustered accessions of *Solanum* spp.

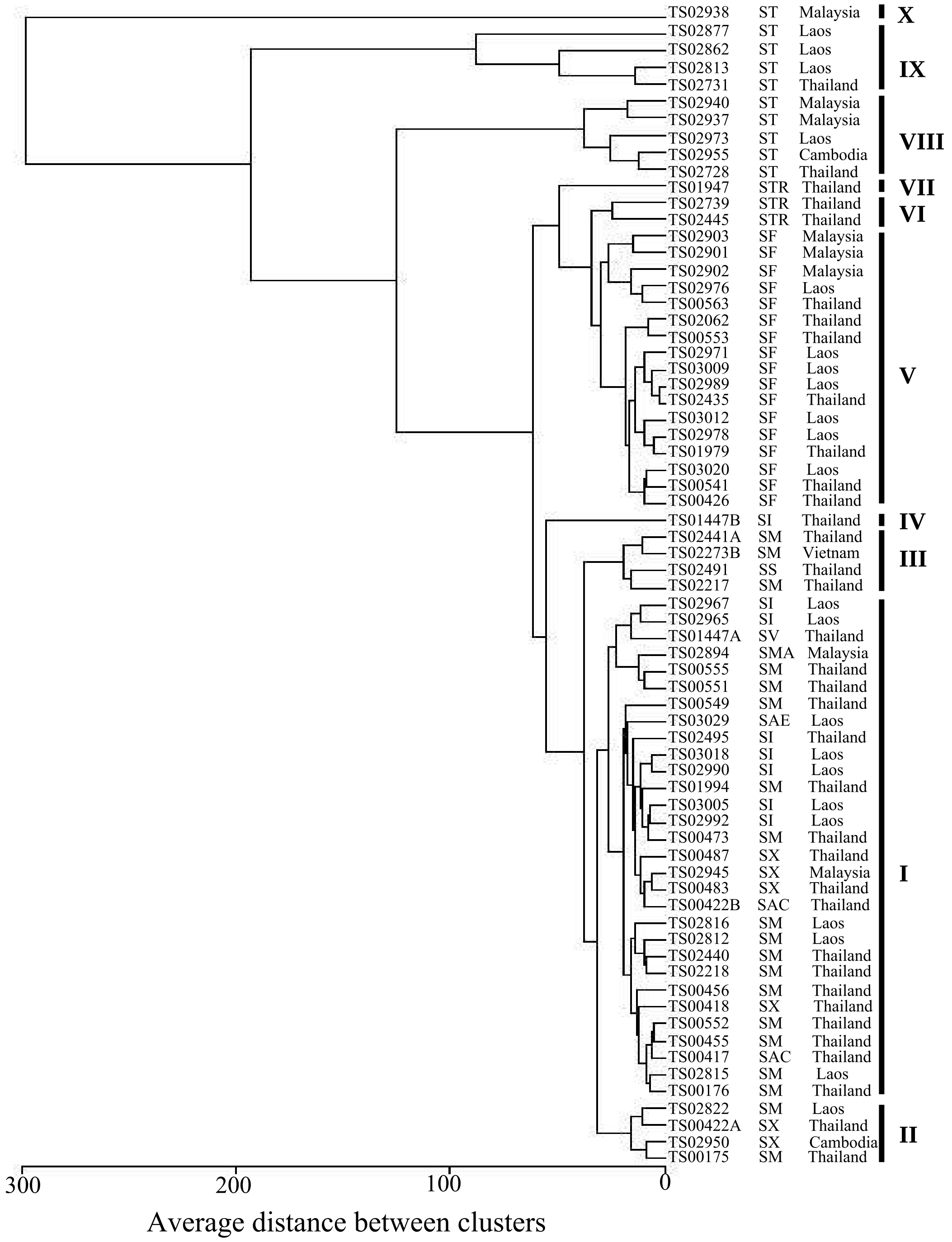

Figure 6 Cluster analysis of the 69 accessions, belonging to *Solanum* spp. based on the 14 ratio scale traits using UPGMA clustering method.

SAC = *S. aculeatissimum,* SAE = *S. aethiopicum,* SF = *S. ferox,*

SI = *S. indicum,* SM = *S. melongena,* SMA = *S. mammosum,*

SS = *S. sanitwongsei,* ST = *S. torvum,* STR = *S. trilobatum,*

SV = *S. viarum,* SX = *S. xanthocarpum*

Table 9 Accessions number of *Solanum* spp. per cluster and subcluster based on ratio scale traits.

Cluster	Subcluster	Accession No.	Species	Country of origin	Population (%)
I	A	TS00176	*S. melongena*	Thailand	15.94
		TS02815	*S. melongena*	Laos	
		TS00417	*S. aculeatissimum*	Thailand	
		TS00455	*S. melongena*	Thailand	
		TS00552	*S. melongena*	Thailand	
		TS00418	*S. xanthocarpum*	Thailand	
		TS00456	*S. melongena*	Thailand	
		TS02218	*S. melongena*	Thailand	
		TS02440	*S. melongena*	Thailand	
		TS02812	*S. melongena*	Laos	
		TS02816	*S. melongena*	Laos	
	B	TS00422-B	*S. aculeatissimum*	Thailand	18.84
		TS00483	*S. xanthocarpum*	Thailand	
		TS02945	*S. xanthocarpum*	Malaysia	
		TS00487	*S. xanthocarpum*	Thailand	
		TS00473	*S. melongena*	Thailand	
		TS02992	*S. indicum*	Laos	
		TS03005	*S. indicum*	Laos	
		TS01994	*S. melongena*	Thailand	
		TS02990	*S. indicum*	Laos	
		TS03018	*S. indicum*	Laos	
		TS02495	*S. xanthocarpum*	Malaysia	
		TS03029	*S. aethiopicum*	Laos	
		TS00549	*S. melongena*	Thailand	
	C	TS00551	*S. melongena*	Thailand	8.70
		TS00555	*S. melongena*	Thailand	

Table 9 (Continued)

Cluster	Subcluster	Accession No.	Species	Country of origin	Population (%)
I	C	TS02894	*S. mammosum*	Malaysia	
		TS01447-A	*S. viarum*	Laos	
		TS02965	*S. indicum*	Laos	
		TS02967	*S. indicum*	Laos	
II		TS00175	*S. melongena*	Thailand	5.80
		TS02950	*S. xanthocarpum*	Cambodia	
		TS00422-A	*S. xanthocarpum*	Thailand	
		TS02822	*S. melongena*	Laos	
III		TS02217	*S. melongena*	Thailand	5.80
		TS02491	*S. sanitwongsei*	Thailand	
		TS02273-B	*S. melongena*	Vietnam	
		TS02441-A	*S. melongena*	Thailand	
IV		TS01447-B	*S. indicum*	Thailand	1.45
V	A	TS00426	*S. ferox*	Thailand	17.39
		TS00541	*S. ferox*	Thailand	
		TS03020	*S. ferox*	Laos	
		TS01979	*S. ferox*	Thailand	
		TS02978	*S. ferox*	Malaysia	
		TS03012	*S. ferox*	Laos	
		TS02435	*S. ferox*	Thailand	
		TS02989	*S. ferox*	Laos	
		TS03009	*S. ferox*	Laos	
		TS02971	*S. ferox*	Laos	
		TS00553	*S. ferox*	Thailand	
		TS02062	*S. ferox*	Thailand	
	B	TS00563	*S. ferox*	Thailand	7.25
		TS02976	*S. ferox*	Laos	

Table 9 (Continued)

Cluster	Subcluster	Accession No.	Species	Country of origin	Population (%)
V	B	TS02902	*S. ferox*	Malaysia	
		TS02901	*S. ferox*	Thailand	
		TS02903	*S. ferox*	Malaysia	
VI		TS02445	*S. trilobatum*	Thailand	2.90
		TS02739	*S. trilobatum*	Thailand	
VII		TS01947	*S. trilobatum*	Thailand	1.45
VIII		TS02728	*S. torvum*	Thailand	7.25
		TS02955	*S. torvum*	Cambodia	
		TS02973	*S. torvum*	Laos	
		TS02937	*S. torvum*	Malaysia	
		TS02940	*S. torvum*	Malaysia	
IX		TS02731	*S. torvum*	Thailand	5.80
		TS02813	*S. torvum*	Laos	
		TS02862	*S. torvum*	Laos	
		TS02877	*S. torvum*	Laos	
X		TS02938	*S. torvum*	Malaysia	1.45

Table 10 The morphological characters of 69 accessions of *Solanum* spp. per cluster and subcluster based on quantitative traits.

Characters \ Cluster/subcluster	I			II	III	IV	V		VI	VII	VIII	IX	X
	A	B	C				A	B					
Germination period (day)	6.00	6.92	7.33	8.00	6.50	11.00	8.42	9.40	7.00	8.00	13.00	15.25	9.00
Cotyledonous leaf width (mm)	8.29	7.57	7.37	8.10	8.58	3.45	5.89	6.35	7.00	6.80	3.34	4.03	4.85
Cotyledon leaf length/width ratio	2.11	2.29	2.35	1.99	1.97	2.39	1.55	1.56	2.59	2.82	2.30	2.43	2.42
Plant breadth (cm)	83.55	94.54	96.33	114.50	62.13	49.00	91.38	112.70	92.75	93.50	128.60	249.50	185.00
Plant branching	9.95	10.15	10.50	9.13	10.13	12.00	10.71	11.00	9.00	9.50	14.90	17.38	16.00
Leaf blade width (cm)	16.13	17.50	21.29	17.91	16.05	14.10	32.85	34.73	10.38	12.50	35.90	34.69	40.50
No. flowers per inflorescence	3.95	6.85	6.00	6.13	5.50	9.00	10.58	10.70	16.00	8.00	82.60	77.63	290.00
Flowering time (day)	57.45	62.00	72.83	58.25	57.75	91.00	108.17	118.40	113.50	152.00	162.20	157.25	151.00
Fruit length (cm)	3.02	2.60	2.90	2.94	4.77	0.94	2.14	3.27	1.05	0.88	1.33	1.22	1.43
Fruit breadth (cm)	3.42	3.14	3.00	3.50	5.26	0.96	2.24	3.03	0.91	0.89	1.32	1.26	1.42
Fruit stalk length (mm)	31.04	24.54	15.25	37.45	25.86	18.10	13.53	14.22	27.18	21.70	16.89	16.43	18.30
Fruit stalk thickness (mm)	5.79	4.76	3.88	5.70	4.99	2.45	3.10	3.79	2.03	1.95	3.25	3.48	3.30

Stratifying the accessions into 10 clusters showed variability among accessions brought about their distinguishing external characteristics. Component accessions per cluster and subcluster were presented in Table 9 and the morphological characters based on quantitative traits per cluster and subcluster was presented in Table 10.

Cluster I is a largest group consisting of 30 homogeneous accessions. This cluster represents the majority (43.48 %) of accessions which had ratio scale traits considered to be similar enough to group them into one cluster.

Cluster I was divided into 3 subclusters. Among the three, subcluster B was considered to be the most diverse with 13 accessions (18.84 %). Subcluster B represented the mixture accessions belonging to *Solanum aethiopicum* (1 accession) collected in Laos, *S. aculeatissimum* (1 accession) collected in Thailand, *S. indicum* (4 accessions) collected in Laos, *S. melongena* (3 accessions) collected in Thailand and *S. xanthocarpum* (4 accessions) collected in Thailand and Malaysia. Subcluster B can be distinguished from the rest (subclusters A and C) by having the intermediate variability for the traits used except for number of fruit per infructescence which is the largest (1.88).

Subcluster A consist of *S. melongena* collected in Thailand (7 accessions), Laos (3 accessions), *S. aculeatissimum* (1 accession) collected in Thailand and *S. xanthocarpum* (1 accession) collected in Thailand .The uniqueness of this subcluster is characterized by having the shortest period to germinate (6 days), the shortest cotyledon leaf length/width ratio (2.11), smallest plant breadth (83.55 cm), the least number of plant branching (9.95), the shortest leaf blade width (16.13 cm), the least number of flower per inflorescence (3.95 flowers) and the shortest period of flowering time (57.95 days). Also, it has the biggest cotyledon leaf width (8.29 mm), the longest fruit length (3.02 cm) and biggest fruit breadth (3.42 cm), the largest fruit stalk length (31.04 mm) and thickest fruit stalk (5.79 mm) when compared with the other subclusters.

Subcluster C consisted of 2 accessions of *S. indicum* and one accession of *S. viarum* collected in Laos, one accession of *S. mammosum* collected in Malaysia and 2 accessions collected in Thailand. This subcluster was separated from the other subcluster by taking the longest time to germinate (7.33 days), the largest cotyledonous leaf length/width ratio (2.35), the biggest plant breadth (96.33 cm), the largest number plant branching (10.50), the bigggest leaf blade width (21.29) and the longest period of flowering time (72.83 days). Furthermore, it has the shortest fruit breadth, only 3.00 cm diameter of the broadest part of the fruit. Also, it has the shortest fruit stalk length (15.25 mm) and fruit stalk thickness (3.88 mm) and the smallest 100 seed weight (0.43 g).

By virtue of their morphological characteristics, these 4 subclusters were related to each other. All of their component accessions exhibited nearly homogeneous ratio traits. This included the cotyledon leaf width, cotyledon leaf length and width ratio, leaf blade width and 100 seeds weight from which the differences in their ranges were at proximity. Cluster I, association of the accessions would be mean intermediate variability for the traits used. More likely, this would be suggested that their morphological characters were nearly similar even if they were different species and taken from different parts of Southeast Asia.

<u>Cluster II</u>: the second cluster accounting for 5.80 % of the total accessions, consisted of 2 accessions of *S. melongena* collected in Thailand and Laos and 2 accessions of *S. xanthocarpum* collected in Thailand and Cambodia. The uniqueness of this cluster is characterized by having the longest fruit stalk length (37.45 mm) and the most of fruit stalk thickness (5.70 mm).

<u>Cluster III</u>: the third cluster covers the 4 accessions (5.80 %). Cluster III consists of 3 accessions of *S. melongena* collected in Thailand (2 accessions) and Vietnam (1 accesion) and only one accessions of *S. sanitwongsei* collected in Thailand. The characteristic traits of this cluster include the shortest period to germinate (6.50 days), the least number of flowers per inflorescence (5.50), the least period of flowering time (57.75 days) and the least number of fruit per influctescence

(single fruit). It has also the widest cotyledonous leaf width (8.58 mm), the longest fruit length (4.77 cm) and widest fruit breadth (5.26 cm).

Cluster IV: the forth cluster is the smallest cluster; there is only one accession (TS014474-B) of *S. melongena* collected in Thailand. The uniqueness of this cluster is characterized by having the smallest plant breadth (49.00 cm).

Cluster V: the fifth cluster is a second largest group consisting of 17 homogeneous accessions, belong to *S. ferox*. This account for the 24.63 % of the total accessions stratified. Cluster V was divided into 2 subclusters. Subcluster A consist of 12 accessions (17.39 %) which 6 accessions collected in Thailand, 5 accessions collected in Laos and one accession in Malaysia. Subcluster B consist of 5 accessions (7.25 %) which 2 accessions collected in Thailand, 2 accessions collected in Malaysia and one accession collected in Laos. Subcluster A was separated from subcluster B by having the 12 bigger ratio scale traits except for the number of fruits per infructescence. Cluster V can be distinguished from the rest by having the least cotyledon leaf length and width ratio and the shortest fruit stalk length (13.87 mm).

Cluster VI consists of 2 accessions which were identified as *S. trilobatum* collected in Thailand. This cluster is unique to have the least of number of primary branches per plant (9) and the shortest leaf blade width (10.38 cm). Furthermore, it has the highest 100 seed weight (0.39 g), on the average.

Cluster VII consists of only one accession of *S. trilobatum* collected in Thailand. This species formed its own separated stratified clusters. It could be recognized from the rest as having the shortest fruit length and fruit width corresponds to 0.88 and 0.89 cm, respectively. Also, it has the smallest fruit stalk thickness (1.95 mm). Furthermore, it has the largest cotyledon leaf length and width ratio (2.82) and largest number of fruit per infructescence (7 fruits).

Cluster VIII includes only one species, *S. torvum,* consisting of 4 accessions which TS02955 collected in Cambodia, TS02973 collected in Laos and TS02937 and

TS02940 collected in Malaysia. This cluster can be distinguished from the rest by having the smallest cotyledon leaf length and width ratio (3.34). Also, it has the longest period of flowering time (162.20 days).

Cluster IX also includes only one species, *S. torvum*, consisting of 4 accessions collected in Thailand (1 accession) and Laos (4 accessions). This unique of this clusters attributed by having the longest time to germinate (15.25 days), the biggest plant breadth (249.50 cm), the largest number of plant branching (17.38) and the smallest 100 seeds weight (0.11 g).

Cluster X includes 1 accession of *S. torvum* from Malaysia. This cluster is separated from the rest which indicated that it has ratio scale traits that are most different from the other clusters. The uniqueness of this cluster is attributed by having the largest leaf breadth (40.40 cm), the largest number of flower per inflorescence (290 flowers) and largest number of fruits per infructescence (7 fruits).

However, the determination of morphological traits was associated with geographical origin basing on quantitative traits for 14 traits. Overall, the results on the accessions show the same species and same origin trend to cluster. For *S. melongena* the major part (approximately 27.54 %) of the variation was found within collection areas, where the major part (approximately 73.68 %) of the variation was found in Thailand. Also the variation of *S. melongena* is presented in the collections from Laos and Vietnam, approximately 21.05 % and 5.26 %, respectively.

S. aculeatissimum presents only in cluster I and the variation was found only in the collections from Thailand (approximately 2.90 %). For *S. xanthocarpum* (10.14 %) belongs to cluster I and II. The variation was found in the collections from Thailand (approximately 57.14 %), Malaysia (approximately 28.57 %) and Cambodia (approximately 14.29 %).

S. aethiopicum, *S. mammosum* and *S. vairum* consist of only one accession each and they were grouped together in Cluster I. *S. aethiopicum* and *S. vairum,* both were collected in Laos, while *S. mammosum* originated from Malaysia. The three species showed homogeneous of the ratio traits in morphological characters especially in fruit shape. This included the cotyledon leaf width, cotyledon leaf length and width ratio, leaf blade width and 100 seeds weight.

Cluster I and IV include *S. indicum*; six of accessions *S. indicum* belong to cluster I collected from Laos (85.71 %), while one accession belongs to cluster IV originated from Thailand (14.29 %). This resulted in the same species but different ratio scale traits and could be seperated. For example the unique of *S. indicum* in cluster IV is characterized by being the smallest plant breadth (49.00 cm) while *S. indicum* in cluster I is characterized by being the biggest plant breadth (97.17 cm).

Moreover, *S. sanitwongsei*, the only one accession collected in Thailand, belongs to cluster III. Its morphological was similar to *S. indicum* collected in Laos (Figure 6).

Cluster V includes 17 accessions of *S. ferox* and is the second largest group (approximately 24.64 %) of the variation found in Southeast Asia, where the major part (approximately 47.06 %) of the variation occur in Thailand, Laos and Malaysia, approximately 35.29 and 17.65 %, respectively. Therefore, the distribution center of *S. ferox* is located in Thailand and Laos due to the fact that this species is consumed in Thailand and Laos but not in Malaysia.

Three accessions of *S. trilobatum* collected in Thailand belong to cluster VI and VII. Based on the ratio scale traits, two accessions in cluster VI, it is unique in its lowest number of primary branches per plant (9) and the smallest leaf leaf blade width (10.38 cm). Furthermore, it has the highest 100 seed weight (0.39 g), on the average. Compared to cluster VII, the one accession displayed the rest as it obtained the shortest fruit length and fruit width corresponds to 0.88 and 0.89 cm, respectively. Also, it has the smallest fruit stalk thickness (1.95 mm). Furthermore, it has the maximum cotyledon leaf length to width ratio.

S. torvum accessions, based on the ratio scale traits can be divided into three clusters. Approximately 14.49 % of the variation was found within collection areas, where the major part (approximately 40 %) of the variation was found in Laos, the rest were found in Malaysia, Thailand and Cambodia, approximately 30, 20 and 10 %, respectively. Furthermore, five accessions, belong to Cluster VIII with 2 accessions collected in Malaysia and 3 accessions collected in Thailand, Cambodia and Laos. This cluster contains more variation in Malaysia.

Therefore, the morphological traits were associated with geographic origin based on quantitative traits for 14 traits. Overall, the results on variation of the accessions showed the same species and origin tend to cluster.

II. Nominal traits (qualitative traits)

The most frequent traits among the 69 accessions in Southeast Asia considered are present in Table 11. The traits of plant growth habit was intermediate (approximately 94.20 %), leaf blade lobbing was intermediate (approximately 39.13 %), leaf blade tip angle was intermediate (approximately 55.07 %), relative style length was long (approximately 97.10 %), style exertion was exertion (approximately 81.16 %), fruit length and breadth ratio was as long as broad (approximately 72.46 %), fruit color at commercial ripeness was green (approximately 68.12 %), fruit color at physiological ripeness was deep yellow (approximately 42.03 %), fruit flesh density was loss (crumbly) (approximately 46.38 %), fruit yiled per plant was low (~ 500 g)(approximately 75.36 %) and seed color was light yellow (approximately 46.38 %). However, this indicateas that most of *Solanum* spp. have intermediate plant growth habit and long relative style length. Furthermore, leaf blade lobbing, fruit color at physiological maturity, fruit flesh density and seed color was more variation depend on species.

However, *S. melongena* is the highest population on plant growth habit (28.49 %), leaf blade lobbing (23.19 %), leaf blade tip angle (18.84 %), relative style length (26.09 %), style exertion (14.49 %), fruit color at physiological ripeness (28.49 %) and fruit yiled per plant (21.74 %). However, *S. ferox* is the highest population on fruit length and breadth ratio (24.64 %), fruit color at commercial ripeness (24.64 %), fruit flesh density (24.64 %) and seed color (24.64 %). In addition, *S. torvum* is the highest population on style exertion (14.49 %).

Therefore, following the most frequent of qualitative trait, *S. melongena* was the major group of 69 accessions of *Solanum* spp. and the second major group was *S. ferox* and the third major group was *S. torvum.*

Table 11 Most frequent qualitative traits in the 69 accessions of *Solanum* spp.

Qualitative traits	Frequency	Species	Population (%)
Plant growth habit	Intermediate (94.20 %)	*S. aethiopicum*	1 accs. (1.45 %)
		S. aculeatissimum	2 accs. (2.90 %)
		S. ferox	17 accs. (24.64 %)
		S. indicum	7 accs. (10.14 %)
		S. mammosum	1 accs. (1.45 %)
		S. melongena	20 accs. (28.49 %)
		S. torvum	10 accs. (14.49 %)
		S. viarum	1 accs. (1.45 %)
		S. xanthocarpum	6 accs. (8.70 %)
Leaf blade lobbing	Intermediate (39.13 %)	*S. aethiopicum*	1 accs. (1.45 %)
		S. aculeatissimum	2 accs. (2.90 %)
		S. melongena	16 accs. (23.19 %)
		S. trilobatum	3 accs. (4.35 %)
		S. xanthocarpum	5 accs. (7.25 %)
Leaf blade tip angle	Intermediate (~75°) (55.07 %)	*S. aethiopicum*	1 accs. (1.45 %)
		S. aculeatissimum	2 accs. (2.90 %)
		S. indicum	4 accs. (5.80 %)
		S. melongena	13 accs. (18.84 %)
		S. trilobatum	3 accs. (4.35 %)
		S. torvum	10 accs. (14.49 %)
		S. xanthocarpum	5 accs. (7.25 %)
Relative style length (mm)	Long (~5) (97.10 %)	*S. aethiopicum*	1 accs. (1.45 %)
		S. aculeatissimum	2 accs. (2.90 %)
		S. ferox	17 accs. (24.64 %)
		S. indicum	7 accs. (10.14 %)
		S. mammosum	1 accs. (1.45 %)
		S. melongena	18 accs. (26.09 %)
		S. sanitwongsei	1 accs. (1.45 %)

Table 11 (Continued)

Nominal traits	Frequency	Species	Population (%)
Relative style length (mm)	Long (~5)	*S. trilobatum*	3 accs. (4.35 %)
		S. torvum	10 accs. (14.49 %)
		S. viarum	1 accs. (1.45 %)
		S. xanthocarpum	6 accs. (8.70 %)
Style exertion	Exert (81.16 %)	*S. aethiopicum*	1 accs. (1.45 %)
		S. aculeatissimum	1 accs. (1.45 %)
		S. ferox	17 accs. (24.64 %)
		S. indicum	7 accs. (10.14 %)
		S. melongena	10 accs. (14.49 %)
		S. sanitwongsei	1 accs. (1.45 %)
		S. trilobatum	3 accs. (4.35 %)
		S. torvum	10 accs. (14.49 %)
		S. viarum	1 accs. (1.45 %)
		S. xanthocarpum	5 accs. (7.25 %)
Fruit length and breadth ratio	As long as board (72.46 %)	*S. aculeatissimum*	1 accs. (1.45 %)
		S. ferox	17 accs. (24.64 %)
		S. indicum	7 accs. (10.14 %)
		S. melongena	6 accs. (8.70 %)
		S. sanitwongsei	1 accs. (1.45 %)
		S. trilobatum	3 accs. (4.35 %)
		S. torvum	10 accs. (14.49 %)
		S. viarum	1 accs. (1.45 %)
		S. xanthocarpum	4 accs. (5.80 %)
Fruit color at commercial ripeness	Green (68.12 %)	*S. aethiopicum*	1 accs. (1.45 %)
		S. aculeatissimum	1 accs. (1.45 %)
		S. ferox	17 accs. (24.64 %)
		S. melongena	8 accs. (11.59 %)
		S. trilobatum	3 accs. (4.35 %)

Table 11 (Continued)

Nominal traits	Frequency	Species	Population (%)
Fruit color at commercial ripeness	Green	*S. torvum*	10 accs. (14.49 %)
		S. viarum	1 accs. (1.45 %)
		S. xanthocarpum	6 accs. (8.70 %)
Fruit color at physiological ripeness	Deep yellow (42.03 %)	*S. aculeatissimum*	2 accs. (2.90 %)
		S. melongena	20 accs. (28.49 %)
		S. viarum	1 accs. (1.45 %)
		S. xanthocarpum	6 accs. (8.70 %)
Fruit flesh density	Loose (crumbly) (46.38 %)	*S. aethiopicum*	1 accs. (1.45 %)
		S. ferox	17 accs. (24.64 %)
		S. melongena	1 accs. (1.45 %)
		S. torvum	10 accs. (14.49 %)
		S. viarum	1 accs. (1.45 %)
		S. xanthocarpum	2 accs. (2.90 %)
Fruit yield per plant (g)	Low (~500) (75.36 %)	*S. aculeatissimum*	1 accs. (1.45 %)
		S. ferox	14 accs. (20.29 %)
		S. indicum	6 accs. (8.70 %)
		S. melongena	15 accs. (21.74 %)
		S. trilobatum	2 accs. (2.90 %)
		S. torvum	10 accs. (14.49 %)
		S. xanthocarpum	4 accs. (5.80 %)
Seed color	Light yellow (46.38 %)	*S. aethiopicum*	1 accs. (1.45 %)
		S. ferox	15 accs. (21.74 %)
		S. indicum	7 accs. (10.14 %)
		S. sanitwongsei	1 accs. (1.45 %)
		S. trilobatum	1 accs. (1.45 %)
		S. torvum	7 accs. (10.14 %)

The similarity coefficient values (8.47) of 69 accessions were divided into 9 clusters by using R-program version 2.6.1. Here, the majority of the accessions is shown in Table 12.

Cluster I: the first cluster is the largest cluster with 19 accessions. This account for the 27.14 % of the total accessions stratified. This cluster represents the majority of mixture accessions belonging to *Solanum melongena*, *S. aculeatissimum* and *S. xanthocarpum.* This cluster is heterogeneous for 10 traits except for plant growth habit. The unique of this cluster is by having the broader than long of fruit length to breadth ratio and brownish yellow seed.

This cluster can be divided into four subclusters. Subcluster A is composed of 2 accessions (2.90 %) belong to *S. melongena* collected from Thailand. This subcluster is characterized by having weak leaf blade lobbing, the acute (~ 45°) of leaf blade tip angle and grey yellow seed. Subcluster B is the only one accession of *S. melongena* collected from Thailand. This subcluster is characterized by having intermediate (~3 mm) relative style length, insert of style exertion and as long as broad fruit length and breadth ratio. Subcluster C is a group of 6 accessions (8.70 %) heterogenous accessions belong to *S. melongena*, *S. aculeatissimum* and *S. xanthocarpum* collected from Thailand (5 accessions) and one accession from Malaysia. This subcluster is heterogenous for 7 traits except for plant growth habit, leaf blade lobbing, relative style length and fruit yield per plant. Subcluster D was considered to be the most diverse with 10 accessions (14.49 %). Subcluster D consisted of *S. melongena* collected in Thailand (7 accessions), Laos (1 accession) and Vietnam (1 accession) and *S. xanthocarpum* collected from Thailand (1 accession).

Cluster II: the second cluster consists of 6 accessions. This account for the 8.70 % of the total accessions stratified. This cluster is a group of 3 accessions belonging to *S. melongena*, 2 accessions belonging to *S. xanthocarpum* and one accessions of *S. aculeatissimum*. This cluster is homogenous for plant habit, style exertion and seed color. The unique of this cluster is having brownish yellow seed.

This cluster can be divided into two subclusters using leaf blade lobbing. Between the two, subcluster A was considered to be the most diversity with 4 accessions (5.80 %). Subcluster A consisted of *S. aculeatissimum* (1 accession) collected in Thailand, *S. melongena* (2 accessions) collected in Thailand and *S. xanthocarpum* (1 accession) collected in Thailand. Subcluster A is characterized by having intermediate leaf blade lobbing. Subclaster B consisted of *S. melongena* (1 accession) collected in Thailand and one accessions of *S. xanthocarpum* collected in Cambodia. This subcluster is characterized by having weak leaf blade lobbing.

Cluster III: the third cluster is a mixture of one accession, belonging to *S. aethiopicum* collected from Laos and 3 accessions belong to *S. trilobatum* collected from Thailand. Cluster III can be distinguished from the rest by having the prostrate plant growth habit, poppy red fruit at physiological maturity and very loose fruit flesh density. This cluster can be divided into 2 subclusters. Subcluster A (*S. aethiopicum*) that can be distinguished from subcluster B (*S. trilobatum*) by having the intermediate plant growth habit, the broader than long fruit length and breadth ratio, yellow orange fruit at physiological maturity, loose (crumbly) fruit flesh density and very low yield per plant.

Cluster IV: the forth cluster is represented by only one accession (TS01447-A). This accession belonged to *S. viarum*, collected from Thailand. This cluster formed its own, separated itself from the rest of the stratified clusters. It could be recognized from the rest as it is having the very strong leaf blade lobbing, the acute (~ 45°) of leaf blade tip angle, intermediate yield per plant and brown black seed.

Cluster V: the fifth cluster is a group of 10 accessions which is homogenous, belong to *S. torvum*, collected from Thailand, Laos, Cambodia and Malaysia. This account for the 14.49 % of the total accessions stratified. It is separated from the other cluster because the fruit color is still green at ripening stage. This cluster can be divided into two subclusters using the seed color. Between the two, subcluster A was considered to be the most diverse with 7 accessions (10.14 %). Subcluster A consisted of *S. torvum* collected in Laos (3 accessions), Cambodia (1 accession) and Malaysia

(3 accessions). Subclaster A is characterized by having light yellow seed. Subclaster B consists of *S. torvum* collected in Thailand (2 accessions) and one accessions collected in Laos. This subcluster is characterized by having grey yellow seed. This cluster is homogenous for 10 traits except seed color. The unique of this cluster is for very strong leaf blade lobbing and green fruit color at riping stage.

Cluster VI: the sixth cluster is the second largest group, consisting of 17 accessions belong to *S. ferox*. This account for the 24.64 % of the total accessions stratified. Except for the yield per plant and seed color, these subclusters are homogenous for the remaining nine nominal traits which were used to describe the accessions. Cluster VI can be divided into four subclusters using yield per plant and seed color. Among them, subcluster C is the largest with 12 component accessions (20.29 %) merged at 100 % similarity which, they were collected from Laos (5 accessions) and Thailand (7 accessions) with low fruit yield per plant and light yellow seed. Subcluster A and D comprise two accessions. Subcluster A is represented by TS02989 and TS02978 collected from Laos. These subcluster having the intermediate fruit yield per plant and light yellow seed. Subcluster D is a group of two homogenous accessions which collected from Malaysia with low fruit yield per plant and grey yellow seed. For subcluster B, is the only one accession collected from Thailand. This subcluster was separated from the other subcluster because it is the only one subcluster with very low fruit yield per plant and light yellow seed.

This cluster can be distinguished from the rest by having the strong leaf blade lobbing, the acute (~ 45°) of leaf blade tip angle and yellow orange fruit at physiological maturity.

Cluster VII is a mixture of accessions, belong to *S. sanitwongsai* and *S. indicum*. This cluster consists of 8 accessions which account for 11.59 % of the total accessions stratified. Cluster VII is homogeneous for the remaining of 7 nominal traits except plant growth habit, leaf blade lobbing, leaf blade angle and yield per plant, these traits can be divided into four subclusters.

Subcluster A is the only one accession of *S. sanitwongsei* collected in Thailand. This subcluster was separated from the other subcluster because it is the only one subcluster with upright plant growth habit and strong leaf blade lobbing, obtuse (~ 110°) leaf blade angle and very low yield per plant. Subcluster B is represented by TS02495 (*S. indicum*) collected from Thailand. The unique of this subcluster is for acute (~ 45°) leaf blade angle and very low yield per plant. Subcluster C is the homogenous of the two accessions of *S. indicum* collected from Laos, this can be separated from subcluster D by having the obtuse (~ 110°) leaf blade angle. Subcluster D is the largest subcluster with 5 accessions collected from Laos merging at 100 % similarity which.

This cluster formed its own, separated stratified clusters. It could be recognized from the rest by very strong leaf blade lobbing, deep yellow fruit at ripening and very loose (spongy) fruit flesh density.

Cluster VIII is a group of three accessions, belong to *S. melongena* collected from Laos. The unique of this cluster by having the purple fruit at ripening, dense fruit flesh density and grey yellow seed.

Cluster IX is the only one accession, belong to *S. mammosum* collected from Malaysia. The unique of this cluster is strong leaf blade lobbing, acute (~ 45°) leaf blade angle, insert style exertion, slightly longer than broad of fruit length to breadth ratio (Appendix A), deep yellow fruit at harvesting, yellow orange fruit at maturity, average density of fruit flesh density and black seed. Hence, Cluster IX was considered to be the last cluster that fuses with the rest of the clusters. This indicated the cluster IX had nominal traits considering being almost different from the other clusters.

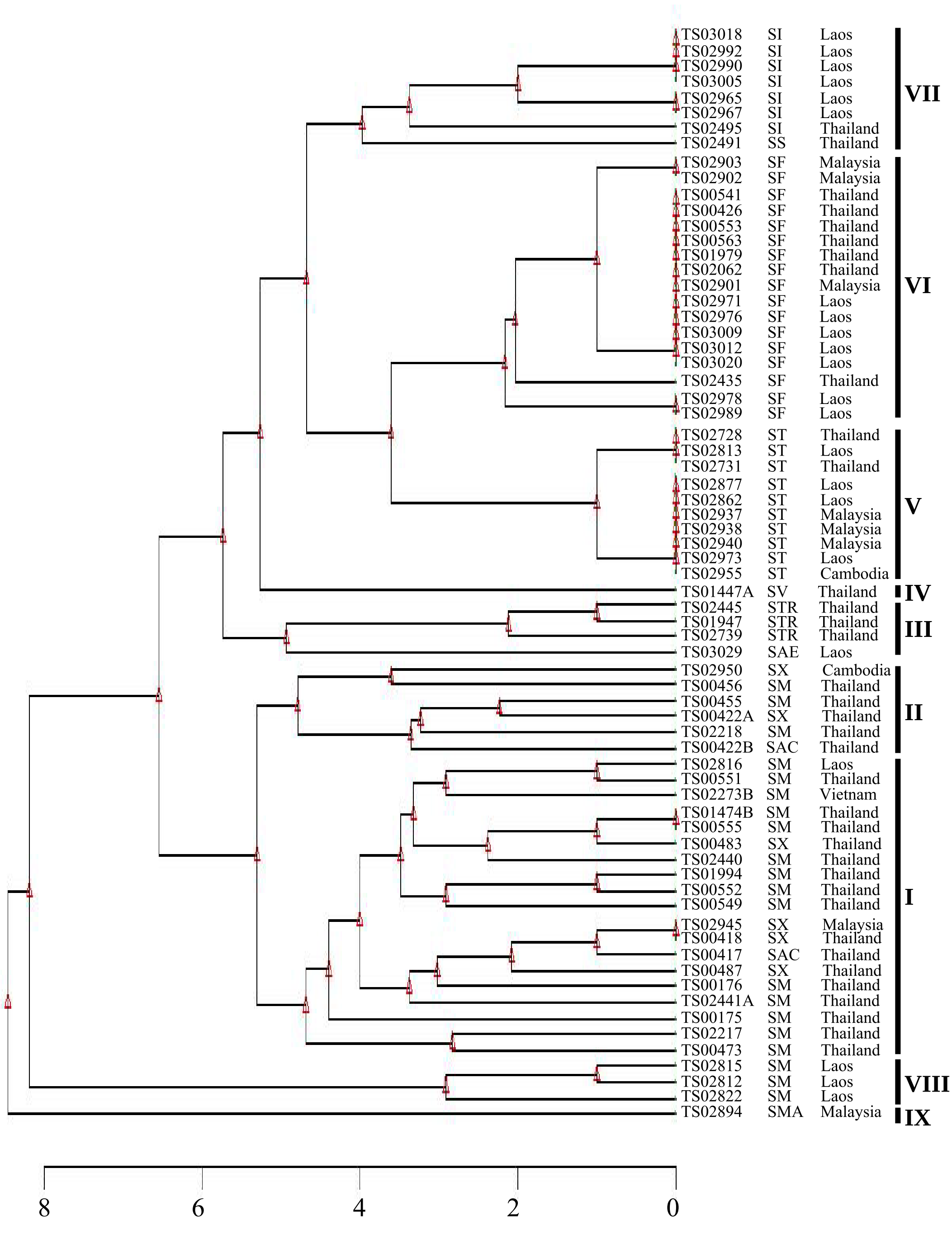

Figure 7 Cluster analysis of the 69 accessions, belonging to *Solanum* spp. based on the 11 nominal traits using UPGMA clustering method.

SAC = *S. aculeatissimum,* SAE = *S. aethiopicum,* SF = *S. ferox,*

SI = *S. indicum,* SM = *S. melongena,* SMA = *S. mammosum,*

SS = *S. sanitwongsei,* ST = *S. torvum,* STR = *S. trilobatum,*

SV = *S. viarum,* SX = *S. xanthocarpum*

Table 12 Accessions number of *Solanum* spp. per cluster and subcluster based on nominal traits.

Cluster	Subcluster	Accession No.	Species	Country of origin	Population (%)
I	A	TS00473	*S. melongena*	Thailand	2.90
		TS02217	*S. melongena*	Thailand	
	B	TS00175	*S. melongena*	Thailand	1.45
	C	TS02441-A	*S. melongena*	Thailand	8.70
		TS00176	*S. melongena*	Thailand	
		TS00487	*S. xanthocarpum*	Thailand	
		TS00417	*S. aculeatissimum*	Thailand	
		TS00418	*S. xanthocarpum*	Thailand	
		TS02945	*S. xanthocarpum*	Malaysia	
	D	TS00549	*S. melongena*	Thailand	14.49
		TS00552	*S. melongena*	Thailand	
		TS01994	*S. melongena*	Thailand	
		TS02440	*S. melongena*	Thailand	
		TS00483	*S. xanthocarpum*	Thailand	
		TS00555	*S. melongena*	Thailand	
		TS01474-B	*S. melongena*	Thailand	
		TS02273-B	*S. melongena*	Vietnam	
		TS00551	*S. melongena*	Thailand	
		TS02816	*S. melongena*	Laos	
II	A	TS00422-B	*S. aculeatissimum*	Thailand	5.80
		TS02218	*S. melongena*	Thailand	
		TS00422-A	*S. xanthocarpum*	Thailand	
		TS00455	*S. melongena*	Thailand	
	B	TS00456	*S. melongena*	Thailand	2.90
		TS02950	*S. xanthocarpum*	Cambodia	

Table 12 (Continued)

Cluster	Subcluster	Accession No.	Species	Country of origin	Population (%)
III	A	TS03029	*S. aethiopicum*	Laos	1.45
	B	TS02739	*S. trilobatum*	Thailand	4.35
		TS01947	*S. trilobatum*	Thailand	
		TS02445	*S. trilobatum*	Thailand	
IV		TS01447-A	*S. viarum*	Thailand	1.45
V	A	TS02955	*S. torvum*	Cambodia	10.14
		TS02973	*S. torvum*	Laos	
		TS02940	*S. torvum*	Malaysia	
		TS02938	*S. torvum*	Malaysia	
		TS02937	*S. torvum*	Malaysia	
		TS02862	*S. torvum*	Laos	
		TS02877	*S. torvum*	Laos	
	B	TS02731	*S. torvum*	Thailand	4.35
		TS02813	*S. torvum*	Laos	
		TS02728	*S. torvum*	Thailand	
VI	A	TS02989	*S. ferox*	Laos	2.90
		TS02978	*S. ferox*	Laos	
	B	TS02435	*S. ferox*	Thailand	1.45
	C	TS03020	*S. ferox*	Laos	20.29
		TS03012	*S. ferox*	Laos	
		TS03009	*S. ferox*	Laos	
		TS02976	*S. ferox*	Laos	
		TS02971	*S. ferox*	Laos	
		TS02901	*S. ferox*	Thailand	
		TS02062	*S. ferox*	Thailand	
		TS01979	*S. ferox*	Thailand	
		TS00563	*S. ferox*	Thailand	

Table 12 (Continued)

Cluster	Subcluster	Accession No.	Species	Country of origin	Population (%)
VI	C	TS00553	*S. ferox*	Thailand	
		TS00426	*S. ferox*	Thailand	
		TS00541	*S. ferox*	Thailand	
		TS02902	*S. ferox*	Malaysia	
		TS02903	*S. ferox*	Malaysia	
VII	A	TS02491	*S. sanitwongsei*	Thailand	1.45
	B	TS02495	*S. indicum*	Thailand	10.14
		TS02967	*S. indicum*	Laos	
		TS02965	*S. indicum*	Laos	
		TS03005	*S. indicum*	Laos	
		TS02990	*S. indicum*	Laos	
		TS02992	*S. indicum*	Laos	
		TS03018	*S. indicum*	Laos	
VIII		TS02822	*S. melongena*	Laos	4.35
		TS02812	*S. melongena*	Laos	
		TS02815	*S. melongena*	Laos	
IX		TS02894	*S. mammosum*	Malaysia	1.45

However, the determination of the morphological traits associated with the geographical origin by using 11qualitative traits was shown the more congruence than using quantitative traits when compared to variation of dendrogram of cluster analysis (Figure 18 and 19). For *S. melongena* the major part (approximately 27.54 %) of the variation was found within collection areas, where the major part (approximately 73.68 %) of the variation was found in Thailand. The variations of *S. melongena* were also found in Laos and Vietnam, approximately 21.05 % and 5.26 %, respectively. Furthermore, *S. melongena* was belonging to cluster I, II and III.

This study was reported the association between geographical origin and morphological traits of *Solanum* species in Southeast Asia. However, the ability to do so, depends on several factors such as details information of geographical coordinates, altitude, latitude and longitude. For this study, we did not include the on-site gathering of any geographical data.

Moreover, the genetic uniformity of multiple accessions sampled from the same site was significant to this study. According to del Rio and Bamberg (2004), the intra-population homogeneity also increases the chance of stable samples from a single site. If a population is heterogeneous, there is a chance of particular phenotypes presented for sampling will be different depending on the particular growing conditions at time of collection. But when the populations are homogenous, any sample size, pattern or timing will be resulted in a stable, representative sample. Within accession uniformity and distinction are needed to reveal the significant correlations of breeding behavior. Inbreeding may greatly reduce gene flow and genetic diversity is reduced within populations, but increase between populations (Lovesless and Hamrick, 1984). Although inbreeding may be more outcrossing among population heterogeneity (Schoen and Brown, 1991). del Rio and Bamberg (2002) confirmed the suspect tailored low heterogeneity within accessions of *S. verrucosum* when compared to the other species (*S. fendleri, S. sucrense* and *S. jamesiie*) showing no significant correlations with in ecogeographic parameters (del Rio and Bamberg, 2002).

2. Genetic relationships of *Solanum* spp. using interspecific hybridization

The degree of hybridization varied with in each combination. Among 169 cross combinations, seventy-three of them were crossable. Percentages of fruit setting ranged from 0 to 98.3. The highest percentages of fruit setting (98.3) were found in the cross between *S. villosum* (TS02600) and *S. americanum* (S00861) (Table 18). However, this is due to the low number of pollinated flowers (58 pollinated flowers; Table 18). In addition, very low fruit setting was observed in many crosses of different species. This result indicates the level of cross compatibility depending on the varieties used and/or on environmental conditions. Furthermore, the reciprocal differences in the success of crosses are common and the frequency of abortion hybrid seed is also high (Table 15 and 18).

1) Cross - compatibility of *S. melongena* and its wild relatives (*S. torvum*, *S. americanum*, *S. villosum* and *S. nigrum*)

When *S. melongena* was used as a female parent, the percentages of fruit setting is higher on the intraspecific hybridization within *S. melongena* (96.2 %) than interspecific hybridization between *S. melongena* and its wild relatives (Table 14 and 15). Percentages of fruit setting between *S. melongena* x *S. torvum* range from 0 to 72 (Table 14). The highest percentages of fruit setting (72 %), was found in the cross between S00022 (collected in India) and S00429 (collected in Thailand), but no plants were obtained even after embryo recuing. They had only the abnormal seedlings (Figure 11).

However, the crosses between *S. melongena* (S00625 collected in South Africa) x *S. torvum* (S00429) and S00809 (collected in Bangladesh) and S00429 could be successful through embryo rescue (Figure 10). In addition, S00625 x S00429 was better than S00809 x S00429 (Table 15). This resulted in the effect of genotype and geographical areas or may be due to variation in environmental conditions (Rao and Rao, 1984).

This result is in agreement with the report of Singh *et al*. (2002), which fruits with seeds of the cross *S. melongena* (Panjab Sadabahar) and *S. torvum* were obtained. In several cases, crosses were only successful if in vitro embryo rescued was employed (McCammon and Honma, 1983; Bletsos *et al*., 2000).

In addition, the protoplast culture and somatic hybridization would be useful in overcoming the pre- and post-fertilization barriers encountered during conventional breeding (Fournier *et al*., 1995). However, *S. torvum* has been reported to use for introgression of disease resistance (Daunay *et al*., 1991; Collonnier *et al*., 2001). Traits of resistance against *Ralstonia* and *Verticillium* wilts have successfully been transferred from *S. torvum* into *S. melongena* by using somatic fusion (Jarl *et al*., 1999; Iwamoto *et al*., 2007).

Furthermore, the cross combinations among *S. melongena* and other three species (*S. americanum*, *S. villosum* and *S. nigrum*), were only successful when *S. melongena* is the female parent. The highest percentages of fruit setting (56.8) were obtained in the cross between S00809 x S00269 (*S. melongena* x *S. americanum*) (Table 14) may not be true hybrid because F_1 hybrid plants have high pollen fertility and morphological characters are not intermediate when compare to their parent (Table 15 and Figure 21). Lower fruit setting is found in S00625 x S00859 (3.6 %) and S00809 x S00865 (9.8 %), which the seeds were abortive. It may be that the ovules begin to develop and produce sufficient auxins to stimulate only fruit development but not the seeds (Lester and Kang, 1998).

The results reveal that *S. melongena* and *S. villosum* crosses are possible. When *S. melongena* was used as female parent, percentage of fruit setting is higher than using *S. villosum* as female parent. However, the accesssion S00809 (collected in Bangladesh) of *S. melongena* was crossable with all accessions of *S. villosum*. The highest percentages of fruit setting (48.3 %) were found in the cross between S00809 and *S. villosum* (S00854 collected in Tanzania) (Table 15) but hybrid plants without seeds were obtained due to abortive of embryo. In addition, the crosses between *S. melongena* and *S. villosum* from S00809 x S00860 and S00809 x TS02600 which may not be the true hybrids because F_1 hybrid plants have high pollen fertility and morphological characters were not intermediate when compare to their parent (Table 15 and Figure 22).

Furthermore, when *S. melongena* was used as male parent, only one accession S00860 of *S. villosum* (collected in Japan) was crossable with all accessions of *S. melongena* may be due to the flower of S00860 is bigger than others accession of *S. villosum*. However, only the hybrid fruits were obtained from the crosses between *S. melongena* and *S. villosum* but their seeds were abortive. Moreover, most of them fell before harvesting stage. In the case of embryo culture, the embryos of hybrid fruits from *S. villosum* x *S. melongena* were rescued but no hybrid plants were obtained (Figure 11). Similarly, the interspecific hybrids have also been made between *S. melongena* and *S. sisymbriifolium* by embryo rescuing but they still fail to develop within a few days (Sharma *et al*., 1984). Moreover, the protoplast culture and somatic hybridization could be useful in overcoming the pre- and post- fertilization barriers (Fournier *et al*., 1995) and was successful in several cases in previous literature. This technique could be useful to rescue the hybrids from *S. villosum* and *S. melongena*.

Although the hybrid fruits were set, most of them fell before harvesting. In case of embryo culture, the embryo of hybrid fruits from the two cross combinations; *S. villosum* (S00860) x *S. melongena* (S00022), *S. villosum* (S00860) x *S. melongena* (S00809) (Figure 11), were fail. Similarly, the interspecific hybrids have also been made between *S. melongena* and *S. sisymbriifolium* by embryo rescuing but they still fail to develop within a few days (Sharma *et al*., 1984).

The crosses between *S. melongena* x *S. nigrum* was successful only the crossing from S00809 x TS02930 which 49.1 % fruit setting (Table 16). The crossing between S00809 x TS02930 was ontained but this may not be true hybrid. This finding is in contrast to result obtained by Singh *et al*. (2002) who reported that *S. nigrum* were not crossable to *S. melongena*. However, interspecific somatic hybrids were developed by fusing protoplast of *S. melongena* with *S. nigrum* L. to transfer herbicide (atrazine) resistant trait from *S. nigrum* is indicated by Southern analysis (Guri and Sink, 1988b).

In addition, some of the mature hybrid fruits are parthenocarpic (Figure 8), Most of them were found in the crosses between *S. melongena* x *S. torvum, S. melongena* x *S. americanum, S. melongena* x *S. villosum* and *S. melongena* x *S. nigrum.* The interspecific crossing among *S. melongena* and other four species (*S. torvum*, *S. americanum*, *S. villosum* and *S. nigrum*), could be produced but some hybrids seeds are abortive (Figure 9), and no hybrid seeds are obtained.

However, interspecific hybridization are considerably more successful when species of the same floral size were involved, crossing using the smaller-flowered species male parent and large-flowered species female parent were generally unsuccessful, presumably due to the inablility of the pollen tubes from the small flower to traverse the long styles of the female parent. Reciprocally, when the larger-flowered species were used as the paternal parent, such a barrier would not exist and hybrid seeds were often obtained (Edmonds and Chweya, 1997).

Moreover, in interspecific hybrids, lack of coordination may cause unbalanced production of growth regulating substances by the endosperm and hence abortion of the embryo, or even unregulated production of nucleases and proteases resulting firstly in autolysis of the endosperm and then digestion of the embryo. The endosperm may thus serve to setect inappropiate hybridization of species or ploidy levels and so prevent waste of resources by producing seeds that would result in sterile hybrids or unthrify subsequent generation (Lester and Kang, 1998).

In addition, the success of gene introgression via sexual hybridization depends on the phylogenetic relationships between species, opportunities for genetic recombination and stability of the introgressed gene. Cytological analyses are usually performed to evaluate the meiotic process in experimental hybrids (Hermsen, 1994).

2) Cross - compatibility of *S. torvum* and other three species (*S. americanum*, *S. villosum* and *S. nigrum*)

These cross combinations among *S. torvum*, *S. americanum*, *S. villosum* and *S. nigrum* were not successful when used *S. torvum* as female parent but when *S. torvum* was used as male parent were successful crossable. These indicated that the recipocal crosses could be overcome the incompatibility crossing barrier (Jansky, 2006). This was also showed the incompatibility in *S. torvum.* Novy and Hanneman (1991) noted that pollen tubes of *S. brevidens* and S. *fernandezianum* were consistently inhibited in the upper portion of the styles of self-incompatible of haploid Tuberosum Group.

When *S. torvum* was used as male parent, the highest percentage of fruit setting (78.0) was obtained in the cross between *S. villosum* and *S. torvum* (TS02600 x S00429) but no hybrid seeds were obtained (Table 17). The cross between *S. americanum* (S00859, collected in Tanzania) and *S. torvum* (S00429, collected in Thailand) gave the fertile hybrid seed. Furthurmore, the abortive hybrid seeds were obtained from the crossing between S00861 (collected in Japan) x S00429 (collected in Thailand) (Table 17). Similarly, the crosses between *S. villosum* (S00854, collected in Tanzania) x *S. torvum* (S00429) yielded the fertile hybrid seeds but no seed was obtained from the crosses between S00860 (collected in Japan) x S00429. This result indicates that the level of cross compatibility depends on the genotype and/or on geographical origins (Hawtin *et al.,* 1997).

However, the crosses between *S. nigrum* and *S. torvum* gave hybrid seeds but no hybrid plants were obtained because of the abortive seeds. Similar to the crosses between *S. villosum* and *S. torvum* hybrid seeds were obtained without hybrid plants. This result due to the chromosome number of *S. villosum* (2n = 48) and *S. nigrum* (2n = 72) were different from *S. torvum* (2n = 24), while *S. americanum* (2n = 24) had a same chromosome number with *S. torvum* (Edmond and Chweya, 1997). In addition, the variation of hybrid plants were obtained depend on the genotype of parents (Singh *et al.*, 2002).

3) Cross - compatibility among *S. americanum*, *S. villosum* and *S. nigrum*

These cross combinations among *S. americanum*, *S. villosum* and *S. nigrum* were successfull in both directions. This indicates that they are closely related which support the former classification that place them together in *Solanum nigrum* Complex (Edmonds and Chweya, 1997). However, the percentages of fruit setting vary among different species combinations. Some crosses produced fruit with viable seeds and some others produced aborted seed (Figure 9).

When *S. americanum* was used as female parent, the crossing of accessions within *S. americanum* produced fruit with viable seeds and hybrid plant. The percentage of fruit setting varies among accessions. This result showed the effect of genotype and phylogenic relationship on cross compatibility (Hawtin *et al.,* 1997). *S. villosum* (S00860 from Japan) is crossable with all accessions of *S. americanum* and hybrid seeds were obtained. The crosses between *S. americanum* x *S. nigrum* and their reciprocals gave hybrid fruits but the percentages of fruit setting, when using *S. americanum* as female parent, was lower than the respective reciprocal. This finding is in contrast to the result obtained by Ganapathi and Rao (1986) who found that the crosses between *S. nigrum* (2n = 6x = 72) and *S. americanum* (2n = 2x = 24) were successful only when *S. nigrum* was used as female parent.

When *S. villosum* was used as female parent, the crossing of accessions within *S. villosum* produced fruit with viable seeds and hybrid plant. All accession of *S. villosum* is crossable with *S. americanum.* The percentage of fruit setting is highest (98.3 %) from crossing between the accessions TS02600 (*S. villosum*) x S00861 (*S. americanum*) (Table 18). Similar to Beg *et al*. (1989) who studied the biosystematic of *S. villosum* subsp. *puniceum* (n = 24) and *S. americanum* (n = 12) in which the interspecific hybrids (n = 18) were obtained using *S. villosum* as the female parent.

The fruits were obtained from the crosses between *S. villosum* and *S. nigrum*, but no hybrid plant was obtained due to the abortive hybrid seeds. Similar to Beg and Khan (1988) who reported that tetraploid *S. villosum* subsp. *puniceum* (2n =

48) was crossed with diploid *S. nigrum* (2n = 24). This finding is in contrast to result obtained by Edmonds (1977) who found that both *S. villosum* and *S. nigrum* crosses within and also between species (recognized in each taxon in morphologically intermediate) gave extremely vigorous and fertile F_1 progeny.

When *S. nigrum* was used as female parent, only one accession of *S. americanum* (S00861) could be crossed with *S. nigrum* (TS02930) and 39.8 % (Table 18) fruit setting with both viable and abortive seeds were obtained. When *S. nigrum* was used as male parent slightly lower fruit setting was obtained. Similarly, only one accession of *S. villosum* could cross with *S. nigrum.* The crossing of *S. nigrum* (TS02930) x *S. villosum* (S00860) gave 22.0 % of fruit setting and obtained hybid seeds but no hybrid plant is obtained.

These results showed that the unsuccessful crosses may be due to the hybridizations involving accessions from distinct geographical origins of *S. villosum*, S00854 (collected in Tanzania) and TS02600 (collected in Kenya) both Africa and TS02930 (*S. nigrum*) from Malaysia. Contrasting with S00860 (*S. villosum* collected in Japan) was successfull crossed with TS02930 (*S. nigrum*). This present finding was in agreement with the report of Ganapathi (1988) who obtained a heptaploid hybrid (2n = 7x = 84) by crossing *S. nigrum* (2n = 6x = 72) with pollen of *S. villosum* (2n = 4x = 48). Moreover, Khan *et al.* (1978) who found that cytogy of hybrids of the cross tetraploid *S. nigrum* x *S. americanum* and their amphidiploids obtained through colchicine treatment revealed that the structural difference between chromosomes of parents plays an important role in diversification of morphological characters of the two taxa and the tetraploid *S. nigrum* and *S. americanum* play an important role in origin and evolution of natural hexaploid *S. nigrum*.

Moreover, interspecific hybridization are considerably more successful when species of the same floral size are involved. Crossing using the smaller-flowered species paternally (male parent) and large-flowered species maternally (female parent) are generally unsuccessful, presumably due to the inablility of the pollen tubes from the small flower to traverse the long styles of the female parent. Reciprocally, when the larger-flowered species were used as male parent, such a barrier would not exist and hybrid seed was often obtained (Edmonds and Chweya, 1997).

However, the occurrence of polyploidy in the section *Solanum* is probably the most efficient barrier to natural hybridization between these species. Successful crosses are more difficult between taxa of different ploidy levels than they are between taxa of the same chromosome number, with interploidy crosses leading to the development of morphologic intermediate but sterile progeny. In contrast with report of Edmonds (1977) who found that such interploidy crosses were not dependent on the use of the higher ploidy level as the maternal parent. Nevertheless, species of differing chromosome levels can be induced to cross and the chromosome number of the resultant progeny can often be doubled experimentally, to restore the fertility of such amphiploid plants (Edmond, 1979).

Table 13 Intra- and interspecific crossability of *Solanum melongena* accessions (S00022, S00388, S00625 and S00809) with *S. torvum* (S00429).

Cross combinations	No. pollinated flowers	No. fruit set	% Fruit setting	No. of seed per fruit	No. of plants obtained
S. melongena and *S. melongena*					
S00022 x S00022	49	25	51.0	906.4	8
S00022 x S00388	27	23	85.2	935.4	8
S00022 x S00625	53	43	81.1	812.2	8
S00022 x S00809	26	25	96.2	1,021.2	8
S00388 x S00022	41	22	53.7	1,140.1	8
S00388 x S00388	14	5	35.7	1,855.0	8
S00388 x S00625	26	11	42.3	1,338.4	8
S00388 x S00809	26	13	50.0	1,724.5	8
S00625 x S00022	35	16	45.7	1,438.5	8
S00625 x S00388	23	9	39.1	1,704.7	8
S00625 x S00625	28	14	50.0	1,213.8	8
S00625 x S00809	13	6	46.2	1,676.5	8
S00809 x S00022	39	33	84.6	869.7	8
S00809 x S00388	31	27	87.1	1,579.4	8
S00809 x S00625	37	30	81.1	1,020.5	8
S00809 x S00809	22	22	100.0	1,365.0	8
S. melongena and *S. torvum*					
S00022 x S00429	50	36	72.0	487.3	-
S00388 x S00429	70	0	0.0	-	-
S00625 x S00429	50	2	4.0	294.5	8
S00809 x S00429	50	9	18.0	2.6	3
S00429 x S00022	40	0	0.0	-	-
S00429 x S00388	50	0	0.0	-	-
S00429 x S00625	50	0	0.0	-	-
S00429 x S00809	64	0	0.0	-	-

Table 14 Interspecific crossability of *Solanum melongena* accessions with *S. americanum* (S00269, S00859, S00861 and S00865).

Cross combinations	No. of pollinated flowers	No. of fruit set	Fruit setting (%)	No. of seed per fruit	No. of plants obtained
S. melongena and *S. americanum*					
S00022 x S00269	50	0	0.0	-	-
S00022 x S00859	50	0	0.0	-	-
S00022 x S00861	54	0	0.0	-	-
S00022 x S00865	50	0	0.0	-	-
S00388 x S00269	33	0	0.0	-	-
S00388 x S00859	50	0	0.0	-	-
S00388 x S00861	50	0	0.0	-	-
S00388 x S00865	50	0	0.0	-	-
S00625 x S00269	50	0	0.0	-	-
S00625 x S00859	28	1	3.6	0.0*	-
S00625 x S00861	50	0	0.0	-	-
S00625 x S00865	50	0	0.0	-	-
S00809 x S00269	50	21	56.8	3.6	8
S00809 x S00859	37	0	0.0	-	-
S00809 x S00861	50	0	0.0	-	-
S00809 x S00865	51	5	9.8	0.0*	-
S00269 x S00022	50	0	0.0	-	-
S00269 x S00388	55	0	0.0	-	-
S00269 x S00625	67	0	0.0	-	-
S00269 x S00809	80	0	0.0	-	-
S00859 x S00022	88	0	0.0	-	-
S00859 x S00388	50	0	0.0	-	-
S00859 x S00625	50	0	0.0	-	-
S00859 x S00809	56	0	0.0	-	-
S00861 x S00022	50	0	0.0	-	-
S00861 x S00388	60	0	0.0	-	-

Table 14 (Continued)

Cross combinations	No. of pollinated flowers	No. of fruit set	Fruit setting (%)	No. of seed per fruit	No. of plants obtained
S00861 x S00625	60	0	0.0	-	-
S00861 x S00809	58	0	0.0	-	-
S00865 x S00022	61	0	0.0	-	-
S00865 x S00388	56	0	0.0	-	-
S00865 x S00625	50	0	0.0	-	-
S00865 x S00809	71	0	0.0	-	-

* All hybrid seeds were abortive.

Table 15 Interspecific crossability of *Solanum melongena* accessions with *S. villosum* (S00854, S00860 and TS02600).

Cross combinations	No. of pollinated flowers	No. of fruit set	Fruit setting (%)	No. of seed per fruit	No. of plants obtained
S. melongena and *S. villosum*					
S00022 x S00854	32	0	0.0	-	-
S00022 x S00860	50	0	0.0	-	-
S00022 x TS02600	50	0	0.0	-	-
S00388 x S00854	50	0	0.0	-	-
S00388 x S00860	50	0	0.0	-	-
S00388 x TS02600	50	0	0.0	-	-
S00625 x S00854	50	0	0.0	-	-
S00625 x S00860	50	0	0.0	-	-
S00625 x TS02600	50	0	0.0	-	-
S00809 x S00854	29	14	48.3	19.1	-
S00809x S00860	50	22	44.0	42.8	8
S00809 x TS02600	50	5	10.0	0.2	7
S00854 x S00022	50	0	0.0	-	-
S00854 x S00388	50	0	0.0	-	-
S00854 x S00625	42	0	0.0	-	-
S00854 x S00809	50	0	0.0	-	-
S00860 x S00022	65	24	36.9	12.08*	-
S00860 x S00388	50	15	30.0	15.07*	-
S00860 x S00625	50	11	22.0	20.09*	-
S00860 x S00809	55	19	34.6	2.53*	-
TS02600 x S00022	50	0	0.0	-	-
TS02600 x S00388	50	0	0.0	-	-
TS02600 x S00625	50	0	0.0	-	-
TS02600 x S00809	50	0	0.0	-	-

* All hybrid seeds were abortive.

Table 16 Interspecific crossability of *Solanum melongena* accessions with *S. nigrum* (TS02930).

Cross combinations	No. of pollinated flowers	No. of fruit set	Fruit setting (%)	No. of seed per fruit	No. of plants obtained
S. melongena and *S. nigrum*					
S00022 x TS02930	55	0	0.0	-	-
S00388 x TS02930	37	0	0.0	-	-
S00625 x TS02930	29	0	0.0	-	-
S00809x TS02930	55	27	49.1	1.4	8
TS02930 x S00022	66	0	0.0	-	-
TS02930x S00388	58	0	0.0	-	-
TS02930 x S00625	52	0	0.0	-	-
TS02930 x S00809	54	0	0.0	-	-

Table 17 Intra- and interspecific crossability of *Solanum torvum* (S00429) with *S. americanum, S. villosum* and *S. nigrum*.

Cross combinations	No. of pollinated flowers	No. of fruit set	Fruit setting (%)	No. of seed per fruit	No. of plants obtained
S. torvum and *S. torvum*					
S00429 x S00429	50	15	30.0	189.2	8
S. torvum and *S. americanum*					
S00429 x S00269	57	0	0.0	-	-
S00429 x S00859	50	0	0.0	-	-
S00429 x S00861	64	0	0.0	-	-
S00429 x S00865	50	0	0.0	-	-
S00269 x S00429	50	0	0.0	-	-
S00859 x S00429	50	7	14.0	2.4	8
S00861 x S00429	60	9	15.0	12.1*	-
S00865 x S00429	50	0	0.0	-	-
S. torvum and *S. villosum*					
S00429 x S00854	50	0	0.0	-	-
S00429 x S00860	50	0	0.0	-	-
S00429 x TS02600	50	0	0.0	-	-
S00854 x S00429	60	8	13.3	1.0	-
S00860 x S00429	70	18	25.7	22.7*	-
TS02600 x S00429	50	39	78.0	0.0	-
S. torvum and *S. nigrum*					
S00429 x TS02930	81	0	0.0	-	-
TS02930 x S00429	90	2	2.2	15.0	-

* All hybrid seeds were abortive.

Table 18 Intra- and interspecific crossability between leafy *Solanum* (*S. americanum, S. villosum* and *S. nigrum*).

Cross combinations	No. of pollinated flowers	No. of fruit set	Fruit setting (%)	No. of seed per fruit	No. of plants obtained
S. americanum and *S. americanum*					
S00269x S00269	81	7	8.6	15.5	8
S00269 x S00859	50	0	0.0	-	-
S00269 x S00861	59	2	3.4	15.5	8
S00269 x S00865	50	0	0.0	-	-
S00859 x S00269	42	0	0.0	-	-
S00859 x S00859	43	0	0.0	-	-
S00859 x S00861	77	24	31.2	19.5	8
S00859 x S00865	78	15	19.2	9.9	7
S00861 x S00269	72	9	12.5	3.7	6
S00861 x S00859	42	0	0.0	-	-
S00861 x S00861	59	34	57.6	29.4	8
S00861 x S00865	50	2	4.0	2.5	5
S00865 x S00269	58	0	0.0	-	-
S00865 x S00859	50	0	0.0	-	-
S00865 x S00861	60	5	8.3	6.8	8
S00865 x S00865	40	0	0.0	-	-
S. americanum and *S. villosum*					
S00269 x S00854	42	5	11.9	11.0	-
S00269 x S00860	53	2	3.8	7.0	-
S00269 x TS02600	50	0	0.0	-	-
S00859 x S00854	40	0	0.0	-	-
S00859 x S00860	54	1	1.9	37.0	8
S00859 x TS2600	50	0	0.0	-	-
S00861 x S00854	60	0	0.0	-	-
S00861 x S00860	87	18	20.7	5.4	7
S00861 x TS02600	50	0	0.0	-	-
S00865 x S00854	50	0	0.0	-	-

Table 18 (Continued)

Cross combinations	No. of pollinated flowers	No. of fruit set	Fruit setting (%)	No. of seed per fruit	No. of plants obtained
S. americanum and *S. villosum*					
S00865 x S00860	52	1	1.9	6.0	-
S00865 x TS02600	50	0	0.0	-	-
S00854 x S00269	60	1	1.7	9.0	5
S00854 x S00859	27	0	0.0	-	-
S00854 x S00861	64	35	54.7	19.5	8
S00854 x S00865	46	11	23.9	5.3	8
S00860 x S00269	56	6	10.7	1.3	-
S00860 x S00859	46	14	30.4	2.5**	5
S00860 x S00861	113	43	38.1	27.1*	-
S00860 x S00865	63	17	27.0	7.1*	-
TS02600 x S00269	50	33	66.0	1.3*	-
TS02600 x S00859	60	34	56.7	4.0**	2
TS02600 x S00861	58	57	98.3	14.2	8
TS02600 x S00865	50	33	66.0	2.0**	7
S. americanum and *S. nigrum*					
S00269 x TS02930	90	2	2.2	18.0	8
S00859 x TS02930	67	0	0.0	-	-
S00861 x TS02930	128	1	0.8	1.0*	-
S00865 x TS02930	63	4	6.4	5.0*	-
TS02930 x S00269	70	0	0.0	-	-
S. villosum and *S. villosum*					
S00854 x S00854	40	0	0.0	-	-
S00854 x S00860	63	22	34.9	14.3	6
S00854 x TS02600	50	0	0.0	-	-
S00860 x S00854	40	0	0.0	-	-
S00860 x S00860	57	51	89.5	34.7	8
S00860 x TS02600	50	0	0.0	-	-
TS02600 x S00854	50	44	88.0	3.0*	-

Table 18 (Continued)

Cross combinations	No. of pollinated flowers	No. of fruit set	Fruit setting (%)	No. of seed per fruit	No. of plants obtained
S. villosum and *S. villosum*					
TS02600 x S00860	40	25	62.5	34.4	8
TS02600 x TS02600	50	8	16.0	0.4	-
S. villosum and *S. nigrum*					
S00854 x TS02930	100	7	7.0	12.5*	-
S00860 x TS02930	114	61	53.5	12.7*	-
TS02600 x TS02930	70	2	2.9	1.5	-
TS02930 x S00854	40	0	0.0	-	-
TS02930 x S00860	50	11	22.0	0.5	-
TS02930 x TS02600	50	0	0.0	-	-
S. nigrum and *S. nigrum*					
TS02930 x TS02930	125	53	42.4	5.4	8

* All hybrid seeds were abortive.

** Some hybrid seeds were abortive.

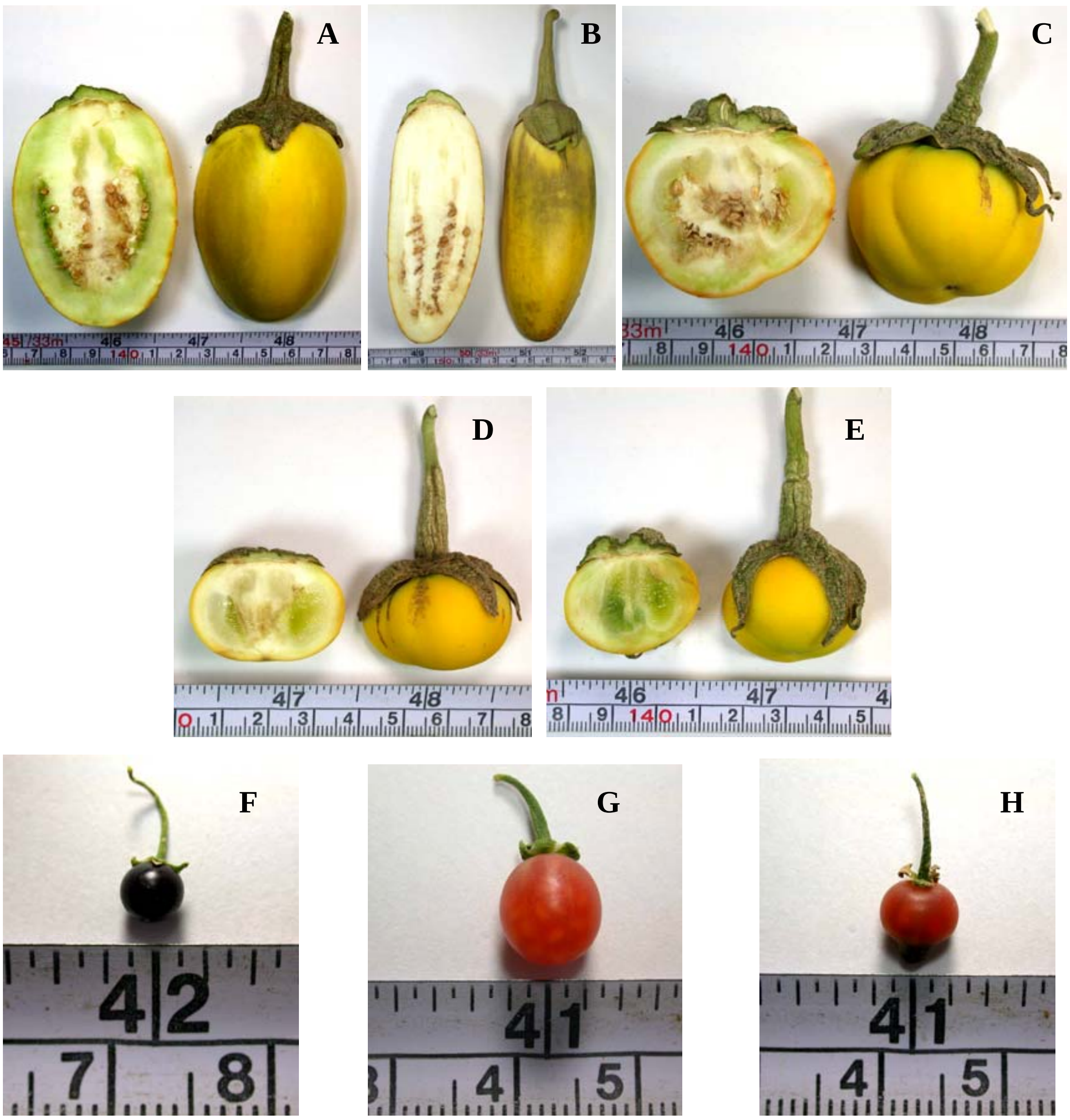

Figure 8 The hybrid fruit between *S. melongena* x *S. torvum*; S00022 x S00429 (66 DAP)(A), S00625 x S00429 (66 DAP) (B) and S00809 x S00429 (66 DAP) (C), *S. melongena* x *S. americanum* (S00809 x S00269: 73 DAP) (D), *S. melongena* x *S. nigrum* (S00809 x TS02930: 81 DAP) (E), *S. americanum* x *S. villosum* (S00269 x S00860: 47 DAP) (F) and *S. villosum* x *S. americanum* (S00853 x S00861: 44 DAP) (G), TS02600 x S00860 (55 DAP)(H).

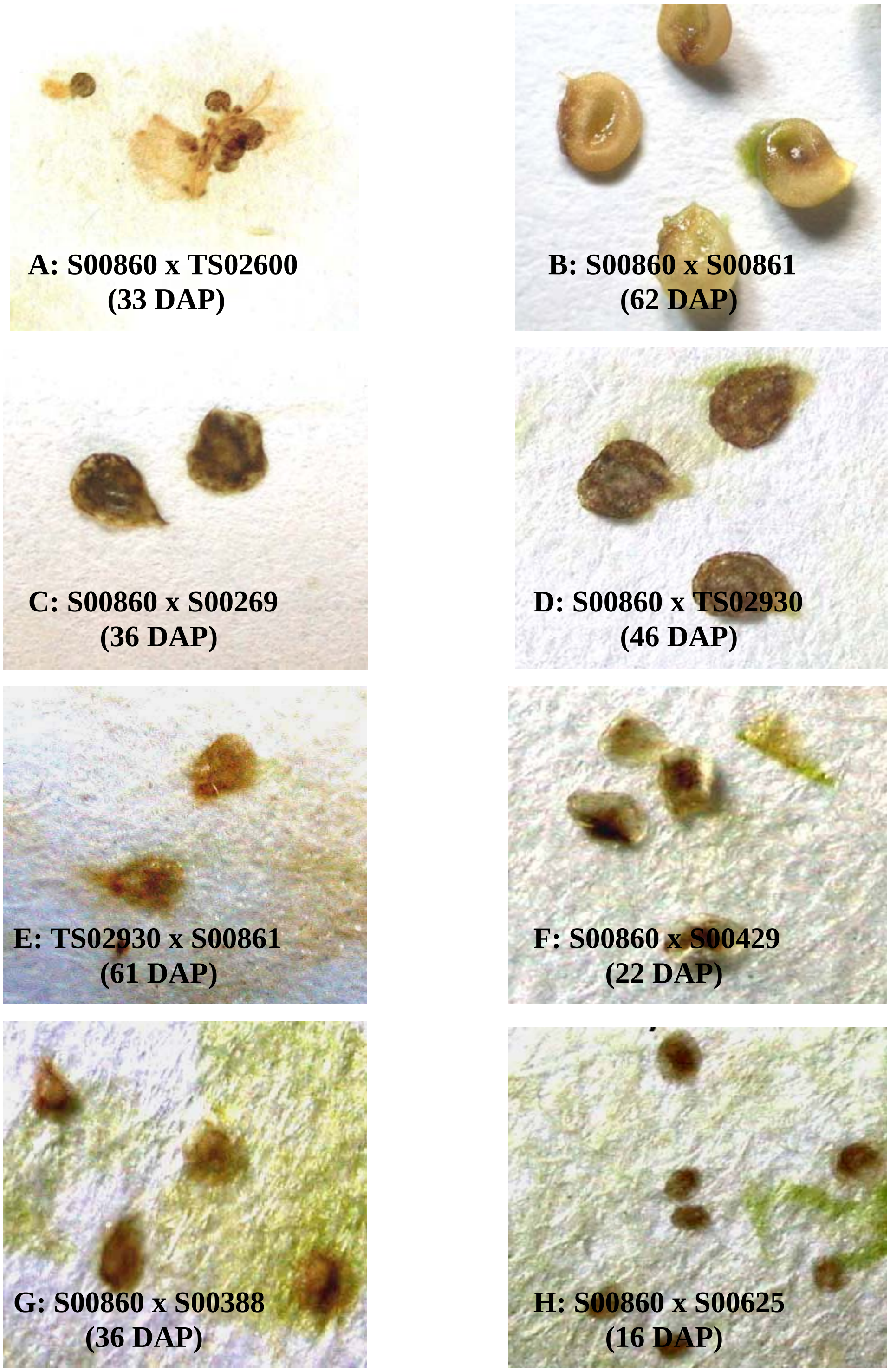

Figure 9 Abortive in seeds crosses between *S. villosum* x *S. villosum* (A), *S. villosum* x *S. americanum* (B and C), *S. villosum* x *S. nigrum* (D), *S. nigrum* x *S. americanum* (E), *S. villosum* x *S. torvum* (F) and *S. villosum* x *S. melongena* (G and H).

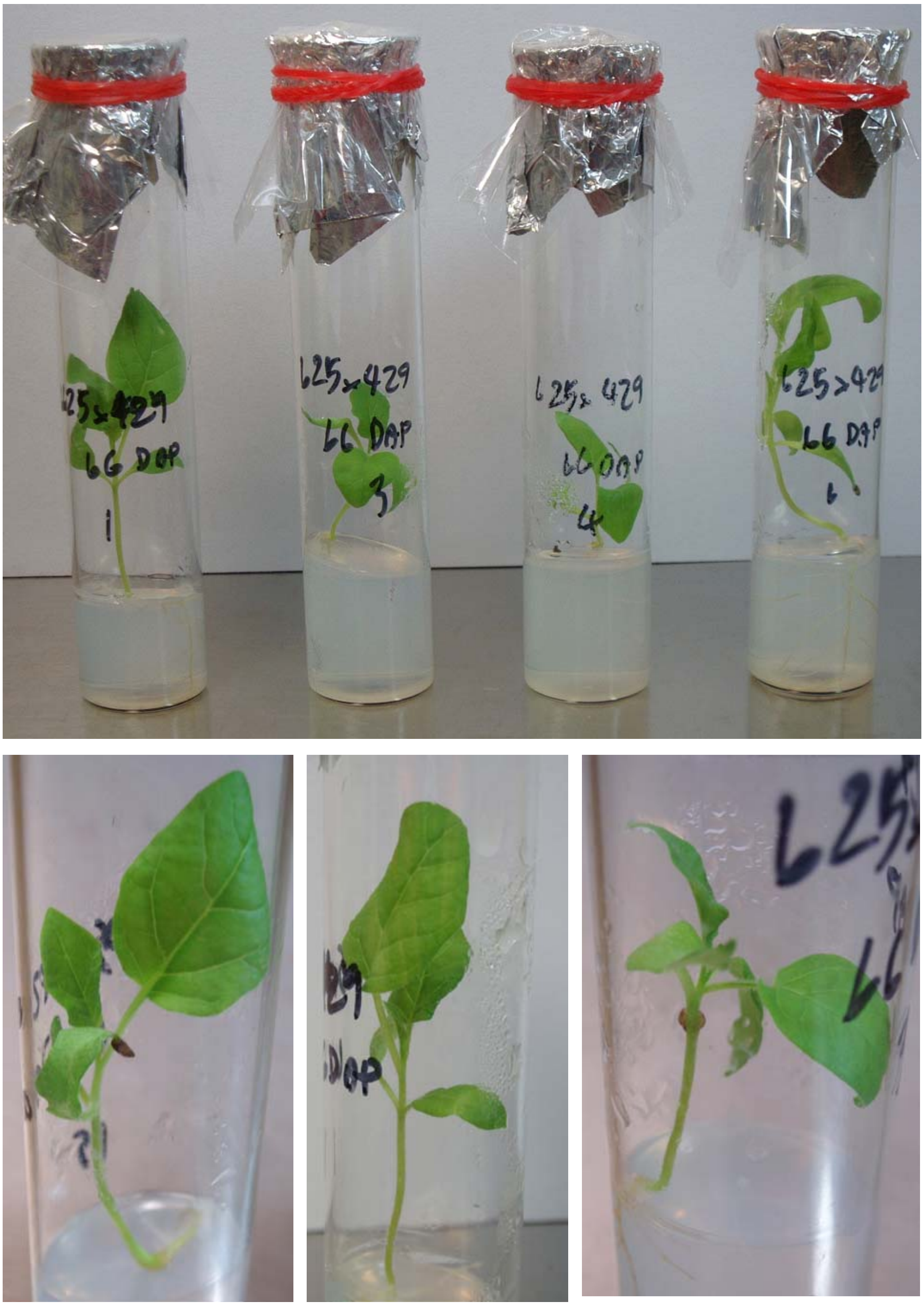

Figure 10 F_1 hybrid plant from *S. melongena* x *S. torvum*, 66 days after pollination by embryo rescued.

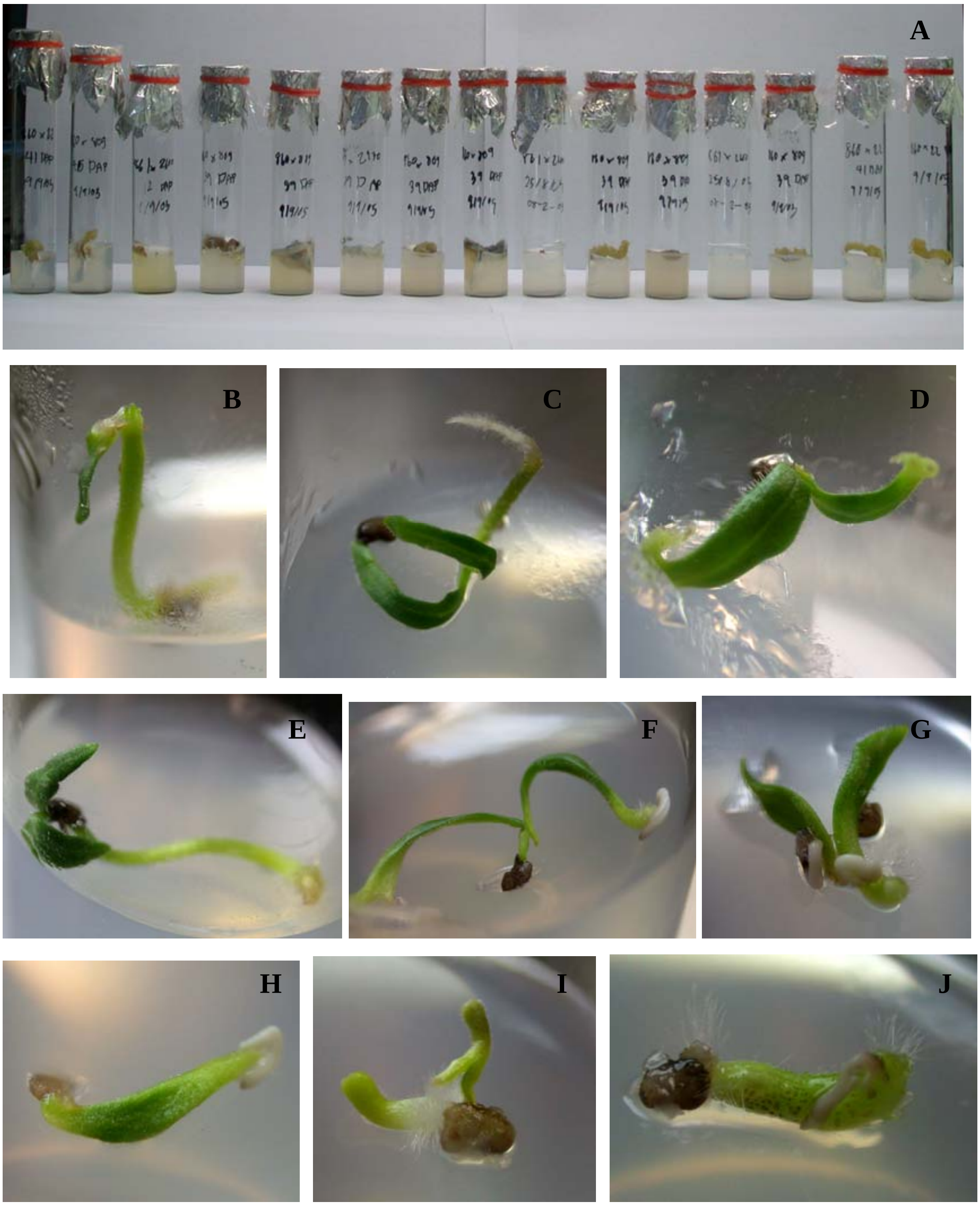

Figure 11 F_1 hybrid seeds from interspecific hybridization between *S. melongena* and its wild relative were not germinate by embryo rescued (A) and the abnormal seedling of F_1 hybrid between *S. melongena* (S00022) x *S. torvum* (S00429) by embryo rescued (B to J).

Confirmation of interspecific hybrids

2.1 Pollen fertility

To confirm that the putative hybrid obtained were truly of interspecific, pollen fertility analysis was performed at flowering stage. Since interspecific and intergeneric hybrid sterility has been reported as a general hybrid barrier in many crops, pollen viability was tested (Yoon, 2003). Almost all pollen grains of interspecific hybrid were not stained by acetocarmine and the size was smaller than their parent (Figure 12).

According to Behera and Singh (2002a; 2002b) who reported that the sterility is typically due to the disharmonius genetic consititution or combination of genes of the hybrids with different types of earliest differentiation to the final stage of meiosis.

The pollen fertility of intra- and inter-specific hybrids between *S. melongena* and its wild relative, and their respective parents were showed in Table 20. The intraspecific hybrids within *S. melongena* had higher pollen viability than the interspecific hybrids between *S. melongena* and *S. torvum* (0.00 %). This result indicate that the F_1 hybrids within *S. melongena* had high pollen viability due to the species with closely related genetic affinity produce fertile hybrids with regular chromosome pairing, while the hybrids of those more distantly related species have meiotic irregularities and are sterile (Marfil *et al*., 2006).

However, the pollen fertility of interspecifc hybrids between *S. melongena* x *S. americanum* (61.09 %), *S. melongena* x *S. villosum* (74.23 and 73.50 %) and *S. melongena* x *S. nigrum* (72.88 %) had high pollen fertility than *S. melongena* x *S. torvum* (0.00 %). This result indicated the hybrids from those species were not true interspecific hybrids because all pollen grains of interspecific hybrid were not stained by acetocarmine and the size was smaller than their parents (Yoon, 2003). According to Gowda *et al*. (1990), hybrids between *S. melongena x S. macrocarpon* are sterile, the investigations revealed that the failure of seed set in hybrids was due to the ovule abortion. In order to overcome the sterility, the colchicine has been applied to the interspecific hybrids.

The pollen fertility of *S. americanum* x *S. torvum* (59.34 %) (Table 21) was lower than their parent but not too much different. This result could not confirm that the hybrids from the crosses between *S. americanum* x *S. torvum* were true hybrids or not; we have to confirm with poildy levels determination and also the morphological characters.

The hybrids wihin *S. americanum* x *S. americnum* gave lower pollen fertility than their parents. Similar results have been obtained for F_1 hybrids from the same species combination (Rajasekaran, 1970; Rangasamy and Kadambavanasundaram, 1974). The low pollen fertility of the F_1 may be attributed to meiotic difficulty arising from hybridity of the nucleus (Isshiki and Kawajiri, 2002).

Pollen of F_1 hybrids between *S. americanum* x *S. villosum* was sterile (~ 0.00 %) (Table 21). The variations in the level of low pollen fertility could be due to either the differences in genetic constitution or cryptic structural differences between the parent chromosomes, which might be too small to be detected cytologically or due to combined effects of both factors (Rao, 1981; Anis *et al*., 1994). Moreover, the hybrids of S00859 x S00860 and its reciprocal between *S. americanum* x *S. villosum* had very high pollen fertility (Table 21), this could be due to both of accessions were very closely related but the ploidy levels determination and the morphological characters have yet to be confirmed.

In cantrast, pollen fertility of the interspecific hybrids between *S. americanum* x *S. nigrum* and *S. villosum* x *S. nigrum* were insignificantly lower than their parents. This also has to confirm the interspecific hybrids by polidy levels determination and the morphological characters.

However, pollen fertility of the intraspecific hybrids of *S. villosum* is high (Table 21). This result shows that the accessions within same species closely related genetic affinity produced fertile hybrids with regular chromosome pairing, while the hybrids of the distantly related species have meiotic irregularities and are sterile (Marfil *et al*., 2006).

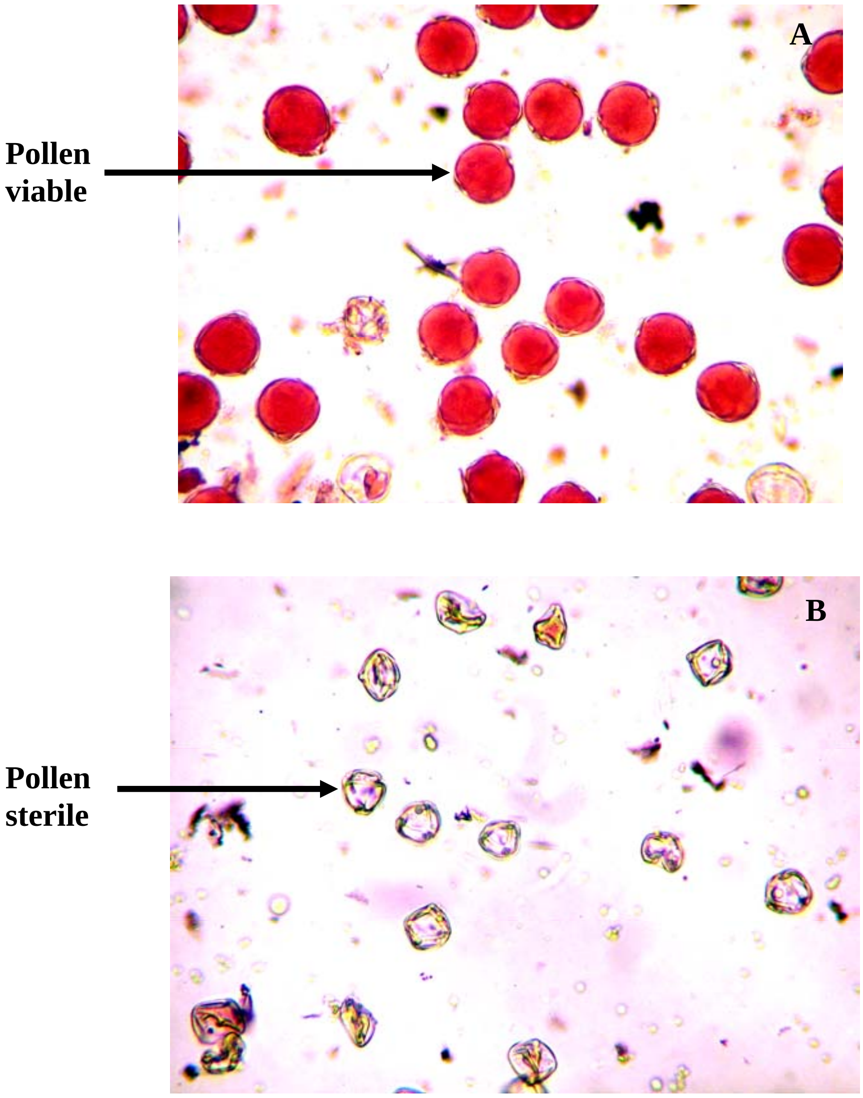

Figure 12 Pollen viability of F_1 hybrid plants. Pollen stainability with acetocarmine was identified as pollen viable (A) and pollen not stainability with acetocarmine was identified as pollen sterile.

Table 19 The pollen fertility of F_1 hybrids within S.*melongena* and F_1 hybrids between its wild relatives, and their respective parents.

Species	Accession No.	Pollen fertility (%)
Parents:		
S. melongena	S00022	77.30
	S00388	78.15
	S00625	76.38
	S00809	76.98
S. torvum	S00429	67.47
S. americanum	S00269	80.91
S. villosum	S00860	85.56
	TS02600	82.81
S. nigrum	TS02930	85.43
Hybrids:		
S. melongena x *S. melongena*	S00022 x S00388	80.45
	S00022 x S00625	80.60
	S00022 x S00809	81.63
	S00388 x S00022	81.98
	S00388 x S00625	80.48
	S00388 x S00809	77.65
	S00625 x S00022	79.82
	S00625 x S00388	79.09
	S00625 x S00809	80.27
	S00809 x S00022	71.56
	S00809 x S00388	78.66
	S00809 x S00625	76.68
S. melongena x *S. torvum*	S00625 x S00429	0.00
	S00625 x S00809	0.00
S. melongena x *S. americanum*	S00809 x S00269	61.09
S. melongena x *S. villosum*	S00809 x S00860	74.23
	S00809 x TS02600	73.50
S. melongena x *S. nigrum*	S00809 x TS02930	72.88

Table 20 The pollen fertility of F_1 hybrids between *S. torvum* and *S. americanum* and their respective parents.

Species	Accession No.	Pollen fertility (%)
Parents:		
S. torvum	S00429	67.47
S. americanum	S00859	64.29
Hybrid:		
S. americanum x *S. torvum*	S00859 x S00429	59.34

Table 21 The pollen fertility of F_1 hybrids between *S. americanum, S. villosum* and *S. nigrum* and their respective parents.

Species	Accession No.	Pollen fertility (%)
Parents:		
S. americanum	S00269	80.91
	S00859	64.29
	S00861	84.33
	S00865	71.38
S. villosum	S00854	78.76
	S00860	85.56
	TS02600	82.81
S. nigrum	TS02930	85.43
Hybrids:		
S. americanum and *S. americanum*	S00269 x S00861	9.84
	S00859 x S00861	14.30
	S00859 x S00865	36.71
	S00861 x S00269	21.89
	S00861 x S00865	34.77
	S00865 x S00861	19.78
S. americanum and *S. villosum*	S00859 x S00860	81.90

Table 21 (Continued)

Species	Accession No.	Pollen fertility (%)
S. americanum and *S. villosum*	S00861 x S00860	0.08
	S00854 x S00269	0.07
	S00854 x S00861	0.04
	S00854 x S00865	0.08
	S00860 x S00859	87.15
	TS02600 x S00859	0.00
	TS02600 x S00861	0.07
	TS02600 x S00865	0.03
S. americanum and *S. nigrum*	S00269 x TS02930	57.14
	TS02930 x S00861	67.38
S. villosum and *S. villosum*	S00854 x S00860	81.97
	TS02600 x S00860	83.88
S. villosum and *S. nigrum*	S00860 x TS02930	77.36

2.2 Ploidy levels determination

The histogram obtained after flow cytometric analysis was reported in Figure 13 to 18. The DNA content of S00022 accession of *S. melongena* was used as internal reference standard for the estimation of nuclear genome size in this studied. The expected for genome size accession S00022 was diploid (2n). The other *Solanum* accessions and their interspecific hybrids were measured with reference to the accession S00022 of *S. melongena*.

The genome sizes of various *Solanum* species showed significant differences (Figure 13 to 18). *S. melongena* (2n), *S. torvum* (2n) and *S. americanum* (2n) had the small genome size, while *S. villosum* (4n) had genome size bigger than *S. melongena*, *S. torvum* and *S. americanum* but still smaller than *S. nigrum* (6n). As expected, the hexaploid (6n) species had more nuclear DNA than tetraploid (4n) and diploid (2n) species. Significant differences in DNA content between cultivated and wild species have been found in some other plant such as *Capsicum annuum* and *C. baccatum* (Bennett and Smith, 1976), *Piper nigrum*, *P. betle* and *P. longum* (Samuel *et al*., 1986), *Glycine* species (Yamamoto and Nagato, 1984) and rice species (Martinez *et al*. 1994).

The histogram of flow cytometer showed the DNA content of their nuclei. In case of *S. melongena* genome size was expected to be diploid. Genome sizes of all accessions of *S. melongena* are shown to be diploid (Figure 13). The interspecific hybrids of *S. melongena* and its wild relative was showed in Figure 13, which the histrogram of hybrids between *S. melongena* x *S. torvum* from S00625 x S00429 and S00809 x S00429, the hybrids between *S. melongena* x *S. villosum* from S00809 x S00860 and their parents. This figure represented the result of the hybrid from S00625 x S00429 and S00809 x S00429 had same level ploidy with their parents. This due to *S. melongena* and *S. torvum* are diploid species when both species were crossed, the hybrids should be diploid. This results confirm that both hybrids are true intertspecific hybrids. In contrast the hybrid between *S. melongena* x *S. villosum* (S00809 x

S00860) showed a same ploidy level with female parent (*S. melongena*) which indicates that the hybrids were not true hybrids.

S. torvum has the expected diploid genome size but the histrogram of accession S00429 genome size was not showed clearly (Figure 13). It might be the leaf sample was too old. These due to the mature organs were usually heavily loaded with polysaccharides, calcium oxalate crystals and other metabolites which decrease the purity of intact nuclei. These contaminants, such as calcium oxalate crystals, have smaller diameters than the nuclei and were difficult to remove by the small-pore-size of nylon mesh (167 µm) used in this protocols. On disruption, cytoplasmic compounds come into contact with nuclei and pose a major obstacle to the purity of nuclei. These contaminants accelerate the degradation of nuclei, increase the viscosity of the samples, and block the fluidic system of the flow cytometer (Lee and Lin, 2005).

S. americanum with diploid expected genome size, there is no significant differences among accessions of these species (Figure 15). The histrogram of hybrids within *S. americanum* and their parents has shown the intermediate between content of their parents. All of histrogram from the intraspecific hybrids showed the same ploidy levels with their parents. This indicates that the intraspecific hybrids within *S. americanum* are true hybrids due to *S. americanum* is diploid species.

S. villosum has tetraploid expected genome size, the genome size of accessions belong to *S. villosum* were significant differences. The histrogram of S00854 (Figure 16), TS002600 (Figure 17) and S00860 (Figure 18) show that S00854 and S00860 had the same genome size and bigger than the genome size of TS002600. This indicated the variation of different genotype within *S. villosum*. However, the differences of genome sizes found can be interpreted as unstable tetraploid. Likewise Martinez *et al*. (1994), who found the differences of genome sizes of accessions of rice in tetraploid species (*Oryza rideyi*).

S. nigrum has hexaploid expected genome size, the histrogram of accession TS02930 of *S. nigrum* showed the hexaploid (Figure 15). This result confirms that *S. nigrum* is hexaploid species and has more nuclear DNA than tetraploid (*S. villosum)* and diploid (*S. melongena*, *S. torvum* and *S. americanum*) species.

The interspecific hybrids among leafy *Solanum* species are shown in Figure 15 to 18. As expected genome size of interspecific hybrid *S. americanum* (2n) and *S. nigrum* (6n) should be tetraploid (4n). The histrogram of S00269 x TS02930 is near to diploid, this indicates that the hybrids are not true hybrids. In contrast the hybrid of TS02930 x S00861 is shown as tetraploid genome size. This indicates that this hybrid is true hybrid.

The genome size of interspecific hybrid *S. villosum* (4n) and *S. americanum* (2n) should be triploid (3n). The histrogram of S00854 x S00269 is near to diploid, this indicates that this hybrid is not true hybrid. In contrast the hybrids of S00854 x S00861 and S00854 x S00865 showed triploid genome size. This indicates that this hybrid is true hybrid (Figure 16). Likewise the interspecific hybrid of *S. villosum* and *S. americanum* are shown in Figure 17. The hybrids of TS02600 x S00861 and TS02600 x S00865 showed the triploid genome size. This indicates that this hybrid is true hybrid. No significant differences are found among accessions of female parent that belonging to *S. villosum*.

The interspecific hybrid between *S. villosum* and *S. americanum* when used *S. villosum* as male and female parent (S00860 x S00859 and S00861 x S00860), showed the same histrogram of intermediate of hybrids even in reciprocal crosses. However, as expected genome size of the interspecific hybrids between *S. villosum* and *S. nigrum* should be pentaploid but the hybrid of S00860 x TS02930 could not confirm (Figure 18). It might be the leaf sample was too old and contaminated with some heavily loaded, which decrease the purity of intact nuclei and could not showed the DNA content of hybrid (Lee and Lin, 2005).

Moreover, an accurate determination of genome size provides basic information for breeders and molecular geneticists. Comparisons of nuclear DNA amount were also useful in cytotaxonomy and evolution. Beacause of its rapid and simple, DNA flow cytometer has become a popular method for ploidy screening, detection of mixoploidy and aneuploidy, cell cycle analysis, assessment of degree of polysomaty, determination of reproductive pathway and estimation of absolute DNA amont to determine size. Therefore, ploidly level determination was useful to confirm hybridity of interspecific hybrids. However, a major drawback to ploidy identification using bulk samples is that bulk samples may mask the presence of aneuploid plants (Lee and Lin, 2005).

Therefore, the induction of polyploidy can overcome crossing barriers resulting from endosperm failure. In intra-specific, intraploidy crosses, viable seeds are produced because the endosperm develops normally. Conversely, in most inter-ploidy crosses, inviable seeds are produced as a result of endosperm failure. How ever, endosperm may also fail to develop adequately in some intraploidy, interspecific crosses, while some interploidy crosses succeed. Therefore, crossing success is predicted by effective ploidy, rather that actual ploidy (Jansky, 2006).

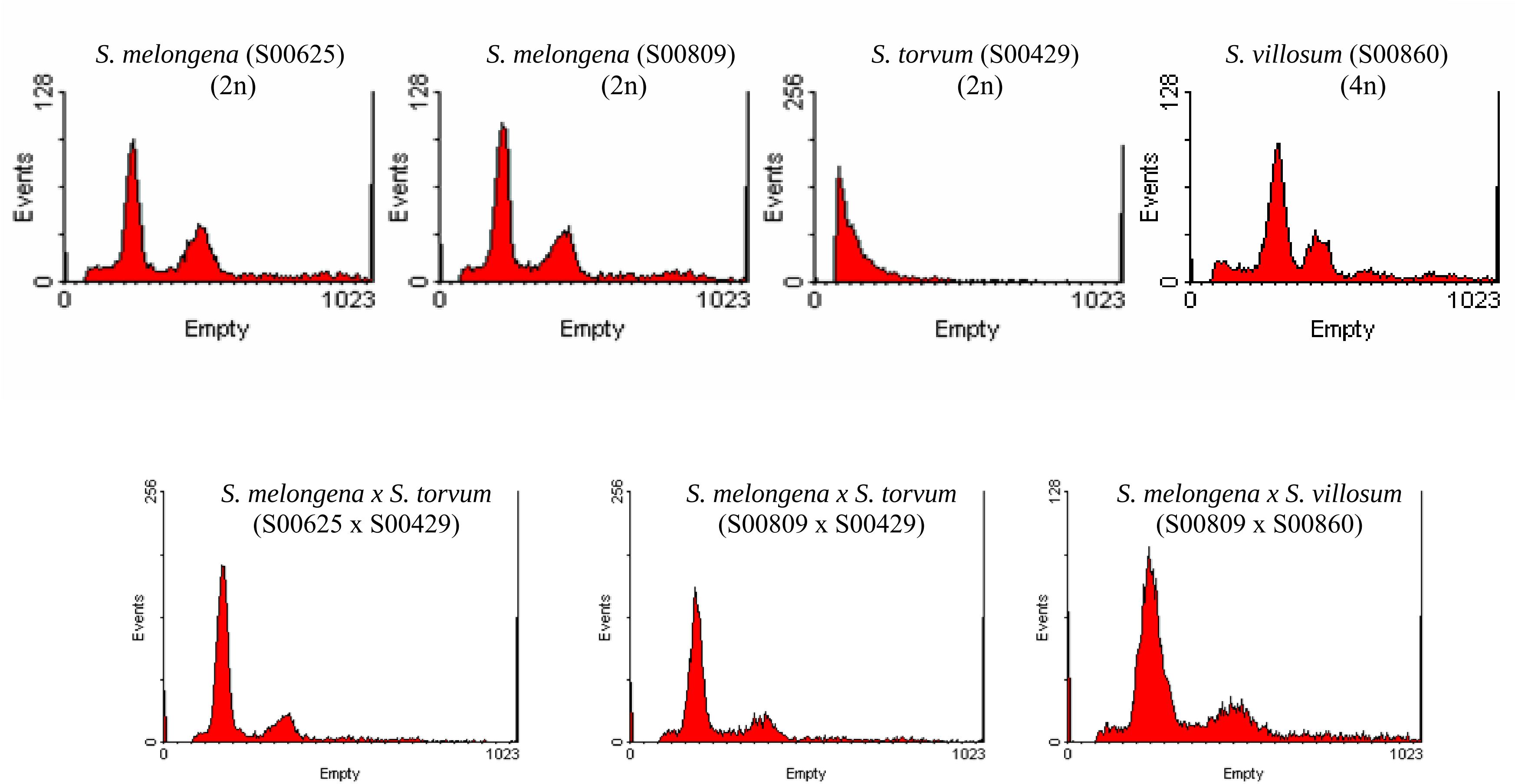

Figure 13 Histrogram of hybrids between *S. melongena* x *S. torvum* and *S. melongena* x *S. villosum* and their parents.

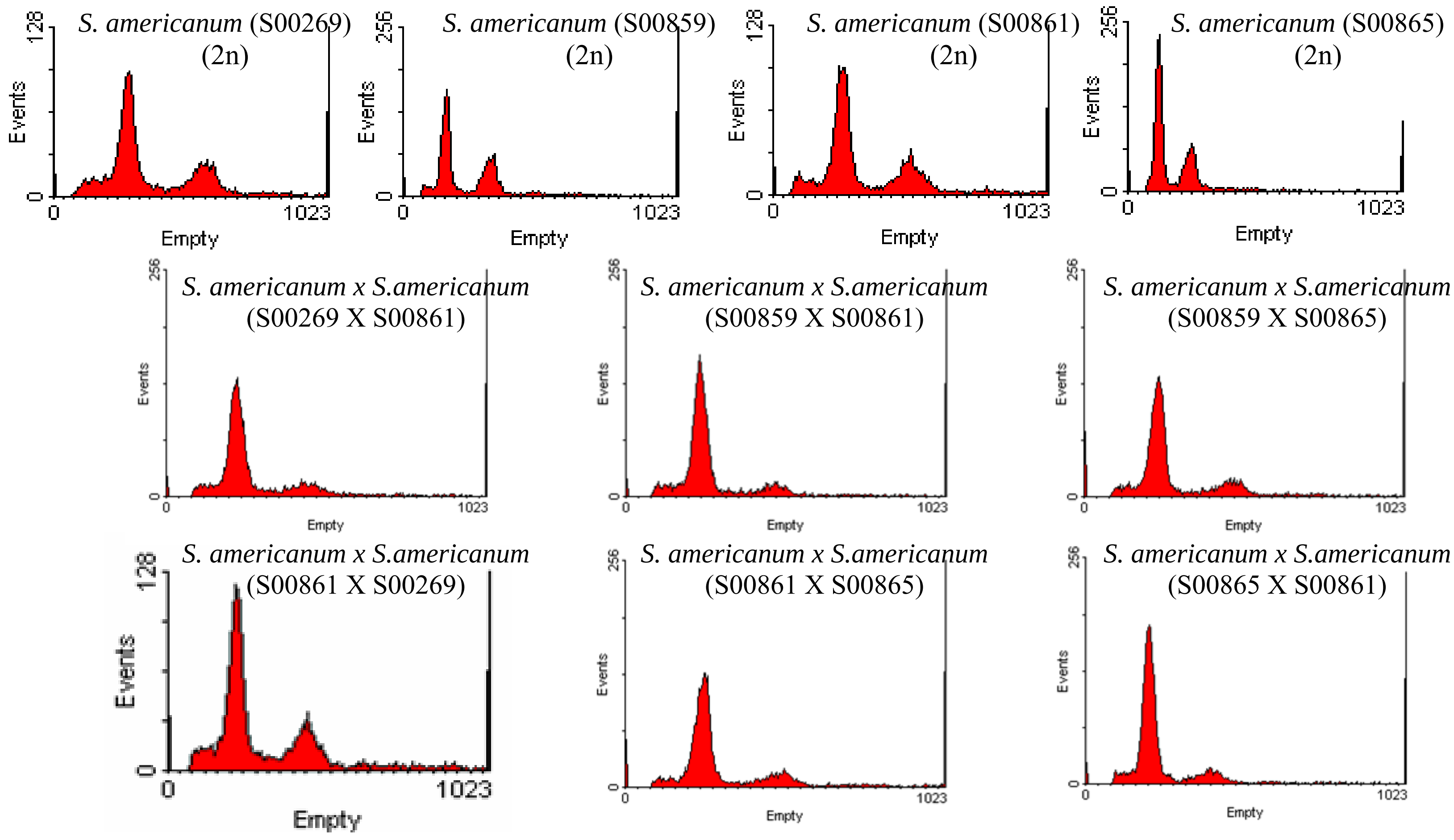

Figure 14 Histrogram of hybrids within *S. americanum* and their parents.

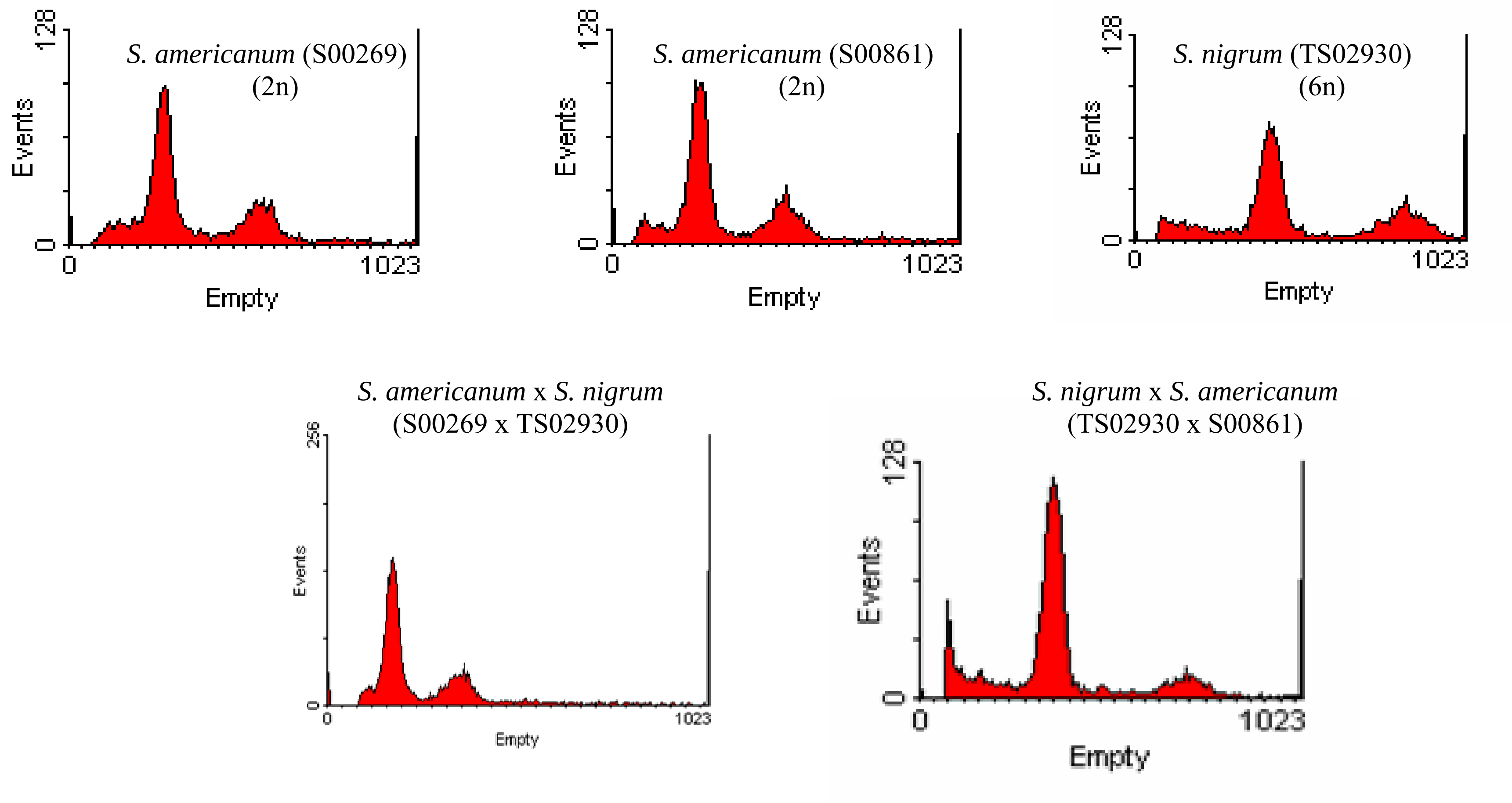

Figure 15 Histrogram of hybrids between *S. americanum* and *S. nigrum* and their parents.

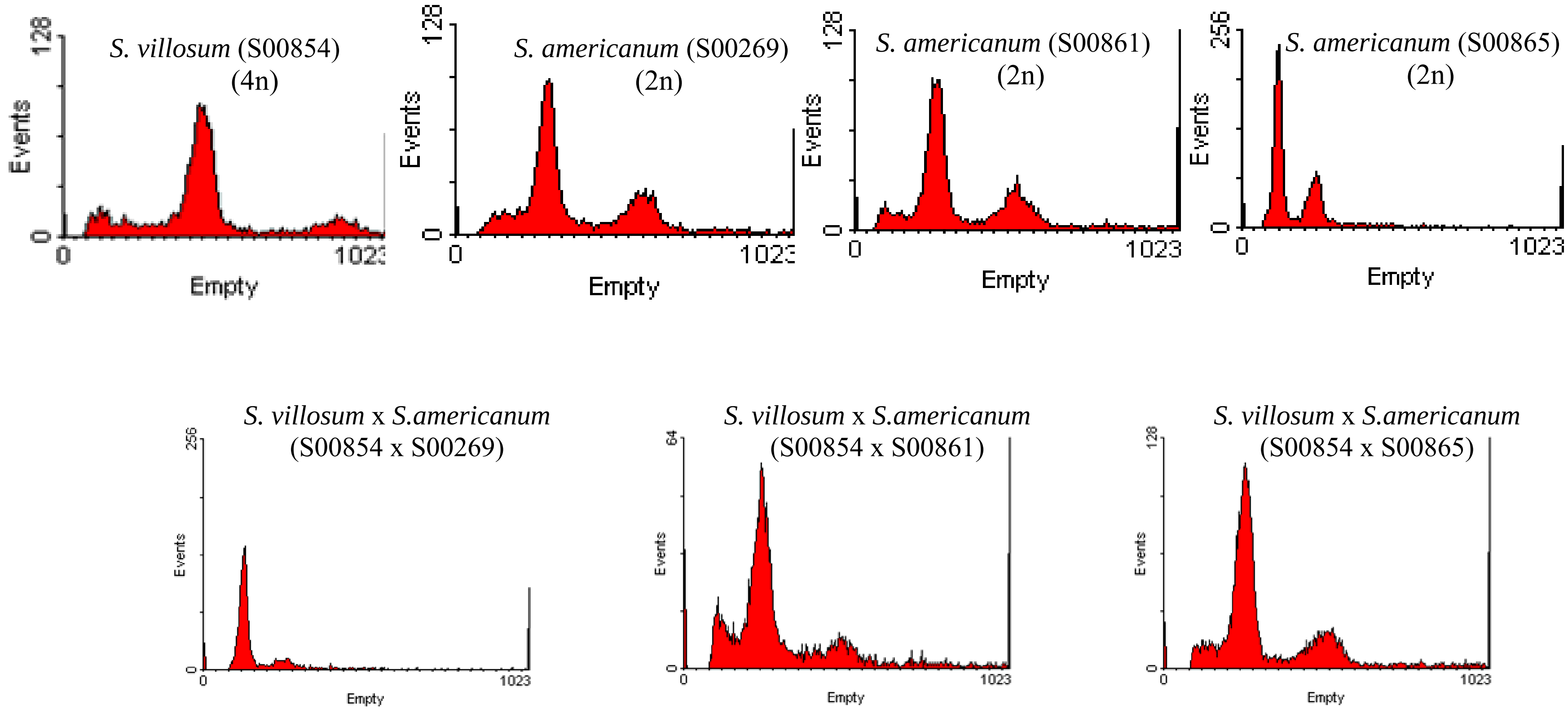

Figure 16 Histrogram of F_1 hybrids within *S. villosum* (S00854) and *S. ameicanum* and their parents.

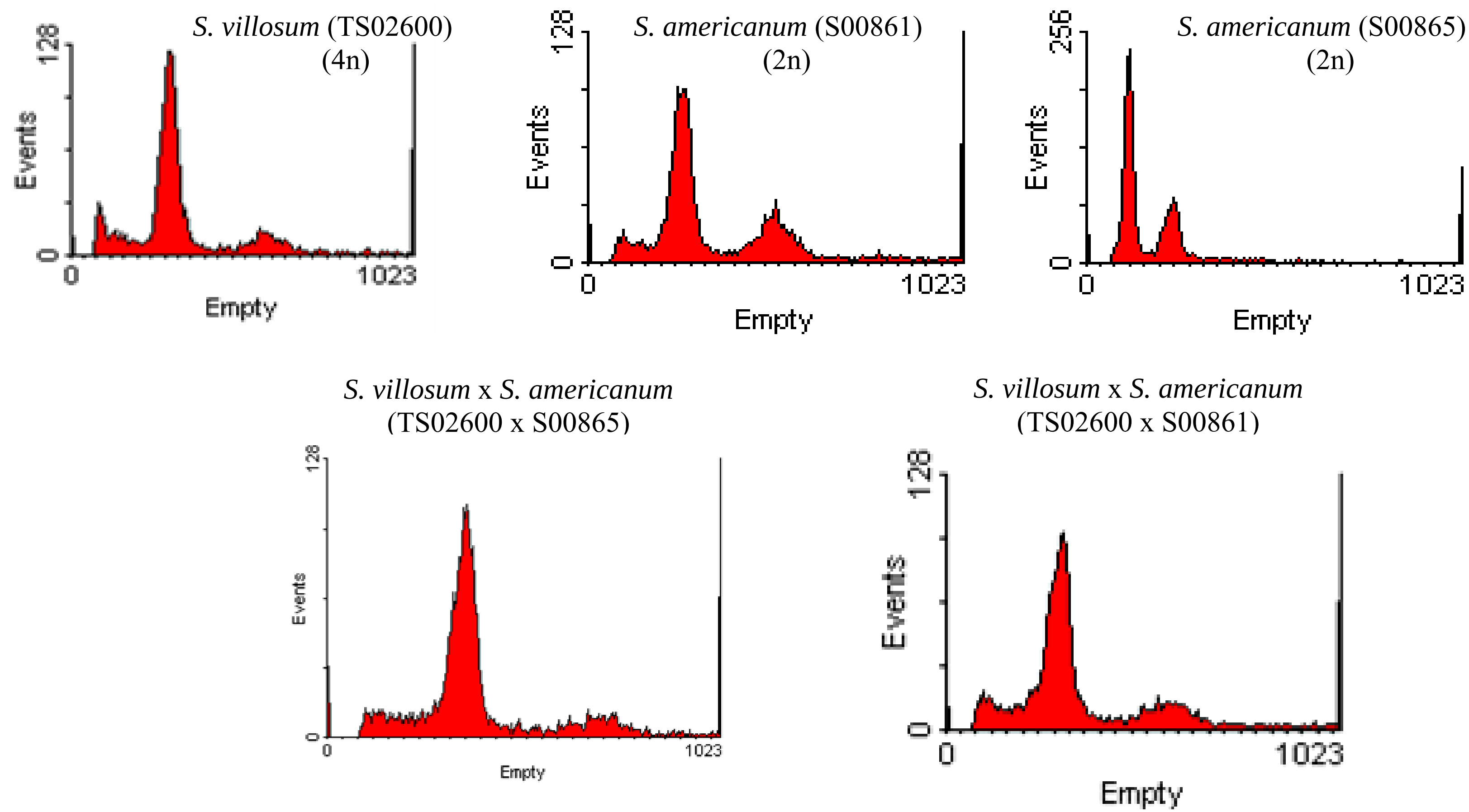

Figure 17 Histrogram of F_1 hybrids within *S. villosum* (TS02600) x *S. americanum* and their parents.

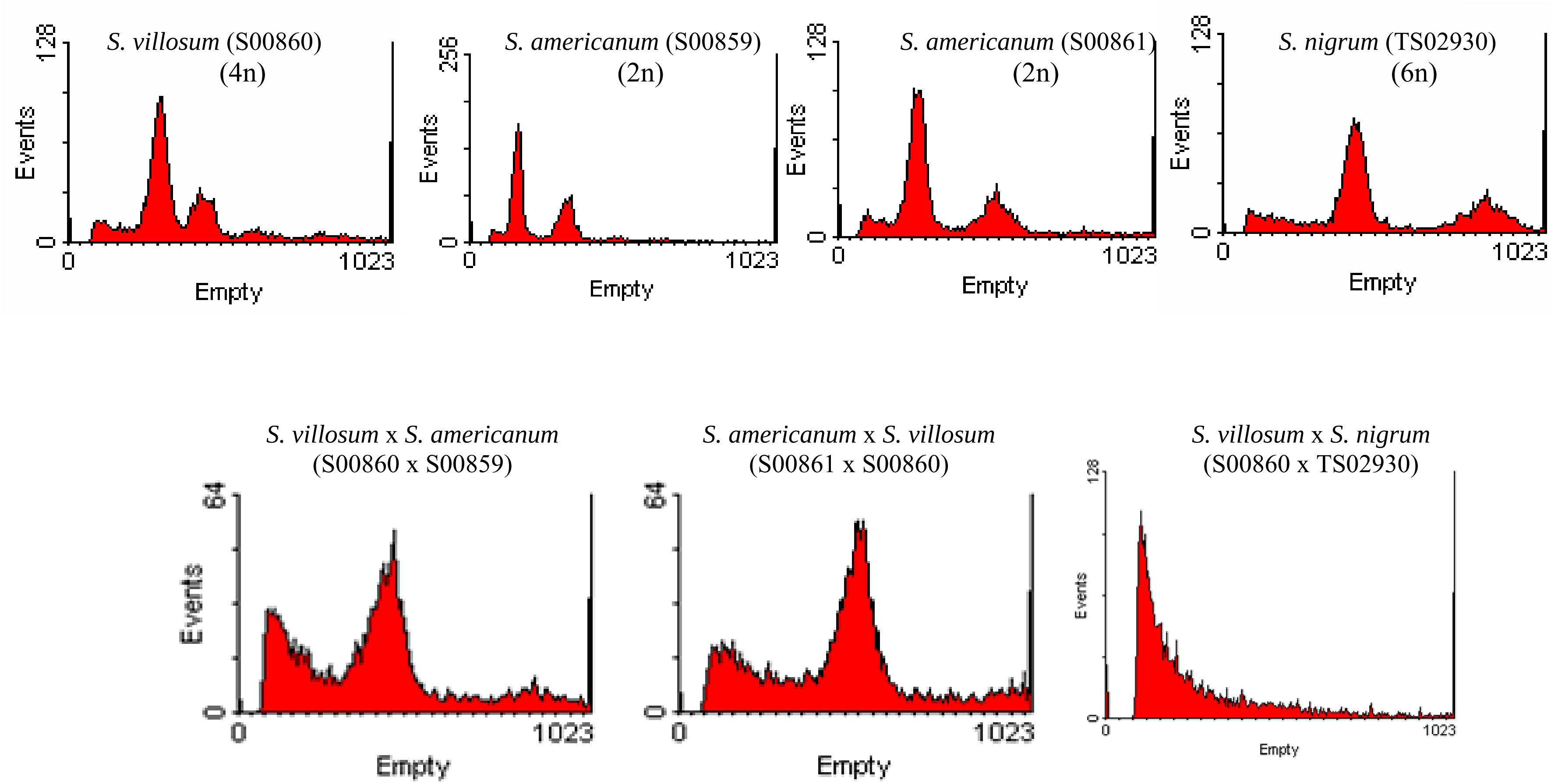

Figure 18 Histrogram of F_1 hybrids between *S. villosum* (S00860) x *S. americanum, S. americnum* x *S. villosum* and *S. villosum* x *S. nigrum* and their parents.

2.3 Morphological characters

The morphological characters of F_1 compare to their parents are shown in Figure 19 to 32. From the morphological observation of F_1 hybrid plants derived from *S. melongena* x *S. melongena*, the F_1 hybrid plants obtained from these crosses grew vigorously and fertile. Their plant size, leaf size, flowering time, fruit size and fruit color characters are intermediate to their parents. This indicates that these characters are controlled by additive genes (Seehalak, 2005). Similar the hybrid plants were obtained from rescuing the embryos of *S. melongena* and *S. torvum*, the morphological characters of F_1 hybrids when compared to their parents are present in Figure 20. Plant hieght, plant breadth, leaf blade length, leaf blade width and flowering time of F_1 hybrid plants are intermediate between their parents. Especially, the leaf blade and flower of F_1 hybrids are similar to *S. torvum* but the number of flowere per inflorescence is less than *S. torvum*. This indicates that the interspecific hybrids between *S. melongena* x *S. torvum* are true hybrids.

The hybrids plant between *S. moleongena* x *S. americanum* (Figure 21), *S. moleongena* x *S. villosum* (Figure 22) and *S. moleongena* x *S. nigrum* (Figure 23), are not true hybrids due to all morphological characters such as plant habit, leaf shape, leaf size and flower exhibited like *S. melongena*.

The crossing within *S. americanum* from S00861 x S00865 (Figure 24), the hybrid plant is low vigor than their parents. Hybrid plant show very low viogor in plant height. According to Bhaduri (1951) who concluded that the hybridization and selection accompanied by gene mutation and segmental interchange of chromosome is the cytogenetical basis of origin of the non-tuberous species complex of *Solanum*.

However, the hybrids plants between *S. americanum* x *S. villosum* (S00861 x S00860) show the intermediate morphological characters when compared to their parents (Figure 25). This indicates that it is a true hybrid.

Moreover, the crosses between *S. americium* x *S. nigrum* (Figure 26), *S. vilosum* x *S. viilosum* (Figure 28), *S. villosum* x *S. americanum* (TS02600 x S00861) (Figure 29), *S. villosum* x *S. americanum* (S00854 x S00861) (Figure 30), *S. villosum* x *S. nigrum* (S00860 x TS2930) (Figure 31) and *S. nigrum* x *S.americanum* (Figure 32), the hybrid plants are morphologically intermediate when compare to the parent. This indicates that these hybrid plants are true hybrids.

In contrast to the crosses between *S. americanum* x *S. torvum* (Figure 27) and *S. villosum* x *S. nigrum* (Figure 31), the obtained planyts are not true hybrid due to their morphological similarity to their female parent.

In this present investigation the interspecific hybrids are highly fertile. The various types of crossability behaviour may be attributed to the different genotypes of the parent (Chopde and Wanjari, 1974).

Therefore, the confirmation of interspecifc hybrids determined by pollen fertility, ploidy level and morphological characters are useful.

S. melongena (S00022) F_1 *S. melongena* (S00809)

S. melongena (S00022) F_1 *S. melongena* (S00809)

S. melongena (S00022) F_1 *S. melongena* (S00809)

S. melongena (S00022) F_1 *S. melongena* (S00809)

Figure 19 Morphological characters of F_1 hybrid crosses within *S. melongena* and their parent.

S. melongena (S00625) F_1 *S. torvum* (S00429)

S. melongena (S00625) F_1 *S. torvum* (S00429)

S. melongena (S00625) F_1 *S. torvum* (S00429)

Figure 20 Morphological characters of F_1hybrid plant obtained from embryo rescue from the crosses between *S. melongena* with *S. torvum* and their parent.

S. melongena (S00809) F_1 *S. americanum* (S00269)

S. melongena (S00809) F_1 *S. americanum* (S00269)

S. melongena (S00809) F_1 *S. americanum* (S00269)

Figure 21 Morphological characters of F_1 hybrid between *S. melongena* with *S. americaum* and their parent.

S. melongena (S00809) | F_1 | *S. villosum* (S00860)

S. melongena (S00809) | F_1 | *S. villosum* (S00860)

S. melongena (S00809) | F_1 | *S. villosum* (S00860)

Figure 22 Morphological characters of F_1 hybrid between *S. melongena* with *S. villosum* and their parent.

S. melongena (S00809) F_1 *S. nigrum* (TS02930)

S. melongena (S00809) F_1 *S. nigrum* (TS02930)

S. melongena (S00809) F_1 *S. nigrum* (TS02930)

Figure 23 Morphological characters of F_1 hybrid between *S. melongena* with *S. nigrum* and their parent.

S. americanum (S00861) F$_1$ *S. americanum* (S00865)

S. americanum (S00861) F$_1$ *S. americanum* (S00865)

S. americanum (S00861) F$_1$ *S. americanum* (S00865)

Figure 24 Morphological characters of F$_1$ hybrid within *S. americanum* and their parent.

S. americanum (S00861) F$_1$ *S. villosum* (S00860)

S. americanum (S00861) F$_1$ *S. villosum* (S00860)

S. americanum (S00861) F$_1$ *S. villosum* (S00860)

Figure 25 Morphological characters of F$_1$ hybrid between *S. americanum* with *S. villosum* and their parent.

S. americanum (S00269) F_1 *S. nigrum* (TS02930)

S. americanum (S00269) F_1 *S. nigrum* (TS02930)

S. americanum (S00269) F_1 *S. nigrum* (TS02930)

Figure 26 Morphological characters of F_1 hybrid between *S. americanum* with *S. nigrum* and their parent.

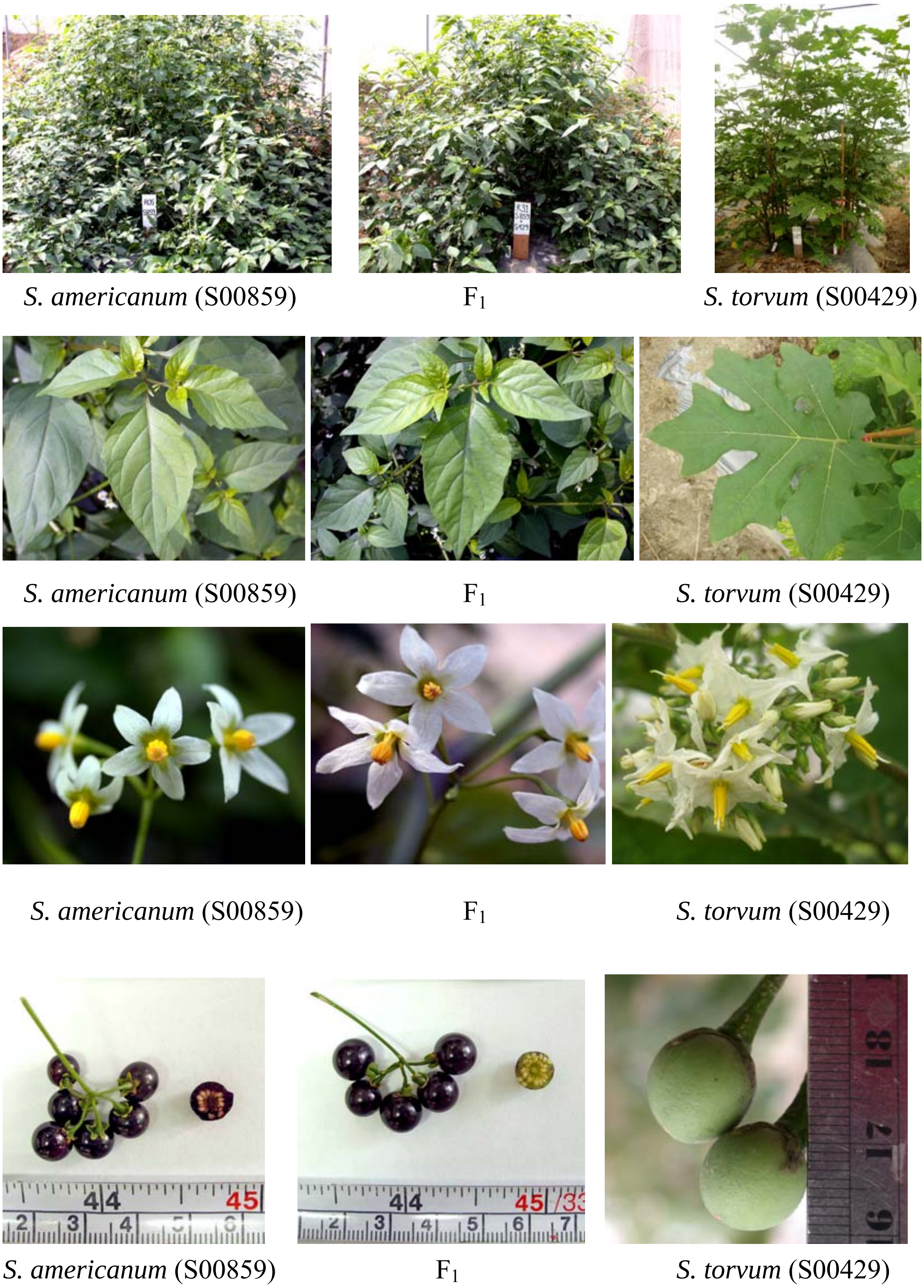

Figure 27 Morphological characters of F_1 hybrid between *S. americanum* with *S. torvum* and their parents.

S. villosum (TS02600) F_1 *S. villosum* (S00860)

S. villosum (TS02600) F_1 *S. villosum* (S00860)

S. villosum (TS02600) F_1 *S. villosum* (S00860)

S. villosum (TS02600) F_1 *S. villosum* (S00860)

Figure 28 Morphological characters of F_1 hybrid within *S. villosum* and their parents.

S. villosum (TS02600) F_1 *S. americanum* (S00861)

S. villosum (TS02600) F_1 *S. americanum* (S00861)

S. villosum (TS02600) F_1 *S. americanum* (S00861)

Figure 29 Morphological characters of F_1 hybrid between *S. villosum* with *S. americanum* and their parents.

S. villosum (S00854) F_1 *S. americanum* (S00861)

S. villosum (S00854) F_1 *S. americanum* (S00861)

S. villosum (S00854) F_1 *S. americanum* (S00861)

Figure 30 Morphological characters of F_1 hybrid between *S. villosum* with *S. americanum* and their parents.

S. villosum (S00860) F_1 *S. nigrum* (TS02930)

S. villosum (S00860) F_1 *S. nigrum* (TS02930)

S. villosum (S00860) F_1 *S. nigrum* (TS02930)

Figure 31 The morphological characters of F_1 hybrid between *S. villosum* with *S. nigrum* and their parents.

S. nigrum (TS02930) F_1 *S. americanum* (S00861)

S. nigrum (TS02930) F_1 *S. americanum* (S00861)

S. nigrum (TS02930) F_1 *S. americanum* (S00861)

Figure 32 The morphological characters of F_1 hybrid between *S. nigrum* with *S. americanum* and their parents.

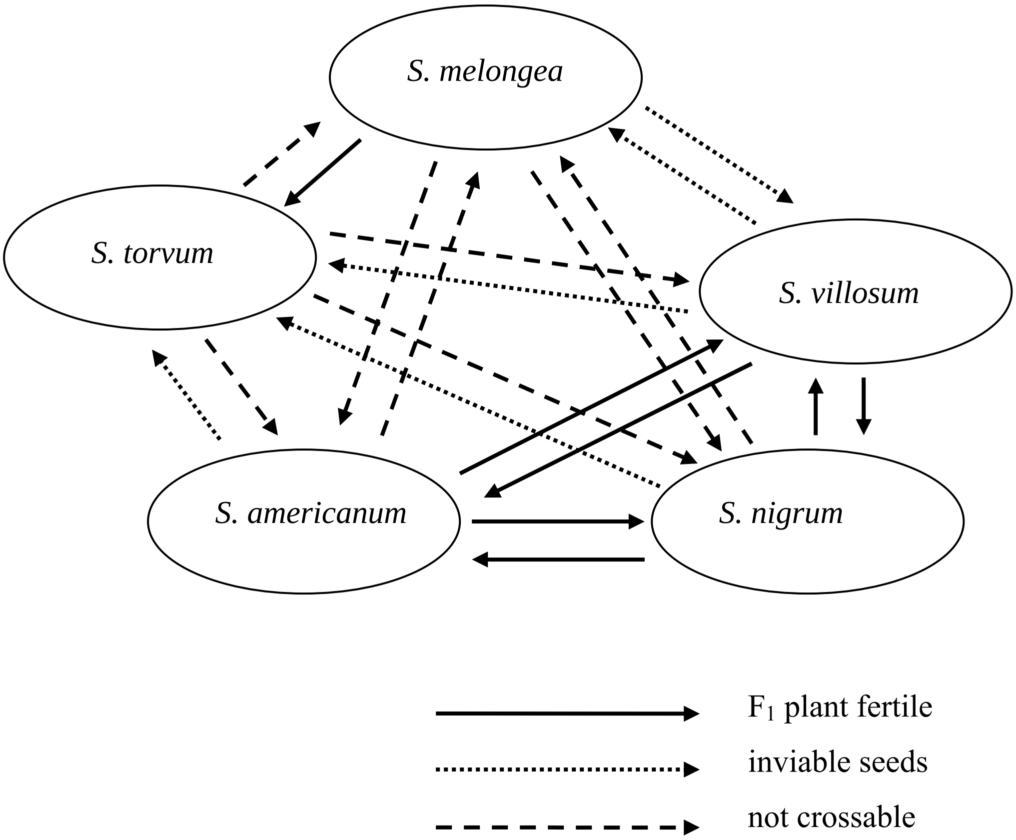

Figure 33 Genetic relationship among cultivated *S. melongena* and other species. Arrow heads point towards female parents.

Therefore, the interspecfic hybridization among *S. melongena* and its wild relatives is applied to determine the genetic relationships. The degree of crossiblility is determined by the percentages of fruit setting and number of seed per fruit and confirmation of the interpecific hybrids were done by pollen fertility, ploidy levels determination and morphological characters. The result showes that *S. torvum* is more closely related to *S. melongena* than the other three species (*S. americanum*, *S. villosum* and *S. nigrum*) (Figure 33) because the cross between *S. melongena* and *S. torvum* was successful and hybrid plants were obtained through embryo rescue (Table 13). Furtheremore, F_1 hybrids showed low pollen fertilly and intermediate charateristics of morphology and ploidy levels when compared to their parents.

For the interspecific crossing among *S. melongena* and other three species (*S. americanum*, *S. villosum* and *S. nigrum, S. villosum* is more closely related to *S. melonegena* than *S. americanum* and *S. nigrum.* This due to the crosses between *S. melongena* and those three species gave hybrid plants but when confirmed the hybridity by pollen fertility, ploidy levels and morphological characters, they were not the true hybrid. In contrast, when used *S. melongena* as male parent, the hybrid fruits were obtained but no viable seeds from the cross between *S. melongena* and *S. villosum.*

Moreover, from the interspecific hybridization among *S. torvum* and the three species (*S. americanum*, *S. villosum* and *S. nigrum*), *S. villosum* is more closely related to *S. torvum* than *S. americanum* and *S. nigrum* when considered the percentages of fruit setting and number of seeds per fruit. *S. villosum* has the higest percentages of fruit setting and number of seeds per fruit when compare to *S. americanum* and *S. nigrum* (Table 17).

Furthermore, from the interspecific hybridization among *S. americanum*, *S. villosum* and *S. nigrum*, we found that *S. americanum* is more closely related to *S. villosum* than *S. nigrum* when considered the percentages of fruit setting and number of seeds per fruit (Table 18).

Therefore, germplasm characterization provides essential, valuable information for breeding programs. Knowledge on genetic diversity and relationships among the *S. melongena* germplasm may play significant role in breeding programs to improve fruit quality and resistance to biotic and abiotic stresses of *S. melongena*. Interspecific hybridization is possible between *Solanum* spp. This may accelerate diversity and increase gene pool for breeding programs. Diversity within germplasm is critical for *S. melongena* breeding programs. However, all F_1 hybrids from interspecific hybridization are sterile which may be overcome by using hormone and/or some chemical such as GA (gibberlleic acid) and colchicines for doubling the set of chromosome.

CONCLUSION

On the basis of finding from the present studies, the following conclusions can be drawn:

1. The morphological characterization of the 89 accessions of *Solanum* spp. collected from Southeast Asia have been done using a standard set of IBPGR, they were identified follows:

    1) *Solanum melongena* L. (38 accessions)
    2) *S. aculeatissimum* (2 accessions)
    3) *S. aethiopicum* (1 accession)
    4) *S. ferox* (17 accessions)
    5) *S. indicum* (8 accessions)
    6) *S. mammosum* (1 accession)
    7) *S. sanitwongsei* (1 accession)
    8) *S. torvum* (11 accessions)
    9) *S. trilobatum* (3 accessions)
    10) *S. viarum* (1 accession)
    11) *S. xanthocarpum* (6 accessions)

2. The *S. melongena* is the major group among 89 accessions of *Solanum* spp. originally collected in Southeast Asia.

3. The result of cluster analysis based on quantitative traits had more variation than qualitative traits. Howevr, both analyses gave almost the same members in each cluster. The variation among the eleven *Solanum* spp. can be attributed to their inherent variation and geographic distribution.

4. Based on success rate of crossing among species, *S. torvum* is more closely related to *S. melongena* than the other three species (*S. americanum*, *S. villosum* and

S. nigrum). For the interspecific crossing among those three species found the *S. americanum* is more closely related to *S. villosum* than *S. nigrum.*

5. The confirmation of interpecific hybrids is verified by pollen fertility showing the lower pollen fertility of F_1 hybrid plant than their parent. F_1 hybrids show intermediate characteristics of morphology and ploidy levels when comapare to their parents.

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APPENDICES

Appendix A

Descriptors of eggplant by IBPGR and modified by AVRDC

AVRDC-GRSU CHARACTERIZATION RECORD SHEET

Crop: EGGPLANT Accession No.:_____________

Sowing Date: __________________Plot No.:__________________

Transplanting Date: _____________ Name:____________________

Location: _____________________Species:___________________

Origin: ____________________

SEEDLING DATA

S110 Germination period (No. of days from sowing till first germination)

S120 Cotyledonous leaf length (mm) (N=10)

S130 Cotyledonous leaf width (mm) (N=10)

S140 Cotyledonous leaf color

3 = Green 5 = Light violet 7 = Violet X = Mixture

S150 Cotyledon length/width ratio

1 = Very low (<2.0) 3 = Low (~2.2) 5 = Intermediate (~2.5)

7 = High (~3.5) 9 = Very high (>5.0) X = Mixture

VEGETATIVE DATA

S210 Plant growth habit

3 = Upright 5 = Intermediate 7 = Prostrate X = Mixture

S215 Stem ridging

0 = Absent 3 = Shallow 5 = Intermediate 7 = Prominent X = Mixture

S216 Spines on stem

0 = Absent 3 = Short 5 = Intermediate 7= Long X = Mixture

S217 Degree of stem pubescence

0 = Absent 1 = Few 2 = Intermediate

3 = Many 4 = Very many X = Mixture

S220 Plant height (cm) (at flowering stage)

1 = Very short (<20) 3 = Short (~30) 5 = Intermediate (~60)

7 = Tall (~100) 9 = Very tall (>150) X = Mixture

S230 Plant breadth (cm) (at flowering stage)

1 = Very narrow (<30) 3 = Narrow (~40) 5 = Intermediate

7 = Broad (~90) 9 = Very strong (>130) X = Mixture

S240 Plant branching (no. of primary branches per plant)

1 = Very weak (~2) 3 = Weak (~5) 5 = Intermediate (~10)

7 = Strong (~20) 9 = Very strong (>30) X = Mixture

S250 Petiole color

1 = Green 2 = Greenish violet 3 = Violet

7 = Dark violet 9 = Dark brown X = Mixture

S260 Petiole length (mm)

0 = None 1 = Very short (<5) 3 = Short (~10)

5 = Intermediate (~30) 7 = Long (~50) 9 = Very long (>100)

X = Mixture

S270 Leaf blade length (cm)

3 = Short (~10) 5 = Intermediate (~20) 7 = Long (~30)

X = Mixture

S280 Leaf blade width (cm) (maximum width)

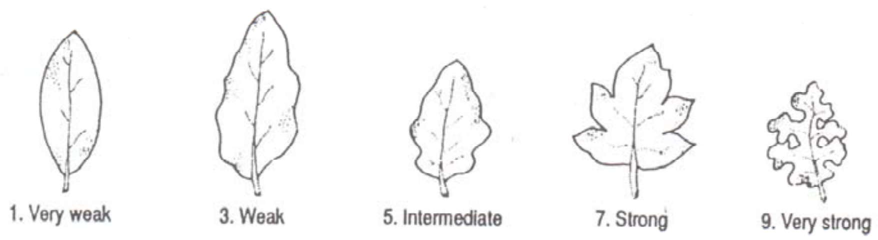
3 = Narrow (~5) 5 = Intermediate (~10) 7 = Wide (~15)

X = Mixture

S290 Leaf blade lobbing

1 = Very weak 3 = Weak 5 = Intermediate 7 = Strong

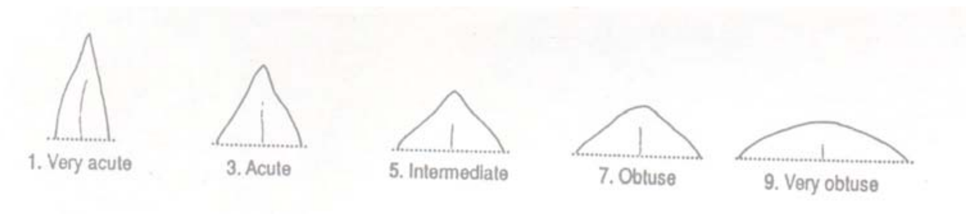
9 = Very strong X = Mixture



S300 Leaf blade tip angle

1 = Very acute (<15^{o}) 3 = Acute (~45^{o}) 5 = Intermediate (~75^{o})

7 = Obtuse (~110^{o}) 9 = Very obtuse (>160^{o}) X = Mixture



S310 Leaf blade color (upper surface)

1 = Light green 3 = Green 5 = Dark green

7 = Greenish violet 9 = Violet X = Mixture

S320 Leaf prickles (No. of leaf prickles on upper surface of the leaf)

0 = None 1 = Very few (1-2) 3 = Few (3-5)

5 = Intermediate (6-10) 7 = Many (11-20) 9 = Very many (>20)

X = Mixture

S330 Leaf hairs (No. of hair per mm2 on lower surface of the leaf)

1 = Very few (<20) 3 = Few (20-50) 5 = Intermediate (50-100)

7 = Many (100-200) 9 = Very many (>200) X = Mixture

INFLORESCENCE DATA

S410 Number of flowers per inflorescence

S420 Flowering time (No. of days from sowing till first flower opening)

S421 Stamen length (cm) (N=5)

________ ________ ________ ________ ________

S422 Petal length (cm) (N=5)

________ ________ ________ ________ ________

S423 Sepal length (cm) (N=5)

________ ________ ________ ________ ________

S430 Number of hermaphrodite flowers per inflorescence

1 = Only one hermaphrodite flower on each inflorescence

2 = Only two hermaphrodite flower on each inflorescence

3 = Only three hermaphrodite flower on each inflorescence

4 = Four or more hermaphrodite flower on each inflorescence, but some flowers functionally male

5 = Four or more hermaphrodite flower on each inflorescence, no functionally male flowers

X = Mixture

S440 Corolla color

1 = Greenish white 3 = White 5 = Pale violet

7 = Light violet 9 = Bluish violet X = Mixture

S450 Relative style length (mm)

3 = Short (~1) 5 = Intermediate (~3) 7 = Long (~5)

X = Mixture

S460 Pollen production

0 = None 3 = Low 5 = Medium 7 = High

X = Mixture

S470 Style exertion

3 = Inserted 5 = Intermediate 7 = Exerted

FRUIT DATA

First harvest date ______________________

Last harvest date ______________________

Fruiting date (date when 50 % of plants have mature fruits)

S510 Fruit length (cm) (from base of calyx to tip of fruit)

1 = Very short (<1) 3 = Short (~2) 5 = Intermediate (~5)

7 = Long (~10) 9 = Very long (>20) X = Mixture

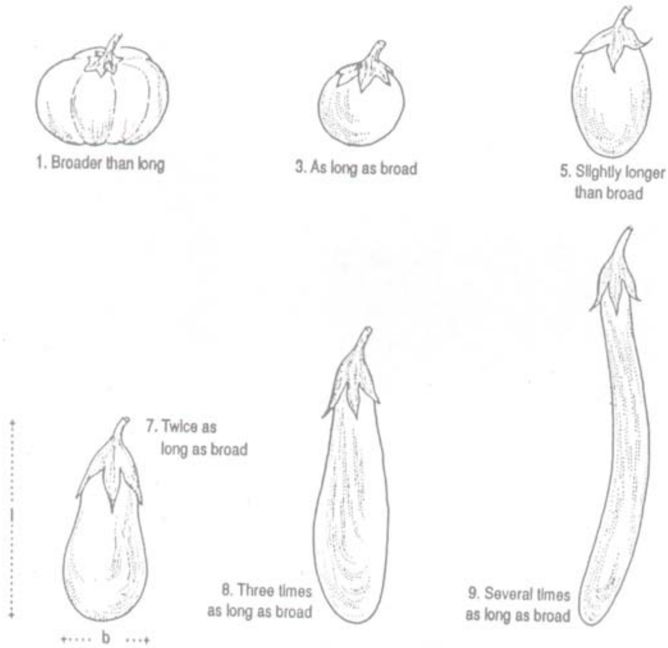
S520 Fruit breadth (cm) (diameter at broadest part)

1 = Very small (<1) 3 = Small (~2) 5 = Intermediate (~3)

7 = Large (~5) 9 = Very large (>10) X = Mixture

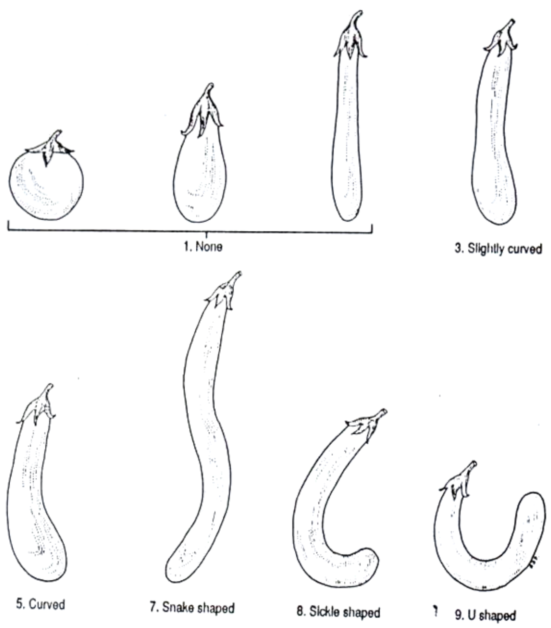
S530 Fruit length/breadth ratio

1 = Broader than long
3 = As long as broad
5 = Slightly longer than broad
7 = Twice as long as broad
8 = Three times as long as broad
9 = Several times as long as broad
X = Mixture



S540 Fruit curvature

1 = None
3 = Slightly curved
5 = Curved
7 = Snake shape
9 = U shaped
X = Mixture



S550 Fruit stalk length (mm)

1 = Very short (<5) 3 = Short (~10) 5 = Intermediate (~25)

7 = Long (~50) 9 = Very long (~75) X = Mixture

S560 Fruit stalk thickness (mm)

1 = Very thin (<1) 3 = Thin (~2) 5 = Intermediate (~3)

7 = Thick (~5) 9 = Very thick (>10) X = Mixture

S570 Fruit stalk prickles

0 = None 1 = Very few (<3) 3 = Few (~5)

5 = Intermediate (~10) 7 = Many (~20) 9 = Very many (>30)

X = Mixture

S580 Fruit shape

3 = About 1/4 way from base to tip

5 = About 1/2 way from base to tip

7 = About 3/4 way from base to tip

X = Mixture

S590 Fruit apex shape

3 = Protruded 5 = Rounded 7 = Depressed X = Mixture

S600 Fruit color at commercial ripeness

1 = Green 2 = Milk white 3 = Deep yellow

4 = Fire red 5 = Scarlet red 6 = Lilac gray

7 = Purple 8 = Purple black 9 = Black X = Mixture

S610 Fruit color distribution at commercial ripeness

1 = Uniform 3 = Mottled 5 = Netted

7 = Striped X = Mixture

S620 Fruit color at physiological ripeness

1 = Green 2 = Deep yellow 3 = Yellow orange

4 = Deep orange 5 = Fired red 6 = Poppy red

7 = Scarlet red 8 = Light brown 9 = Black

X = Mixture

S630 Fruit position

1 = Erect 3 = Semi-erect 5 = Horizontal

7 = Semi-pendant 9 = Pendant X = Mixture

S640 Fruit calyx length (N=10)

_____ _____ _____ _____ _____ _____ _____ _____ _____ _____

S650 Fruit calyx prickles (N=10)

0 = None　1 = Very few (<3)　3 = Few (~5)

5 = Intermediate (~10)　7 = Many (~20)　9 = Very many (>30)

X = Mixture

S660 Fruit cross section

1 = Circular, no grooves　3 = Elliptic, no grooves

5 = Few grooves (~4)　7 = Many grooves (~8)

9 = Very irregular　X = Mixture

S680 Number of locules per fruit (N=10)

_____ _____ _____ _____ _____ _____ _____ _____ _____ ____

S690 Fruit flesh density

1 = Very loose (spongy)　3 = Loose (crumbly)　5 = Average density

7 = Dense　9 = Very dense　X = Mixture

S700 Number of fruit per inflorescence

_____ _____ _____ _____ _____ _____ _____ _____ _____ _____

S710 Number of fruit per plant

_____ _____ _____ _____ _____ _____ _____ _____ _____ _____

S720 Fruit yield per plant (gm)

1 = Very low (<250)　3 = Low (~500)　5 = Intermediate (~1000)

7 = High (~2500)　9 = Very high (>5000)　X = Mixture

S730 Fruit flavor

3 = Bitter　5 = Intermediate　7 = Sweet　X = Mixture

S760 Varietal mixture condition

0 = Pure　3 = Slight mixture　5 = Medium mixture　7 = Serious mixture

S770 Flesh browning (after cutting)

1 = Immediate browning 0 ~ 1 minute　2 = > 1 ~ 3 minute

3 = > 3 ~ 5 minute　4 = > 5 ~ 7 minute

5 = > 7 ~ 9 minute　6 = > 9 ~ 12 minute

7 = > 12 ~ 15 minute　8 = > 15 ~ 20 minute

9 = > 20 ~ 30 minute　10 = > 30 minute

S900 Harvest procedure

1 = Bulk	2 = 2 sub-accessions	3 = 3 sub-accessions

SEED DATA

S810 Seed color

1 = White	2 = Light yellow	3 = Grey yellow
4 = Brownish yellow	5 = Brown	6 = Brown black
9 = Black	X = Mixture	

S820 Number of seeds per fruit

0 = None	1 = Very few (<10)	3 = Few (~50)
5 = Intermediate (~100)	7 = Many (~300)	
9 = Very many (>500)	X = Mixture	

S825 Seed density

3 = Scarce	5 = Intermediate	7 = Dense

S830 Seed Size (mm)

3 = Small (~2)	5 = Intermediate (~3)	7 = Large (~4)
X = Mixture		

S840 100 seeds weight (g)

Appendix Table A1 Characterization of 91 accessions of *Solanum* spp. based on quantitative data in the morphological analysis.

Temporary No.	Species	Identified	Germination period	Cotyledonous leaf length	Cotyledonous leaf length	Cotyledon leaf length/width ratio	Plant height	Plant breadth
TS00175	*S. melongena*	*S. melongena*	8	15.50	7.85	1.97	97.00	118.00
TS00176	*S. melongena*	*S. melongena*	5	23.95	8.60	2.78	68.50	83.00
TS00177	*S. melongena*	*S. melongena*	8	17.50	8.85	1.98	55.00	90.00
TS00178	*S. melongena*	*S. melongena*	5	21.30	10.30	2.07	74.50	89.00
TS00179-A	*S. melongena*	*S. melongena*	7	18.65	8.50	2.19	65.00	85.50
TS00179-B	*S. melongena*	*S. melongena*	7	18.05	9.00	2.01	61.50	98.00
TS00417	*S. aculeatissimum*	*S. aculeatissimum*	7	18.45	8.45	2.18	77.50	86.50
TS00418	*S. aculeatissimum*	*S. xanthocarpum*	7	19.00	7.40	2.57	81.50	75.50
TS00422-A	*S. aculeatissimum*	*S. xanthocarpum*	7	18.80	9.00	2.09	87.00	105.00
TS00422-B	*S. aculeatissimum*	*S. aculeatissimum*	7	18.80	9.00	2.09	77.50	98.00
TS00426	*S. stramonifilium*	*S. ferox*	8	11.10	6.30	1.76	70.00	78.50
TS00455	*S. parkinsonii*	*S. melongena*	5	19.60	8.90	2.20	76.50	86.50
TS00456	*S. parkinsonii*	*S. melongena*	5	21.75	9.55	2.28	66.50	77.50
TS00473	*S. parkinsonii*	*S. melongena*	5	20.65	8.10	2.55	68.50	91.00
TS00483	*S. aculeatissimum*	*S. xanthocarpum*	7	15.35	7.00	2.19	69.50	99.00
TS00487	*S. aculeatissimum*	*S. xanthocarpum*	7	16.20	6.90	2.35	78.50	105.00
TS00541	*S. stramonifilium*	*S. ferox*	9	7.90	5.85	1.35	83.00	87.00
TS00549	*S. linociera*	*S. melongena*	8	18.75	6.70	2.80	76.00	96.50
TS00551	*S. linociera*	*S. melongena*	8	17.30	8.35	2.07	71.00	96.50

Appendix Table A1 (Continued)

Temporary No.	Species	Identified	Germination period	Cotyledonous leaf length	Cotyledonous leaf length	Cotyledon leaf length/width ratio	Plant height	Plant breadth
TS00552	*S. linociera*	*S. melongena*	5	17.35	8.20	2.12	72.50	85.00
TS00553	*S. linociera*	*S. ferox*	8	9.50	6.30	1.51	122.00	90.50
TS00555	*S. linociera*	*S. melongena*	5	19.55	9.65	2.03	79.00	95.50
TS00563	*S. stramonifilium*	*S. ferox*	10	11.10	7.50	1.48	113.00	113.50
TS01321	*S. ferox*	*S. melongena*	5	24.85	9.50	2.62	94.50	96.00
TS01322	*S. melongena*	*S. melongena*	4	26.65	9.75	2.73	76.50	86.00
TS01447-A	*S. anguivi*	*S. viarum*	8	13.25	4.80	2.76	72.00	103.00
TS01447-B	*S. anguivi*	*S. indicum*	11	8.25	3.45	2.39	57.00	49.00
TS01947	*S. indicum*	*S. trilobatum*	8	19.15	6.80	2.82	191.50	193.50
TS01979	*S. stramonifilium*	*S. ferox*	9	10.20	6.45	1.58	63.00	97.50
TS01994	*S. linociera*	*S. melongena*	5	18.40	7.25	2.54	67.50	92.00
TS02062	*S. stramonifilium*	*S. ferox*	11	10.90	5.95	1.83	103.00	92.50
TS02216	*S. parkinsonii*	*S. melongena*	5	19.80	9.75	2.03	71.50	70.50
TS02217	*S. parkinsonii*	*S. melongena*	7	18.75	8.65	2.17	67.00	68.50
TS02218	*S. parkinsonii*	*S. melongena*	7	18.35	8.95	2.05	73.50	84.50
TS02245	*S. melongena*	*S. melongena*	13	10.40	5.00	2.08	49.00	81.00
TS02246	*S. melongena*	*S. melongena*	7	20.80	10.00	2.08	90.00	83.50
TS02247	*S. melongena*	*S. melongena*	5	22.20	9.15	2.43	59.50	54.00
TS02268	*S. undatum*	*S. melongena*	7	19.45	8.50	2.29	38.50	48.00
TS02273-A	*S. melongena*	*S. melongena*	7	14.55	8.70	1.67	30.00	41.00

Appendix Table A1 (Continued)

Temporary No.	Species	Identified	Germination period	Cotyledonous leaf length	Cotyledonous leaf length	Cotyledon leaf length/width ratio	Plant height	Plant breadth
TS02273-B	*S. melongena*	*S. melongena*	7	14.55	8.70	1.67	43.00	62.00
TS02435	*S. ferox*	*S. ferox*	8	8.30	5.30	1.57	92.50	94.50
TS02440	*S. seaforthianum*	*S. melongena*	8	11.50	7.50	1.53	72.50	82.00
TS02441-A	*S. seaforthianum*	*S. melongena*	5	17.15	8.70	1.97	44.00	57.00
TS02441-B	*S. seaforthianum*	*S. melongena*	5	17.15	8.70	1.97	39.00	42.00
TS02445	*S. trilobatum*	*S. trilobatum*	7	18.35	7.40	2.48	272.50	95.00
TS02491	*S. trilobatum*	*S. sanitwongsei*	7	17.20	8.25	2.08	63.00	61.00
TS02495	*S. trilobatum*	*S. indicum*	9	13.90	6.40	2.17	92.50	93.50
TS02728	*S. torvum*	*S. torvum*	13	7.95	4.00	1.99	237.50	136.50
TS02731	*S. torvum*	*S. torvum*	10	7.70	3.25	2.37	235.00	244.50
TS02739	*S. trilobatum*	*S. trilobatum*	7	17.80	6.60	2.70	204.50	90.50
TS02812	*S. melongena*	*S. melongena*	5	16.95	8.70	1.95	63.00	82.50
TS02813	*S. torvum*	*S. torvum*	16	7.60	2.90	2.62	237.50	242.50
TS02815	*S. torvum*	*S. melongena*	5	14.50	7.50	1.93	77.00	82.00
TS02816	*S. melongena*	*S. melongena*	7	12.25	7.40	1.66	70.50	94.00
TS02821	*S. melongena*	*S. melongena*	5	16.05	8.55	1.88	73.00	82.00
TS02822	*S. melongena*	*S. melongena*	8	14.30	7.85	1.82	80.00	112.00
TS02862	*S. torvum*	*S. torvum*	21	9.50	3.75	2.53	247.50	201.00
TS02877	*S. torvum*	*S. torvum*	14	13.60	6.20	2.19	210.00	310.00
TS02894	*S. mammosum*	*S. mammosum*	8	21.65	7.95	2.72	77.50	94.50

Appendix Table A1 (Continued)

Temporary No.	Species	Identified	Germination period	Cotyledonous leaf length	Cotyledonous leaf length	Cotyledon leaf length/width ratio	Plant height	Plant breadth
TS02901	*S. ferox*	*S. ferox*	9	10.30	5.45	1.89	100.50	102.00
TS02902	*S. ferox*	*S. ferox*	9	9.05	6.80	1.33	108.00	125.50
TS02903	*S. ferox*	*S. ferox*	11	10.10	5.65	1.79	114.50	109.50
TS02906	*S. indicum*	*S. torvum*	16	6.30	3.45	1.83	212.50	215.00
TS02937	*S. torvum*	*S. torvum*	14	6.00	2.75	2.18	210.00	135.00
TS02938	*S. torvum*	*S. torvum*	9	11.75	4.85	2.42	203.00	185.00
TS02939	*S. torvum*	*S. melongena*	5	22.20	8.20	2.71	80.00	80.50
TS02940	*S. torvum*	*S. torvum*	17	7.95	3.65	2.18	251.50	132.50
TS02945	*S. xanthocarpum*	*S. xanthocarpum*	7	16.65	7.95	2.09	72.50	94.50
TS02946	*S. xanthocarpum*	*S. melongena*	7	16.55	8.15	2.03	37.50	56.50
TS02950	*S. macrocapon*	*S. xanthocarpum*	9	15.90	7.70	2.06	79.00	123.00
TS02955	*S. torvum*	*S. torvum*	14	8.20	3.05	2.69	245.00	126.50
TS02965	*S. sisymbrifolium*	*S. indicum*	8	14.50	7.05	2.06	99.50	99.00
TS02967	*S. ferox*	*S. indicum*	7	15.70	6.40	2.45	92.50	89.50
TS02971	*S. ferox*	*S. ferox*	7	9.05	6.20	1.46	85.00	88.50
TS02973	*S. torvum*	*S. torvum*	7	8.00	3.25	2.46	250.00	112.50
TS02976	*S. sisymbrifolium*	*S. ferox*	8	8.35	6.35	1.31	106.00	113.00
TS02978	*S. ferox*	*S. ferox*	9	8.70	4.80	1.81	87.00	99.00
TS02989	*S. ferox*	*S. ferox*	8	10.30	5.75	1.79	91.00	95.00
TS02990	*S. sisymbrifolium*	*S. indicum*	7	16.40	7.95	2.06	101.50	89.50

Appendix Table A1 (Continued)

Temporary No.	Species	Identified	Germination period	Cotyledonous leaf length	Cotyledonous leaf length	Cotyledon leaf length/width ratio	Plant height	Plant breadth
TS02992	*S. sisymbrifolium*	*S. indicum*	7	16.35	7.60	2.15	111.50	90.50
TS03005	*S. sisymbrifolium*	*S. indicum*	7	16.70	7.55	2.21	93.00	95.00
TS03009	*S. ferox*	*S. ferox*	8	8.55	6.20	1.38	100.50	91.00
TS03012	*S. ferox*	*S. ferox*	8	8.65	6.30	1.37	137.50	100.50
TS03018	*S. sisymbrifolium*	*S. indicum*	7	16.65	7.15	2.33	107.50	89.50
TS03020	*S. ferox*	*S. ferox*	8	6.55	5.30	1.24	57.00	82.00
TS03029	*S. aethiopicum*	*S. aethiopicum*	7	19.50	8.80	2.22	103.50	95.00
TS03049	*S. melongena*	*S. melongena*	13	20.45	7.95	2.57	82.00	86.00
TS03052	*S. melongena*	*S. melongena*	13	18.65	8.30	2.25	74.50	86.50
TS03053	*S. melongena*	*S. melongena*	16	16.65	7.65	2.18	72.50	84.50

Appendix Table A1 (Continued)

Temporary No.	Plant branching	Petiole length	Leaf blade length	Leaf blade width	No. of flowers/inflorescence	Flowering time	Fruit length	Fruit breadth
TS00175	10.50	134.00	24.80	16.55	6.00	58	2.57	3.19
TS00176	10.50	105.00	20.80	15.00	4.50	61	2.67	2.32
TS00177	10.00	108.00	24.40	19.45	3.50	62	7.02	10.26
TS00178	8.50	136.00	28.20	21.10	3.00	62	6.13	8.91
TS00179-A	10.50	97.00	22.10	16.75	3.50	58	5.88	9.65
TS00179-B	10.00	12.35	21.60	15.75	4.50	48	5.31	7.98
TS00417	8.50	107.00	18.60	16.75	3.00	59	3.37	3.35
TS00418	8.00	101.00	20.40	15.10	3.00	61	2.56	2.53
TS00422-A	10.50	115.50	21.80	19.00	4.00	55	3.89	4.68
TS00422-B	8.50	145.00	23.90	20.60	6.00	55	3.48	3.80
TS00426	10.50	162.50	31.50	29.50	12.00	110	2.28	2.30
TS00455	11.00	113.50	22.50	16.20	2.50	61	3.61	4.99
TS00456	14.00	96.00	20.10	13.20	4.00	52	3.90	3.16
TS00473	12.50	96.50	23.10	16.90	6.00	62	2.95	4.22
TS00483	8.50	99.50	18.70	14.00	5.50	58	2.47	3.73
TS00487	9.00	107.00	19.40	14.55	7.00	62	2.58	2.83
TS00541	10.50	150.00	34.00	31.00	9.00	110	2.12	2.26
TS00549	9.00	112.00	26.00	21.20	5.50	67	2.59	3.01
TS00551	9.50	121.00	23.45	19.80	3.50	68	3.41	4.26

Appendix Table A1 (Continued)

Temporary No.	Plant branching	Petiole length	Leaf blade length	Leaf blade width	No. of flowers/inflorescence	Flowering time	Fruit length	Fruit breadth
TS00552	9.00	98.50	21.00	17.15	4.00	62	2.95	3.71
TS00553	12.00	183.50	33.85	34.75	8.50	123	2.09	2.49
TS00555	9.50	104.50	23.15	20.10	3.00	67	3.11	4.06
TS00563	9.50	220.00	32.00	31.15	7.50	107	2.61	2.18
TS01321	8.50	133.50	27.25	18.85	2.50	55	10.87	5.10
TS01322	10.50	111.50	27.95	19.90	5.00	48	14.75	6.09
TS01447-A	10.50	174.50	15.00	18.25	4.00	73	2.51	2.92
TS01447-B	12.00	79.00	13.70	14.10	9.00	91	0.94	0.96
TS01947	9.50	62.50	9.75	12.50	8.00	152	0.88	0.89
TS01979	12.00	164.00	34.00	33.15	10.00	107	2.26	2.31
TS01994	8.50	100.00	25.40	19.60	6.00	69	2.27	3.04
TS02062	11.50	188.50	30.90	36.50	11.50	118	2.36	2.41
TS02216	13.00	103.50	20.00	13.60	3.50	55	4.04	5.01
TS02217	12.00	106.50	22.80	17.55	3.50	62	4.59	5.64
TS02218	10.00	116.50	21.80	16.55	1.50	55	4.06	4.72
TS02245	8.00	172.00	33.80	25.40	3.00	81	32.50	4.61
TS02246	10.00	14.15	24.30	19.75	3.00	64	3.11	3.51
TS02247	10.00	126.00	21.55	17.25	5.00	61	22.50	5.26
TS02268	7.50	65.00	19.60	13.65	3.50	42	3.28	4.15

Appendix Table A1 (Continued)

Temporary No.	Plant branching	Petiole length	Leaf blade length	Leaf blade width	No. of flowers/inflorescence	Flowering time	Fruit length	Fruit breadth
TS02273-A	9.50	54.50	14.25	11.35	3.00	44	2.42	2.80
TS02273-B	9.00	46.00	18.25	15.30	2.50	54	2.11	2.28
TS02435	11.00	218.50	32.50	33.50	9.00	100	2.42	2.49
TS02440	7.50	117.50	19.00	15.50	6.50	59	2.36	3.03
TS02441-A	8.50	106.00	19.75	14.70	10.50	50	2.54	2.94
TS02441-B	9.50	94.00	17.85	13.20	6.00	55	3.06	3.24
TS02445	9.00	70.00	9.50	10.25	12.00	124	0.90	0.77
TS02491	11.00	118.50	16.45	16.65	5.50	65	9.85	10.20
TS02495	13.00	99.00	16.15	15.80	9.00	62	9.15	9.45
TS02728	15.50	187.50	40.50	37.00	94.00	166	1.32	1.33
TS02731	18.00	185.00	37.50	34.25	82.50	153	1.18	1.17
TS02739	9.00	70.50	10.00	10.50	20.00	103	1.21	1.05
TS02812	11.50	117.50	25.30	18.90	5.00	53	2.64	3.63
TS02813	17.50	202.50	38.00	37.00	73.50	160	1.17	1.25
TS02815	9.00	119.00	19.30	16.50	5.00	58	2.60	3.08
TS02816	10.50	132.50	22.70	16.55	4.50	51	2.58	3.09
TS02821	10.50	137.50	26.25	20.60	3.50	73	5.58	7.16
TS02822	7.50	152.50	25.00	18.50	5.00	58	2.64	3.44
TS02862	15.00	205.00	37.50	33.50	57.50	165	1.26	1.30

Appendix Table A1 (Continued)

Temporary No.	Plant branching	Petiole length	Leaf blade length	Leaf blade width	No. of flowers/inflorescence	Flowering time	Fruit length	Fruit breadth
TS02877	19.00	170.00	36.50	34.00	97.00	151	1.27	1.32
TS02894	7.50	225.50	26.60	28.40	5.50	69	6.56	4.73
TS02901	12.00	175.00	38.00	35.00	12.00	130	7.14	6.13
TS02902	10.50	235.00	38.50	35.50	6.00	112	2.34	2.53
TS02903	11.50	212.50	40.50	40.50	17.00	129	2.55	2.47
TS02906	19.00	200.00	40.00	33.50	71.00	165	1.19	1.33
TS02937	16.00	195.00	36.25	38.00	64.00	151	1.38	1.41
TS02938	16.00	227.50	39.75	40.50	290.00	151	1.43	1.42
TS02939	9.50	166.00	24.50	20.25	3.50	54	9.31	5.42
TS02940	13.00	180.00	34.50	32.50	63.00	166	1.40	1.35
TS02945	9.00	88.50	18.00	13.75	5.00	59	2.19	2.19
TS02946	9.50	67.50	14.80	12.85	3.00	52	2.48	2.52
TS02950	8.00	120.00	27.60	17.60	9.50	62	2.68	2.70
TS02955	14.00	155.00	37.25	34.50	89.00	168	1.32	1.30
TS02965	13.00	142.50	22.10	23.00	10.50	78	0.94	1.03
TS02967	13.00	129.00	18.80	18.20	9.50	82	0.89	1.02
TS02971	8.00	205.00	31.75	32.50	14.50	103	1.62	1.74
TS02973	16.00	227.50	38.00	37.50	103.00	160	1.24	1.22
TS02976	11.50	160.00	34.00	31.50	11.00	114	1.74	1.83

Appendix Table A1 (Continued)

Temporary No.	Plant branching	Petiole length	Leaf blade length	Leaf blade width	No. of flowers/inflorescence	Flowering time	Fruit length	Fruit breadth
TS02978	11.00	210.00	34.75	35.25	8.50	110	2.29	2.37
TS02989	10.50	185.00	33.50	35.00	9.00	100	2.20	2.11
TS02990	12.00	119.50	18.35	17.95	11.00	67	0.96	1.01
TS02992	12.00	128.50	18.45	18.60	10.00	62	0.96	0.99
TS03005	11.50	103.00	16.80	15.00	8.00	62	1.05	0.97
TS03009	8.50	175.00	30.00	30.50	10.00	100	2.23	2.35
TS03012	14.00	205.00	34.75	34.00	16.00	112	1.98	2.18
TS03018	12.50	128.00	17.75	14.85	8.00	66	1.13	1.10
TS03020	9.00	145.00	28.50	28.50	9.00	105	1.88	1.93
TS03029	6.00	109.50	34.50	24.65	2.00	55	2.05	4.49
TS03049	11.00	153.00	28.25	26.70	5.00	59	16.50	7.32
TS03052	10.50	153.00	28.75	19.10	4.50	58	32.00	6.08
TS03053	11.00	105.50	17.85	13.00	1.50	61	24.55	30.35

Appendix Table A1 (Continued)

Temporary No.	Fruit stalk length	Fruit stalk thickness	Fruit calyx length	No. of fruits/infructescence	100 seeds weight
TS00175	33.95	5.05	12.05	1.00	0.30
TS00176	31.50	3.90	11.30	1.00	0.35
TS00177	23.55	14.90	39.35	1.00	0.48
TS00178	33.90	10.15	36.80	1.00	0.40
TS00179-A	24.50	12.30	30.30	1.00	0.40
TS00179-B	33.20	10.30	25.40	1.00	0.37
TS00417	22.75	8.45	15.00	1.00	0.31
TS00418	31.55	3.80	13.70	1.00	0.31
TS00422-A	42.45	6.65	20.20	1.00	0.36
TS00422-B	27.35	5.95	14.80	1.00	0.34
TS00426	14.95	3.15	9.55	1.00	0.17
TS00455	25.40	5.15	18.50	1.00	0.36
TS00456	26.40	7.90	10.35	1.00	0.33
TS00473	28.55	5.30	22.40	1.00	0.37
TS00483	21.45	5.45	15.25	1.00	0.31
TS00487	27.20	6.30	17.35	1.00	0.30
TS00541	12.95	2.60	6.90	2.00	0.15
TS00549	37.20	5.00	10.95	1.00	0.34
TS00551	13.00	5.50	13.95	1.00	0.34
TS00552	26.95	7.75	17.75	1.00	0.24

Appendix Table A1 (Continued)

Temporary No.	Fruit stalk length	Fruit stalk thickness	Fruit calyx length	No. of fruits/infructescence	100 seeds weight
TS00553	12.90	2.10	9.25	1.00	0.16
TS00555	4.18	5.00	19.45	1.00	0.40
TS00563	8.00	4.90	6.60	1.50	0.18
TS01321	21.70	7.90	32.10	1.50	0.41
TS01322	33.95	7.20	23.85	1.00	0.51
TS01447-A	20.45	3.35	5.00	1.00	0.31
TS01447-B	18.10	2.45	5.95	2.50	0.26
TS01947	21.70	1.95	2.25	7.00	0.33
TS01979	12.40	3.85	7.30	1.50	0.19
TS01994	26.55	5.75	13.20	1.00	0.24
TS02062	12.00	4.15	9.30	1.00	0.18
TS02216	25.65	7.25	20.50	1.00	0.36
TS02217	18.05	8.15	16.95	1.00	0.33
TS02218	40.70	7.45	18.70	1.00	0.33
TS02245	28.40	9.35	27.75	1.00	0.51
TS02246	41.30	7.40	26.80	1.00	0.36
TS02247	23.90	10.40	27.30	1.00	0.40
TS02268	28.55	5.65	16.45	2.50	0.32
TS02273-A	24.75	6.05	19.00	2.00	0.35
TS02273-B	27.90	3.60	12.50	1.00	0.33

Appendix Table A1 (Continued)

Temporary No.	Fruit stalk length	Fruit stalk thickness	Fruit calyx length	No. of fruits/infructescence	100 seeds weight
TS02435	16.95	3.30	9.55	1.00	0.15
TS02440	39.30	5.95	17.65	1.00	0.24
TS02441-A	29.40	4.00	13.60	1.00	0.28
TS02441-B	38.45	4.90	13.95	1.00	0.26
TS02445	23.90	1.15	2.45	1.50	0.42
TS02491	28.10	4.20	5.75	1.00	0.27
TS02495	19.15	4.40	5.10	1.50	0.24
TS02728	15.25	3.55	6.45	9.00	0.13
TS02731	15.55	3.30	4.95	5.50	0.11
TS02739	30.45	2.90	4.05	3.50	0.35
TS02812	35.35	4.05	17.00	1.00	0.26
TS02813	16.50	3.00	4.45	4.50	0.11
TS02815	26.70	3.85	15.90	1.00	0.30
TS02816	34.85	5.45	13.45	1.50	0.30
TS02821	42.95	14.60	35.55	1.00	0.31
TS02822	37.65	7.30	22.00	1.00	0.37
TS02862	15.55	3.60	5.05	3.50	0.10
TS02877	18.10	4.00	5.40	7.00	0.12
TS02894	4.55	4.55	9.45	1.00	0.96
TS02901	20.85	4.05	11.05	1.00	0.19

Appendix Table A1 (Continued)

Temporary No.	Fruit stalk length	Fruit stalk thickness	Fruit calyx length	No. of fruits/infructescence	100 seeds weight
TS02902	16.65	4.00	7.85	1.00	0.15
TS02903	12.90	4.00	6.75	1.00	0.14
TS02906	18.60	2.75	3.55	3.00	0.12
TS02937	16.60	3.45	5.55	1.50	0.12
TS02938	18.30	3.30	6.05	7.00	0.12
TS02939	11.95	10.50	27.50	1.00	0.46
TS02940	18.50	2.95	4.70	6.50	0.12
TS02945	24.30	3.95	9.75	1.00	0.28
TS02946	14.05	4.45	11.80	1.00	0.30
TS02950	35.75	3.80	15.30	1.00	0.27
TS02955	17.40	3.00	4.50	8.00	0.12
TS02965	25.30	2.35	6.05	2.50	0.28
TS02967	24.05	2.55	6.05	2.00	0.31
TS02971	13.90	3.15	10.30	2.00	0.12
TS02973	16.70	3.30	4.85	3.50	0.11
TS02976	12.70	2.00	7.25	1.00	0.16
TS02978	13.70	3.55	9.20	2.00	0.17
TS02989	15.55	3.00	8.60	2.00	0.17
TS02990	21.55	3.40	6.30	4.00	0.27
TS02992	26.20	3.20	4.80	3.00	0.27

Appendix Table A1 (Continued)

Temporary No.	Fruit stalk length	Fruit stalk thickness	Fruit calyx length	No. of fruits/infructescence	100 seeds weight
TS03005	25.10	3.30	5.90	4.50	0.32
TS03009	14.95	3.70	9.35	1.50	0.18
TS03012	11.35	2.50	9.35	1.00	0.17
TS03018	17.45	3.85	4.95	3.00	0.29
TS03020	10.70	2.10	9.10	1.50	0.16
TS03029	16.95	6.05	12.80	1.50	0.39
TS03049	31.15	12.50	27.75	1.00	0.52
TS03052	65.35	11.75	47.40	1.00	0.48
TS03053	32.15	6.85	18.85	1.00	0.20

Appendix Table A2 Characterization of 91 accessions of *Solanum* spp. based on qualitative data in the morphological analysis.

Temporary No.	Plant growth habit	Leaf blade lobbing	Leaf blade angle	Relative style length	Style exertion	Fruit length/ breadth ratio	Fruit color at commercial ripeness
TS00175	intermediate	intermediate	intermediate	intermediate	insert	as long as broad	intermediate
TS00176	intermediate	intermediate	intermediate	long	intermediate	as long as broad	green
TS00177	intermediate	intermediate	intermediate	long	exert	broader than long	green
TS00178	intermediate	intermediate	intermediate	long	intermediate	broader than long	purple
TS00179-A	intermediate	intermediate	intermediate	long	intermediate	broader than long	green
TS00179-B	intermediate	intermediate	intermediate	long	exert	broader than long	green
TS00417	intermediate	intermediate	intermediate	long	exert	as long as broad	milk white
TS00418	intermediate	intermediate	intermediate	long	exert	as long as broad	green
TS00422-A	intermediate	intermediate	obtuse	long	exert	broader than long	green
TS00422-B	intermediate	intermediate	intermediate	long	intermediate	broader than long	green
TS00426	intermediate	strong	very acute	long	exert	as long as broad	green
TS00455	intermediate	intermediate	intermediate	long	exert	broader than long	milk white
TS00456	intermediate	weak	intermediate	long	exert	slightly longer than broad	milk white
TS00473	intermediate	weak	very acute	long	exert	broader than long	green
TS00483	intermediate	intermediate	intermediate	long	intermediate	broader than long	green
TS00487	intermediate	intermediate	intermediate	long	exert	as long as broad	green
TS00541	intermediate	strong	very acute	long	exert	as long as broad	green
TS00549	intermediate	intermediate	obtuse	long	insert	broader than long	green
TS00551	intermediate	intermediate	intermediate	long	exert	broader than long	milk white

Appendix Table A2 (Continued)

Temporary No.	Plant growth habit	Leaf blade lobbing	Leaf blade angle	Relative style length	Style exertion	Fruit length/ breadth ratio	Fruit color at commercial ripeness
TS00552	intermediate	intermediate	obtuse	long	intermediate	broader than long	milk white
TS00553	intermediate	strong	very acute	long	exert	as long as broad	green
TS00555	intermediate	intermediate	intermediate	long	intermediate	broader than long	milk white
TS00563	intermediate	strong	very acute	long	exert	as long as broad	green
TS01321	intermediate	intermediate	intermediate	long	exert	mixture	mixture
TS01322	intermediate	intermediate	intermediate	long	exert	twice as long as broad	purple
TS01447-A	intermediate	strong	very acute	long	exert	broader than long	green
TS01447-B	intermediate	strong	intermediate	long	exert	broader than long	deep yellow
TS01947	prostrate	strong	intermediate	long	exert	as long as broad	fire red
TS01979	intermediate	strong	very acute	long	exert	as long as broad	green
TS01994	intermediate	intermediate	obtuse	long	intermediate	broader than long	green
TS02062	intermediate	strong	very acute	long	exert	as long as broad	green
TS02216	intermediate	weak	very acute	long	exert	broader than long	milk white
TS02217	intermediate	weak	very acute	long	exert	broader than long	green
TS02218	intermediate	intermediate	obtuse	long	exert	as long as broad	milk white
TS02245	intermediate	intermediate	very acute	long	exert	slightly longer than broad	purple
TS02246	intermediate	intermediate	intermediate	long	exert	broader than long	purple
TS02247	intermediate	weak	obtuse	long	exert	several times as long as broad	milk white
TS02268	intermediate	weak	intermediate	long	intermediate	broader than long	green
TS02273-A	intermediate	weak	obtuse	long	exert	broader than long	green

Appendix Table A2 (Continued)

Temporary No.	Plant growth habit	Leaf blade lobbing	Leaf blade angle	Relative style length	Style exertion	Fruit length/ breadth ratio	Fruit color at commercial ripeness
TS02273-B	intermediate	weak	intermediate	long	intermediate	broader than long	milk white
TS02435	intermediate	strong	very acute	long	exert	as long as broad	green
TS02440	intermediate	intermediate	intermediate	long	insert	broader than long	green
TS02441-A	intermediate	intermediate	obtuse	long	exert	broader than long	green
TS02441-B	intermediate	intermediate	intermediate	long	exert	broader than long	green
TS02445	prostrate	intermediate	intermediate	long	exert	as long as broad	green
TS02491	upright	strong	obtuse	long	exert	broader than long	deep yellow
TS02495	upright	very strong	very acute	long	exert	broader than long	deep yellow
TS02728	intermediate	very strong	intermediate	long	exert	as long as broad	green
TS02731	intermediate	very strong	intermediate	long	exert	as long as broad	green
TS02739	prostrate	intermediate	intermediate	long	exert	as long as broad	green
TS02812	intermediate	intermediate	intermediate	long	exert	broader than long	purple
TS02813	intermediate	very strong	intermediate	long	exert	as long as broad	green
TS02815	intermediate	intermediate	intermediate	long	exert	broader than long	purple
TS02816	intermediate	intermediate	intermediate	long	exert	broader than long	milk white
TS02821	intermediate	intermediate	intermediate	long	exert	broader than long	purple
TS02822	intermediate	intermediate	intermediate	long	intermediate	broader than long	purple
TS02862	intermediate	very strong	intermediate	long	exert	as long as broad	green
TS02877	intermediate	very strong	intermediate	long	exert	as long as broad	green
TS02894	upright	strong	very acute	long	intermediate	slightly longer than broad	deep yellow

Appendix Table A2 (Continued)

Temporary No.	Plant growth habit	Leaf blade lobbing	Leaf blade angle	Relative style length	Style exertion	Fruit length/ breadth ratio	Fruit color at commercial ripeness
TS02901	intermediate	strong	very acute	long	exert	as long as broad	green
TS02902	intermediate	strong	very acute	long	exert	as long as broad	green
TS02903	intermediate	strong	very acute	long	exert	as long as broad	green
TS02906	intermediate	strong	intermediate	long	exert	as long as broad	green
TS02937	intermediate	very strong	intermediate	long	exert	as long as broad	green
TS02938	intermediate	very strong	intermediate	long	exert	as long as broad	green
TS02939	intermediate	weak	intermediate	long	insert	slightly longer than broad	green
TS02940	intermediate	very strong	intermediate	long	exert	as long as broad	green
TS02945	intermediate	intermediate	intermediate	long	exert	as long as broad	green
TS02946	intermediate	intermediate	obtuse	long	intermediate	as long as broad	green
TS02950	intermediate	weak	intermediate	long	exert	as long as broad	green
TS02955	intermediate	very strong	intermediate	long	exert	as long as broad	green
TS02965	intermediate	very strong	obtuse	long	exert	broader than long	deep yellow
TS02967	intermediate	very strong	obtuse	long	exert	as long as broad	deep yellow
TS02971	intermediate	strong	very acute	long	exert	as long as broad	green
TS02973	intermediate	strong	intermediate	long	exert	as long as broad	green
TS02976	intermediate	strong	very acute	long	exert	as long as broad	green
TS02978	intermediate	strong	very acute	long	exert	slightly longer than broad	green
TS02989	intermediate	strong	very acute	long	exert	as long as broad	green
TS02990	intermediate	very strong	intermediate	long	exert	broader than long	deep yellow

Appendix Table A2 (Continued)

Temporary No.	Plant growth habit	Leaf blade lobbing	Leaf blade angle	Relative style length	Style exertion	Fruit length/ breadth ratio	Fruit color at commercial ripeness
TS02992	intermediate	very strong	intermediate	long	exert	broader than long	green
TS03005	intermediate	very strong	intermediate	long	exert	broader than long	deep yellow
TS03009	intermediate	strong	very acute	long	exert	as long as broad	green
TS03012	intermediate	strong	very acute	long	exert	as long as broad	green
TS03018	intermediate	very strong	intermediate	long	exert	broader than long	deep yellow
TS03020	intermediate	strong	very acute	long	exert	as long as broad	green
TS03029	upright	intermediate	intermediate	long	exert	broader than long	scarlet red
TS03049	intermediate	intermediate	intermediate	long	exert	slightly longer than broad	purple
TS03052	intermediate	intermediate	intermediate	long	exert	slightly longer than broad	purple
TS03053	intermediate	intermediate	obtuse	long	intermediate	broader than long	green

Appendix Table A2 (Continued)

Temporary No.	Fruit color at physiological ripeness	Fruit fresh density	Fruit yield per plant	Seed color
TS00175	deep yellow	average density	low	brownish yellow
TS00176	yellow orange	loose	low	grey yellow
TS00177	deep yellow	very dense	intermediate	brownish yellow
TS00178	yellow orange	dense	intermediate	brownish yellow
TS00179-A	yellow orange	very dense	high	brownish yellow
TS00179-B	deep yellow	dense	very high	brownish yellow
TS00417	deep yellow	average density	low	brownish yellow
TS00418	deep yellow	average density	low	brownish yellow
TS00422-A	deep yellow	dense	high	brownish yellow
TS00422-B	deep yellow	average density	high	brownish yellow
TS00426	yellow orange	average density	low	light yellow
TS00455	deep yellow	dense	high	brownish yellow
TS00456	deep yellow	average density	intermediate	brownish yellow
TS00473	deep yellow	dense	intermediate	grey yellow
TS00483	deep yellow	average density	low	brownish yellow
TS00487	deep yellow	loose	low	brownish yellow
TS00541	yellow orange	loose	low	light yellow
TS00549	deep yellow	dense	intermediate	brownish yellow
TS00551	deep yellow	dense	low	brownish yellow
TS00552	deep yellow	dense	low	brownish yellow
TS00553	yellow orange	average density	low	light yellow

Appendix Table A2 (Continued)

Temporary No.	Fruit color at physiological ripeness	Fruit fresh density	Fruit yield per plant	Seed color
TS00555	deep yellow	average density	low	brownish yellow
TS00563	yellow orange	average density	low	light yellow
TS01321	deep yellow	mixture	high	brownish yellow
TS01322	deep yellow	very loose	very high	brownish yellow
TS01447-A	deep yellow	very loose	intermediate	brown black
TS01447-B	yellow orange	loose	low	light yellow
TS01947	fires red	loose	low	light yellow
TS01979	yellow orange	loose	low	light yellow
TS01994	deep yellow	dense	low	brownish yellow
TS02062	yellow orange	average density	low	light yellow
TS02216	deep yellow	dense	low	grey yellow
TS02217	deep yellow	average density	low	grey yellow
TS02218	deep yellow	average density	high	brownish yellow
TS02245	deep yellow	very loose	intermediate	brown
TS02246	yellow orange	average density	intermediate	grey yellow
TS02247	deep yellow	very loose	high	brownish yellow
TS02268	deep yellow	very dense	very high	brownish yellow
TS02273-A	deep yellow	dense	high	grey yellow
TS02273-B	deep yellow	dense	low	grey yellow
TS02435	yellow orange	average density	very low	light yellow
TS02440	deep yellow	average density	low	grey yellow

Appendix Table A2 (Continued)

Temporary No.	Fruit color at physiological ripeness	Fruit fresh density	Fruit yield per plant	Seed color
TS02441-A	deep yellow	average density	low	grey yellow
TS02441-B	deep yellow	average density	low	brownish yellow
TS02445	scarlet red	very loose	low	grey yellow
TS02491	deep orange	loose	very low	light yellow
TS02495	deep orange	loose	very low	light yellow
TS02728	deep yellow	loose	low	grey yellow
TS02731	deep yellow	loose	low	grey yellow
TS02739	scarlet red	very loose	intermediate	grey yellow
TS02812	deep yellow	dense	low	grey yellow
TS02813	deep yellow	loose	low	grey yellow
TS02815	deep yellow	loose	low	brownish yellow
TS02816	deep yellow	dense	low	grey yellow
TS02821	deep yellow	very dense	low	grey yellow
TS02822	deep yellow	very dense	low	grey yellow
TS02862	deep yellow	loose	low	light yellow
TS02877	deep yellow	loose	low	light yellow
TS02894	yellow orange	very loose	low	black
TS02901	yellow orange	loose	low	light yellow
TS02902	yellow orange	loose	low	grey yellow
TS02903	yellow orange	average density	low	grey yellow
TS02906	deep yellow	loose	low	grey yellow

Appendix Table A2 (Continued)

Temporary No.	Fruit color at physiological ripeness	Fruit fresh density	Fruit yield per plant	Seed color
TS02937	deep yellow	loose	low	light yellow
TS02938	deep yellow	loose	low	light yellow
TS02939	deep yellow	average density	very high	brownish yellow
TS02940	deep yellow	loose	low	light yellow
TS02945	deep yellow	average density	low	brownish yellow
TS02946	deep yellow	average density	very high	light yellow
TS02950	deep yellow	loose	high	brownish yellow
TS02955	deep yellow	loose	low	light yellow
TS02965	deep orange	loose	low	light yellow
TS02967	deep orange	very loose	low	light yellow
TS02971	yellow orange	loose	low	light yellow
TS02973	deep yellow	loose	low	light yellow
TS02976	yellow orange	average density	low	light yellow
TS02978	yellow orange	loose	low	light yellow
TS02989	yellow orange	loose	intermediate	light yellow
TS02990	deep orange	loose	low	light yellow
TS02992	deep orange	loose	low	light yellow
TS03005	deep orange	loose	low	light yellow
TS03009	yellow orange	loose	low	light yellow
TS03012	yellow orange	average density	low	light yellow
TS0301	deep orange	loose	low	light yellow

Appendix Table A2 (Continued)

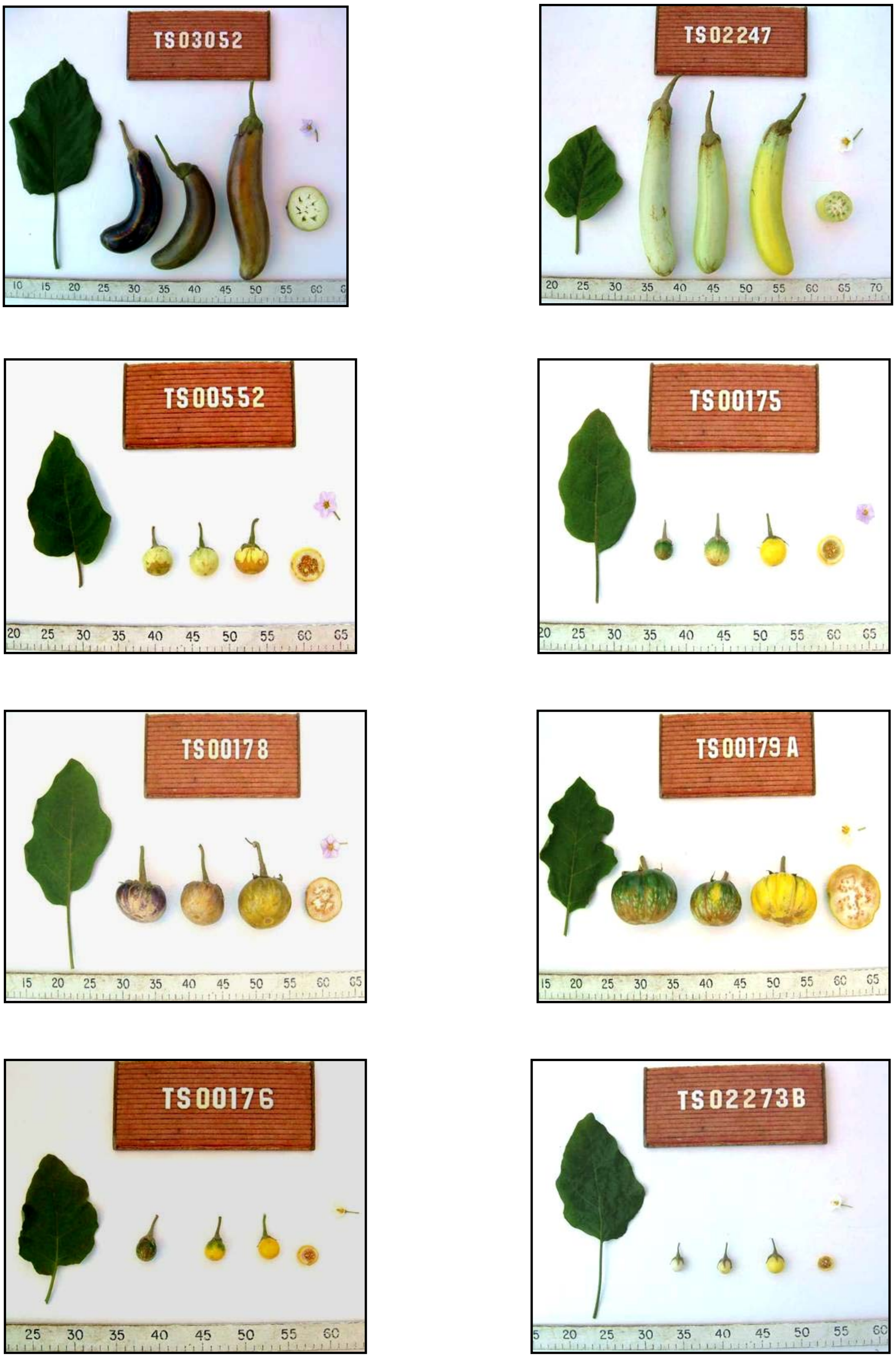
Temporary No.	Fruit color at physiological ripeness	Fruit fresh density	Fruit yield per plant	Seed color
TS03020	yellow orange	loose	low	light yellow
TS03029	scarlet red	loose	very low	light yellow
TS03049	deep yellow	very loose	intermediate	brownish yellow
TS03052	deep yellow	very loose	very high	grey yellow
TS03053	deep yellow	average density	low	light yellow

Appendix Table A3 Identification of 11 accessions of *Solanum* spp.

Identified	Accessions	Country of origin	Remark
Solanum spp.	TS00513	Thailand	not germinated
	TS00540	Thailand	not germinated
	TS00550	Thailand	not germinated
	TS00554	Thailand	not germinated
	TS02818	Laos	not germinated
	TS02843	Laos	not germinated
	TS02941	Malaysia	not germinated
	TS03050	Cambodia	not germinated
	TS03051	Cambodia	not germinated
Lycopersicon sp.	TS00491	Vietnam	
Capsicum sp.	TS02271	Thailand	

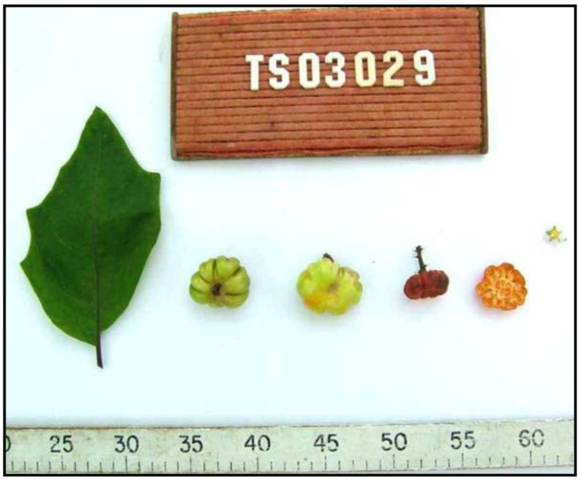
Appendix Table A4 List of morphological characters used for the cluster analysis of 91 accessions belonging to *Solanum* spp.

Characters	Descriptor	Characteristic code
	Ratio scale traits	
Characters	Descriptor	Characteristic code
Seedling	Germination period (day)	S110
	Cotyledonous leaf length (mm)	S120
	Cotyledonous leaf width (mm)	S130
	Cotyledon leaf length/width ratio	S150
Vegetative	Plant height (cm)	S220
	Plant breadth (cm)	S230
	Plant branching	S240
	Petiole length (mm)	S260
	Leaf blade length (cm)	S270
	Leaf blade width (cm)	S280
Inflorescence	Number of flowers per inflorescence (flower)	S410
	Flowering time (day)	S420
Fruit	Fruit length (cm)	S510
	Fruit breadth (cm)	S520
	Fruit stalk length (mm)	S550
	Fruit stalk thickness (mm)	S560
	Fruit calyx length	S640
	Number of fruits per infructescence (fruit)	S700
Seed	100 seeds weight (g)	S840
	Nominal traits	
Characters	Descriptor	Characteristic code
Vegetative	Plant growth habit	S210
	Leaf blade lobbing	S290
	Leaf blade tip angle	S300
Inflorescence	Relative style length (mm)	S450
	Style Exertion	S470
	Fruit length/breadth ratio	S530
	Fruit color at commercial ripeness	S600
	Fruit color at physiological ripeness	S620
	Fruit flesh density	S690
	Fruit yield per plant (g)	S720
Seed	Seed color	S810

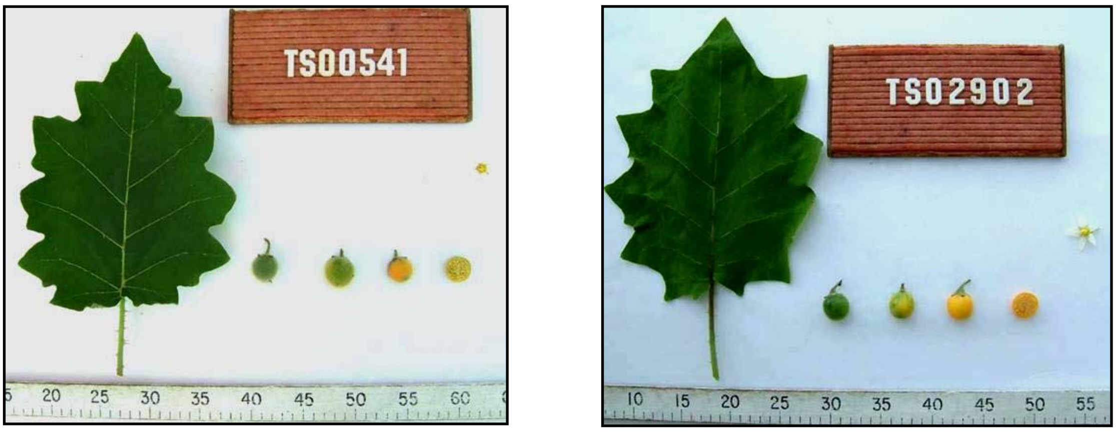


Appendix Figure A1 Morphological characters of *Solanum melongena*.

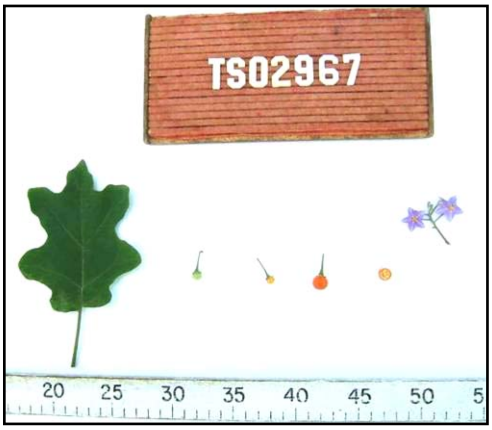
Appendix Figure A2 Morphological characters of *Solanum aculeatissimum*.

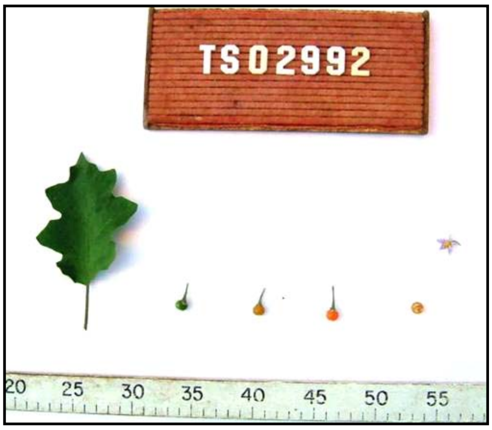


Appendix Figure A3 Morphological characters of *Solanum aethiopicum*.

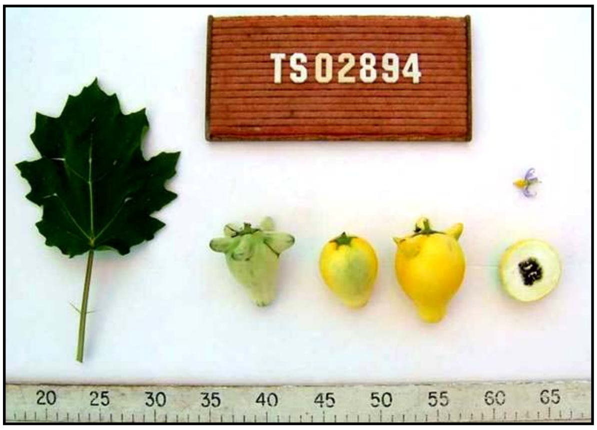


Appendix Figure A4 Morphological characters of *Solanum ferox*.

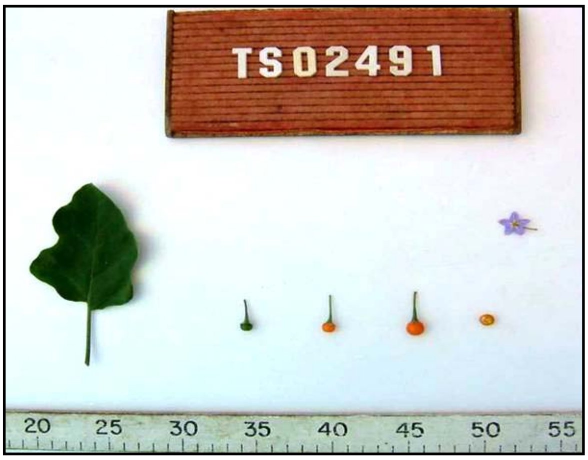




Appendix Figure A5 Morphological characters of *Solanum indicum*.

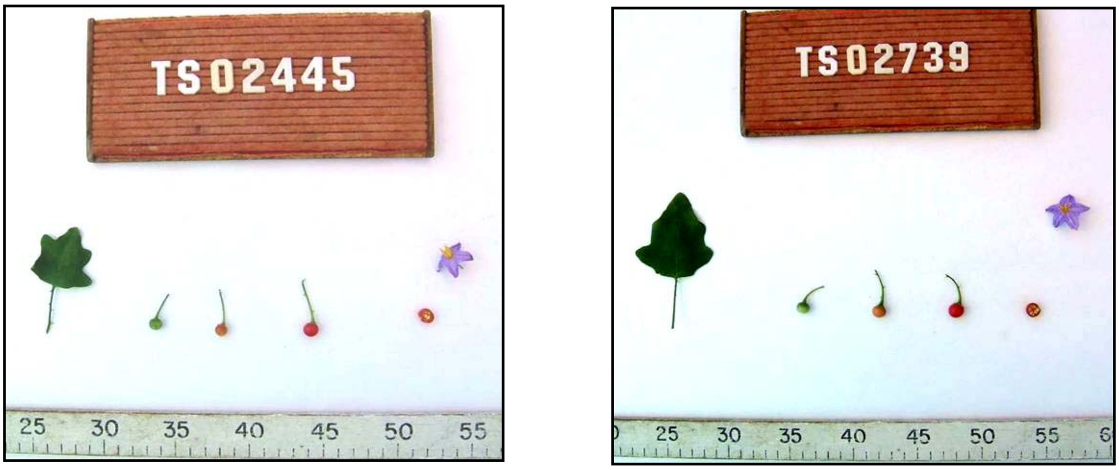


Appendix Figure A6 Morphological characters of *Solanum mammosum*.



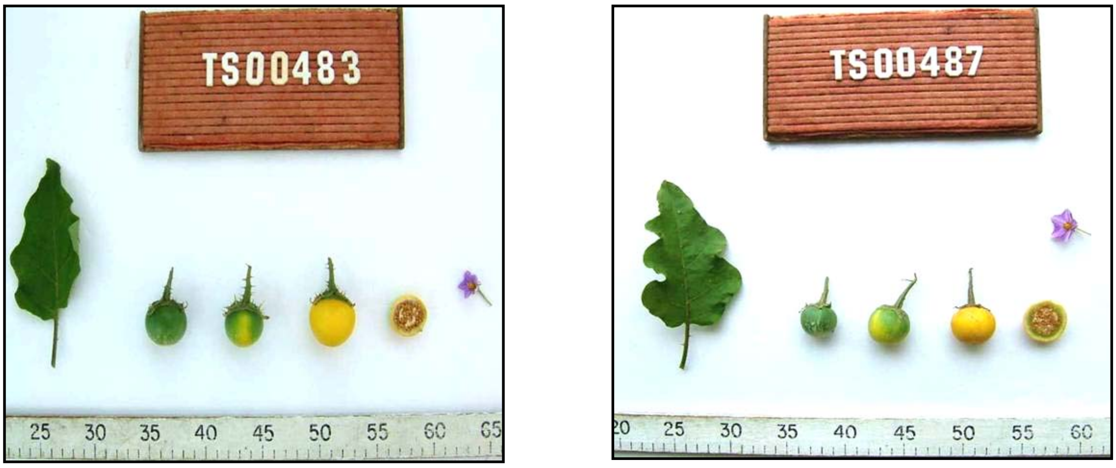
Appendix Figure A7 Morphological characters of *Solanum sanitwongsei*.

Appendix Figure A8 Morphological characters of *Solanum torvum*.



Appendix Figure A9 Morphological characters of *Solanum trilobatum*.

Appendix Figure A10 Morphological characters of *Solanum viarum*.



Appendix Figure A11 Morphological characters of *Solanum xanthocarpum*.

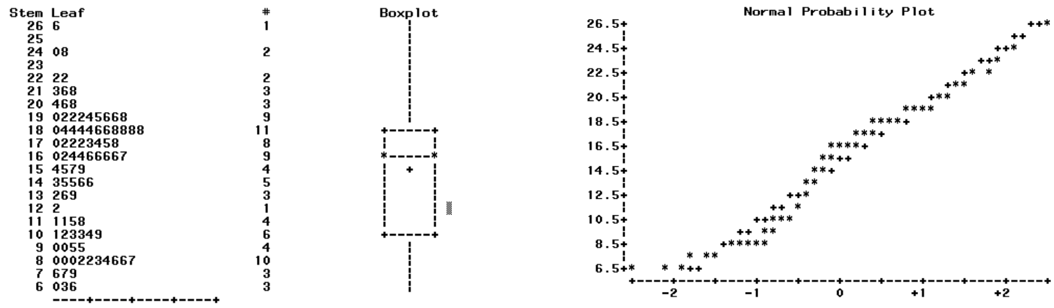
Appendix B

Identification of species outliers of quantitative traits

Moment			
N	91	Sum Weights	91
Mean	15.0456044	Sum Observations	1369.15
Std Deviation	4.9271394	Variance	24.2767027
Skewness	-0.1208002	Kurtosis	-0.9236123
Uncorrected SS	22784.5925	Corrected SS	2184.90324
Coeff Variation	32.7480324	Std Error Mean	0.51650455
Median	16.35000	Range	20.65000
Mode	16.65000	Interquartile Range	8.45000
Student's t	29.12966	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.952218	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
6.00	1	1.1	1.1	12.25	1	1.1	34.1	18.05	1	1.1	67.0
6.30	1	1.1	2.2	13.25	1	1.1	35.2	18.35	2	2.2	69.2
6.55	1	1.1	3.3	13.60	1	1.1	36.3	18.40	1	1.1	70.3
7.60	1	1.1	4.4	13.90	1	1.1	37.4	18.45	1	1.1	71.4
7.70	1	1.1	5.5	14.30	1	1.1	38.5	18.65	2	2.2	73.6
7.90	1	1.1	6.6	14.50	2	2.2	40.7	18.75	2	2.2	75.8
7.95	2	2.2	8.8	14.55	2	2.2	42.9	18.80	2	2.2	78.0
8.00	1	1.1	9.9	15.35	1	1.1	44.0	19.00	1	1.1	79.1
8.20	1	1.1	11.0	15.50	1	1.1	45.1	19.15	1	1.1	80.2
8.25	1	1.1	12.1	15.70	1	1.1	46.2	19.25	2	2.2	82.4
8.30	1	1.1	13.2	15.90	1	1.1	47.3	19.45	1	1.1	83.5
8.35	1	1.1	14.3	16.05	1	1.1	48.4	19.50	1	1.1	84.6
8.55	1	1.1	15.4	16.20	1	1.1	49.5	19.55	1	1.1	85.7
8.65	1	1.1	16.5	16.35	1	1.1	50.5	19.60	1	1.1	86.8
8.70	1	1.1	17.6	16.40	1	1.1	51.6	19.80	1	1.1	87.9
9.05	2	2.2	19.8	16.55	1	1.1	52.7	20.45	1	1.1	89.0
9.50	2	2.2	22.0	16.65	3	3.3	56.0	20.65	1	1.1	90.1
10.10	1	1.1	23.1	16.70	1	1.1	57.1	20.80	1	1.1	91.2
10.20	1	1.1	24.2	16.95	1	1.1	58.2	21.30	1	1.1	92.3
10.30	2	2.2	26.4	17.15	2	2.2	60.4	21.65	1	1.1	93.4
10.40	1	1.1	27.5	17.20	1	1.1	61.5	21.75	1	1.1	94.5
10.90	1	1.1	28.6	17.30	1	1.1	62.6	22.20	2	2.2	96.7
11.10	2	2.2	30.8	17.35	1	1.1	63.7	23.95	1	1.1	97.8
11.50	1	1.1	31.9	17.50	1	1.1	64.8	24.85	1	1.1	98.9
11.75	1	1.1	33.0	17.80	1	1.1	65.9	26.65	1	1.1	100.0



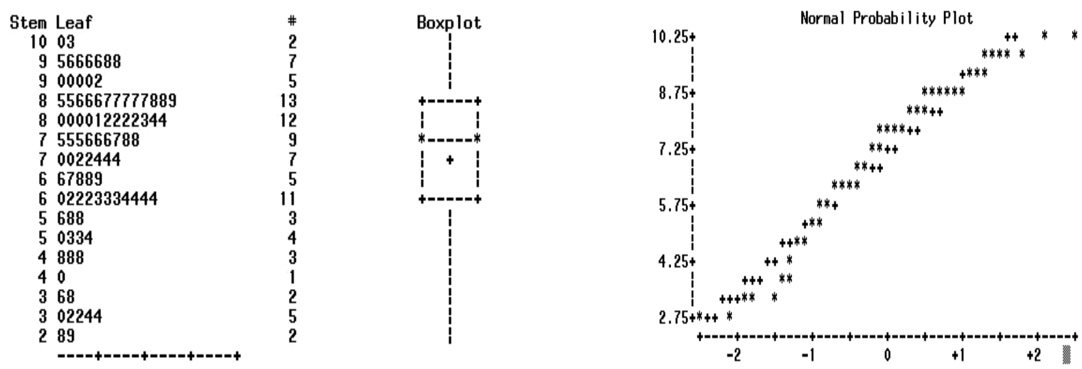
Appendix Figure B1 Selected items from PROC UNIVARIATE output for cotyledonous leaf length with the analysis of the *Solanum* spp. dataset.

Moments

N	91	Sum Weights	91
Mean	7.16373626	Sum Observations	651.9
Std Deviation	1.87320382	Variance	3.50889255
Skewness	-0.6972857	Kurtosis	-0.2399741
Uncorrected SS	4985.84	Corrected SS	315.80033
Coeff Variation	26.1484196	Std Error Mean	0.19636512
Median	7.500000	Range	7.55000
Mode	8.700000	Interquartile Range	2.45000
Student's t	36.48172	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.942359	Pr < W	0.0005

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
2.75	1	1.1	1.1	6.45	1	1.1	34.1	8.30	1	1.1	68.1
2.90	1	1.1	2.2	6.60	1	1.1	35.2	8.35	1	1.1	69.2
3.05	1	1.1	3.3	6.70	1	1.1	36.3	8.45	1	1.1	70.3
3.25	2	2.2	5.5	6.80	2	2.2	38.5	8.50	2	2.2	72.5
3.45	2	2.2	7.7	6.90	1	1.1	39.6	8.55	1	1.1	73.6
3.65	1	1.1	8.8	7.00	1	1.1	40.7	8.60	1	1.1	74.7
3.75	1	1.1	9.9	7.05	1	1.1	41.8	8.65	1	1.1	75.8
4.00	1	1.1	11.0	7.15	1	1.1	42.9	8.70	5	5.5	81.3
4.80	2	2.2	13.2	7.25	1	1.1	44.0	8.80	1	1.1	82.4
4.85	1	1.1	14.3	7.40	3	3.3	47.3	8.85	1	1.1	83.5
5.00	1	1.1	15.4	7.50	3	3.3	50.5	8.90	1	1.1	84.6
5.30	2	2.2	17.6	7.55	1	1.1	51.6	8.95	1	1.1	85.7
5.45	1	1.1	18.7	7.60	1	1.1	52.7	9.00	3	3.3	89.0
5.65	1	1.1	19.8	7.65	1	1.1	53.8	9.15	1	1.1	90.1
5.75	1	1.1	20.9	7.70	1	1.1	54.9	9.50	1	1.1	91.2
5.85	1	1.1	22.0	7.85	2	2.2	57.1	9.55	1	1.1	92.3
5.95	1	1.1	23.1	7.95	4	4.4	61.5	9.60	2	2.2	94.5
6.20	3	3.3	26.4	8.10	1	1.1	62.6	9.65	1	1.1	95.6
6.30	3	3.3	29.7	8.15	1	1.1	63.7	9.75	2	2.2	97.8
6.35	1	1.1	30.8	8.20	2	2.2	65.9	10.00	1	1.1	98.9
6.40	2	2.2	33.0	8.25	1	1.1	67.0	10.30	1	1.1	100.0



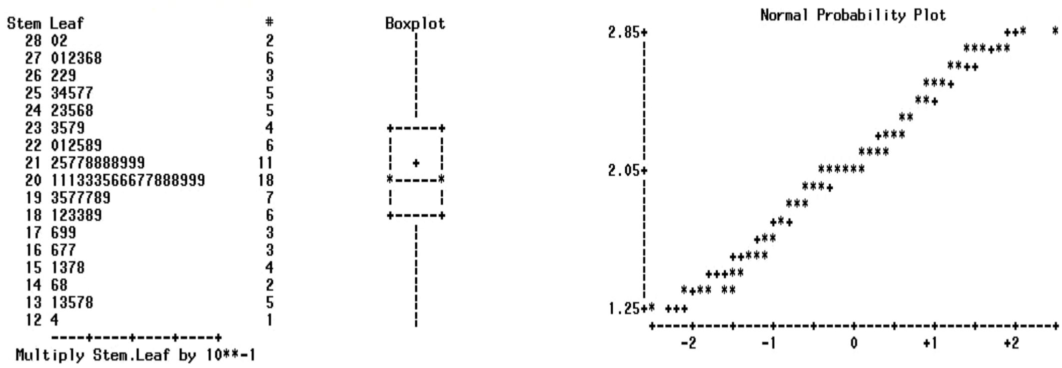
Appendix Figure B2 Selected items from PROC UNIVARIATE output for cotyledonous leaf width with the analysis of the *Solanum* spp. dataset.

Moments

N	91	Sum Weights	91
Mean	2.09901099	Sum Observations	191.01
Std Deviation	0.3864455	Variance	0.14934012
Skewness	-0.171446	Kurtosis	-0.398448
Uncorrected SS	414.3727	Corrected SS	13.440611
Coeff Variation	18.4108372	Std Error Mean	0.0405105
Median	2.080000	Range	1.58000
Mode	2.180000	Interquartile Range	0.49000
Student's t	51.814	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.974205	Pr < W	0.0674

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
1.24	1	1.1	1.1	1.97	3	3.3	31.9	2.35	1	1.1	74.7
1.31	1	1.1	2.2	1.98	1	1.1	33.0	2.37	1	1.1	75.8
1.33	1	1.1	3.3	1.99	1	1.1	34.1	2.39	1	1.1	76.9
1.35	1	1.1	4.4	2.01	3	3.3	37.4	2.42	1	1.1	78.0
1.37	1	1.1	5.5	2.03	3	3.3	40.7	2.43	1	1.1	79.1
1.38	1	1.1	6.6	2.05	1	1.1	41.8	2.45	1	1.1	80.2
1.46	1	1.1	7.7	2.06	3	3.3	45.1	2.46	1	1.1	81.3
1.48	1	1.1	8.8	2.07	2	2.2	47.3	2.48	1	1.1	82.4
1.51	1	1.1	9.9	2.08	3	3.3	50.5	2.53	1	1.1	83.5
1.53	1	1.1	11.0	2.09	3	3.3	53.8	2.54	1	1.1	84.6
1.57	1	1.1	12.1	2.12	1	1.1	54.9	2.55	1	1.1	85.7
1.58	1	1.1	13.2	2.15	1	1.1	56.0	2.57	2	2.2	87.9
1.66	1	1.1	14.3	2.17	2	2.2	58.2	2.62	2	2.2	90.1
1.67	2	2.2	16.5	2.18	4	4.4	62.6	2.69	1	1.1	91.2
1.76	1	1.1	17.6	2.19	3	3.3	65.9	2.70	1	1.1	92.3
1.79	2	2.2	19.8	2.20	1	1.1	67.0	2.71	1	1.1	93.4
1.81	1	1.1	20.9	2.21	1	1.1	68.1	2.72	1	1.1	94.5
1.82	1	1.1	22.0	2.22	1	1.1	69.2	2.73	1	1.1	95.6
1.83	2	2.2	24.2	2.25	1	1.1	70.3	2.76	1	1.1	96.7
1.88	1	1.1	25.3	2.28	1	1.1	71.4	2.78	1	1.1	97.8
1.89	1	1.1	26.4	2.29	1	1.1	72.5	2.80	1	1.1	98.9
1.93	1	1.1	27.5	2.33	1	1.1	73.6	2.82	1	1.1	100.0
1.95	1	1.1	28.6								

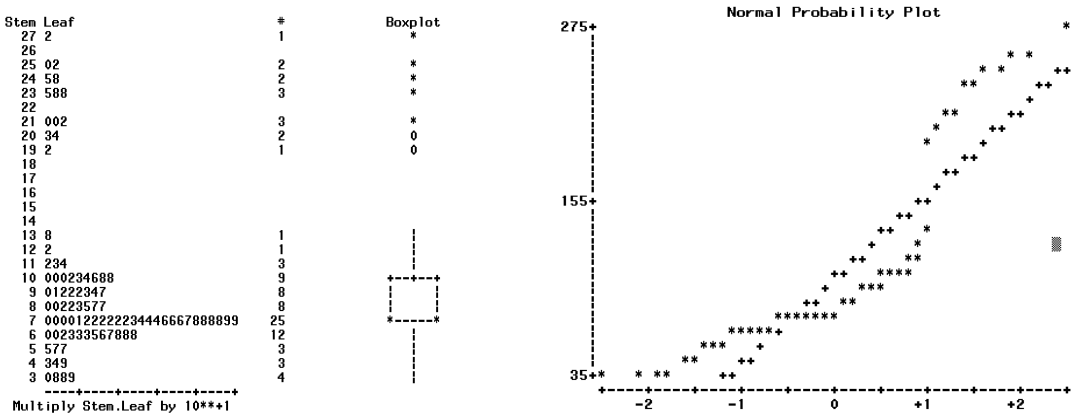


Appendix Figure B3 Selected items from PROC UNIVARIATE output for cotyledon leaf length/width ratio with the analysis of the *Solanum* spp. dataset.

Moment			
N	91	Sum Weights	91
Mean	101.351648	Sum Observations	9223
Std Deviation	58.609797	Variance	3435.1083
Skewness	1.63476194	Kurtosis	1.54409599
Uncorrected SS	1243926	Corrected SS	309159.747
Coeff Variation	57.8281636	Std Error Mean	6.14397615
Median	79.0000	Range	242.50000
Mode	72.5000	Interquartile Range	34.00000
Student's t	16.4961	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.749695	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
30.0	1	1.1	1.1	73.0	1	1.1	37.4	101.5	1	1.1	73.6
37.5	1	1.1	2.2	73.5	1	1.1	38.5	103.0	1	1.1	74.7
38.5	1	1.1	3.3	74.5	2	2.2	40.7	103.5	1	1.1	75.8
39.0	1	1.1	4.4	76.0	1	1.1	41.8	106.0	1	1.1	76.9
43.0	1	1.1	5.5	76.5	2	2.2	44.0	107.5	1	1.1	78.0
44.0	1	1.1	6.6	77.0	1	1.1	45.1	108.0	1	1.1	79.1
49.0	1	1.1	7.7	77.5	3	3.3	48.4	111.5	1	1.1	80.2
55.0	1	1.1	8.8	78.5	1	1.1	49.5	113.0	1	1.1	81.3
57.0	2	2.2	11.0	79.0	2	2.2	51.6	114.5	1	1.1	82.4
59.5	2	2.2	13.2	80.0	2	2.2	53.8	122.0	1	1.1	83.5
61.5	1	1.1	14.3	81.5	1	1.1	54.9	137.5	1	1.1	84.6
63.0	3	3.3	17.6	82.0	1	1.1	56.0	191.5	1	1.1	85.7
65.0	1	1.1	18.7	83.0	1	1.1	57.1	203.0	1	1.1	86.8
66.5	1	1.1	19.8	85.0	1	1.1	58.2	204.5	1	1.1	87.9
67.0	1	1.1	20.9	87.0	2	2.2	60.4	210.0	2	2.2	90.1
67.5	1	1.1	22.0	90.0	1	1.1	61.5	212.5	1	1.1	91.2
68.5	2	2.2	24.2	91.0	1	1.1	62.6	235.0	1	1.1	92.3
69.5	1	1.1	25.3	92.5	3	3.3	65.9	237.5	2	2.2	94.5
70.0	1	1.1	26.4	93.0	1	1.1	67.0	245.0	1	1.1	95.6
70.5	2	2.2	28.6	94.5	1	1.1	68.1	247.5	1	1.1	96.7
71.0	1	1.1	29.7	97.0	1	1.1	69.2	250.0	1	1.1	97.8
71.5	1	1.1	30.8	99.5	1	1.1	70.3	251.5	1	1.1	98.9
72.0	1	1.1	31.9	100.5	2	2.2	72.5	272.5	1	1.1	100.0
72.5	4	4.4	36.3								



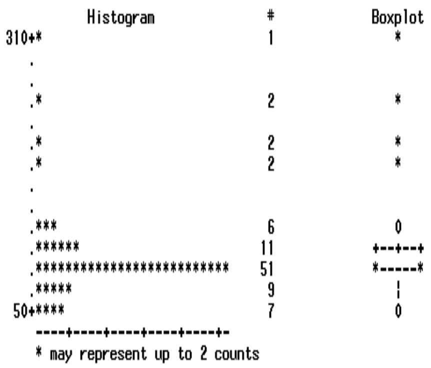
Appendix Figure B4 Selected items from PROC UNIVARIATE output for plant height with the analysis of the *Solanum* spp. dataset.

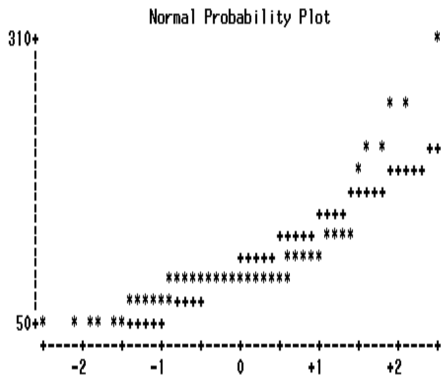
Moments

N	91	Sum Weights	91
Mean	100.587912	Sum Observations	9153.5
Std Deviation	42.6048115	Variance	1815.16996
Skewness	2.61354531	Kurtosis	8.51379161
Uncorrected SS	1084096.75	Corrected SS	163365.297
Coeff Variation	42.3557967	Std Error Mean	4.46619779
Median	91.0000	Range	269.00000
Mode	82.0000	Interquartile Range	19.50000
Student's t	22.52205	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.712039	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
41.0	1	1.1	1.1	85.0	1	1.1	30.8	100.5	1	1.1	74.7
42.0	1	1.1	2.2	85.5	1	1.1	31.9	102.0	1	1.1	75.8
48.0	1	1.1	3.3	86.0	2	2.2	34.1	103.0	1	1.1	76.9
49.0	1	1.1	4.4	86.5	3	3.3	37.4	105.0	2	2.2	79.1
54.0	1	1.1	5.5	87.0	1	1.1	38.5	109.5	1	1.1	80.2
56.5	1	1.1	6.6	88.5	1	1.1	39.6	112.0	1	1.1	81.3
57.0	1	1.1	7.7	89.0	1	1.1	40.7	112.5	1	1.1	82.4
61.0	1	1.1	8.8	89.5	3	3.3	44.0	113.0	1	1.1	83.5
62.0	1	1.1	9.9	90.0	1	1.1	45.1	113.5	1	1.1	84.6
68.5	1	1.1	11.0	90.5	3	3.3	48.4	118.0	1	1.1	85.7
70.5	1	1.1	12.1	91.0	2	2.2	50.5	123.0	1	1.1	86.8
75.0	1	1.1	13.2	92.0	1	1.1	51.6	125.5	1	1.1	87.9
75.5	1	1.1	14.3	92.5	1	1.1	52.7	126.5	1	1.1	89.0
76.5	1	1.1	15.4	93.5	1	1.1	53.8	132.5	1	1.1	90.1
77.5	1	1.1	16.5	94.0	1	1.1	54.9	135.0	1	1.1	91.2
78.5	1	1.1	17.6	94.5	3	3.3	58.2	136.5	1	1.1	92.3
80.5	1	1.1	18.7	95.0	4	4.4	62.6	185.0	1	1.1	93.4
81.0	1	1.1	19.8	95.5	1	1.1	63.7	193.5	1	1.1	94.5
82.0	4	4.4	24.2	96.0	1	1.1	64.8	201.0	1	1.1	95.6
82.5	1	1.1	25.3	96.5	2	2.2	67.0	215.0	1	1.1	96.7
83.0	1	1.1	26.4	97.5	1	1.1	68.1	242.5	1	1.1	97.8
83.5	1	1.1	27.5	98.0	2	2.2	70.3	244.5	1	1.1	98.9
84.5	2	2.2	29.7	99.0	3	3.3	73.6	310.0	1	1.1	100.0





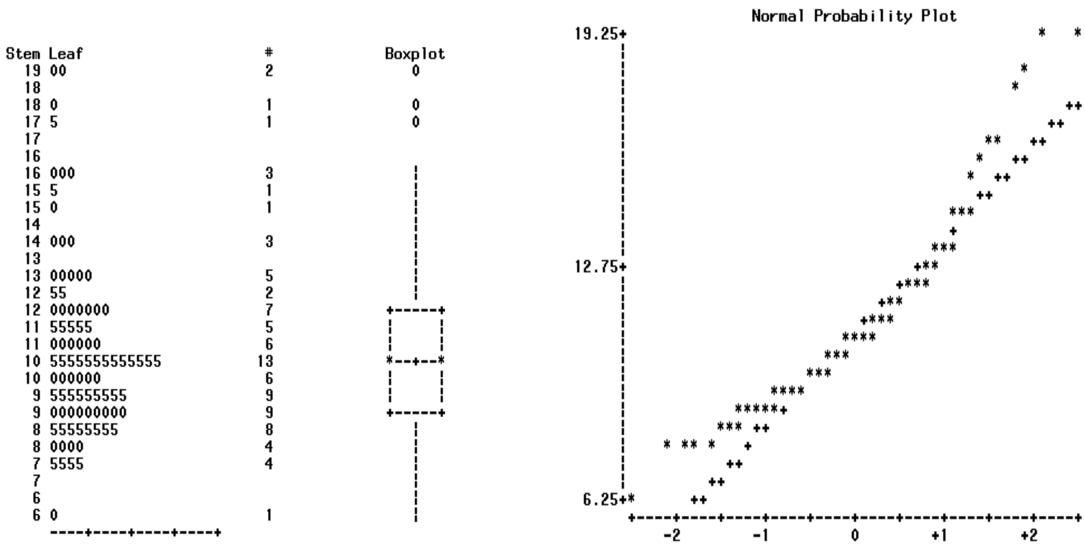
Appendix Figure B5 Selected items from PROC UNIVARIATE output for plant breadth with the analysis of the *Solanum* spp. dataset.

Moments

N	91	Sum Weights	91
Mean	10.8846154	Sum Observations	990.5
Std Deviation	2.61308345	Variance	6.82820513
Skewness	1.19734687	Kurtosis	1.51747615
Uncorrected SS	11395.75	Corrected SS	614.538462
Coeff Variation	24.0071271	Std Error Mean	0.27392558
Median	10.50000	Range	13.00000
Mode	10.50000	Interquartile Range	3.00000
Student's t	39.73567	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.907385	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
6.0	1	1.1	1.1	10.5	13	14.3	59.3	15.0	1	1.1	91.2
7.5	4	4.4	5.5	11.0	6	6.6	65.9	15.5	1	1.1	92.3
8.0	4	4.4	9.9	11.5	5	5.5	71.4	16.0	3	3.3	95.6
8.5	8	8.8	18.7	12.0	7	7.7	79.1	17.5	1	1.1	96.7
9.0	9	9.9	28.6	12.5	2	2.2	81.3	18.0	1	1.1	97.8
9.5	9	9.9	38.5	13.0	5	5.5	86.8	19.0	2	2.2	100.0
10.0	6	6.6	45.1	14.0	3	3.3	90.1				



Appendix Figure B6 Selected items from PROC UNIVARIATE output for plant branching with the analysis of the *Solanum* spp. dataset.

Moments

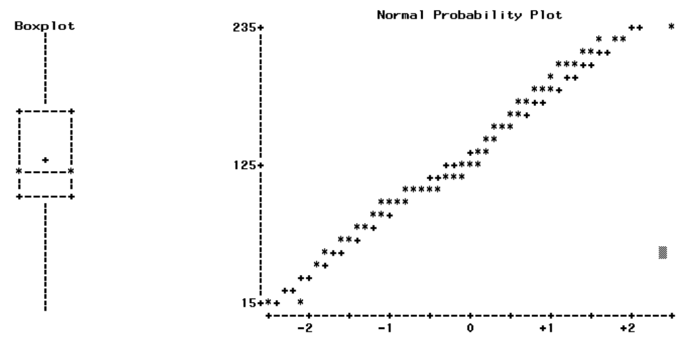
N	91	Sum Weights	91
Mean	134.78022	Sum Observations	12265
Std Deviation	49.1693332	Variance	2417.62333
Skewness	0.08358999	Kurtosis	-0.3412104
Uncorrected SS	1870665.5	Corrected SS	217586.099
Coeff Variation	36.4811196	Std Error Mean	5.15434664
Median	126.0000	Range	222.65000
Mode	205.0000	Interquartile Range	71.50000
Student's t	26.14885	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.973675	Pr < W	0.0618

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
12.35	1	1.1	1.1	106.50	1	1.1	31.9	152.50	1	1.1	64.8
14.15	1	1.1	2.2	107.00	2	2.2	34.1	153.00	2	2.2	67.0
46.00	1	1.1	3.3	108.00	1	1.1	35.2	155.00	1	1.1	68.1
54.50	1	1.1	4.4	109.50	1	1.1	36.3	160.00	1	1.1	69.2
62.50	1	1.1	5.5	111.50	1	1.1	37.4	162.50	1	1.1	70.3
65.00	1	1.1	6.6	112.00	1	1.1	38.5	164.00	1	1.1	71.4
67.50	1	1.1	7.7	113.50	1	1.1	39.6	166.00	1	1.1	72.5
70.00	1	1.1	8.8	115.50	1	1.1	40.7	170.00	1	1.1	73.6
70.50	1	1.1	9.9	116.50	1	1.1	41.8	172.00	1	1.1	74.7
79.00	1	1.1	11.0	117.50	2	2.2	44.0	174.50	1	1.1	75.8
85.00	1	1.1	12.1	118.50	1	1.1	45.1	175.00	2	2.2	78.0
88.50	1	1.1	13.2	119.00	1	1.1	46.2	180.00	1	1.1	79.1
94.00	1	1.1	14.3	119.50	1	1.1	47.3	183.50	1	1.1	80.2
96.00	1	1.1	15.4	120.00	1	1.1	48.4	185.00	2	2.2	82.4
96.50	1	1.1	16.5	121.00	1	1.1	49.5	187.50	1	1.1	83.5
97.00	1	1.1	17.6	126.00	1	1.1	50.5	188.50	1	1.1	84.6
98.50	1	1.1	18.7	128.00	1	1.1	51.6	195.00	1	1.1	85.7
99.00	1	1.1	19.8	128.50	1	1.1	52.7	200.00	1	1.1	86.8
99.50	1	1.1	20.9	129.00	1	1.1	53.8	202.50	1	1.1	87.9
100.00	1	1.1	22.0	132.50	1	1.1	54.9	205.00	3	3.3	91.2
101.00	1	1.1	23.1	133.50	1	1.1	56.0	210.00	1	1.1	92.3
102.50	1	1.1	24.2	134.00	1	1.1	57.1	212.50	1	1.1	93.4
103.00	1	1.1	25.3	136.00	1	1.1	58.2	218.50	1	1.1	94.5
103.50	1	1.1	26.4	137.50	1	1.1	59.3	220.00	1	1.1	95.6
104.50	1	1.1	27.5	142.50	1	1.1	60.4	225.50	1	1.1	96.7
105.00	1	1.1	28.6	145.00	2	2.2	62.6	227.50	2	2.2	98.9
105.50	1	1.1	29.7	150.00	1	1.1	63.7	235.00	1	1.1	100.0
106.00	1	1.1	30.8								

Stem	Leaf	#
23	5	1
22	0688	4
21	028	3
20	02555	5
19	5	1
18	045588	6
17	02455	5
16	0246	4
15	02335	5
14	255	3
13	24468	5
12	0016889	7
11	0224668889	10
10	00123445666778	14
9	466789	6
8	58	2
7	009	3
6	258	3
5	4	1
4	6	1
3		
2		
1	24	2

Multiply Stem.Leaf by 10**+1

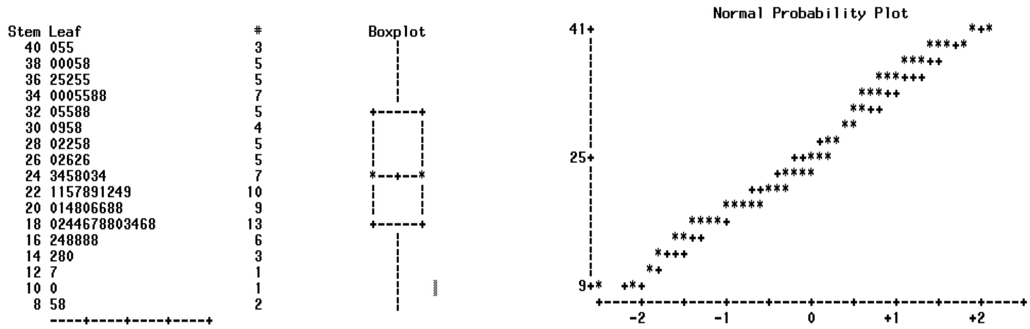


Appendix Figure B7 Selected items from PROC UNIVARIATE output for petiole length with the analysis of the *Solanum* spp. dataset.

Moments			
N	91	Sum Weights	91
Mean	25.606044	Sum Observations	2330.15
Std Deviation	7.94419717	Variance	63.1102686
Skewness	0.20074929	Kurtosis	-0.8783733
Uncorrected SS	65345.8475	Corrected SS	5679.92418
Coeff Variation	31.0246955	Std Error Mean	0.83277814
Median	24.30000	Range	31.00000
Mode	34.00000	Interquartile Range	14.20000
Student's t	30.74774	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.960513	Pr < W	0.0074

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
9.50	1	1.1	1.1	20.40	1	1.1	31.9	27.95	1	1.1	63.7
9.75	1	1.1	2.2	20.80	1	1.1	33.0	28.20	1	1.1	64.8
10.00	1	1.1	3.3	21.00	1	1.1	34.1	28.25	1	1.1	65.9
13.70	1	1.1	4.4	21.55	1	1.1	35.2	28.50	1	1.1	67.0
14.25	1	1.1	5.5	21.60	1	1.1	36.3	28.75	1	1.1	68.1
14.80	1	1.1	6.6	21.80	2	2.2	38.5	30.00	1	1.1	69.2
15.00	1	1.1	7.7	22.10	2	2.2	40.7	30.90	1	1.1	70.3
16.15	1	1.1	8.8	22.50	1	1.1	41.8	31.50	1	1.1	71.4
16.45	1	1.1	9.9	22.70	1	1.1	42.9	31.75	1	1.1	72.5
16.80	1	1.1	11.0	22.80	1	1.1	44.0	32.00	1	1.1	73.6
17.75	1	1.1	12.1	22.90	1	1.1	45.1	32.50	1	1.1	74.7
17.85	2	2.2	14.3	23.10	1	1.1	46.2	33.50	1	1.1	75.8
18.00	1	1.1	15.4	23.15	1	1.1	47.3	33.80	1	1.1	76.9
18.25	1	1.1	16.5	23.45	1	1.1	48.4	33.85	1	1.1	78.0
18.35	1	1.1	17.6	23.90	1	1.1	49.5	34.00	3	3.3	81.3
18.45	1	1.1	18.7	24.30	1	1.1	50.5	34.50	2	2.2	83.5
18.60	1	1.1	19.8	24.40	1	1.1	51.6	34.75	2	2.2	85.7
18.70	1	1.1	20.9	24.50	1	1.1	52.7	36.25	1	1.1	86.8
18.75	1	1.1	22.0	24.80	1	1.1	53.8	36.50	1	1.1	87.9
18.80	1	1.1	23.1	25.00	1	1.1	54.9	37.25	1	1.1	89.0
19.00	1	1.1	24.2	25.30	1	1.1	56.0	37.50	2	2.2	91.2
19.30	1	1.1	25.3	25.40	1	1.1	57.1	38.00	3	3.3	94.5
19.40	1	1.1	26.4	26.00	1	1.1	58.2	38.50	1	1.1	95.6
19.60	1	1.1	27.5	26.25	1	1.1	59.3	39.75	1	1.1	96.7
19.75	1	1.1	28.6	26.60	1	1.1	60.4	40.00	1	1.1	97.8
20.00	1	1.1	29.7	27.25	1	1.1	61.5	40.50	2	2.2	100.0
20.10	1	1.1	30.8	27.60	1	1.1	62.6				



Appendix Figure B8 Selected items from PROC UNIVARIATE output for leaf blade length with the analysis of the *Solanum* spp. dataset

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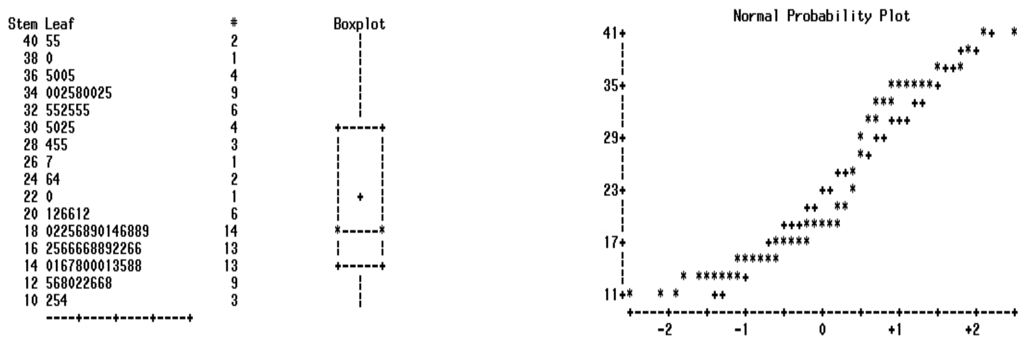
Moments

N	91	Sum Weights	91
Mean	22.439011	Sum Observations	2041.95
Std Deviation	8.66281261	Variance	75.0443223
Skewness	0.60726343	Kurtosis	-1.1081018
Uncorrected SS	52573.3275	Corrected SS	6753.98901
Coeff Variation	38.6060358	Std Error Mean	0.90810951
Median	19.00000	Range	30.25000
Mode	16.55000	Interquartile Range	16.00000
Student's t	36.48172	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.879876	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
10.25	1	1.1	1.1	16.65	1	1.1	34.1	23.00	1	1.1	64.8
10.50	1	1.1	2.2	16.75	2	2.2	36.3	24.65	1	1.1	65.9
11.35	1	1.1	3.3	16.90	1	1.1	37.4	25.40	1	1.1	67.0
12.50	1	1.1	4.4	17.15	1	1.1	38.5	26.70	1	1.1	68.1
12.65	1	1.1	5.5	17.25	1	1.1	39.6	28.40	1	1.1	69.2
12.85	1	1.1	6.6	17.55	1	1.1	40.7	28.50	1	1.1	70.3
13.00	1	1.1	7.7	17.60	1	1.1	41.8	29.50	1	1.1	71.4
13.20	2	2.2	9.9	17.95	1	1.1	42.9	30.50	1	1.1	72.5
13.60	1	1.1	11.0	18.20	1	1.1	44.0	31.00	1	1.1	73.6
13.65	1	1.1	12.1	18.25	1	1.1	45.1	31.15	1	1.1	74.7
13.75	1	1.1	13.2	18.50	1	1.1	46.2	31.50	1	1.1	75.8
14.00	1	1.1	14.3	18.60	1	1.1	47.3	32.50	2	2.2	78.0
14.10	1	1.1	15.4	18.85	1	1.1	48.4	33.15	1	1.1	79.1
14.55	1	1.1	16.5	18.90	1	1.1	49.5	33.50	3	3.3	82.4
14.70	1	1.1	17.6	19.00	1	1.1	50.5	34.00	2	2.2	84.6
14.85	1	1.1	18.7	19.10	1	1.1	51.6	34.25	1	1.1	85.7
14.95	1	1.1	19.8	19.45	1	1.1	52.7	34.50	1	1.1	86.8
15.00	2	2.2	22.0	19.60	1	1.1	53.8	34.75	1	1.1	87.9
15.10	1	1.1	23.1	19.75	1	1.1	54.9	35.00	2	2.2	90.1
15.30	1	1.1	24.2	19.80	1	1.1	56.0	35.25	1	1.1	91.2
15.50	1	1.1	25.3	19.90	1	1.1	57.1	35.50	1	1.1	92.3
15.75	1	1.1	26.4	20.10	1	1.1	58.2	36.50	1	1.1	93.4
15.80	1	1.1	27.5	20.25	1	1.1	59.3	37.00	2	2.2	95.6
16.20	1	1.1	28.6	20.60	2	2.2	61.5	37.50	1	1.1	96.7
16.50	1	1.1	29.7	21.10	1	1.1	62.6	38.00	1	1.1	97.8
16.55	3	3.3	33.0	21.20	1	1.1	63.7	40.50	2	2.2	100.0



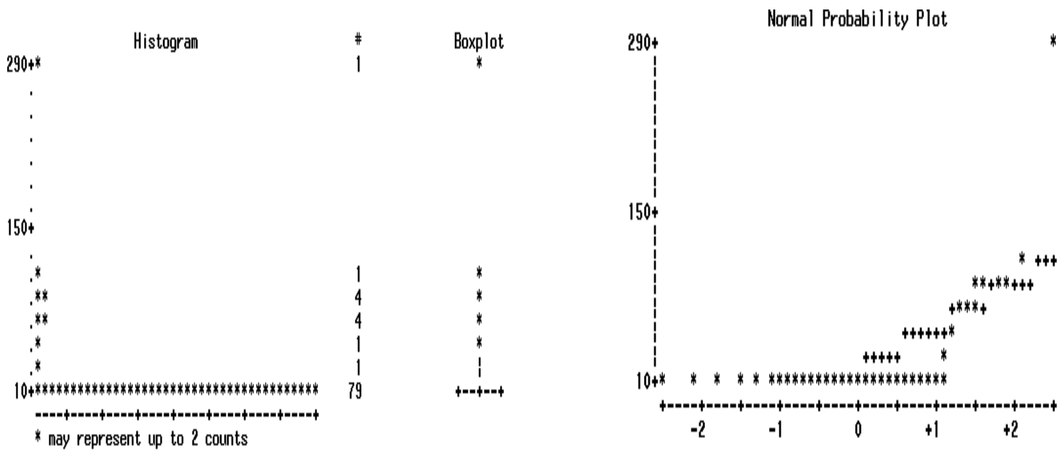
Appendix Figure B9 Selected items from PROC UNIVARIATE output for leaf blade width with the analysis of the *Solanum* spp. dataset.

Moments

N	91	Sum Weights	91
Mean	17.6043956	Sum Observations	1602
Std Deviation	37.3846757	Variance	1397.61398
Skewness	4.97008252	Kurtosis	31.6017022
Uncorrected SS	153987.5	Corrected SS	125785.258
Coeff Variation	212.359893	Std Error Mean	3.91897887
Median	6.00000	Range	289.00000
Mode	3.00000	Interquartile Range	7.00000
Student's t	4.492087	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.41137	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
1.0	1	1.1	1.1	7.5	1	1.1	57.1	20.0	1	1.1	87.9
1.5	2	2.2	3.3	8.0	3	3.3	60.4	57.5	1	1.1	89.0
2.0	2	2.2	5.5	8.5	2	2.2	62.6	63.0	1	1.1	90.1
2.5	3	3.3	8.8	9.0	6	6.6	69.2	64.0	1	1.1	91.2
3.0	8	8.8	17.6	9.5	2	2.2	71.4	71.0	1	1.1	92.3
3.5	8	8.8	26.4	10.0	3	3.3	74.7	73.5	1	1.1	93.4
4.0	4	4.4	30.8	10.5	2	2.2	76.9	82.5	1	1.1	94.5
4.5	4	4.4	35.2	11.0	2	2.2	79.1	89.0	1	1.1	95.6
5.0	7	7.7	42.9	11.5	1	1.1	80.2	94.0	1	1.1	96.7
5.5	4	4.4	47.3	12.0	3	3.3	83.5	97.0	1	1.1	97.8
6.0	6	6.6	53.8	14.5	1	1.1	84.6	103.0	1	1.1	98.9
6.5	1	1.1	54.9	16.0	1	1.1	85.7	290.0	1	1.1	100.0
7.0	1	1.1	56.0	17.0	1	1.1	86.8				



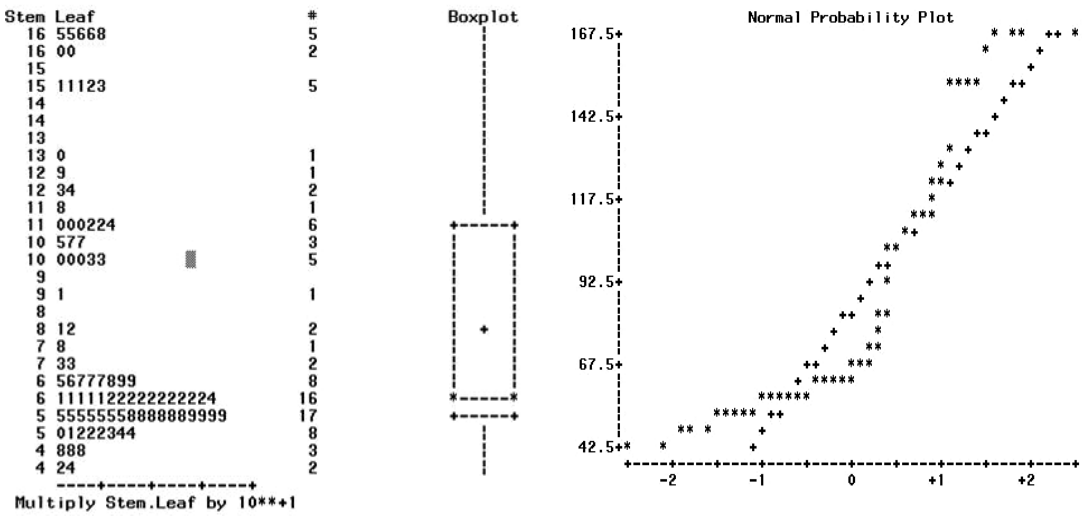
Appendix Figure B10 Selected items from PROC UNIVARIATE output for number of flowers per inflorescence with the analysis of the *Solanum* spp. dataset.

Moments

N	91	Sum Weights	91
Mean	84.032967	Sum Observations	7647
Std Deviation	36.8463629	Variance	1357.65446
Skewness	1.04774583	Kurtosis	-0.2088122
Uncorrected SS	764789	Corrected SS	122188.901
Coeff Variation	43.8475091	Std Error Mean	3.86254835
Median	64.00000	Range	126.00000
Mode	62.00000	Interquartile Range	52.00000
Student's t	21.75584	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.819023	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
42	1	1.1	1.1	66	1	1.1	52.7	112	2	2.2	80.2
44	1	1.1	2.2	67	3	3.3	56.0	114	1	1.1	81.3
48	3	3.3	5.5	68	1	1.1	57.1	118	1	1.1	82.4
50	1	1.1	6.6	69	2	2.2	59.3	123	1	1.1	83.5
51	1	1.1	7.7	73	2	2.2	61.5	124	1	1.1	84.6
52	3	3.3	11.0	78	1	1.1	62.6	129	1	1.1	85.7
53	1	1.1	12.1	81	1	1.1	63.7	130	1	1.1	86.8
54	2	2.2	14.3	82	1	1.1	64.8	151	3	3.3	90.1
55	7	7.7	22.0	91	1	1.1	65.9	152	1	1.1	91.2
58	6	6.6	28.6	100	3	3.3	69.2	153	1	1.1	92.3
59	4	4.4	33.0	103	2	2.2	71.4	160	2	2.2	94.5
61	5	5.5	38.5	105	1	1.1	72.5	165	2	2.2	96.7
62	10	11.0	49.5	107	2	2.2	74.7	166	2	2.2	98.9
64	1	1.1	50.5	110	3	3.3	78.0	168	1	1.1	100.0
65	1	1.1	51.6								



Appendix Figure B11 Selected items from PROC UNIVARIATE output flowering time with the analysis of the *Solanum* spp. dataset.

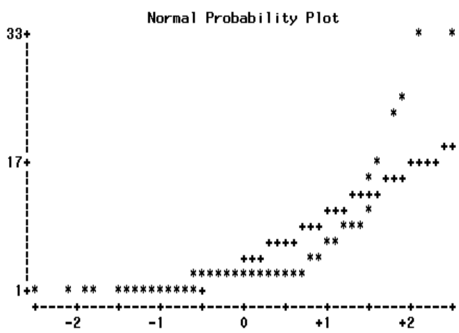
Moments

N	91	Sum Weights	91
Mean	4.38032967	Sum Observations	398.61
Std Deviation	5.86443432	Variance	34.3915899
Skewness	3.38536066	Kurtosis	12.1698385
Uncorrected SS	4841.2863	Corrected SS	3095.24309
Coeff Variation	133.881118	Std Error Mean	0.61475976
Median	2.550000	Range	31.62000
Mode	0.940000	Interquartile Range	2.15000
Student's t	7.125271	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.539347	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
0.88	1	1.1	1.1	1.88	1	1.1	26.4	2.55	1	1.1	50.5
0.89	1	1.1	2.2	1.98	1	1.1	27.5	2.56	1	1.1	51.6
0.90	1	1.1	3.3	2.05	1	1.1	28.6	2.57	1	1.1	52.7
0.94	2	2.2	5.5	2.09	1	1.1	29.7	2.58	2	2.2	54.9
0.96	2	2.2	7.7	2.11	1	1.1	30.8	2.59	1	1.1	56.0
1.05	1	1.1	8.8	2.12	1	1.1	31.9	2.60	1	1.1	57.1
1.13	1	1.1	9.9	2.19	1	1.1	33.0	2.61	1	1.1	58.2
1.17	1	1.1	11.0	2.20	1	1.1	34.1	2.64	2	2.2	60.4
1.18	1	1.1	12.1	2.23	1	1.1	35.2	2.67	1	1.1	61.5
1.19	1	1.1	13.2	2.26	1	1.1	36.3	2.68	1	1.1	62.6
1.21	1	1.1	14.3	2.27	1	1.1	37.4	2.95	2	2.2	64.8
1.24	1	1.1	15.4	2.28	1	1.1	38.5	3.06	1	1.1	65.9
1.26	1	1.1	16.5	2.29	1	1.1	39.6	3.08	1	1.1	67.0
1.27	1	1.1	17.6	2.34	1	1.1	40.7	3.11	2	2.2	69.2
1.32	2	2.2	19.8	2.36	2	2.2	42.9	3.28	1	1.1	70.3
1.38	1	1.1	20.9	2.42	2	2.2	45.1	3.37	1	1.1	71.4
1.40	1	1.1	22.0	2.47	1	1.1	46.2	3.41	1	1.1	72.5
1.43	1	1.1	23.1	2.48	1	1.1	47.3	3.48	1	1.1	73.6
1.62	1	1.1	24.2	2.51	1	1.1	48.4	3.61	1	1.1	74.7
1.74	1	1.1	25.3	2.54	1	1.1	49.5	3.89	1	1.1	75.8
3.90	1	1.1	76.9	6.56	1	1.1	85.7	10.87	1	1.1	93.4
4.04	1	1.1	78.0	7.02	1	1.1	86.8	14.75	1	1.1	94.5
4.06	1	1.1	79.1	7.14	1	1.1	87.9	16.50	1	1.1	95.6
4.59	1	1.1	80.2	8.62	1	1.1	89.0	22.50	1	1.1	96.7
5.31	1	1.1	81.3	9.15	1	1.1	90.1	24.55	1	1.1	97.8
5.58	1	1.1	82.4	9.31	1	1.1	91.2	32.00	1	1.1	98.9
5.88	1	1.1	83.5	9.85	1	1.1	92.3	32.50	1	1.1	100.0
6.13	1	1.1	84.6								

```
Stem Leaf                                          #     Boxplot
  32 05                                            2        *
  30
  28
  26
  24 6                                             1        *
  22 5                                             1        *
  20
  18
  16 5                                             1        *
  14 8                                             1        *
  12
  10 9                                             1        *
   8 6238                                          4        0
   6 1601                                          4        0
   4 016369                                        6        +
   2 0011122233333444455556666666666770011113445699 46    +-----+
   0 999990001222223333444679                     24    +-----+
     ----+----+----+----+----+----+----+----+----+-
```



Appendix Figure B12 Selected items from PROC UNIVARIATE output fruit length with the analysis of the *Solanum* spp. dataset.

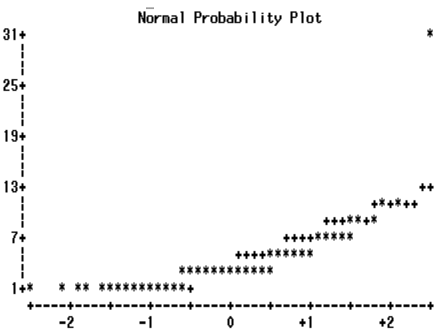
Moments

N	91	Sum Weights	91
Mean	3.70846154	Sum Observations	337.47
Std Deviation	3.59841568	Variance	12.9485954
Skewness	4.83374224	Kurtosis	33.1884785
Uncorrected SS	2416.8681	Corrected SS	1165.37358
Coeff Variation	97.0325737	Std Error Mean	0.37721646
Median	2.920000	Range	29.58000
Mode	1.300000	Interquartile Range	2.78000
Student's t	9.831123	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.594796	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
0.77	1	1.1	1.1	2.32	1	1.1	36.3	4.06	1	1.1	69.2
0.89	1	1.1	2.2	2.35	1	1.1	37.4	4.15	1	1.1	70.3
0.96	1	1.1	3.3	2.37	1	1.1	38.5	4.22	1	1.1	71.4
0.97	1	1.1	4.4	2.41	1	1.1	39.6	4.26	2	2.2	73.6
0.99	1	1.1	5.5	2.47	1	1.1	40.7	4.49	1	1.1	74.7
1.01	1	1.1	6.6	2.49	2	2.2	42.9	4.61	1	1.1	75.8
1.02	1	1.1	7.7	2.52	1	1.1	44.0	4.68	1	1.1	76.9
1.03	1	1.1	8.8	2.53	2	2.2	46.2	4.72	1	1.1	78.0
1.05	1	1.1	9.9	2.70	1	1.1	47.3	4.73	1	1.1	79.1
1.10	1	1.1	11.0	2.80	1	1.1	48.4	4.99	1	1.1	80.2
1.17	1	1.1	12.1	2.83	1	1.1	49.5	5.01	1	1.1	81.3
1.22	1	1.1	13.2	2.92	1	1.1	50.5	5.10	1	1.1	82.4
1.25	1	1.1	14.3	2.94	1	1.1	51.6	5.26	1	1.1	83.5
1.30	2	2.2	16.5	3.01	1	1.1	52.7	5.42	1	1.1	84.6
1.32	1	1.1	17.6	3.03	1	1.1	53.8	5.64	1	1.1	85.7
1.33	2	2.2	19.8	3.04	1	1.1	54.9	6.08	1	1.1	86.8
1.35	1	1.1	20.9	3.08	1	1.1	56.0	6.09	1	1.1	87.9
1.41	1	1.1	22.0	3.09	1	1.1	57.1	6.11	1	1.1	89.0
1.42	1	1.1	23.1	3.16	1	1.1	58.2	6.13	1	1.1	90.1
1.74	1	1.1	24.2	3.19	1	1.1	59.3	7.16	1	1.1	91.2
1.83	1	1.1	25.3	3.24	1	1.1	60.4	7.32	1	1.1	92.3
1.93	1	1.1	26.4	3.35	1	1.1	61.5	7.98	1	1.1	93.4
2.11	1	1.1	27.5	3.44	1	1.1	62.6	8.91	1	1.1	94.5
2.18	2	2.2	29.7	3.51	1	1.1	63.7	9.45	1	1.1	95.6
2.19	1	1.1	30.8	3.63	1	1.1	64.8	9.65	1	1.1	96.7
2.26	1	1.1	31.9	3.71	1	1.1	65.9	10.20	1	1.1	97.8
2.28	1	1.1	33.0	3.73	1	1.1	67.0	10.26	1	1.1	98.9
2.30	1	1.1	34.1	3.80	1	1.1	68.1	30.35	1	1.1	100.0
2.31	1	1.1	35.2								

```
Stem Leaf                                      #          Boxplot
  30 4                                         1             *
  28
  26
  24
  22
  20
  18
  16
  14
  12
  10 23                                        2             0
   8 0946                                      4             0
   6 111123                                    6             |
   4 1223356777001346                         16          +-----+
   2 12223333344455555578899000112224456778   38          *--+--*
   0 890000000122233333444789                 24          +-----+
     ----+----+----+----+----+----+----+---
```

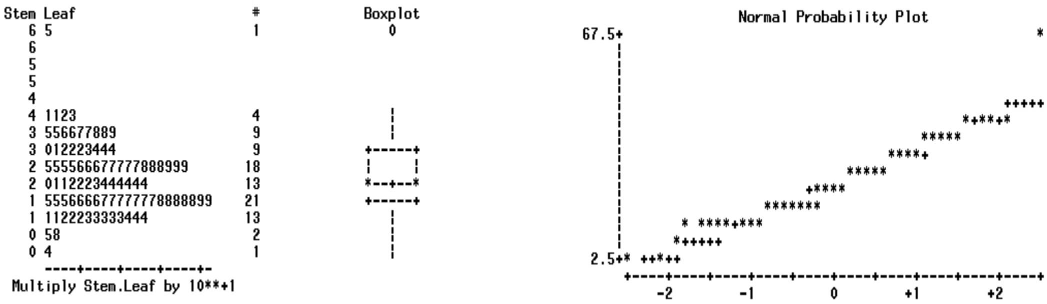


Appendix Figure B13 Selected items from PROC UNIVARIATE output fruit breadth with the analysis of the *Solanum* spp. dataset.

Moments			
N	91	Sum Weights	91
Mean	23.8723077	Sum Observations	2172.38
Std Deviation	10.0929974	Variance	101.868596
Skewness	0.84621927	Kurtosis	1.86764
Uncorrected SS	61027.8974	Corrected SS	9168.17362
Coeff Variation	42.2791022	Std Error Mean	1.05803361
Median	23.90000	Range	61.17000
Mode	15.55000	Interquartile Range	13.95000
Student's t	22.5629	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.954032	Pr < W	0.0028

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
4.18	1	1.1	1.1	18.30	1	1.1	37.4	27.90	1	1.1	69.2
4.55	1	1.1	2.2	18.50	1	1.1	38.5	28.10	1	1.1	70.3
8.00	1	1.1	3.3	18.60	1	1.1	39.6	28.40	1	1.1	71.4
10.70	1	1.1	4.4	19.15	1	1.1	40.7	28.55	2	2.2	73.6
11.35	1	1.1	5.5	20.45	1	1.1	41.8	29.40	1	1.1	74.7
11.95	1	1.1	6.6	20.85	1	1.1	42.9	30.45	1	1.1	75.8
12.00	1	1.1	7.7	21.45	1	1.1	44.0	31.15	1	1.1	76.9
12.40	1	1.1	8.8	21.55	1	1.1	45.1	31.50	1	1.1	78.0
12.70	1	1.1	9.9	21.70	2	2.2	47.3	31.55	1	1.1	79.1
12.90	2	2.2	12.1	22.75	1	1.1	48.4	32.15	1	1.1	80.2
12.95	1	1.1	13.2	23.55	1	1.1	49.5	33.20	1	1.1	81.3
13.00	1	1.1	14.3	23.90	2	2.2	51.6	33.90	1	1.1	82.4
13.70	1	1.1	15.4	24.05	1	1.1	52.7	33.95	2	2.2	84.6
13.90	1	1.1	16.5	24.30	1	1.1	53.8	34.85	1	1.1	85.7
14.05	1	1.1	17.6	24.50	1	1.1	54.9	35.35	1	1.1	86.8
14.95	2	2.2	19.8	24.75	1	1.1	56.0	35.75	1	1.1	87.9
15.25	1	1.1	20.9	25.10	1	1.1	57.1	35.85	1	1.1	89.0
15.55	3	3.3	24.2	25.30	1	1.1	58.2	37.20	1	1.1	90.1
16.50	1	1.1	25.3	25.40	1	1.1	59.3	37.30	1	1.1	91.2
16.60	1	1.1	26.4	25.65	1	1.1	60.4	37.65	1	1.1	92.3
16.65	1	1.1	27.5	26.20	1	1.1	61.5	38.45	1	1.1	93.4
16.70	1	1.1	28.6	26.40	1	1.1	62.6	39.30	1	1.1	94.5
16.95	2	2.2	30.8	26.55	1	1.1	63.7	40.70	1	1.1	95.6
17.40	1	1.1	31.9	26.70	1	1.1	64.8	41.30	1	1.1	96.7
17.45	1	1.1	33.0	26.95	1	1.1	65.9	42.45	1	1.1	97.8
18.05	1	1.1	34.1	27.20	1	1.1	67.0	42.95	1	1.1	98.9
18.10	2	2.2	36.3	27.35	1	1.1	68.1	65.35	1	1.1	100.0



Appendix Figure B14 Selected items from PROC UNIVARIATE output fruit stalk length with the analysis of the *Solanum* spp.dataset.

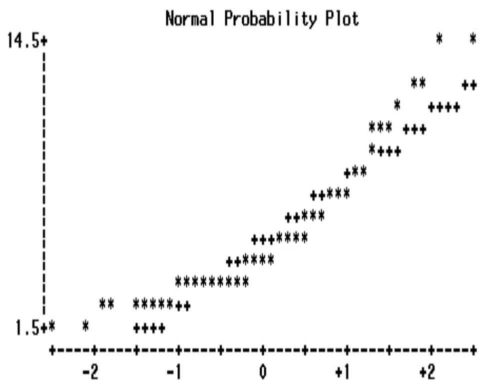
Moments

N	91	Sum Weights	91
Mean	5.29230769	Sum Observations	481.6
Std Deviation	2.85938924	Variance	8.17610684
Skewness	1.40549337	Kurtosis	1.82096638
Uncorrected SS	3284.625	Corrected SS	735.849615
Coeff Variation	54.0291572	Std Error Mean	0.29974544
Median	4.150000	Range	13.75000
Mode	3.300000	Interquartile Range	3.50000
Student's t	17.65601	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.869522	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
1.15	1	1.1	1.1	3.85	3	3.3	40.7	6.80	1	1.1	75.8
1.95	1	1.1	2.2	3.90	1	1.1	41.8	6.85	1	1.1	76.9
2.00	1	1.1	3.3	3.95	1	1.1	42.9	7.20	1	1.1	78.0
2.10	2	2.2	5.5	4.00	4	4.4	47.3	7.25	1	1.1	79.1
2.35	1	1.1	6.6	4.05	2	2.2	49.5	7.30	1	1.1	80.2
2.45	1	1.1	7.7	4.15	1	1.1	50.5	7.40	1	1.1	81.3
2.50	1	1.1	8.8	4.20	1	1.1	51.6	7.45	1	1.1	82.4
2.55	1	1.1	9.9	4.40	1	1.1	52.7	7.75	1	1.1	83.5
2.60	1	1.1	11.0	4.45	1	1.1	53.8	7.90	2	2.2	85.7
2.75	1	1.1	12.1	4.55	1	1.1	54.9	8.00	1	1.1	86.8
2.90	1	1.1	13.2	4.90	2	2.2	57.1	8.15	1	1.1	87.9
2.95	1	1.1	14.3	5.00	2	2.2	59.3	8.45	1	1.1	89.0
3.00	3	3.3	17.6	5.05	1	1.1	60.4	9.35	1	1.1	90.1
3.15	2	2.2	19.8	5.15	1	1.1	61.5	10.15	1	1.1	91.2
3.20	1	1.1	20.9	5.30	1	1.1	62.6	10.30	1	1.1	92.3
3.30	5	5.5	26.4	5.45	2	2.2	64.8	10.40	1	1.1	93.4
3.35	1	1.1	27.5	5.50	1	1.1	65.9	10.50	1	1.1	94.5
3.40	1	1.1	28.6	5.65	1	1.1	67.0	11.75	1	1.1	95.6
3.45	1	1.1	29.7	5.75	1	1.1	68.1	12.30	1	1.1	96.7
3.55	2	2.2	31.9	5.95	2	2.2	70.3	12.50	1	1.1	97.8
3.60	2	2.2	34.1	6.05	2	2.2	72.5	14.60	1	1.1	98.9
3.70	1	1.1	35.2	6.30	1	1.1	73.6	14.90	1	1.1	100.0
3.80	2	2.2	37.4	6.65	1	1.1	74.7				

```
Stem Leaf                      #        Boxplot
  14 69                        2           0
  13
  12 35                        2           0
  11 8                         1           |
  10 2345                      4           |
   9 4                         1           |
   8 024                       3           |
   7 22344899                  8           |
   6 00003688                  8        +-----+
   5 0002344568               10        |  +  |
   4 00000002244699           14        *-----*
   3 00002223333344466667888889 26      +-----+
   2 00114456689              11           |
   1 2                         1           |
     ----+----+----+----+----+-
```



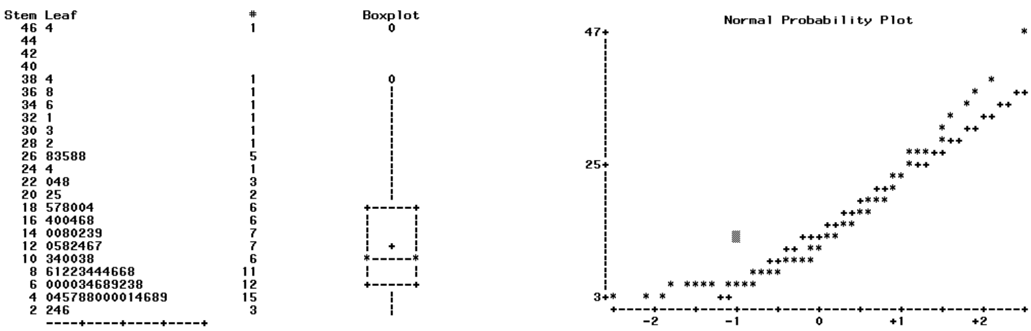
Appendix Figure B15 Selected items from PROC UNIVARIATE output fruit stalk thickness with the analysis of the *Solanum* spp. dataset.

Moments

N	91	Sum Weights	91
Mean	13.9027473	Sum Observations	1265.15
Std Deviation	9.24256867	Variance	85.4250757
Skewness	1.25069173	Kurtosis	1.46238094
Uncorrected SS	5277.3175	Corrected SS	7688.25681
Coeff Variation	66.4801604	Std Error Mean	0.96888446
Median	11.30000	Range	45.15000
Mode	6.05000	Interquartile Range	12.40000
Student's t	14.34923	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.889731	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
2.25	1	1.1	1.1	9.10	1	1.1	35.2	16.95	1	1.1	69.2
2.45	1	1.1	2.2	9.20	1	1.1	36.3	17.00	1	1.1	70.3
3.55	1	1.1	3.3	9.25	1	1.1	37.4	17.35	1	1.1	71.4
4.05	1	1.1	4.4	9.30	1	1.1	38.5	17.65	1	1.1	72.5
4.45	1	1.1	5.5	9.35	2	2.2	40.7	17.75	1	1.1	73.6
4.50	1	1.1	6.6	9.45	1	1.1	41.8	18.50	1	1.1	74.7
4.70	1	1.1	7.7	9.55	2	2.2	44.0	18.70	1	1.1	75.8
4.80	1	1.1	8.8	9.75	1	1.1	45.1	18.85	1	1.1	76.9
4.85	1	1.1	9.9	10.30	1	1.1	46.2	19.00	2	2.2	79.1
4.95	2	2.2	12.1	10.35	1	1.1	47.3	19.45	1	1.1	80.2
5.00	1	1.1	13.2	10.95	1	1.1	48.4	20.20	1	1.1	81.3
5.05	1	1.1	14.3	11.05	1	1.1	49.5	20.50	1	1.1	82.4
5.10	1	1.1	15.4	11.30	1	1.1	50.5	22.00	1	1.1	83.5
5.40	1	1.1	16.5	11.80	1	1.1	51.6	22.40	1	1.1	84.6
5.55	1	1.1	17.6	12.05	1	1.1	52.7	23.85	1	1.1	85.7
5.75	1	1.1	18.7	12.50	1	1.1	53.8	25.40	1	1.1	86.8
5.90	1	1.1	19.8	12.80	1	1.1	54.9	26.80	1	1.1	87.9
5.95	1	1.1	20.9	13.20	1	1.1	56.0	27.30	1	1.1	89.0
6.05	3	3.3	24.2	13.45	1	1.1	57.1	27.50	1	1.1	90.1
6.30	1	1.1	25.3	13.60	1	1.1	58.2	27.75	2	2.2	92.3
6.45	1	1.1	26.4	13.70	1	1.1	59.3	29.15	1	1.1	93.4
6.60	1	1.1	27.5	13.95	2	2.2	61.5	30.30	1	1.1	94.5
6.75	1	1.1	28.6	14.80	1	1.1	62.6	32.10	1	1.1	95.6
6.90	1	1.1	29.7	15.00	1	1.1	63.7	35.55	1	1.1	96.7
7.25	1	1.1	30.8	15.25	1	1.1	64.8	36.80	1	1.1	97.8
7.30	1	1.1	31.9	15.30	1	1.1	65.9	39.35	1	1.1	98.9
7.85	1	1.1	33.0	15.90	1	1.1	67.0	47.40	1	1.1	100.0
8.60	1	1.1	34.1	16.45	1	1.1	68.1				



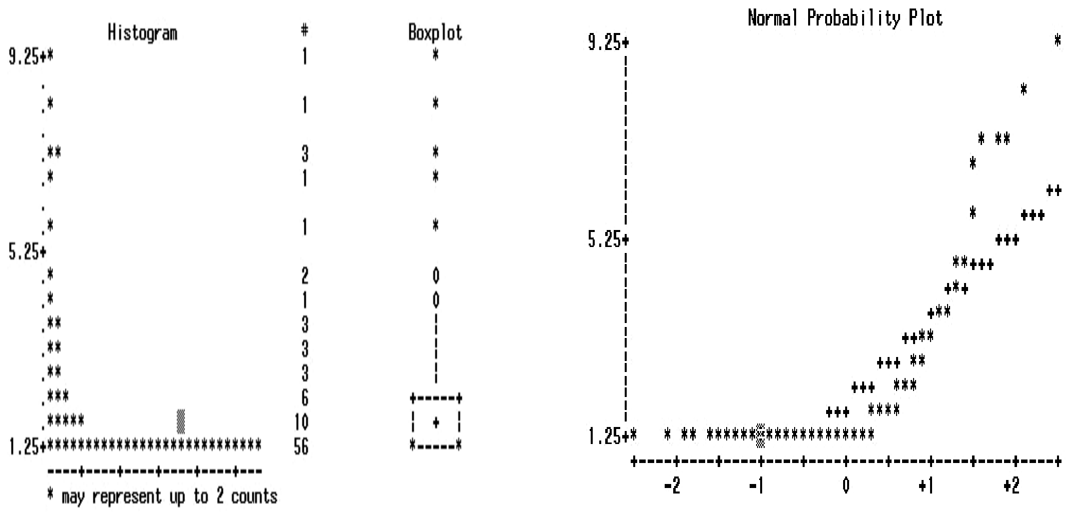
Appendix Figure B16 Selected items from PROC UNIVARIATE output fruit calyx length with the analysis of the *Solanum* spp. dataset.

Moments

N	91	Sum Weights	91
Mean	1.9010989	Sum Observations	173
Std Deviation	1.7547076	Variance	3.07899878
Skewness	2.40938523	Kurtosis	5.33929971
Uncorrected SS	606	Corrected SS	277.10989
Coeff Variation	92.2996486	Std Error Mean	0.18394334
Median	1.000000	Range	8.00000
Mode	1.000000	Interquartile Range	1.00000
Student's t	10.33524	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.585958	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
1.0	56	61.5	61.5	3.5	3	3.3	89.0	6.5	1	1.1	94.5
1.5	10	11.0	72.5	4.0	1	1.1	90.1	7.0	3	3.3	97.8
2.0	6	6.6	79.1	4.5	2	2.2	92.3	8.0	1	1.1	98.9
2.5	3	3.3	82.4	5.5	1	1.1	93.4	9.0	1	1.1	100.0
3.0	3	3.3	85.7								



Appendix Figure B17 Selected items from PROC UNIVARIATE output number of fruits per infructescence with the analysis of the *Solanum* spp. dataset.

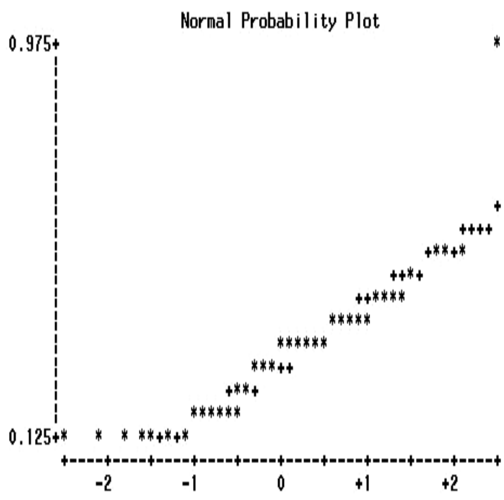
Moments

N	91	Sum Weights	91
Mean	0.28472527	Sum Observations	25.91
Std Deviation	0.1287404	Variance	0.01657409
Skewness	1.5763815	Kurtosis	7.05596144
Uncorrected SS	8.8689	Corrected SS	1.49166813
Coeff Variation	45.2156554	Std Error Mean	0.01349566
Median	0.300000	Range	0.86000
Mode	0.120000	Interquartile Range	0.18000
Student's t	21.09754	Pr > |t|	<.0001
Sign	45.5	Pr >= |M|	<.0001
Signed Rank	2093	Pr >= |S|	<.0001
Shapiro-Wilk (W)	0.878049	Pr < W	<0.0001

Frequency Counts

		Percents				Percents				Percents	
Value	Count	Cell	Cum	Value	Count	Cell	Cum	Value	Count	Cell	Cum
0.10	1	1.1	1.1	0.24	4	4.4	36.3	0.36	4	4.4	81.3
0.11	3	3.3	4.4	0.26	3	3.3	39.6	0.37	3	3.3	84.6
0.12	7	7.7	12.1	0.27	4	4.4	44.0	0.39	1	1.1	85.7
0.13	1	1.1	13.2	0.28	3	3.3	47.3	0.40	4	4.4	90.1
0.14	1	1.1	14.3	0.29	1	1.1	48.4	0.41	1	1.1	91.2
0.15	3	3.3	17.6	0.30	5	5.5	53.8	0.42	1	1.1	92.3
0.16	3	3.3	20.9	0.31	6	6.6	60.4	0.46	1	1.1	93.4
0.17	4	4.4	25.3	0.32	2	2.2	62.6	0.48	2	2.2	95.6
0.18	3	3.3	28.6	0.33	6	6.6	69.2	0.51	2	2.2	97.8
0.19	2	2.2	30.8	0.34	3	3.3	72.5	0.52	1	1.1	98.9
0.20	1	1.1	31.9	0.35	4	4.4	76.9	0.96	1	1.1	100.0

```
Stem Leaf                     #     Boxplot
   9 6                        1        *
   9
   8
   8
   7
   7
   6
   6
   5
   5 112                      3        |
   4 688                      3        |
   4 000012                   6        |
   3 555566667779            12     +------+
   3 0000011111122333333444  22     *------*
   2 66677778889             11     |  +   |
   2 04444                    5     |      |
   1 55566677778889          15     +------+
   1 0111222222234           13        |
     ----+----+----+----+--
 Multiply Stem.Leaf by 10**-1
```



Appendix Figure B18 Selected items from PROC UNIVARIATE output 100 seeds weight with the analysis of the *Solanum* spp. dataset.

CURRICULUM VITAE

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WORK PLACE	**:**	-
AWARDS	**:**	-
SCHORLARSHIP	**:**	Return Inturn in the Genetic Resources and Seed Unit, Asian Vegetable Research and Development Center (AVRDC) - The World Vegetable Center, Taiwan from 2005-2006