Association Mapping of SSR Markers to *Tomato Spotted Wilt Virus* Resistance in Cultivated Peanuts

by

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Abstract

Tomato Spotted Wilt Virus (TSWV), one of the most serious diseases in peanut, is transmitted by thrips (*Franklinieila occidentalis*). The mechanism of TSWV resistance and relevant genes in peanut are still unknown. Breeding and selection of resistant genotypes is the optimal method to manage TSWV in peanut. In order to more efficiently breed resistant cultivars, marker assisted selection should be implemented in breeding program. Therefore, the objectives of this study are to screen the U.S. peanut mini core collection to identify genotypes that are resistant to TSWV; to examine genetic diversity and population structure in the U.S. peanut mini core collection by SSR markers, and to conduct an association mapping of SSR markers to TSWV resistance in cultivated peanuts. One hundred eighteen genotypes of the U.S. peanut mini-core germplasm collection were used for screening for TSWV resistance by mechanical inoculation and ELISA assay. One hundred and thirty-three SSR markers were applied for genotyping the panel of 104 peanut genotypes. Two genotypes, PI356004 and PI493880, were identified as resistant to TSWV based on the data from mechanical inoculation, ELISA, and field evaluation. Four subpopulations were classified by population structure analysis, and corresponded to botanical varieties to a certain extent. Association mapping analysis indicated that the five markers, pPGPseq5D5, GM1135, GM1991, TC23C08, and TC24C06, were consistently associated with visual symptoms by four models, Q model, PCA model, Q+K model, and PCA+K model. These identified markers accounts for 36.4% of the phenotypic variance for TSWV resistance. Moreover, pPGPseq5D5 and GM1991 were both associated with visual symptoms and ELISA resulting in a high R^2. These highly resistant genotypes along with their associated markers could be used for the development of TSWV-resistant cultivars in peanut breeding programs.

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List of Abbreviations

AFLP	amplified fragment length polymorphism
AMOVA	analysis of molecular variance
ANOVA	analysis of variance
CAF	correlated allele frequencies
DAP	days after planting
DAS-ELISA	double antibody sandwich enzyme-linked immunosorbent assay
DPI	days postinoculation
EDTA	ethylenediaminetetraacetic acid
ELISA	enzyme-linked immunosorbent assay
EST	expressed sequence tag
F*st*	Fixation index
GenAlEx	genetic analysis in Excel
GLM	general linear model
GWAS	genome-wide association study
HR	hypersensitive response
ICRISAT	International Crops Research for the Semi-Arid Tropics
InDel	insertion and deletion
ISSR	inter simple sequence repeat
LD	linkage disequilibrium

MAS	marker-assisted selection
MCMC	Markov Chain Monte Carlo
MLM	mixed linear model
mM	millimolar
ng	nanogram
ORF	open reading frame
PC	principal component
PCA	principal component analysis
PCR	polymerase chain reaction
PIC	polymorphic information content
QTL	quantitative trait loci
RAPD	random amplified polymorphic DNA
RCB	randomized complete block
RdRp	RNA-dependent RNA polymerase
RFLP	restriction fragment length polymorphism
RIL	recombinant inbred line
S.W.E.A.T	spotted wilt eradication action team
SAS	Statistical Analysis Software
SCoT	start codon targeted polymorphism
SNP	single nucleotide polymorphism
SPAGeDi	Spatial Pattern Analysis of Genetic Diversity
SSR	simple sequence repeat
TSWV	tomato spotted wilt virus

UPGMA	unweighted pair group method with arithmetic average
USDA	United States Department of Agriculture
wt/vol	weight per volume
ΔK	second order rate of change of the likelihood
μl	microliter

CHAPTER ONE

LITERATURE REVIEW

INTRODUCTION OF PEANUT

The peanut (*Arachis hypogaea*) is a species in the legume or “bean” family (Fabaceae). It is widely grown throughout the tropical, subtropical, and warm areas of the world, and it is well-suited for growing in sandy soils. With 50% oil content, peanut is considered a typical oilseed crop (Worthington et al., 1972), and peanut oil is a major factor contributing to the economic value of peanut.

The peanut probably originated in South America, the center of origin most possibly being Brazil and Peru, where more than 10 wild species are found (Acquaah, 2012). In the 15th century, Spanish explorers introduced peanut into Spain, and then spread through Europe. In the 16th century, peanut spread from Europe to Africa by slave ship, and then reached North America via the slave trade. In the 18th century, peanut was planted in China, and then it spread to India and Japan. It took about 300 years to spread peanut to different areas all over the world (Stalker, 1997).

Worldwide, the production of peanut is about 30 million metric tons per year. China is the largest producer in the world followed by India and the U.S. (Soyatech, 2012). Worldwide peanut exports are around 1.25 million metric tons. The U.S., Argentina and China are three principal peanut exporters in the world. The exports of the U.S. is between 200,000 and 250,000 metric tons per year. Global average peanut yields have increased because of technological advances. The average yield was 849 kg ha^{-1} in 1961, and increased to 1774 kg ha^{-1} in 2011 (FAOSTAT, 2014).

Georgia (46%) is the largest producer of peanut in the U.S., followed by Florida (13%), Alabama (11%), Texas (9%), South Carolina (8%), and North Carolina (7%). These six states covered about 94% of all peanut grown in the U.S. in 2014. There are around 7,000 peanut farmers in these major producing regions (National Peanut Board, 2016).

Peanut is propagated commercially through seeds and the seeding time is in the spring, from late April to early June. The genus *Arachis* contains about 70 species (Krapovickas and Gregory, 1994), and almost of them are diploid with either an A genome or a B genome. Cultivated peanut is an allotetraploid ($2n = 4x = 40$) originating through the cross of two ancient diploid species, probably A. *duranensis* (A-genome) and A. *ipaensis* (B-genome) (Milla et al., 2005).

There are four market types for peanuts in USA – Runner, Virginia, Spanish, and Valencia. The market type is classified based on growth habit, seed and pod size. Runners have become the main peanut type grown in the U.S. since the early 1970's. Runners, accounting for 80% of national production, are grown mainly in Georgia, Alabama, Florida, Texas and Oklahoma. About 54% of this market type is used for making peanut butter. Virginias, accounting for about 15% of national production, are grown mainly in southeastern Virginia, North Carolina, South Carolina, and West Texas. Spanish, accounting for 4% of national production, are grown mainly in Oklahoma and Texas. This market type has higher oil content than the other types which is an advantage for oil production. Valencia, accounting for less than one percent of national production, are grown mainly in New Mexico (Soyatech, 2012).

INTRODUCTION OF TOMATO SPOTTED WILT VIRUS

Tomato spotted wilt virus (TSWV) is a species of the *Tospovirus* genus which is the only group known to infect both plants and insects in the family Bunyaviridae (Francki, et al., 1991). TSWV infects a wide range of crops and impacts agriculture in tropical and subtropical areas (Pappu et al., 2009). Tomato spotted wilt virus is the most economically important of more than 25 known tospoviruses, because its host range is more than 1,000 plant species (Scholthof et al., 2011). Host plants of TSWV include bean, lettuce, peanut, pepper, potato, tobacco, tomato and numerous ornamental species (Pappu, 2008).

Spotted wilt was first identified on tomato (*Solanum tuberosum* L.) in Australia in 1915 (Brittlebank, 1919), and was first reported to be caused by a virus in 1930 (SAMUEL et al., 1930). TSWV was first found on peanut in the United States in 1971 in southern Texas, but the disease has caused serious damage since 1984 (ACES, 1998). TSWV caused a yield reduction of up to 95% in Texas since 1986. The incidence of TSWV has been found to be up to 100% in sample fields through a survey of peanut fields in 10 counties of Georgia (Camann, 1995). The damage to peanut resulting from TSWV was estimated at more than $44 million in 1995 in

Georgia, approximately doubling the financial loss experienced by Georgia farmers in 1994 (Williams-Woodward, J, 2001).

The particles of TSWV are near pleiomorphic, 80-120 nm in diameter. It has a tripartite genome composed of three single-stranded RNAs labeled as L, M, and S (Adkins, 2000). The tripartite genome of TSWV contains five ORFs (Open Reading Frame) and uses a negative and ambisense coding strategy (Soellick et al., 2000). The S and M RNAs are ambisense and have two ORFs in their genome organization, while the L RNA is in negative polarity and only has one ORF (Jain et al., 1998). Due to this genome organization, TSWV is difficult to control and manage, because it recombines with related viruses to create genome heterogeneity when it faces new challenges. (Qiu et al., 1998). The L RNA (~9kb) codes for the RNA-dependent RNA polymerase (RdRp) of ~330 kDa (van Poelwuk et al., 1993). The M RNA (~4.8 kb) codes for a nonstructural protein (NSm) of 33.6 kDa, which plays an important role for viral movement among cells. (Kormelink et al., 1994). M RNA also codes for G1 (78 kDa) and G2 (58 kDa), which are the precursors of the membrane glycoproteins (Kormelink et al., 1992). The S RNA (~3kb) codes for the nonstructural protein NSs and the major component of the nucleocapsid N proteins. The NSs is a silencing suppressor directed contrary to the plant RNA silencing system, and the N protein combines with RNA to form homoligomeric structures (Bucher et al., 2003). The RdRp is known to perform together with host-encoded factors (Sin and McNulty, 2005), and must be cotransported with the viral RNA to permit transcription and replication in the freshly infected cells (Soellick et al., 2000). The G1 protein of TSWV and a 50-kDa protein of thrips collaborate with a receptor-mediated endocytosis and may allow TSWV entry to thrips midgut cells (Medeiros et al., 2000). Moreover, the G2 protein also combines with a 94-kDa protein of thrips (Kikkert et al., 1998). The N protein, which interacts with one of the two viral glycoproteins, may play a role in controlling the transcription and replication. It has been commonly used to induce resistance to pathogen-derived virus (Yang and Campus, 2004). The first example for transgenic resistance to TSWV was achieved by introducing the TSWV N protein gene into *Nicotiana tabacum* plants (Gielen et al., 1991).

TSWV is transmitted by thrips. Thrips are a hemimetabolous insect with a small, cylindrical and slender body. Their size ranges from 0.5 to 5.0 mm long (Lewis, 1997; Triplehorn and Borror, 2005). Worldwide, at least ten species of thrips are reported to be vectors of TSWV (Jones, 2005). The western flower thrips (*Franklinieila occidentalis*) and the tobacco thrips (*F. fusca*), are two major vectors occurring in most peanut producing areas of the U.S. (Lowry et al., 1992). The life cycle of thrips contains six major stages, which include an egg stage, two wingless larval stages, two non-feeding pupal stages, and an adult stage (Whitfield et al., 2005; Riley et al., 2011). It takes thrips about 20-30 days to develop from egg to adult depending on the environmental conditions (Ananthakrishnan, 1993; Whitfield et al., 2005). Thrips can be infected by tospovirus at any phase of development. However, thrips must acquire the virus at first instar larvae stage in order for adults to successfully transmit the virus to plants. (Moritz et al., 2004). There is a positive correlation between the ability of thrips to acquire TSWV and the thrips age. Adults transmit the virus from infected salivary glands, and uninfected adults will not transmit the virus (Groves et al., 2003). Adult thrips do not transmit the virus to progeny, however, overlapping stages in life cycle may lead to virus spread (Lewis, 1997). In Alabama, the peak of thrips populations on peanuts is about 2 to 4 weeks after seedling emergence and weakens sharply after 6 weeks. Feeding damage on peanut seedlings is more obvious at this stage because their growth is slow. The feeding damage will be suppressed when peanuts begin rapid growth (Austin Hagan, et al., 1998).

TOMATO SPOTTED WILT ON PEANUT

Symptoms of tomato spotted wilt are variable among different hosts and even in a single host species. Symptoms in certain crops are obvious only under certain environmental conditions. For example, in tobacco, more and earlier developmental symptoms occur at 20°C when compared to 15°C. Generally, if plants are older, the infection will cause less symptoms compared to young plants. For example, the degree of stunting in tobacco is less when older plants are infected. Symptoms may occur from 3 to 14 days after inoculation in general, however, symptoms may not occur for several weeks under some conditions (Kucharek et al., 1990). TSWV causes a wide range of symptoms on peanut. These include concentric ringspots; different chlorosis on leaflets; stunting of all above-ground plant parts; small and/or misshapen carpophores, pods, and kernels; and reddish discoloration and cracking of the seed coats (Halliwel and Philley, 1974). The severity ranges from slight spotting on a few leaves to serious stunting and even death. The reduction of yield, pods, and kernel size caused by TSWV will decrease, as the time of initial symptoms appearance is delayed. (Culbreath et al., 1992). Roots commonly show various degrees of necrosis as a symptom, which can lead to death (Culbreath, 1991). Infected plants may also show no symptoms. Based on immunoassays of root tissue from field-grown plants, incidence of asymptomatic infections is the same as the incidence based on visible symptoms (Culbreath et al., 1992b).

A spotted wilt eradication action team (S.W.E.A.T.) (researchers from Florida and Georgia for improving the management of spotted wilt on peanut) has identified several management techniques for reducing yield and quality losses due to TSWV. These include cultivar selection, planting date, plant population, row pattern, tillage system, and application of phorate in the furrow. Some peanut cultivars such as' Florunner', 'Georgia Runner', 'SunOleic 97R', and 'GK-7' were extremely susceptible to TSWV (Culbreath et al., 2003). Some resistance sources have been identified from screening peanut germplasm collection and breeding lines, and three generations of TSWV-resistant peanut cultivars have been released. In general, the third generation TSWV resistant cultivars had significantly lower TSWV incidence, higher yield, and better grade (Branch and Culbreath, 2011; Branch, 2013). Although the incidence of TSWV and severity of spotted wilt are significant lower than susceptible cultivars such as 'Florunner', none of these resistant cultivars is immune to TSWV. They still get significant infection under high TSWV pressure. Planting date is an important factor for reducing TSWV infection (Mitchell et al., 1991). Disease incidence is higher in early plantings than when plantings are delayed until after mid-May (Brown et al., 1995). This may due to the larger population of thrips during April than May (Culbreath et al., 1999). It was reported that there was a negative correlation between TSWV incidence and plant population density, that is to say a lower plant density leads to more TSWV infection than a denser plant spacing (Gorbet and Shokes, 1994). Moreover, Brown et al. (1996) reported that the effect of plant spacing became more significant when TSWV incidence became greater. It was reported that a twin-row pattern with 18 to 25 cm spacing between paired rows lead to higher yield and an approximate 25 to 30% reduction of TSWV incidence compared to single-row planting patterns (Baldwin et al., 1997). Brown et al. (1996) reported lower thrips populations and less thrips feeding injury in no-tilled plots compared to conventionally tilled plots. Insecticide application is ineffective in preventing TSWV infection (Todd and Culbreath, 1995; Todd et al., 1995), but it was reported that application of phorate insecticide in-furrow showed consistent, low level inhibition against TSWV (Brown, 1999). There was a hypothesis that phorate may induce peanut genes responsible for defense against pathogens (Gallo-Meagher and Chengalrayan, 2001).

With regard to host-plant resistant genes responsible for TSWV, genotypes of tomato and pepper with dominant genes *Sw-5* and *Tsw*, respectively, confer resistance to TSWV by exhibiting a hypersensitive response (HR) (Stevens et al., 1991; Boiteux and Avila, 1994; Moury et al., 1997). HR leads to rapid death of cells at virus entry sites, thus, limits virus spread to other cells in the plant. In contrast, no such genes have been found with resistance to TSWV in peanut, and the mechanisms of resistance in peanut remains unknown. Recently, Shrestha et al. (2013) reported that they used thrips-mediated transmission to evaluate four resistant genotypes and a susceptible genotype in greenhouse. The results showed that some resistant genotypes had reduced viral loads (fewer TSWV N-gene copies) than the susceptible genotype, and the incidence of TSWV on the susceptible genotype was significantly higher than on resistance genotypes. However, Sundaraj et al. (2014) used mechanical inoculation to evaluate another four resistant genotypes and the same susceptible genotype in the field, but the results were different from Shrestha et al. (2013). In contrast, the results showed that the incidence of TSWV and estimation of TSWV nucleocapsid (N) gene copies did not reveal significant differences between resistant and susceptible genotypes. Thereby Sundaraj et al (2014) concluded that the resistance observed in the field could be not only a reaction to the effects of the virus on the host plant but also the interactions between thrips and peanut.

PEANUT GENETIC DIVERSITY AND MOLECULAR MARKERS

Genetic diversity plays an important role in plant breeding. Information about genetic diversity has a significant influence on the effectiveness of plant breeding for further crop improvement (Hallauer and Miranda, 1981; Hoisington et al., 1999). Even though cultivated peanut genotypes show various morphological, physiological and agronomic traits, the genetic diversity of cultivated peanut is low, as resulting from the single hybridization event between two ancient diploid species, such as *Arachis duranensis* (A genome) and *Arachis ipaensis* (B genome)(Burow et al., 2009; Nagy et al., 2012; Shirasawa et al., 2013). As a result of low genetic diversity in cultivated peanuts, a very limited number of polymorphic DNA markers have been detected. This has made peanut molecular research, such as genetic mapping, marker-assisted selection, resistance gene cloning, and crop evolutionary studies lagged behind other crops (He et al., 2003). With the ongoing peanut genome project, development and applications of molecular markers have steadily progressed.

Microsatellites, also known as simple sequence repeats (SSR), is a motif consisting of one to six bases sequences repeating a number of times, and dispersed throughout the genomes frequently and randomly (Tang et al., 2007). Until now, SSR markers have been the most widely used DNA marker to describe genetic diversity in germplasm collections of crops because of their high degree of polymorphism, high abundance, codominant expression, ease of use, readily transferable and relatively low cost (Vignal et al., 2002; Weber, 1990). The advantages of SSRs over other markers will become more obvious when they are used to track desirable traits in large scale breeding programs and as anchor points for map-based gene cloning (He et al., 2003). SSR markers have been developed using sequences derived from SSR-enriched genomic libraries and expressed sequence tags (ESTs), but the level of polymorphism is very low in cultivated peanut and high in wild peanut (Hopkins et al., 1999; He et al., 2003; Moretzsohn et al., 2004; Liang et al., 2009; Song et al., 2010; Zhang et al., 2012; Wang et al., 2012; Koilkonda et al., 2012). They have been used in detecting the genetic diversity for the U.S., Chinese and ICRISAT peanut mini-core collections (Cuc et al., 2008; XiaoPing et al., 2010; Moretzsohn et al., 2013), and construction of genetic linkage maps (Varshney et al., 2009; Hong et al., 2010; Qin et al., 2012; Nagy et al., 2012; Gautami et al., 2012; Shirasawa et al., 2013). To date, these existing maps do not have adequate markers to be highly useful for the genetic studies, and there is still a great need for development of novel SSR markers.

Single nucleotide polymorphism (SNP) is a single base pair position in genomic DNA, where a high substitution rate has been shown among individual samples in a population (Brookes, 1999). More recently, SNP markers have attracted high attention because of automatic genotyping, various of analysis method, and high density of genetic map (Khlestkina and Salina, 2006). However, most SNPs are bi-allelic, thus, making a low PIC value as illustrated in wheat with 0.27±0.23 (Somers et al., 2003). The functional SNP markers, detected from *FAD2A* and *FAD2B* genes by a real-time PCR genotyping (Barkley et al., 2009, 2011), have been used to screen the U.S. mini-core collection (Wang et al., 2013). In 2012, the first SNP marker-based genetic map was successfully constructed for the AA genome in wild peanut (Nagy et al., 2012). Afterwards, a SNP genetic map was constructed in cultivated peanut in 2014 (Zhou et al., 2014).

Other types of molecular markers, such as random amplified polymorphic DNA (RAPD) (Williams et al., 1990; Burow et al., 1996; Subramanian et al., 2000), amplified fragment length polymorphism (AFLP) (He and Prakash, 1997; Vos et al., 1995; Herselman et al., 2004), inter simple sequence repeat (ISSR) markers (Zietkiewicz et al., 1994; Raina et al., 2001), restriction fragment length polymorphism (RFLP) (Halward et al., 1991; Garcia et al., 1995), insertion and deletion (InDel) (Liu et al., 2015), start codon targeted polymorphism (SCoT) (Xiong et al., 2011), also have been developed and used for studying the genetic diversity and association study in cultivated peanut, but they have been used less widely than the SSR and SNP platforms.

ASSOCIATION MAPPING IN CULTIVATED PEANUTS

A quantitative trait locus (QTL) is a section of DNA which correlates with variation in a quantitative phenotype. The QTL normally links to, or contains, the genes that control the phenotype. The goal of QTL mapping is to identify markers for marker-assisted selection (MAS) which could enhance the efficiency of selection in plant breeding (Li et al., 2011). There are two approaches in genetic mapping. One is traditional bi-parental mapping whose populations derive from crosses of two individual genotypes. However, the restricted recombination events limit the genetic resolution. Moreover, the bi-parental mapping approach requires more time and effort to create large enough populations. In addition, it requires more steps to precisely pinpoint the location of the QTL or clone the gene. Another approach is association mapping, which uses the recombination events from many lineages, and exploits relationships between markers and traits in a much broader germplasm. The first step in association mapping is to identify the markers with unequal distribution of alleles among the individuals for a trait, and then we can identify the markers that have association with a particular trait of interest (Schafer and Hawkins, 1998). In association mapping, the cost of time and money is much lower compared with traditional mapping, and the precision of QTL location is much higher. Moreover, since association analysis is conducted using broad germplasm with a diverse genetic background, it’s more efficient to identify association between markers and traits ((Zeng et al., 2009). Association mapping relies on linkage disequilibrium (LD) resulting from physical linkage between markers and trait loci.

However, unlike a population such as F_2 or RIL (recombinant inbred line), the observed LD in a natural or breeding population also could be caused by nonlinkage factors like genetic drift, selection and population admixture (Jannink and Walsh, 2002; Flint-Garcia et al., 2003; Mackay and Powell, 2007). Thus, LD could be observed between unlinked loci, which could cause false positive associations. The number of false association can be reduced by comprising the population structure and kinship relatedness among individuals (Stich et al., 2008). In addition, this problem also can be partially solved by using random mating populations. In some degree, the LD between QTLs and unlinked markers could decrease, as the recombination rate increases (Zeng et al., 2009).

Association analysis was first applied in human to identify loci responsible for certain diseases (Risch and Merikangas, 1996). In plants, this method was first used to identify associations with flowering time in maize (Thornsberry et al., 2001). So far, association mapping has been applied in over ten plant species, such as glutinous phenotype and yield in rice (Olsen and Purugganan, 2002; Agrama et al., 2007), heading date and flowing time in perennial ryegrass (Skøt et al., 2005, 2007), late blight resistance in potato (Malosetti et al., 2007), salt tolerance in wild barley (Ivandic et al., 2003) and fiber traits in cotton (Kantartzi and Stewart, 2008). In peanut, the first attempt at association mapping was reported by Wang et al. (2011). In this study, 81 SSR markers and two functional SNP markers from *FAD2* were applied in 94 *Arachis hypogaea* mini core collection germplasm accessions for association mapping of seed quality traits in peanut. YAN et al., (2013) applied 64 SSR markers in 136 accessions and found 4 markers associated with quality traits based on 3-years phenotyping data. More recently, a genome-wide association study (GWAS) in peanut has been reported, in which 300 genotypes were tested for 36 traits including biotic and abiotic resistances, seed quality and yield. (Pandey et al., 2014).

OBJECTIVES

The goal of this research was to screen the U.S. peanut mini core collection for TSWV resistance and detect the QTL responsible for the resistance. In particular, the objectives of this research were to

1. Evaluate the resistance for TSWV in the U.S. peanut mini core germplasm collection by mechanical inoculation in greenhouse and compare greenhouse results to field evaluation;
2. Examine genetic diversity and population structure in the U.S. peanut mini core collection by SSR markers;
3. Conduct association mapping of SSR markers to TSWV resistance in cultivated peanuts.

REFERENCES

ACES (Alabama Cooperative Extension System): Tomato Spotted Wilt Virus on Peanuts. 1998. [online] Available at: http://www.aces.edu/pubs/docs/A/ANR-0574/ANR-0574.pdf.

Acquaah, G. 2012. Principles of Plant Genetics and Breeding: Second Edition.

Adkins, S. 2000. Tomato spotted wilt virus-positive steps towards negative success. Mol. Plant Pathol. 1(3): 151–157.

Agrama, H.A., G.C. Eizenga, and W. Yan. 2007. Association mapping of yield and its components in rice cultivars. Mol. Breed. 19(4): 341–356.

Ananthakrishnan, T.N. 1993. Bionomics of Thrips. Annu. Rev. Entomol. 38(1): 71–92.

Anderson, W.F., C.C. Holbrook, and a. K. Culbreath. 1996. Screening the Peanut Core Collection for Resistance to Tomato Spotted Wilt Virus. Peanut Sci. 23: 57–61.

Baldwin, J., J.B. Jr, A. Culbreath, and S. Brown. 1997. Twin versus single row patterns for peanut production. Proc. Am. Peanut Res. Ed. Soc (Vol. 29, p. 20).

Barkley, N.A., K.D.C. Chamberlin, M.L. Wang, and R.N. Pittman. 2009. Development of a real-time PCR genotyping assay to identify high oleic acid peanuts (Arachis hypogaea L.). Mol. Breed. 25(3): 541–548.

Barkley, N.A., M.L. Wang, and R.N. Pittman. 2011. A real-time PCR genotyping assay to detect FAD2A SNPs in peanuts (Arachis hypogaea L.). Electron. J. Biotechnol. 14(1): 1–9.

Boiteux, L., and A. De Avila. 1994. Inheritance of a resistance specific to tomato spotted wilt tospovirus in Capsicum chinense “PI 159236.” Euphytica.

Branch, W. 2013. Registration of “Georgia-12Y”peanut. J. Plant Regist.

Branch, W., and A. Culbreath. 2011. Registration of “Georgia-10T”peanut. J. Plant Regist.

Brittlebank, C.C. 1919. Tomato diseases. J. Dep. Agric. Victoria. 17: 1348–1352.

Brookes, A.J. 1999. The essence of SNPs. Gene 234(2): 177–186.

Brown, S. 1999. Tomato spotted wilt of peanut: Identifying and avoiding high-risk situations. Cooperative Extension Service, The University of Georgia College of Agriculture.

Brown, S.L., Todd, J.W. and Culbreath, A.K., 1995. Effect of selected cultural practices on incidence of tomato spotted wilt virus and populations of thrips vectors in peanuts. Tospoviruses and Thrips of Floral and Vegetable Crops 431, pp.491-498.

Bucher, E., Sijen, T., de Haan, P., Goldbach, R. and Prins, M., 2003. Negative-strand tospoviruses and tenuiviruses carry a gene for a suppressor of gene silencing at analogous genomic positions. Journal of Virology, 77(2), pp.1329-1336.

Burow, M.D., C.E. Simpson, M.W. Faries, J.L. Starr, and A.H. Paterson. 2009. Molecular biogeographic study of recently described B- and A-genome Arachis species, also providing new insights into the origins of cultivated peanut. Genome 52(2): 107–119.

Burow, M.D., C.E. Simpson, A.H. Paterson, and J.L. Starr. 1996. Identification of peanut (Arachis hypogaea L.) RAPD markers diagnostic of root-knot nematode (Meloidogyne arenaria (Neal) Chitwood) resistance. Mol. Breed. 2(4): 369–379.

Camann, M. a. 1995. Spatial and Temporal Patterns of Spotted Wilt Epidemics in Peanut. Phytopathology 85: 879.

Cuc, L.M., E.S. Mace, J.H. Crouch, V.D. Quang, T.D. Long, and R.K. Varshney. 2008. Isolation and characterization of novel microsatellite markers and their application for diversity assessment in cultivated groundnut (Arachis hypogaea). BMC Plant Biol. 8(1): 55.

Culbreath, A.K., Csinos, A.S., Brenneman, T.B., Demski, J.W. and Todd, J.W., 1991. Association of tomato spotted wilt virus with foliar chlorosis of peanut in Georgia. Plant Disease, 75(8), pp.863-863.

Culbreath, A.K., Todd, J.W. and Brown, S.L., 2003. Epidemiology and management of tomato spotted wilt in peanut. Annual review of phytopathology, 41(1), pp.53-75.

Culbreath, A.K., Todd, J.W. and Demski, J.W., 1992. Productivity of Florunner peanut infected with tomato spotted wilt virus. Peanut Science, 19(1), pp.11-14.

Culbreath, A.K., Todd, J.W. and Demski, J.W., 1992. Comparison of hidden and apparent spotted wilt epidemics in peanut. In Proc. Am. Peanut Res. Ed. Soc (Vol. 24, p. 39).

Culbreath, a. K., J.W. Todd, D.W. Gorbet, S.L. Brown, J. a. Baldwin, H.R. Pappu, C.C. Holbrook, and F.M. Shokes. 1999. Response of Early, Medium, and Late Maturing Peanut Breeding Lines to Field Epidemics of Tomato Spotted Wilt. Peanut Sci. 26(2): 100–106.

Flint-Garcia, S.A., J.M. Thornsberry, and E.S. Buckler. 2003. Structure of linkage disequilibrium in plants. Annu. Rev. Plant Biol. 54: 357–74.

Francki, R.I.B., Fauquet, G.M., Knudson, D.L. et al. 1991. Classification and nomenclature of viruses: fifth report of the International Committee on Taxonomy of Viruses. Arch Virol 2: 223–233.

Food and Agricultural Organization of the United Nations 2014. [Online]. Available http://faostat.fao.org

Gallo-Meagher, M., Chengalrayan, K., Davis, J.M. and McDonald, G.E., 2001. Phorateinduced peanut genes that may condition acquired resistance to tomato spotted wilt. Proc. Am. Peanut Res. Edu. Soc, 33, p.29.

Garcia, G.M., H.T. Stalker, and G. Kochert. 1995. Introgression analysis of an interspecific hybrid population in peanuts (Arachis hypogaea L.) using RFLP and RAPD markers. Genome 38(1): 166–176.

Gautami, B., D. Foncéka, M.K. Pandey, M.C. Moretzsohn, V. Sujay, H. Qin, Y. Hong, I. Faye, X. Chen, A. BhanuPrakash, T.M. Shah, M.V.C. Gowda, S.N. Nigam, X. Liang, D.A. Hoisington, B. Guo, D.J. Bertioli, J.-F. Rami, and R.K. Varshney. 2012. An international reference consensus genetic map with 897 marker loci based on 11 mapping populations for tetraploid groundnut (Arachis hypogaea L.). PLoS One 7(7): e41213.

Gielen, J.J.L., P. de Haan, A.J. Kool, D. Peters, M.Q.J.M. van Grinsven, and R.W. Goldbach. 1991. Engineered Resistance to Tomato Spotted Wilt Virus, a Negative–Strand RNA Virus. Bio/Technology 9(12): 1363–1367.

Gorbet, D.W. and Shokes, F.M., 1994. Plant spacing and tomato spotted wilt virus. In Proc. Am. Peanut Res. Educ. Soc (Vol. 26, p. 50).

Groves, R.L., J.F. Walgenbach, J.W. Moyer, and G.G. Kennedy. 2003. Seasonal dispersal patterns of Frankliniella fusca (Thysanoptera: Thripidae) and tomato spotted wilt virus occurrence in central and eastern North Carolina. J. Econ. Entomol. 96(1): 1–11.

Hallauer, A.R. and Miranda, J.B., 1958. Fo. 1988. Quantitative genetics in maize breeding. Iowa State Univ Press, Ames, IA. Jenkins, JN, WL Parrott, JC McCarty Jr & RL Shepherd, 1988a. Registration of three noncommercial germplasm lines of upland cotton tolerant to tobacco budworm. Crop Sci, 28, p.869.

Halliwel. RS and Philley, G., 1974. Spotted wilt of peanut in Texas. Plant Disease Reporter, 58(1), pp.23-25.

Halward, T., H. Stalker, E. Larue, and G. Kochert. 1991. Genetic variation detectable with molecular markers among unadapted germ-plasm resources of cultivated peanut and related wild species. Genome 34(1965): 1013–1020.

He, G., R. Meng, M. Newman, G. Gao, R.N. Pittman, and C.S. Prakash. 2003. Microsatellites as DNA markers in cultivated peanut (Arachis hypogaea L .). 6: 1–6.

He, G., and C.S. Prakash. Identification of polymorphic DNA markers in cultivated peanut (Arachis hypogaea L.). Euphytica 97(2): 143–149.

Herselman, L., R. Thwaites, F.M. Kimmins, B. Courtois, P.J.A. Van Der Merwe, and S.E. Seal. 2004. Identification and mapping of AFLP markers linked to peanut (Arachis hypogaea L.) resistance to the aphid vector of groundnut rosette disease. Theor. Appl. Genet. 109(7): 1426–1433.

Hoisington, D., M. Khairallah, T. Reeves, J.M. Ribaut, B. Skovmand, S. Taba, and M. Warburton. 1999. Plant genetic resources: what can they contribute toward increased crop productivity? p. 5937–5943. *In* Proceedings of the National Academy of Sciences of the United States of America.

Hong, Y., X. Chen, X. Liang, H. Liu, G. Zhou, S. Li, S. Wen, C.C. Holbrook, and B. Guo. 2010. A SSR-based composite genetic linkage map for the cultivated peanut (Arachis hypogaea L.) genome. BMC Plant Biol. 10: 17.

Hopkins, M., A. Casa, T. Wang, and S. Mitchell. 1999. Discovery and characterization of polymorphic simple sequence repeats (SSRs) in peanut. Crop Sci. 39: 1243–1247.

Ivandic, V., W.T.B. Thomas, E. Nevo, Z. Zhang, and B.P. Forster. 2003. Associations of simple sequence repeats with quantitative trait variation including biotic and abiotic stress tolerance in Hordeum spontaneum. Plant Breed. 122(4): 300–304.

Jain, R.K., S.S. Pappu, H.R. Pappu, A.K. Culbreath, and J.W. Todd. 1998. Molecular Diagnosis of Tomato Spotted Wilt Tospovirus Infection of Peanut and Other Field and Greenhouse Crops. Plant Dis. 82(8): 900–904.

Jannink, J.L. and Walsh, B., 2002. Association mapping in plant populations. Quantitative genetics, genomics and plant breeding, pp.59-68.

Jones, D.R., 2005. Plant viruses transmitted by thrips. European Journal of Plant Pathology, 113(2), pp.119-157.

Kantartzi, S.K., and J.M. Stewart. 2008. Association analysis of fibre traits in Gossypium arboreum accessions. Plant Breed. 127(2): 173–179.

Khlestkina, E.K., and E.A. Salina. 2006. SNP markers: Methods of analysis, ways of development, and comparison on an example of common wheat. Russ. J. Genet. 42(6): 585–594.

Kikkert, M., C. Meurs, F. van de Wetering, S. Dorfmüller, D. Peters, R. Kormelink, and R. Goldbach. 1998. Binding of Tomato Spotted Wilt Virus to a 94-kDa Thrips Protein. Phytopathology 88(1): 63–9.

Koilkonda, P., S. Sato, S. Tabata, K. Shirasawa, H. Hirakawa, H. Sakai, S. Sasamoto, A. Watanabe, T. Wada, Y. Kishida, H. Tsuruoka, T. Fujishiro, M. Yamada, M. Kohara, S. Suzuki, M. Hasegawa, H. Kiyoshima, and S. Isobe. 2012. Large-scale development of expressed sequence tag-derived simple sequence repeat markers and diversity analysis in Arachis spp. Mol. Breed. 30(1): 125–138.

Kormelink, R., P. de Haan, C. Meurs, D. Peters, and R. Goldbach. 1992. The nucleotide sequence of the M RNA segment of tomato spotted wilt virus, a bunyavirus with two ambisense RNA segments. J. Gen. Virol. 73 (Pt 11(11): 2795–804.

Kormelink, R., M. Storms, J. Van Lent, D. Peters, and R. Goldbach. 1994. Expression and subcellular location of the NSM protein of tomato spotted wilt virus (TSWV), a putative viral movement protein. Virology 200(1): 56–65.

Krapovickas, A., and W.C. Gregory. 1994. TAXONOMIA DEL GENERO “ARACHIS (LEGUMINOSAE).” Bonplandia 8(1/4): 1–186.

Kucharek, T., Brown, L., Johnson, F. and Funderburk, J., 1990. Tomato spotted wilt virus of agronomic vegetable, and ornamental crops. Circular-Florida Cooperative Extension

Service (USA).

Lewis, T., 1997. Thrips as crop pests. Cab International.

Li, X., Y. Wei, K.J. Moore, R. Michaud, D.R. Viands, J.L. Hansen, A. Acharya, and E.C. Brummer. 2011. Association Mapping of Biomass Yield and Stem Composition in a Tetraploid Alfalfa Breeding Population. Plant Genome J. 4(1): 24.

Liang, X., X. Chen, Y. Hong, H. Liu, G. Zhou, S. Li, and B. Guo. 2009. Utility of EST-derived SSR in cultivated peanut (Arachis hypogaea L.) and Arachis wild species. BMC Plant Biol. 9: 35.

Liu, L., P.M. Dang, and C.Y. Chen. 2015. Development and Utilization of InDel Markers to Identify Peanut (Arachis hypogaea) Disease Resistance. Front. Plant Sci. 6: 1–11.

Lowry, V.K., Smith, J.W. and Mitchell, F.L., 1992. Life-fertility tables for Frankliniella fusca (Hinds) and F. occidentals (Pergande) (Thysanoptera: Thripidae) on peanut. Annals of the Entomological Society of America, 85(6), pp.744-754..

Mackay, I., and W. Powell. 2007. Methods for linkage disequilibrium mapping in crops. Trends Plant Sci. 12(2): 57–63.

Malosetti, M., C.G. Van Der Linden, B. Vosman, and F.A. Van Eeuwijk. 2007. A mixed-model approach to association mapping using pedigree information with an illustration of resistance to Phytophthora infestans in potato. Genetics 175(2): 879–889.

Medeiros, R.B., Ullman, D.E., Sherwood, J.L. and German, T.L., 2000. Immunoprecipitation of a 50-kDa protein: a candidate receptor component for tomato spotted wilt tospovirus

(Bunyaviridae) in its main vector, Frankliniella occidentalis. Virus research, 67(2), pp.109-118.

Milla, S.R., T.G. Isleib, and H.T. Stalker. 2005. Taxonomic relationships among Arachis sect. Arachis species as revealed by AFLP markers. Genome 48(1): 1–11.

Mitchell, F.L., Smith Jr, J.W., Crumey, C.R. and Stewart, J.W., 1991. Management of tomato spotted wilt virus in south Texas peanut fields. In Proc. Am. Peanut Res. Educ. Soc (Vol. 23, p. 76).

Moretzsohn, M.C., E.G. Gouvea, P.W. Inglis, S.C.M. Leal-Bertioli, J.F.M. Valls, and D.J. Bertioli. 2013. A study of the relationships of cultivated peanut (Arachis hypogaea) and its most closely related wild species using intron sequences and microsatellite markers. Ann. Bot. 111(1): 113–26.

Moretzsohn, M. de C., M.S. Hopkins, S.E. Mitchell, S. Kresovich, J.F.M. Valls, and M.E. Ferreira. 2004. Genetic diversity of peanut (Arachis hypogaea L.) and its wild relatives based on the analysis of hypervariable regions of the genome. BMC Plant Biol. 4: 11.

Moritz, G., Kumm, S. and Mound, L., 2004. Tospovirus transmission depends on thrips ontogeny. Virus research, 100(1), pp.143-149.

Moury, B., Palloix, A., Selassie, K.G. and Marchoux, G., 1997. Hypersensitive resistance to tomato spotted wilt virus in three Capsicum chinense accessions is controlled by a single gene and is overcome by virulent strains. Euphytica, 94(1), pp.45-52.

Nagy, E.D., Y. Guo, S. Tang, J.E. Bowers, R.A. Okashah, C.A. Taylor, D. Zhang, S. Khanal, A.F. Heesacker, N. Khalilian, A.D. Farmer, N. Carrasquilla-Garcia, R.V. Penmetsa, D. Cook, H.T. Stalker, N. Nielsen, P. Ozias-Akins, and S.J. Knapp. 2012. A high-density genetic map of Arachis duranensis, a diploid ancestor of cultivated peanut. BMC Genomics 13: 469.

National Peanut Board: Peanut Country, U.S.A. 2016. [online]. Avalible at: http://nationalpeanutboard.org/the-facts/peanut-country-u-s-a/.

Olsen, K.M., and M.D. Purugganan. 2002. Molecular evidence on the origin and evolution of glutinous rice. Genetics 162(2): 941–950.

Pandey, M.K., H.D. Upadhyaya, A. Rathore, V. Vadez, M.S. Sheshshayee, M. Sriswathi, M. Govil, A. Kumar, M.V.C. Gowda, S. Sharma, F. Hamidou, V.A. Kumar, P. Khera, R.S. Bhat, A.W. Khan, S. Singh, H. Li, E. Monyo, H.L. Nadaf, G. Mukri, S.A. Jackson, B. Guo, X. Liang, and R.K. Varshney. 2014. Genomewide association studies for 50 agronomic traits in peanut using the “reference set” comprising 300 genotypes from 48 countries of the semi-arid tropics of the world. PLoS One 9(8).

Pappu, H.R. 2008. Encyclopedia of Virology. Elsevier.

Pappu, H.R., R.A.C. Jones, and R.K. Jain. 2009. Global status of tospovirus epidemics in diverse cropping systems: Successes achieved and challenges ahead. Virus Res. 141(2): 219–236.

van Poelwuk, F., K. Boye, R. Oosterling, D. Peters, and R. Goldbach. 1993. Detection of the L Protein of Tomato Spotted Wilt Virus. Virology 197(1): 468–470.

Pritchard, J.K., M. Stephens, and P. Donnelly. 2000. Inference of population structure using multilocus genotype data. Genetics 155(2): 945–959.

Qin, H., S. Feng, C. Chen, Y. Guo, S. Knapp, A. Culbreath, G. He, M.L. Wang, X. Zhang, C.C. Holbrook, P. Ozias-Akins, and B. Guo. 2012. An integrated genetic linkage map of cultivated peanut (Arachis hypogaea L.) constructed from two RIL populations. Theor. Appl. Genet. 124(4): 653–664.

Qiu, W.P., S.M. Geske, C.M. Hickey, and J.W. Moyer. 1998. Tomato spotted wilt Tospovirus genome reassortment and genome segment-specific adaptation. Virology 244(1): 186–94.

Raina, S.N., V. Rani, T. Kojima, Y. Ogihara, K.P. Singh, and R.M. Devarumath. 2001. RAPD and ISSR fingerprints as useful genetic markers for analysis of genetic diversity, varietal identification, and phylogenetic relationships in peanut (Arachis hypogaea) cultivars and wild species. Genome 44(5): 763–772.

Riley, D.G., S. V. Joseph, R. Srinivasan, and S. Diffie. 2011. Thrips Vectors of Tospoviruses. J. Integr. Pest Manag. 2(1): 1–10.

Risch, N., and K. Merikangas. 1996. The future of genetic studies of complex human diseases. Science 273(5281): 1516–1517.

SAMUEL, G., J. G. BALD, and , H. A. PITTMAN. 1930. Investigations on ’spotted wilt ' of Tomatoes. Aust. Counc. Sci. Ind. Res. Bull. 44.

Schafer, A.J., and J.R. Hawkins. 1998. DNA variation and the future of human genetics. Nat. Biotechnol. 16(1): 33–9.

Scholthof, K.B.G., S. Adkins, H. Czosnek, P. Palukaitis, E. Jacquot, T. Hohn, B. Hohn, K.

Saunders, T. Candresse, P. Ahlquist, C. Hemenway, and G.D. Foster. 2011. Top 10 plant viruses in molecular plant pathology. Mol. Plant Pathol. 12(9): 938–954.

Shirasawa, K., D.J. Bertioli, R.K. Varshney, M.C. Moretzsohn, S.C.M. Leal-Bertioli, M. Thudi, M.K. Pandey, J.-F. Rami, D. Foncéka, M.V.C. Gowda, H. Qin, B. Guo, Y. Hong, X. Liang, H. Hirakawa, S. Tabata, and S. Isobe. 2013. Integrated consensus map of cultivated peanut and wild relatives reveals structures of the A and B genomes of Arachis and divergence of the legume genomes. DNA Res. 20(2): 173–84.

Shrestha, A., R. Srinivasan, S. Sundaraj, A.K. Culbreath, D.G. Riley, C. AK, and R. DG. 2013. Second generation peanut genotypes resistant to thrips-transmitted tomato spotted wilt virus exhibit tolerance rather than true resistance and differentially affect thrips fitness. J. Econ. Entomol. 106(2): 587–596.

Sin, S.H., McNulty, B.C., Kennedy, G.G. and Moyer, J.W., 2005. Viral genetic determinants for thrips transmission of Tomato spotted wilt virus. Proceedings of the National Academy of Sciences of the United States of America, 102(14), pp.5168-5173.

Sk ø t, L., M.O. Humphreys, I. Armstead, S. Heywood, K.P. Sk ø t, R. Sanderson, I.D. Thomas, K.H. Chorlton, and N.R.S. Hamilton. 2005. An association mapping approach to identify flowering time genes in natural populations of Lolium perenne (L.). Mol. Breed. 15(3): 233–245.

Sk ø t, L., J. Humphreys, M.O. Humphreys, D. Thorogood, J. Gallagher, R. Sanderson, I.P. Armstead, and I.D. Thomas. 2007. Association of candidate genes with flowering time and water-soluble carbohydrate content in Lolium perenne (L.). Genetics 177(1): 535–547.

Soellick, T., J.F. Uhrig, G.L. Bucher, J.W. Kellmann, and P.H. Schreier. 2000. The movement protein NSm of tomato spotted wilt tospovirus (TSWV): RNA binding, interaction with the TSWV N protein, and identification of interacting plant proteins. Proc. Natl. Acad. Sci. U. S. A. 97(5): 2373–2378.

Somers, D.J., R. Kirkpatrick, M. Moniwa, and A. Walsh. 2003. Mining single-nucleotide polymorphisms from hexaploid wheat ESTs. Genome / Natl. Res. Counc. Canada = Génome / Cons. Natl. Rech. Canada 46(3): 431–7.

Song, G.Q., M.J. Li, H. Xiao, X.J. Wang, R.H. Tang, H. Xia, C.Z. Zhao, and Y.P. Bi. 2010. EST sequencing and SSR marker development from cultivated peanut (Arachis hypogaea L.). Electron. J. Biotechnol. 13(3): 1–9.

Soyatech: The U.S. Market 2012. [Online]. Available at http://www.soyatech.com/peanut_facts.htm

Stalker, H.T. 1997. Peanut (Arachis hypogaea L.). F. Crop. Res. 53(1-3): 205–217.

Stevens, M.R., Scott, S.J. and Gergerich, R.C., 1991. Inheritance of a gene for resistance to tomato spotted wilt virus (TSWV) from Lycopersicon peruvianum Mill. Euphytica, 59(1), pp.9-17.

Stich, B., J. Möhring, H.-P. Piepho, M. Heckenberger, E.S. Buckler, and A.E. Melchinger. 2008. Comparison of mixed-model approaches for association mapping. Genetics 178(3): 1745–54.

Subramanian, V., S. Gurtu, R.C. Nageswara Rao, and S.N. Nigam. 2000. Identification of DNA polymorphism in cultivated groundnut using random amplified polymorphic DNA (RAPD) assay. Genome 43(4): 656–660.

Sundaraj, S., R. Srinivasan, A.K. Culbreath, D.G. Riley, and H.R. Pappu. 2014. Host Plant Resistance Against Tomato spotted wilt virus in Peanut (Arachis hypogaea) and Its Impact on Susceptibility to the Virus, Virus Population Genetics, and Vector Feeding Behavior and Survival. Phytopathology 104(2): 202–210.

Tang, R., G. Gao, L. He, Z. Han, S. Shan, R. Zhong, C. Zhou, J. Jiang, Y. Li, and W. Zhuang. 2007. Genetic Diversity in Cultivated Groundnut Based on SSR Markers. J. Genet. Genomics 34(5): 449–459.

Thornsberry, J.M., M.M. Goodman, J. Doebley, S. Kresovich, D. Nielsen, and E.S. Buckler. 2001. Dwarf8 polymorphisms associate with variation in flowering time. Nat. Genet. 28(july): 286–289.

Todd, J.W., Culbreath, A.K., Chamberlin, J.R., Beshear, R.J. and Mullinix, B.G., 1995. Colonization and population dynamics of thrips in peanuts in the southern United States. In Thrips biology and management (pp. 453-460). Springer US.

Todd, J.W., Culbreath, A.K. and Brown, S.L., 1995. Dynamics of vector populations and progress of spotted wilt disease relative to insecticide use in peanuts. Tospoviruses and Thrips of Floral and Vegetable Crops 431, pp.483-490.

Triplehorn, C.A.J., Borror, N.F., Triplehorn, D.J.C.A. and Johnson, N.F., 2005. Borror and

DeLong's introduction to the study of insects (No. QL463 B69 2005).

Varshney, R.K., D.J. Bertioli, M.C. Moretzsohn, V. Vadez, L. Krishnamurthy, R. Aruna, S.N. Nigam, B.J. Moss, K. Seetha, K. Ravi, G. He, S.J. Knapp, and D.A. Hoisington. 2009. The first SSR-based genetic linkage map for cultivated groundnut (Arachis hypogaea L.). Theor. Appl. Genet. 118(4): 729–39.

Vignal, A., D. Milan, M. SanCristobal, and A. Eggen. A review on SNP and other types of molecular markers and their use in animal genetics. Genet. Sel. Evol. 34(3): 275–305.

Vos, P., R. Hogers, M. Bleeker, M. Reijans, T. van de Lee, M. Hornes, A. Frijters, J. Pot, J. Peleman, and M. Kuiper. 1995. AFLP: a new technique for DNA fingerprinting. Nucleic Acids Res. 23(21): 4407–14.

Wang, M.L., C.Y. Chen, B. Tonnis, N. a. Barkley, D.L. Pinnow, R.N. Pittman, J. Davis, C.C. Holbrook, H.T. Stalker, and G. a. Pederson. 2013. Oil, fatty acid, flavonoid, and resveratrol content variability and FAD2A functional SNP genotypes in the U.S. peanut mini-core collection. J. Agric. Food Chem. 61(11): 2875–2882.

Wang, H., R.V. Penmetsa, M. Yuan, L. Gong, Y. Zhao, B. Guo, A.D. Farmer, B.D. Rosen, J. Gao, S. Isobe, D.J. Bertioli, R.K. Varshney, D.R. Cook, and G. He. 2012. Development and characterization of BAC-end sequence derived SSRs, and their incorporation into a new higher density genetic map for cultivated peanut (Arachis hypogaea L.). BMC Plant Biol. 12(1): 10.

Wang, M.L., S. Sukumaran, N. a. Barkley, Z. Chen, C.Y. Chen, B. Guo, R.N. Pittman, H.T.

Stalker, C.C. Holbrook, G. a. Pederson, and J. Yu. 2011. Population structure and marker-trait association analysis of the US peanut (Arachis hypogaea L.) mini-core collection. Theor. Appl. Genet. 123(8): 1307–1317.

Weber, J.L. 1990. Informativeness of human (dC-dA)n.(dG-dT)n polymorphisms. Genomics 7(4): 524–30.

Whitfield, A.E., Ullman, D.E. and German, T.L., 2005. Tospovirus-thrips interactions. Annu. Rev. Phytopathol., 43, pp.459-489.

Williams, J.G., A.R. Kubelik, K.J. Livak, J.A. Rafalski, and S. V Tingey. 1990. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. Nucleic Acids Res. 18(22): 6531–5.

Williams-Woodward, J. 2001. 2000 Georgia plant disease loss estimates. Univ. Georgia Coop. Ext. Serv. Pub. Path. 01-001, Athens, GA.

Worthington, R.E., R.O. Hammons, and J.R. Allison. 1972. Varietal differences and seasonal effects on fatty acid composition and stability of oil from 82 peanut genotypes. J. Agric. Food Chem. 20(3): 729–730.

XiaoPing, R., Z. XiaoJie, L. BoShou, L. Yong, H. JiaQuan, C. YuNing, and J. HuiFang. 2010. Analysis of genetic diversity in ICRISAT mini core collection of peanut (Arachis hypogaea L.) by SSR markers. Sci. Agric. Sin. 43(14): 2848–2858.

Xiong, F., R. Zhong, Z. Han, J. Jiang, L. He, W. Zhuang, and R. Tang. 2011. Start codon targeted polymorphism for evaluation of functional genetic variation and relationships in cultivated peanut (Arachis hypogaea L.) genotypes. Mol. Biol. Rep. 38(5): 3487–94.

YAN, M., HAN, S.Y., DONG, W.S., HUANG, B.Y., LIU, H., ZHANG, Z.X., XU, J., SUN, Z.Q., DU, P., SHANG, F.S. and ZHANG, X.Y., 2013. Association analysis betweeen quality traits and SSR markers in major peanut cultivars developed in China. Journal of Plant Genetic Resources, 14(6), pp.1064-1071.

Yang, H., and T. Campus. 2004. Field Evaluation of Tomato spotted wilt virus Resistance in Transgenic Peanut (Arachis hypogaea). Plant Dis. (March): 259–264.

Zeng, L., W.R. Meredith, O.A. Guti??rrez, and D.L. Boykin. 2009. Identification of associations between SSR markers and fiber traits in an exotic germplasm derived from multiple crosses among Gossypium tetraploid species. Theor. Appl. Genet. 119(1): 93–103.

Zhang, J., S. Liang, J. Duan, J. Wang, S. Chen, Z. Cheng, Q. Zhang, X. Liang, and Y. Li. 2012. De novo assembly and characterisation of the transcriptome during seed development, and generation of genic-SSR markers in peanut (Arachis hypogaea L.). BMC Genomics 13(1): 90.

Zhou, X., Y. Xia, X. Ren, Y. Chen, L. Huang, S. Huang, B. Liao, Y. Lei, L. Yan, and H. Jiang. 2014. Construction of a SNP-based genetic linkage map in cultivated peanut based on large scale marker development using next-generation double-digest restriction-site-associated DNA sequencing (ddRADseq). BMC Genomics 15(1): 351.

Zietkiewicz, E., A. Rafalski, and D. Labuda. 1994. Genome fingerprinting by simple sequence repeat (SSR)-anchored polymerase chain reaction amplification. Genomics 20(2): 176–83.

CHAPTER TWO

SCREENING THE U.S. PEANUT MINI CORE COLLECTION FOR *TOMATO SPOTTED WILT VIRUS* RESISTANCE BY MECHANICAL INOCULATION

ABSTRACT

Tomato spotted wilt virus (TSWV), one of the most serious diseases in peanut, is transmitted by thrips. It reduced yield of peanut up to 95% in Texas in 1986. No genotype has been shown to be completely immune to TSWV, especially when thrips pressure is high. Although the use of TSWV tolerant varieties is the primary tool for managing TSWV the mechanism of TSWV resistance and relevant genes in peanut are still unknown. The objective of this study is to identify the genotypes resistant to TSWV in the U.S. peanut mini core collection. One hundred eighteen genotypes of the U.S. peanut mini-core germplasm collection were used for screening for TSWV resistance under natural conditions in small field plot experiments, and a greenhouse experiment to specifically study TSWV susceptibility using mechanical inoculation and ELISA assay. Mechanical inoculation was used to study effects of the virus on the selected genotypes without confounding effects of thrips. Two genotypes, PI356004 and PI493880 were identified as resistant to TSWV based on the data from mechanical inoculation, ELISA, and field

evaluation. These highly resistant genotypes can be used to identify resistance genes and to develop TSWV-resistant cultivars in peanut breeding programs, and to conduct basic research on resistance mechanisms and genetics of resistance.

INTRODUCTION

Tomato spotted wilt virus (TSWV) is a species of the *Tospovirus* genus which is the only group known to infect both plants and insects in the family Bunyaviridae (Francki, et al., 1991). TSWV is the most widespread and destructive member in the *Tospovirus* genus (Sherwood et al., 2001). TSWV infects a wide range of crops, and impacts agriculture in tropical and subtropical areas (Pappu et al., 2009). The virus was first found in the U.S. in the 1980s in Texas, and then spread across the southern United States (Camann, 1995). TSWV has become a major restriction to peanut production in Alabama, Florida, Georgia, Mississippi, North Carolina and Texas (Mandal et al., 2002). The damage to peanut resulted from TSWV valued at least $44 million in 1995 in Georgia alone (Williams-Woodward, J, 2001).

TSWV causes a wide range of symptoms on peanut. These include concentric ringspots; various patterns of chlorosis on leaflets; stunting of above-ground plant parts; small and/or misshapen carpophores, pods, and kernels; and reddish discoloration and cracking of the seed coats (Halliwel and Philley, 1974). The severity of symptoms range from slight spotting on a few leaves to serious stunting and plant death. The reduction of yield, pods, and kernel size caused by TSWV symptoms are more severe in young plants. (Culbreath et al., 1992). Roots of infected plants commonly show various degrees of necrosis, which can lead to death (Culbreath, 1991).

TSWV is transmitted by several species of thrips; no mechanical transmission or seed transmission occurs in natural epidemic. The western flower thrips (*Franklinieila occidentalis*) and the tobacco thrips (*F. fusca*), are the two major vectors that occur in most peanut producing areas of the United States (Lowry et al., 1992). Thrips can be infected by tospovirus at any phase of development, however, thrips must acquire the virus as a first instar larvae in order to transmit the virus as an adult. Insecticides do not kill thrips before they are able to transmit the virus to plants, therefore, suppression of TSWV in the field is very challenging.

In order to reduce the loss resulted from TSWV, selection of resistant genotypes in breeding programs and use of genetically resistant cultivars is the optimal method of disease management. The objectives of this study were to evaluate the resistance to TSWV in the mini core collection of peanut germplasm in small field plot trials and by mechanical inoculation in the greenhouse. A limited number of cultivars with moderate levels of resistance to TSWV have been released and evaluated under field conditions in previous study (Anderson et al., 1996), and showed that the incidence of TSWV varied significantly among years, and the response of cultivars in the field may not indicate an accurate level of genetic resistance (Mandal et al.,2002). Due to this we evaluated the mini core collection under both field conditions, and in a greenhouse study using mechanical inoculation to evaluate susceptibility of the mini core genotypes in the greenhouse condition without confounding environmental and thrips related effects.

MATERIALS AND METHODS

Genotypes. One hundred and eighteen peanut accessions from the USDA peanut germplasm collection in Griffin, GA were used in this study, in which 104 genotypes were selected from the US peanut mini-core collection and additional 14 genotypes were selected to present two botanical types (*hirsut*a var.and *aequatoriana* var.) that are not presenting in the mini-core collection (Table 2.1). ‘Georgia Green’ has been commonly used as a susceptible standard in TSWV evaluations. It had a moderate field resistance to TSWV, but it is much more susceptible to TSWV compared to most recent released cultivars. Therefore, Georgia green was employed as a susceptible control in this study.

Peanut genotypes were grown in the greenhouse at the temperature of 25 to 30 °C, and 60 to 90% relative humidity. Nine seeds per genotype were sown in a plastic seedling trays (3.10" x 3.10" x 2.33" per cell) containing all-purpose professional growing mix consisting of Canadian sphagnum teat moss, coarse perlite, vermiculite, and dolomitic limestone (Sun Gro Horticulture, Agawam, MA).

Phenotyping in the field. One hundred and eighteen selected peanut genotypes were planted in the field at Auburn University, Wiregrass Research and Extension Center at Headland, AL in a randomized complete block (RCB) design with 3 replicates in 2013, 2014, and 2015. Visual assessment of TSWV in the field was made using the Florida 1-10 scoring system (Chiteka et al., 1988), and then the data were reported as a percentage in this study.

Source of viral inoculum. TSWV-infected peanut (*Arachis hypogaea*) leaves were collected from Auburn University, the Wiregrass Research and Extension Center, Headland, Alabama. Presence of TSWV in the leaf samples was confirmed by ImmunoStrip test from Agdia Inc. (Elkhart, IN) (Baker et al., 2007). The virus was transmitted mechanically to tobacco (*Nicotiana tabacum*) maintained in greenhouse. Transmission of TSWV to tobacco was confirmed by ImmunoStrip test as well. The tobacco leaves with obvious symptom were used as the source of inoculum to study the responses of peanut genotypes to TSWV by mechanical inoculation.

Mechanical inoculation. Peanut plants at two- to three-leaf stage (7 to 9 days after planting [DAP]) were dusted with Carborundum. Inoculum (1 ml per plant) was applied by rubbing both surfaces of the leaf with cotton swab. After inoculation, the sap and carborundum were rinsed off of the seedlings with distilled water and kept in the greenhouse under the same environmental conditions as previously mentioned.

Infected tobacco leaves were collected and ground into a sap in fresh cold 0.01M potassium phosphate buffer, pH 7.0, including 0.2% sodium sulfite and 0.01M 2-mercaptoethanol, using a chilled pestle and mortar at the ratio of 1:6 of tissue/buffer. Celite 545 (Fisher Scientific, Fair Lawn, NJ) and Carborundum 320 grit (Fisher Scientific) were added to the sap at a concentration of 1% and 2%, respectively. The sap was kept on ice until the inoculation was completed.

To monitor uncontrolled TSWV spread by thrips, 10 uninoculated Georgia Green plants were randomly placed around inoculated plants in the greenhouse throughout the study and to minimize thrips population, the application of insecticide was conducted approximately once every two weeks. No instance of uncontrolled TSWV was identified in this study from the uninoculated Georgia Green sentinel plants.

Symptom observation, TSWV detection, and data analysis in greenhouse. Inoculated plants were observed daily for symptom development. Plants were considered to have localized infection when chlorotic rings or concentric rings developed only on the inoculated leaves, and without any symptoms on new leaves. The plants were considered to be systemically infected when the symptoms developed on new emerging leaves. The plants were monitored in the greenhouse for 40 days after inoculation. The percentage of infected plants was recorded at 40 days postinoculation (DPI).

At 40 DPI, 0.2 g of roots was collected from every plant to assay by double antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) using TSWV-specific antiserum (Agdia). Each ELISA plate contained a blank buffer control, two negative controls, and a positive control supplied by AgDia. Positive plant is defined if the ELISA value after subtracting from blank buffer control is four times greater than the average value of negative controls. The positive plants were recorded as “1” and negative plants were recorded as ‘0”. For those of the positive genotypes, if none or only one of the nine plants was detected positive for TSWV infection, the replicated test was conducted to confirm the results. Data were analyzed by ANOVA procedures of SAS Proc Glimmix (SAS Institute Inc., Version 9.4, Cary, NC).

Results

A total of 1038 tested peanut plants from 118 selected genotypes and 9 control plants of 'Georgia Green' were screened by mechanical inoculation for TSWV resistance in greenhouse (Table 2.2). All 9 'Georgia Green' control plants showed visual symptoms in the observation period. Of the 1038 plants, 549 plants were infected by TSWV based on ELISA result (Table 2.3) which is about 53% of susceptibility. The overall TSWV susceptibilities among six botanical types are not differential as 57% for*aequatoriana*; 55% for *fastigiata*; 56% for *hirsuta*; 50% for *hypogaea*; 63% for *peruviana*, and 53% for *vulgaris*, respectively (Table 2.3). No significant difference in the TSWV resistance response was identified among the 6 botanical types (Table 2.4). However, a distinct difference was identified among genotypes with $P < 0.0001$.

Not all plants infected by the virus based on ELISA detection showed symptoms, but the correlation coefficient between visual symptoms and ELISA results was 0.73, indicating the visual symptoms and ELISA results were highly consistent. In term of differences of visual symptoms and ELISA test, paired t-test showed significantly different ($p< 0.0001$). However, the correlation coefficients among the visual symptoms in the greenhouse and the field evaluation results were small ranging from -0.06 to 0.24 (Table 2.5). The results also revealed that there was a big variability of TSWV incidence in field among years. The incidences of TSWV infection ranged from 0.7% in 2014 to 7.0% in 2015 (Table 2.5).

Among 118 tested genotypes, 6 genotypes were tested as ELISA negative, and 9 genotypes were found as only having one ELISA positive plant in the first initial mechanical inoculation screening. The greenhouse experiments were repeated a second time on these 15 genotypes to confirm the initial results. Four genotypes, PI356004, PI493880, PI355271, and PI496401, had no infection (Table 2.6). Of which, PI356004 and PI493880 were identified as new resistant sources to TSWV based on the results from visual symptom, ELISA, and three year field evaluations.

Discussion

Mechanical inoculation in greenhouse resulted in differential disease responses of TSWV in terms of percent transmission among 118 tested genotypes. Botanical types were classified based on morphological characteristics, such as flower on main stem, order of vegetative and reproductive branches, growth habit and period, dormancy, number of seeds per pod, et al. This study showed there was no statistical differences in TSWV resistance among 6 botanical varieties based on ELISA detection in the greenhouse study. Our result demonstrated that no morphological characteristic of peanut plants associated with degree of TSWV incidence in the field, which was agreement with Anderson’s report (Anderson et al., 1996).

Another interesting observation from this study was dealing with symptom development in peanut genotypes. TSWV infected plants did not always develop symptoms of the virus or show any other indication of reduced plant vigor. This phenomenon may be due to different mechanism of plants defense mediating virus-plant interactions. The most common mechanism of natural resistance to virus in plant is the hypersensitive response (HR). HR leads to rapid death of cells at virus entry sites, thus, limiting viral infections by killing cells surrounding viral infections, and producing local lesions that prevent further spread of the virus through the plant. This response caused by a specific recognition of the virus, and this is based on matching gene products of plant and the virus. Dominant genes *Sw-5* and *Tsw* have been found in tomato and pepper, respectively, and have been conferred to have the resistance to TSWV by exhibiting HR (Stevens et al., 1991; Boiteux and Avila, 1994; Moury et al., 1997). The genotypes, which showed no symptoms and which virus was not detected in our study, may have such genes leading to HR. With HR the cells of the site of inoculation died rapidly, and the virus could not move to other cells in the plant. Hence, these plants not only had no symptoms, but also had no virus detection by ELISA. Another virus resistant mechanism is post-transcriptional gene silencing, also known as RNA silencing. It was found in plants, fungi, and some animal species, and it suppressed foreign genetic elements such as viruses and transposons through a specific RNA breakdown mechanism (Goldbach et al., 2003). However, the S RNA genome segment of TSWV encodes a silencing suppressor called NSs protein, which targets the plant RNA silencing system and causes virus symptom expressions (Bucher et al., 2003). For the genotypes infected with virus but without symptoms, a reasonable explanation is that these genotypes have the gene which could suppress the S RNA of TSWV expression or prevent the NSs protein to interfere plant silencing system but it needs further experiment to proof that.

TSWV is only transmitted by thrips in the field, and tobacco thrips (*Franklinieila fusca*) is the most common vector of TSWV occurring on peanut. The incidence of TSWV in the field was much lower than in the greenhouse, which could be caused by a variety of factors. The timing of thrips flights into crop fields in the spring relative to the age and susceptibility of the crop plants determines final incidence of TSWV in crop fields (Morsello et al., 2010; Chappell et al., 2013).Transmission in the field is also determined by the thrips-plant-virus interactions, whereas in the greenhouse effects produced by thrips-virus and thrips-plant interactions was eliminated to study only the susceptibility of the genotypes to TSWV infection. Therefore, in addition to environmental factors, thrips-plant interactions may also influence field results. Some plant factors that might deter thrips feeding responsible for virus transmission include physiological differences in nutrient contents and morphological traits such as leaflet thickness and wax content (Bergh and Blanc, 1997; Kogel et al., 1997; Brown et al., 2002). In the mechanical inoculation method, the amount of the virus for each plant is relative uniform. However, the plants acquired the virus from thrips randomly depending on the number and the preference of thrips. Temperature, which is also a factor that might influence the virus movement and expression in the plants is more variable in the field (Stumpf and Kennedy, 2007). Plant age can also influence virus transmission (Culbreath et al., 1992). In the greenhouse young peanut plants were inoculated, whereas, timing of thrips flights into the field may have occurred when plants were more mature.

In this study, we found four genotypes, PI356004, PI493880, PI355271, and PI496401, that had no infection in greenhouse experiment. PI355271 and PI496401 had incidence in the field evaluation, which indicated that the peanut plants have different responses to mechanical inoculation and thrips inoculation. A similar phenomenon was observed in the breeding line ICGV-86388 as it was reported as one of the most resistant by mechanical inoculation, but was susceptible to thrips inoculation (Nascimento et al., 2006), therefore, other factors due to environment or thrips may be involved in TSWV resistance in these varieties. PI356004 and PI493880 had no TSWV incidence in the field in any of three years. The data strongly suggested that these two PIs could be new resistant sources of TSWV. The results from this experiment provide an initial step towards identifying genotypes exhibiting TSWV resistant and tolerant phenotypes that can be used in future breeding efforts and in studies to characterize genes regulating these important traits. Future studies are needed to further evaluate TSWV resistance in these lines, and to study other pest-related and agronomical important traits such as thrips resistance, disease resistance, seed quality and yield.

REFERENCES

Anderson, W.F., C.C. Holbrook, and a. K. Culbreath. 1996. Screening the Peanut Core Collection for Resistance to Tomato Spotted Wilt Virus. Peanut Sci. 23: 57–61.

Baker, C.A., Davison, D. and Jones, L., 2007. Impatiens necrotic spot virus and Tomato spotted wilt virus diagnosed in Phalaenopsis orchids from two Florida nurseries. Plant Disease, 91(11), pp.1515-1515.

Bergh, C.J. and Le Blanc, J.P.R., 1997. Performance of western flower thrips (Thysanoptera: Thripidae) on cultivars of miniature rose. Journal of economic entomology, 90(2), pp.679-688.

Boiteux, L., and A. De Avila. 1994. Inheritance of a resistance specific to tomato spotted wilt tospovirus in Capsicum chinense “PI 159236.” Euphytica.

Brown, A.S.S., Simmonds, M.S. and Blaney, W.M., 2002. Relationship between nutritional composition of plant species and infestation levels of thrips. Journal of chemical ecology, 28(12), pp.2399-2409.

Bucher, E., Sijen, T., de Haan, P., Goldbach, R. and Prins, M., 2003. Negative-strand tospoviruses and tenuiviruses carry a gene for a suppressor of gene silencing at analogous genomic positions. Journal of Virology, 77(2), pp.1329-1336.

Camann, M. a. 1995. Spatial and Temporal Patterns of Spotted Wilt Epidemics in Peanut. Phytopathology 85: 879.

Chappell, T.M., A.L.P. Beaudoin, and G.G. Kennedy. 2013. Interacting virus abundance and transmission intensity underlie tomato spotted wilt virus incidence: an example weather-based model for cultivated tobacco. PLoS One 8(8): e73321.

Chiteka, Z.A., D.W. Gorbet, D.A. Knauft, F.M. Shokes, and T.A. Kucharek. 1988. Components of Resistance to Late Leafspot in Peanut. II. Correlations Among Components and Their Significance in Breeding for Resistance 1. Peanut Sci. 15(2): 76–81.

Culbreath, A.K., Csinos, A.S., Brenneman, T.B., Demski, J.W. and Todd, J.W., 1991. Association of tomato spotted wilt virus with foliar chlorosis of peanut in Georgia. Plant Disease, 75(8), pp.863-863.

Culbreath, A.K., Todd, J.W. and Demski, J.W., 1992. Productivity of Florunner peanut infected with tomato spotted wilt virus. Peanut Science, 19(1), pp.11-14.

Francki, R.I.B., Fauquet, G.M., Knudson, D.L. et al. 1991. Classification and nomenclature of viruses: fifth report of the International Committee on Taxonomy of Viruses. Arch Virol 2: 223–233.

Goldbach, R., E. Bucher, and M. Prins. 2003. Resistance mechanisms to plant viruses: an overview. Virus Res. 92(2): 207–212.

HALLIWEL. RS and Philley, G., 1974. Spotted wilt of peanut in Texas. Plant Disease Reporter, 58(1), pp.23-25.

Kogel, W., Hoek, M. and Mollema, C., 1997. Variation in performance of western flower thrips populations on susceptible and partially resistant cucumber. Entomologia Experimentalis et

Applicata, 83(1), pp.73-80.

Lowry, V.K., Smith, J.W. and Mitchell, F.L., 1992. Life-fertility tables for Frankliniella fusca (Hinds) and F. occidentals (Pergande) (Thysanoptera: Thripidae) on peanut. Annals of the Entomological Society of America, 85(6), pp.744-754..

Mandal, B., Pappu, H.R., Culbreath, A.K., Holbrook, C.C., Gorbet, D.W. and Todd, J.W., 2002. Differential response of selected peanut (Arachis hypogaea) genotypes to mechanical inoculation by Tomato spotted wilt virus. Plant disease, 86(9), pp.939-944.

Morsello, S.C., A.L.P. Beaudoin, R.L. Groves, B.A. Nault, and G.G. Kennedy. 2010. The influence of temperature and precipitation on spring dispersal of Frankliniella fusca changes as the season progresses. Entomol. Exp. Appl. 134(3): 260–271.

Moury, B., Palloix, A., Selassie, K.G. and Marchoux, G., 1997. Hypersensitive resistance to tomato spotted wilt virus in three Capsicum chinense accessions is controlled by a single gene and is overcome by virulent strains. Euphytica, 94(1), pp.45-52.

Pappu, H.R., R.A.C. Jones, and R.K. Jain. 2009. Global status of tospovirus epidemics in diverse cropping systems: Successes achieved and challenges ahead. Virus Res. 141(2): 219–236.

Sherwood, J.L., German, T.L., Whitfield, A.E., Moyer, J.W. and Ullman, D.E., 2001. Tospoviruses. Encyclopedia of Plant Pathology. John Wiley and Sons, New York, 1346, pp.1034-1040.

Stevens, M.R., Scott, S.J. and Gergerich, R.C., 1991. Inheritance of a gene for resistance to tomato spotted wilt virus (TSWV) from Lycopersicon peruvianum Mill. Euphytica, 59(1), pp.9-17.

Stumpf, C.F., and G.G. Kennedy. 2007. Effects of tomato spotted wilt virus isolates, host plants, and temperature on survival, size, and development time of Frankliniella occidentalis. Entomol. Exp. Appl. 123(2): 139–147.

Table 2.1. One hundred and eighteen accessions used for evaluation of TSWV resistance and their origin and botanical varieties.

Code	PI no.	Botanical variety	Origin	Code	PI no.	Botanical variety	Origin
G-001	PI152146	*fastigiata*	Uruguay	G-036	PI196622	*hypogaea*	Cote D'Ivoire
G-002	PI158854	*fastigiata*	China	G-037	PI196635	*hypogaea*	Madagascar
G-003	PI200441	*fastigiata*	Japan	G-038	PI240560	*hypogaea*	South Africa
G-004	PI259617	*fastigiata*	Cuba	G-039	PI259658	*hypogaea*	Cuba
G-005	PI259836	*fastigiata*	Malawi	G-040	PI259851	*hypogaea*	Malawi
G-006	PI262038	*fastigiata*	Brazil	G-041	PI268586	*hypogaea*	Zambia
G-007	PI290566	*fastigiata*	India	G-042	PI268696	*hypogaea*	South Africa
G-008	PI290620	*fastigiata*	Argentina	G-043	PI268755	*hypogaea*	Zambia
G-009	PI295730	*fastigiata*	India	G-044	PI268806	*hypogaea*	Zambia
G-010	PI313129	*fastigiata*	Taiwan	G-045	PI268868	*hypogaea*	Sudan
G-011	PI337406	*fastigiata*	Paraguay	G-046	PI268996	*hypogaea*	Zambia
G-012	PI339960	*fastigiata*	Argentina	G-047	PI270786	*hypogaea*	Zambia
G-013	PI343398	*fastigiata*	Israel	G-048	PI270905	*hypogaea*	Zambia
G-014	PI356004	*fastigiata*	Argentina	G-049	PI270907	*hypogaea*	Zambia
G-015	PI429420	*fastigiata*	Zimbabwe	G-050	PI274193	*hypogaea*	Bolivia
G-016	PI471954	*fastigiata*	Zimbabwe	G-051	PI290536	*hypogaea*	India
G-017	PI478850	*fastigiata*	Uganda	G-052	PI290594	*hypogaea*	India
G-018	PI482189	*fastigiata*	Zimbabwe	G-053	PI292950	*hypogaea*	South Africa
G-019	PI502040	*fastigiata*	Peru	G-054	PI295250	*hypogaea*	Israel
G-020	PI475863	*fastigiata*	Bolivia	G-055	PI295309	*hypogaea*	Israel
G-021	PI475918	*fastigiata*	Bolivia	G-056	PI296550	*hypogaea*	Israel
G-022	PI476025	*fastigiata*	Peru	G-057	PI296558	*hypogaea*	Israel
G-023	PI493329	*fastigiata*	Argentina	G-058	PI298854	*hypogaea*	South Africa
G-024	PI493356	*fastigiata*	Argentina	G-059	PI319768	*hypogaea*	Israel
G-025	PI493547	*fastigiata*	Argentina	G-060	PI323268	*hypogaea*	Pakistan
G-026	PI493581	*fastigiata*	Argentina	G-061	PI325943	*hypogaea*	Venezuela
G-027	PI493631	*fastigiata*	Argentina	G-062	PI331297	*hypogaea*	Argentina
G-028	PI493693	*fastigiata*	Argentina	G-063	PI331314	*hypogaea*	Argentina
G-029	PI493717	*fastigiata*	Argentina	G-064	PI337293	*hypogaea*	Brazil
G-030	PI493729	*fastigiata*	Argentina	G-065	PI337399	*hypogaea*	Morocco
G-031	PI493880	*fastigiata*	Argentina	G-066	PI343384	*hypogaea*	Israel
G-032	PI493938	*fastigiata*	Argentina	G-067	PI355268	*hypogaea*	Mexico
G-033	PI159786	*hypogaea*	Senegal	G-068	PI355271	*hypogaea*	Mexico
G-034	PI162655	*hypogaea*	Uruguay	G-069	PI370331	*hypogaea*	Israel
G-035	PI162857	*hypogaea*	Sudan	G-070	PI372271	*hypogaea*	Unknown

Table 2.1. Continued

Code	PI no.	Botanical variety	Origin	Code	PI no.	Botanical variety	Origin
G-071	PI372305	*hypogaea*	Nigeria	G-088	PI270998	*vulgaris*	Zambia
G-072	PI399581	*hypogaea*	Nigeria	G-089	PI271019	*vulgaris*	Zambia
G-073	PI442768	*hypogaea*	Zimbabwe	G-090	PI288146	*vulgaris*	India
G-074	PI461434	*hypogaea*	China	G-091	PI290560	*vulgaris*	India
G-075	PI471952	*hypogaea*	Zimbabwe	G-092	PI403813	*vulgaris*	Argentina
G-076	PI476636	*hypogaea*	Nigeria	G-093	PI407667	*vulgaris*	Thailand
G-077	PI481795	*hypogaea*	Mozambique	G-094	PI478819	*vulgaris*	India
G-078	PI482120	*hypogaea*	Zimbabwe	G-095	PI476432	*hypogaea*	Nigeria
G-079	PI494795	*hypogaea*	Zambia	G-096	PI497517	*fastigiata*	Brazil
G-080	PI496401	*hypogaea*	Burkina Faso	G-097	PI497639	*fastigiata*	Ecuador
G-081	PI496448	*hypogaea*	Burkina Faso	G-098	PI497318	*hypogaea*	Bolivia
G-082	PI504614	*hypogaea*	Colombia	G-099	PI497395	*hypogaea*	Bolivia
G-083	PI338338	*peruviana*	Venezuela	G-100	PI494018	*vulgaris*	Argentina
G-084	PI502111	*peruviana*	Peru	G-101	PI494034	*vulgaris*	Argentina
G-085	PI502120	*peruviana*	Peru	G-102	PI288210	*vulgaris*	India
G-086	PI155107	*vulgaris*	Uruguay	G-103	PI371521	*hypogaea*	Israel
G-087	PI157542	*vulgaris*	China	G-104	PI461427	*hypogaea*	China

Table2.2. Means of evaluation values for visual symptoms, ELISA test, and field resistance of TSWV in 118 selected genotypes.

	Greenhouse (%)		Field (%)		
PI no.	**Visual**	**ELISA**	**2015**	**2014**	**2013**
PI152146	77.8	77.8	10.0	0.0	0.0
PI158854	44.4	44.4	0.0	3.3	10.0
PI200441	44.4	44.4	6.7	0.0	0.0
PI259617	88.9	88.9	6.7	0.0	0.0
PI259836	87.5	87.5	0.0	0.0	10.0
PI262038	44.4	44.4	0.0	0.0	0.0
PI290566	11.1	11.1	0.0	0.0	0.0
PI290620	0.0	33.3	3.3	0.0	0.0
PI295730	100.0	100.0	6.7	3.3	0.0
PI313129	62.5	62.5	13.3	0.0	30.0
PI337406	0.0	33.3	0.0	0.0	0.0
PI339960	75.0	75.0	10.0	3.3	20.0
PI343398	44.4	44.4	0.0	0.0	0.0
PI356004	0.0	0.0	0.0	0.0	0.0
PI429420	33.3	33.3	0.0	0.0	0.0
PI471954	12.5	100.0	10.0	0.0	0.0
PI478850	77.8	77.8	0.0	0.0	0.0
PI482189	0.0	22.2	0.0	0.0	0.0
PI502040	33.3	33.3	16.7	0.0	0.0
PI475863	66.7	66.7	6.7	0.0	0.0
PI475918	77.8	77.8	3.3	0.0	0.0
PI476025	55.6	55.6	3.3	3.3	0.0
PI493329	22.2	88.9	0.0	0.0	10.0
PI493356	55.6	55.6	0.0	0.0	40.0
PI493547	55.6	55.6	3.3	0.0	0.0
PI493581	55.6	100.0	0.0	0.0	0.0
PI493631	100.0	100.0	6.7	0.0	0.0
PI493693	22.2	22.2	6.7	0.0	0.0
PI493717	22.2	22.2	10.0	0.0	0.0
PI493729	88.9	88.9	30.0	0.0	10.0
PI493880	0.0	0.0	0.0	0.0	0.0
PI493938	0.0	11.1	0.0	0.0	0.0
PI159786	50.0	50.0	13.3	0.0	50.0
PI162655	44.4	44.4	3.3	0.0	0.0
PI162857	100.0	100.0	10.0	0.0	0.0

Table2.2. Continued

	Greenhouse (%)		Field (%)		
PI no.	Visual	ELISA	2015	2014	2013
PI196622	77.8	77.8	6.7	0.0	0.0
PI196635	44.4	44.4	10.0	0.0	0.0
PI240560	11.1	11.1	0.0	0.0	0.0
PI259658	11.1	33.3	13.3	0.0	0.0
PI259851	77.8	88.9	0.0	0.0	0.0
PI268586	0.0	44.4	0.0	6.7	10.0
PI268696	11.1	11.1	0.0	0.0	0.0
PI268755	37.5	37.5	0.0	3.3	10.0
PI268806	33.3	33.3	0.0	0.0	0.0
PI268868	11.1	11.1	6.7	0.0	10.0
PI268996	88.9	88.9	10.0	0.0	40.0
PI270786	55.6	55.6	6.7	0.0	0.0
PI270905	11.1	11.1	26.7	0.0	0.0
PI270907	66.7	100.0	6.7	0.0	10.0
PI274193	44.4	44.4	23.3	0.0	0.0
PI290536	88.9	88.9	3.3	0.0	10.0
PI290594	77.8	77.8	6.7	0.0	10.0
PI292950	66.7	66.7	43.3	0.0	20.0
PI295250	55.6	55.6	33.3	0.0	10.0
PI295309	0.0	33.3	0.0	0.0	20.0
PI296550	11.1	75.0	0.0	0.0	0.0
PI296558	0.0	66.7	0.0	3.3	0.0
PI298854	0.0	100.0	0.0	0.0	0.0
PI319768	33.3	33.3	3.3	6.7	0.0
PI323268	33.3	33.3	10.0	0.0	0.0
PI325943	0.0	66.7	3.3	0.0	10.0
PI331297	0.0	44.4	0.0	0.0	0.0
PI331314	0.0	11.1	0.0	0.0	10.0
PI337293	11.1	11.1	13.3	0.0	10.0
PI337399	33.3	66.7	0.0	0.0	0.0
PI343384	88.9	88.9	3.3	3.3	0.0
PI355268	88.9	88.9	0.0	0.0	10.0
PI355271	0.0	0.0	13.3	0.0	0.0
PI370331	11.1	11.1	6.7	0.0	0.0
PI372271	44.4	44.4	6.7	0.0	10.0
PI372305	22.2	22.2	30.0	0.0	0.0

Table2.2. Continued

	Greenhouse (%)		Field (%)		
PI no.	Visual	ELISA	2015	2014	2013
PI399581	50.0	75.0	6.7	0.0	20.0
PI442768	44.4	44.4	6.7	0.0	0.0
PI461434	87.5	87.5	6.7	0.0	0.0
PI471952	25.0	25.0	6.7	13.3	20.0
PI476636	22.2	22.2	3.3	3.3	10.0
PI481795	88.9	100.0	3.3	0.0	0.0
PI482120	44.4	44.4	0.0	0.0	0.0
PI494795	33.3	33.3	0.0	0.0	0.0
PI496401	0.0	0.0	20.0	3.3	20.0
PI496448	50.0	50.0	3.3	0.0	0.0
PI504614	66.7	88.9	3.3	0.0	.
PI338338	88.9	88.9	6.7	0.0	20.0
PI502111	66.7	66.7	0.0	0.0	0.0
PI502120	33.3	33.3	3.3	6.7	0.0
PI155107	37.5	37.5	0.0	0.0	0.0
PI157542	75.0	75.0	0.0	0.0	0.0
PI270998	25.0	25.0	30.0	0.0	20.0
PI271019	0.0	22.2	0.0	0.0	0.0
PI288146	0.0	88.9	0.0	0.0	0.0
PI290560	87.5	87.5	0.0	0.0	0.0
PI403813	66.7	66.7	16.7	0.0	0.0
PI407667	66.7	66.7	0.0	3.3	0.0
PI478819	0.0	55.6	6.7	0.0	0.0
PI476432	33.3	33.3	3.3	0.0	20.0
PI497517	50.0	50.0	3.3	0.0	0.0
PI497639	55.6	55.6	0.0	0.0	10.0
PI497318	87.5	87.5	53.3	0.0	0.0
PI497395	57.1	57.1	43.3	0.0	20.0
PI494018	44.4	44.4	0.0	3.3	30.0
PI494034	0.0	0.0	0.0	0.0	0.0
PI288210	66.7	66.7	6.7	0.0	0.0
PI371521	44.4	44.4	0.0	0.0	0.0
PI461427	0.0	0.0	0.0	0.0	0.0
PI576613	0.0	66.7	0.0	.	10.0
GRIF14051	22.2	55.6	13.3	.	0.0
PI576634	55.6	88.9	0.0	.	0.0

Table2.2. Continued

	Greenhouse (%)		Field (%)		
PI no.	Visual	ELISA	2015	2014	2013
PI648241	11.1	11.1	50.0	.	30.0
PI648250	16.7	16.7	3.3	.	0.0
PI576616	0.0	55.6	0.0	.	20.0
PI648249	33.3	33.3	13.3	.	0.0
PI648242	66.7	66.7	0.0	.	10.0
PI648245	100.0	100.0	0.0	.	10.0
GRIF12579	85.7	100.0	3.3	.	0.0
PI576614	57.1	57.1	3.3	.	0.0
GRIF12545	25.0	25.0	26.7	.	0.0
PI576636	44.4	44.4	3.3	.	0.0
PI576637	33.3	66.7	13.3	.	0.0

Table 2.3. Comparison of *Tomato spotted wilt virus* (TSWV) infection within 6 botanical varieties.

Botanical varieties	Number of genotypes	Number of plants tested	Number of infection	Percentage of susceptible	Standard Error
aequatoriana	7	59	35	0.57	0.11
fastigiata	34	302	165	0.55	0.05
hirsuta	7	61	34	0.56	0.11
hypogaea	55	485	243	0.50	0.04
peruviana	3	27	17	0.63	0.17
vulgaris	12	104	55	0.53	0.09
Total	118	1038	549	0.53	0.03

Table 2.4. Analysis of variance (ANOVA) for 6 botanical varieties and 118 genotypes.

Source	DF	Sum of Squares	Mean Square	F Ratio	P-value
Botanical varieties	5	0.096	0.019	0.217	0.955
Error	112	9.917	0.089		
Total	117	10.013			

Table 2.5. Correlation coefficients for disease rating of TSWV between visual symptoms and field evaluation in 2013, 2014, and 2015.

	Visual symptoms	2015 in field	2014 in field	2013 in field
Visual symptoms	1			
2015 in field	0.09 <0.0001	1		
2014 in field	-0.06 <0.0001	-0.09 <0.0001	1	
2013 in field	0.08 <0.0001	0.24 0.19	0.14 <0.0001	1
Mean	42.0%	7.0%	0.7%	5.6%

Table 2.6. The four genotypes identified as new resistant sources to TSWV and their means of disease rating in greenhouse and field tests.

PI no.	Botanical varieties	Visual	ELISA1	ELISA2	2013 field	2014 field	2015 field
PI356004	fastigiata	0	0	0	0	0	0
PI493880	fastigiata	0	0	0	0	0	0
PI355271	hypogaea	0	0	0	0	0	13%
PI496401	hypogaea	0	0	0	20%	3%	20%

CHAPTER THREE

POPULATION STRUCTURE AND ASSCOCIATION ANALYSIS OF THE U.S. PEANUT MINI CORE COLLECTION BY SSR MARKERS

ABSTRACT

Tomato spotted wilt virus (TSWV) is one of the most serious diseases in peanut. In order to more efficiently breed cultivars resistant to TSWV, marker assisted selection (MAS) should be implemented in breeding program. Association mapping is one type of genetic mapping that can exploit relationships between markers and traits from many lineages. The objectives of this study are to examine genetic diversity and population structure in the U.S. peanut mini core collection by SSR markers, and to conduct an association mapping of SSR markers to TSWV resistance in cultivated peanuts. One hundred and thirty-three SSR markers were used for genotyping the 104 genotypes from the U.S. peanut mini core collection. Four subpopulations were classified by population structure analysis, and they corresponded to botanical varieties to a certain extent. Association mapping analysis indicated that the five markers, pPGPseq5D5, GM1135, GM1991, TC23C08, and TC24C06, were consistently associated with visual symptoms by four models, Q model, PCA model, Q+K model, and PCA+K model. These identified markers could explain

totally 36.4% of the phenotypic variance. Moreover, pPGPseq5D5 and GM1991 are associated with both visual symptoms and ELISA in resulting in a high R^2. These markers have potential to be used in a marker-assisted selection program in breeding peanut for resistance to TSWV.

INTRODUCTION

Peanut (*Arachis hypogaea*) is a species in the family Fabaceae, the legume family, which is grown through the tropical, subtropical, and warm areas of the world. Peanut is a typical oil crop, which contains 50% oil on average. Peanut probably originated in South America, the center of origin most possible being Brazil and Peru, where more than 10 wild species were found (Acquaah, 2012).

The cultivated peanut is an allotetraploid (2n = 4x = 40) originated through hybridization of two ancient diploid species, probably A. *duranensis* (A-genome) and A. *ipaensis* (B-genome) (Milla et al., 2005). It contains two subspecies, *A. hypogaea* ssp. *hypogaea* and *A. hypogaea* ssp. *fastigiata.* The ssp. *hypogaea* consists of botanical varieties '*hypogaea'* and '*hirsuta*', the ssp. *fastigiata* consists of botanical varieties '*fastigiata'*, '*vulgaris*', '*peruviana*', and '*aequatoriana* (Krapovickas and Rigoni, 1960).

Tomato spotted wilt virus (TSWV) is a species of the *Tospovirus* genus, and only transmitted by thrips. The virus has caused serious damage on peanut in U.S. since 1984. The damage to peanut resulted from TSWV valued at least $44 million in 1995 just in Georgia (Williams-Woodward, J, 2001). No genotype is totally immune to TSWV under high thrips pressure, the resistant mechanism and gene in peanut are also unknown for now. In order to reduce the loss resulted from TSWV, selection of resistant genotypes in breeding program is the optimal method.

Simple sequence repeat (SSR) markers have been the most widely used DNA marker because of their high degree of polymorphism, highly abundant, codominant inheritance, easy use, readily transferable and relatively low cost (Vignal et al., 2002; Weber, 1990). The advantages of SSR over other markers will become more significant when they are used to track desirable traits in large scale breeding programs and as anchor points for map-based gene cloning (He et al., 2003).

Association mapping is one type of genetic mapping and can easily detect quantitative trait loci (QTL) with relatively large effects on phenotype. It is applied to much broader germplasm than single population trait mapping. In peanut, the first attempt at association mapping was reported for seed quality traits by using SSR markers and SNP markers in 2011 (Wang et al., 2011). More recently, a genome wide association study in peanut including 300 genotypes and identified 524 significant associations for 36 traits which could be used in improving biotic and abiotic stress resistance, seed quality and yield (Pandey et al., 2014).

However, no research on SSR marker association in peanut has been reported for resistance to TSWV in peanut. Therefore, it is vital to conduct association mapping to identify QTL for resistance to TSWV in peanut. The objectives of this research were: (1) to examine genetic diversity and population structure in the mini core collection by SSR markers; (2) to determine whether the population structure is associated with botanical varieties; and (3) to identify whether the employed SSR markers are associated with TSWV through association mapping.

MATERIALS AND METHODS

Plant material and DNA extraction. A total of 104 genotypes of *Arachis hypogaea L.* of the U.S. peanut mini core collection (Table 2.1) were included in the experiment. These genotypes included 4 botanical varieties, *fastigiata, hypogaea, peruviana,* and *vulgaris.* The seeds from each genotype were used to extract DNA by following the method of Dang and Chen (2013). A Nano-Drop 2000c spectrophotometer (Nano Drop Technologies, USA) was used to evaluate the quality and concentration of all DNA. All DNA samples were dissolved and diluted in 0.1 TE (1 mM Tris, 0.1 mM EDTA, pH 8.0) to a final concentration of 10 ng/µl for use in PCR.

Genotyping with SSR markers. A total of 133 SSR markers from previously published literatures (He et al., 2003, 2005, 2006; Ferguson et al., 2004; Moretzsohn et al., 2005; Budiman et al., 2006; Gimenes, 2007; Cuc et al., 2008; Leal-Bertioli et al., 2009; Nagy et al., 2010; Macedo et al., 2012) were employed for genotyping the diversity panel. The name and source for the 133 polymorphic SSR markers are listed in Table 3.1. PCR conditions were applied: 95 ^{o}C for 5 min, 35 cycles of 95 ^{o}C for 30 s, 55 ^{o}C for 30s, 72 ^{o}C for 30 s, and 1 cycle at 72 ^{o}C for 5 min. PCR products were analyzed on a 7% polyacrylamide gel using a LICOR 4300 DNA Analyzer (LICOR Biosciences, Lincoln, NE).

DNA marker profile. Alleles produced from each genotype were scored based on size comparison to a molecular weight ladder. Powermarker version 3.25 (Liu and Muse, 2005) was used to calculate Chord distance (Cavalli-Sforza and Edwards, 1967) among genotypes, to compute molecular diversity statistics, and to calculate polymorphism information content (PIC) for each marker. The gene diversity is calculated based on the formula: D = 1 - $\sum_{u=1}^{k} p_u^2$. PIC is another closely related diversity measurement, which was calculated based on the formula (Botstein et al., 1980): PIC = 1 - $\sum_{u=1}^{k} p_u^2$ - $\sum_{u=1}^{k-1} \sum_{v=u+1}^{k} 2p_u^2 p_v^2$. SPAGeDi version 1.3 (Hardy et al., 2009) was used to calculate a kinship matrix.

Population structure analysis. The program STRUCTURE version 2.2.3 (Pritchard et al., 2000; Falush et al., 2003) was used to detect the population structure and to assign individuals to subpopulations. This program employs model-based clustering in which a Bayesian approach identifies cluster based on compliance with Hardy-Weinberg equilibrium and linkage equilibrium. In this study, the STRUCTURE program was run 10 times for each subpopulation (K) value, ranging from K = 2 to K = 10, with admixture model, using 20,000 replicates for burn-in and 20,000 replicates for Markov Chain Monte Carlo (MCMC) procedures for each runs. The initial boundary of two and ten for K was set because of the current sample size and the outcome that we did find an optimal K between these boundaries. Analyses were conducted with correlated allele frequencies (CAF) for the putative populations. The final population subgroups were determined based on the second order rate of change of the likelihood function (ΔK)

(Evanno et al., 2005), which was calculated using an application on the STRUCTURE Harvester website (Earl and vonHoldt, 2011).

The genetic distances among the subgroups were calculated as Nei's minimum distance and pairwise F_{st} by PowerMarker. GenAlEx version 6.5 (Peakall and Smouse, 2012) was used to do analysis of molecular variance (AMOVA) and principal component analysis (PCA). In AMOVA, the significance of each variation was estimated non-parametrically using 999 permutations. We partitioned the genetic variance within and among the populations suggested by STRUCTURE. PCA was conducted to construct a plot of the most significant axes for validating the genetic structure. The unweighted pair group method with arithmetic average (UPGMA) tree was constructed by MEGA version 6.0 (Tamura et al., 2013) with 100 replications of bootstrapping.

Model comparison and association analysis. The marker-trait association was tested in TASSEL version 5.2 (Bradbury et al., 2007). Four mixed models with subpopulation membership percentage or PCA as fixed covariates and kinship as a random effect were used in TASSEL (Yu et al., 2006). Q and PCA used the general linear model (GLM): $Y = M\alpha + Qw$ or $Pw + e$, where Y is phenotypic score, $M\alpha$ is marker effects, Qw or Pw represents population structure or PCA dimension, and e is the error term. Q+K and PCA+K used mixed linear model (MLM): $Y = M\alpha + Qw$ or $Pw + Ku + e$, where Ku represents familial relatedness. Phenotype data was TSWV infection rate tested by ELISA and visual symptoms.

Results

Profile of SSR markers. 133 SSR markers were utilized to investigate 104 genotypes from the U.S. peanut mini core collection. A total of 1122 alleles were scored, the number of alleles per locus ranged from 2 to 30, with an average of 8.44 alleles per locus (Table 3.2). The major allele frequency for each locus ranged from 0.15 to 0.97, with an average of 0.42 per locus. The PIC for each locus ranged from 0.05 to 0.91, with an average PIC of 0.64. The TC23H10, pPGPseq2D12B, and pPGSseq17E1 loci were the most informative, with more than 20 alleles being amplified for each of these loci. The gene diversity is another closely related diversity measurement, which is calculated based on the formula: $D = 1 - \sum_{u=1}^{k} p_u^2$. The gene diversity for each locus ranged from 0.06 to 0.92, with an average of 0.68.

Population structure and genetic diversity. Based on ΔK information from STRUCTURE analysis, we chose $K = 4$ as optimal grouping (Fig 3.1). Out of 10 runs for $K = 4$, the run with highest likelihood value was selected to assign the posterior membership coefficients (Q) to each genotype. A graphical bar plot was generated with Q (Fig. 3.2). The four subpopulations were named G1, G2, G3, and G4 which contained 25, 18, 25, and 36 genotypes, respectively (Table 3.3). The level of genetic diversity within G2 (0.68) was highest following by G3 (0.62), G1 (0.59), and G4 (0.57) (Table 3.4). The fixation index (F_{st}) with G1 (0.27) was highest followed by G4 (0.26), G3 (0.22), and G2 (0.04) was the lowest. In addition, the genetic distance among these four subpopulations measured by Nei's minimum distance and F_{st} were consistent, the genetic distance between G1 and G4 (0.24 and 0.43) was the largest, and the genetic distance between G2 and G4 (0.16 and 0.34) was the smallest (Table 3.5). The result of principal component analysis (Fig. 3.3) showed that G1 and G3 were well separated from G4, but G2 was not well separated by principal component 1 (PC1). G1 and G3 were well separated, but G2 and G4 were not well separated by principal component 2 (PC2). The results from STRUCTURE analysis and principal analysis were consistent.

The UPGMA (unweighted pair group method with arithmetic average) tree analysis clustered 104 genotypes into four branches (B1, B2, B3, and B4) (Fig. 3.4) based on DNA marker data. First, B1 contained 24 genotypes with 23 genotypes from subpopulation G1 and one genotype from subpopulation G2. Second, B2 contained 2 genotypes that were both from subpopulation G2. Third, B3 contained 31 genotypes with 23 genotypes from subpopulation G3, 2 genotypes from subpopulations G1, 5 genotypes from subpopulations G2, and one genotypes from subpopulation G4. Finally, B4 contained 47 genotypes with 35 genotypes from subpopulation G4, one genotype from subpopulation G1, 10 genotypes from subpopulation G2, and 2 genotypes from subpopulation G3. The results from UPGMA tree analysis were generally consistent with the results from STRUCTURE and PCA analysis with some exceptions.

The AMOVA showed highly significant ($P < 0.0001$) differentiation among subpopulations G1, G2, G3, and G4, with 41.56% of the total genetic variance being attributed to differences among these four subpopulation (Table 3.6). The AMOVA for botanical varieties also showed highly significant differentiation among *fastigiata, hypogaea*, *peruviana,* and *vulgaris*, with

21.21% of the total genetic variance being attributed to differences among these four botanical varieties (Table 3.7).

Population structure with botanical variety. Among 104 genotypes, there were four botanical varieties, *fastigiata* (fa), *hypogaea* (hy), *peruviana* (pr), and *vulgaris* (vu), which were classified based on morphological data. In contrast, the four subpopulations were assigned according to SSR allelic variation. From the distribution frequency, 56% of the var. *fastigiata* were classified into subpopulation G1, 67% of the var. *peruviana* were classified into subpopulation G2, 75% of the var. *vulgaris* were classified into subpopulation G3, and 58% of the var. *hypogaea* were classified into subpopulation G4 (Fig.3.7 and 3.8). In spite of some discrepancies, the population structure is obviously associated with the botanical variety.

Model comparison and association analysis. Four mixed models were used to test association between 133 SSR markers and ELISA result or visual symptoms for TSWV infection. We selected markers with P value < 0.05 as markers significantly associated with TSWV resistance. For ELISA detected presence of virus, PCA model found eight significantly associated markers; Q model detected four significantly associated markers; PCA+K and Q+K models found only three significantly associated markers (Table 3.8). TC23H10, GM1991, and pPGPseq5D5 were found as significantly associated markers across all tested four models for ELISA. For visual symptoms, PCA model also found eleven significantly associated markers; PCA+K model found eight significantly associated markers; Q and Q+K models found five significantly associated markers (Table 3.8). TC23C08, TC24C06, GM1135, GM1991, and pPGPseq5D5 were detected by all four models as significantly associated markers for visual symptoms. The proportion of total variance explained by each significant marker (R^2) ranged from 3.8% to 10.9%, with an average R^2 of 6.4%. Four markers, GM1991, pPGPseq5D5, TC30D04, and pPGSseq16C6, were found for both traits in PCA model. However, the two markers, GM1991, pPGPseq5D5 were consistently detected by four models for both traits.

Discussion

Profile of SSR markers. Evaluation of molecular diversity accelerates the identification of diverse germplasm for use in map construction and genetic enhancement of specific traits in peanut. The average number of alleles per locus revealed in this study was 8.44, which was lower than 12.3 alleles from a previous study on the peanut mini core collection (Belamkar et al., 2011), but very close to 8.1 and 7.9 reported from other studies (Kottapalli et al., 2007; Wang et al., 2011). It was found that 68% genetic diversity across 133 loci was observed among the 104 peanut genotypes screened in this study (Table 3.4). This is a significantly higher level of polymorphism than previously reported within the cultivated peanut gene pool (Dwivedi et al., 2001; He and Prakash, 2001). The PIC scores trended to be high with about 80% of loci having a PIC value ≥ 0.5. Such high values of PIC was due to pre-selected polymorphic markers used for genotyping. The high level of genetic diversity of the US peanut mini-core collection revealed by SSR markers suggested that the mini-core collection is suitable for association mapping in general in which high diverse panel is desirable.

Population structure and genetic diversity with botanical variety. Structure analysis can estimate the number of subpopulations, the degree of admixture among subpopulations, and the genetic relatedness among genotypes. In this study, structure analysis assigned the collection into four subpopulations (G1-G4). According to the pairwise F_{st} among the subpopulations, highest diversity was observed between G1 and G4, and the lowest was observed between G2 and G4. Hence, it could be inferred that G1 and G4 subpopulations have diverged to a greater extent as compared to G2 and G4 subpopulations.

The genetic structure of the four subpopulations was confirmed using an AMOVA, where 41.56% of the variation was explained by the division into the four subpopulations. This finding indicated that the different subpopulations could contain unique alleles or genotypes and the data can discriminate among taxa, especially the more distant taxa. Similar results were also obtained by Cidade et al. (2013). The AMOVA for the botanical variety of peanut germplasm demonstrated that 21.21% of the total genetic variance can be attributed to difference among botanical varieties as compared to 16.87% from previous study which divided botanical variety into three subgroups, *hypogaea*, *fastigiata,* and mixed subgroup (Belamkar et al., 2011). These results support a conclusion from a previous study that botanical variety is a poor indicator of genetic diversity (Mace et al., 2006).

The relationship of genotypes by PCA was consistent with the membership from structure analysis. G1, G3, and G4 could be well separated by PC1 and PC2, while G2 was dispersed around the cross of PC1 and PC2 (Fig. 3.3). The graphical bar plot for structure analysis showed more than half the genotypes in G2 also had a large proportion membership for other subpopulations (Fig. 3.2). In UPGMA tree analysis, the collection was clustered into four branches (B1-B4) (Fig. 3.4). In general, subpopulations identified by STRUCTURE corresponded to a genetic cluster on the phylogeny, 96% of the genotypes of B1 were from G1, all genotypes of B2 were from G2, 74% genotypes of B3 were from G3, and 74% genotypes of B4 were from G4. Moreover, the subpopulation identified by STRUCTURE was also obviously associated with botanical variety (G1/ *fastigiata*, G2/ *peruviana*, G3/ *vulgaris*, G4/ *hypogaea*). However, only three genotypes from *peruviana* were applied in this study, PI502111 (G-84) and PI502120 (G-85) from Peru were grouped in subpopulation G2 with more than 95% proportion of G2, and they were also clustered in B2 in UPGMA tree analysis. PI338338 (G-83) from Venezuela was identified in subpopulation G3 with 51% proportion of G3 and 40% proportion of G2, and it was clustered in B3 in UPGMA tree analysis. These three genotypes from *peruviana* were divided into two group by STRUCTURE and UPGMA might be due to the different origin. In UPGMA tree analysis, B2 was first separated from other three branches. This phenomenon might be due to the lack of genotypes from *peruviana*. In addition, B4 (G4/ *hypogaea*) was separated from B1 (G1/ *fastigiata*) and B3 (G3/ *vulgaris*). These branches were consistent with the classification for botanical variety because botanical variety *hypogaea* is in the subspecies *hypogaea*, while botanical variety *fastigiata* and *vulgaris* are in the subspecies *fastigiata*. Hence, there is an obvious association within botanical variety, population structure, and group identified from distance-based methods (UPGMA, PCA).

Marker-trait association analysis. Association mapping has been applied in over ten plant species, and it has been applied in peanut since 2011. This is the first study to identify association with TSWV resistance through mechanical inoculation in peanut. The markers found by visual symptoms and ELISA through mechanical inoculation were different in our study. This phenomenon was due to unknown mechanism of TSWV resistance in peanut and complex environment factors. In this study, we found five markers, TC23C08, TC24C06, GM1135, GM1991, and pPGPseq5D5, were associated with visual symptoms across all four models, with R^2 of 9.9%, 8.8%, 7.7%, 5.5%, and 4.9%, respectively. We also found three markers, pPGPseq5D5, GM1991, and TC23H10, associated with ELISA result in all four models, with R^2 of 9.3%, 6.2% and 5.3%, respectively. Moreover, marker pPGPseq5D5 and GM1991 were common for both traits with relative high R^2 value. Although the mapping panel size and the number of SSR markers used in this were very limited, the results clearly demonstrated that peanut species with existing linkage disequilibrium and diversity is suitable for association mapping. With the ongoing peanut genome project, more DNA markers will be developed, which will pave the road to genome-wide association mapping for desirable traits in cultivated peanut.

REFERENCES

Acquaah, G. 2012. Principles of Plant Genetics and Breeding: Second Edition.

Belamkar, V., M.G. Selvaraj, J.L. Ayers, P.R. Payton, N. Puppala, and M.D. Burow. 2011. A first insight into population structure and linkage disequilibrium in the US peanut minicore collection. Genetica 139(4): 411–429.

Botstein, D., R.L. White, M. Skolnick, and R.W. Davis. 1980. Construction of a genetic linkage map in man using restriction fragment length polymorphisms. Am. J. Hum. Genet. 32(3): 314–31.

Bradbury, P.J., Z. Zhang, D.E. Kroon, T.M. Casstevens, Y. Ramdoss, and E.S. Buckler. 2007. TASSEL: Software for association mapping of complex traits in diverse samples. Bioinformatics 23(19): 2633–2635.

Budiman, M.A., Jones, J.I.T., Citek, R.W., Warek, U., Bedell, J.A. and Knapp, S.J., 2006. Methylation-filtered and shotgun genomic sequences for diploid and tetraploid peanut taxa. GenBank Available at http://www. ncbi. nlm. nih. gov.

Cavalli-Sforza, L.L., and a W.F. Edwards. 1967. Phylogenetic analysis. Models and estimation procedures. Am. J. Hum. Genet. 19(3 Pt 1): 233–257.

Cidade, F.W., B.B. Vigna, F.H. de Souza, J.F.M. Valls, M. Dall’Agnol, M.I. Zucchi, T.T. de Souza-Chies, and A.P. Souza. 2013. Genetic variation in polyploid forage grass: assessing the molecular genetic variability in the Paspalum genus. BMC Genet. 14: 50.

Cuc, L.M., E.S. Mace, J.H. Crouch, V.D. Quang, T.D. Long, and R.K. Varshney. 2008. Isolation and characterization of novel microsatellite markers and their application for diversity assessment in cultivated groundnut (Arachis hypogaea). BMC Plant Biol. 8(1): 55.

Dang, P.M., and C.Y. Chen. 2013. Modified method for combined DNA and RNA isolation from peanut and other oil seeds. Mol. Biol. Rep. 40(2): 1563–1568.

Dwivedi, S.L., S. Gurtu, S. Chandra, W. Yuejin, and S.N. Nigam. 2001. Assessment of genetic diversity among selected groundnut germplasm. I: RAPD analysis. Plant Breed. 120(4): 345–349.

Earl, D.A., and B.M. vonHoldt. 2011. STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. Conserv. Genet. Resour. 4(2): 359–361.

Evanno, G., S. Regnaut, and J. Goudet. 2005. Detecting the number of clusters of individuals using the software STRUCTURE: A simulation study. Mol. Ecol. 14(8): 2611–2620.

Falush, D., M. Stephens, and J.K. Pritchard. 2003. Inference of Population Structure Using Multilocus Genotype Data: Linked Loci and Correlated Allele Frequencies. Genetics 164(4): 1567–1587.

Ferguson, M.E., M.D. Burow, S.R. Schulze, P.J. Bramel, A.H. Paterson, S. Kresovich, and S. Mitchell. 2004. Microsatellite identification and characterization in peanut (A. hypogaea L.). Theor. Appl. Genet. 108(6): 1064–70.

Gimenes, M.A., Hoshino, A.A., Barbosa, A.V., Palmieri, D.A. and Lopes, C.R., 2007.

Characterization and transferability of microsatellite markers of the cultivated peanut (Arachis hypogaea). BMC Plant Biology, 7(1), p.1.

Hardy, O.J., Vekemans, X. and Cartwright, R.A., 2009. SPAGeDi 1.3 a program for spatial pattern analysis of genetic diversity. Program manual. Universite Libre de Bruxelles, Brussels, Belgium.

He, G., R. Meng, H. Gao, B. Guo, G. Gao, M. Newman, R.N. Pittman, and C.S. Prakash. 2005. Simple sequence repeat markers for botanical varieties of cultivated peanut (Arachis hypogaea L.). Euphytica 142(1-2): 131–136.

He, G., R. Meng, M. Newman, G. Gao, R.N. Pittman, and C.S. Prakash. 2003. Microsatellites as DNA markers in cultivated peanut (Arachis hypogaea L .). 6: 1–6.

He, G., and C. Prakash. 2001. Evaluation of genetic relationships among botanical varieties of cultivated peanut (Arachis hypogaea L.) using AFLP markers. Genet. Resour. Crop Evol. 48(4): 347–352.

He, G., F.E. Woullard, I. Marong, and B.Z. Guo. 2006. Transferability of Soybean SSR Markers in Peanut (Arachis hypogaea L.). Peanut Sci. 33(1): 22–28.

Krapovickas, A. and Rigoni, V.A., 1960. The nomenclature of the subspecies and varieties of A. hypogaea L. Revista de Investigaciones Agricoles, 14, pp.198-228.

Kottapalli, K.R., M.D. Burow, G. Burow, J. Burke, and N. Puppala. 2007. Molecular characterization of the U.S. peanut mini core collection using microsatellite markers. Crop Sci. 47(4): 1718–1727.

Leal-Bertioli, S.C.M., A.C.V.F. José, D.M.T. Alves-Freitas, M.C. Moretzsohn, P.M. Guimarães, S. Nielen, B.S. Vidigal, R.W. Pereira, J. Pike, A.P. Fávero, M. Parniske, R.K. Varshney, and D.J. Bertioli. 2009. Identification of candidate genome regions controlling disease resistance in Arachis. BMC Plant Biol. 9: 112.

Liu, K., and S. V Muse. 2005. PowerMarker: an integrated analysis environment for genetic marker analysis. Bioinformatics 21(9): 2128–9.

Mace, E.S., D.T. Phong, H.D. Upadhyaya, S. Chandra, and J.H. Crouch. 2006. SSR analysis of cultivated groundnut (Arachis hypogaea L.) germplasm resistant to rust and late leaf spot diseases. Euphytica 152(3): 317–330.

Macedo, S.E., M.C. Moretzsohn, S.C. M Leal-Bertioli, D.M. Alves, E.G. Gouvea, V.C. Azevedo, and D.J. Bertioli. 2012. Development and characterization of highly polymorphic long TC repeat microsatellite markers for genetic analysis of peanut. BMC Res. Notes 5(1): 86.

Milla, S.R., T.G. Isleib, and H.T. Stalker. 2005. Taxonomic relationships among Arachis sect. Arachis species as revealed by AFLP markers. Genome 48(1): 1–11.

Moretzsohn, M.C., L. Leoi, K. Proite, P.M. Guimarães, S.C.M. Leal-Bertioli, M.A. Gimenes, W.S. Martins, J.F.M. Valls, D. Grattapaglia, and D.J. Bertioli. 2005. A microsatellite-based, gene-rich linkage map for the AA genome of Arachis (Fabaceae). Theor. Appl. Genet. 111(6): 1060–71.

Nagy, E.D., Y. Chu, Y. Guo, S. Khanal, S. Tang, Y. Li, W.B. Dong, P. Timper, C. Taylor, P.

Ozias-Akins, C. Corley Holbrook, V. Beilinson, N.C. Nielsen, H. Thomas Stalker, and S.J. Knapp. 2010. Recombination is suppressed in an alien introgression in peanut harboring Rma, a dominant root-knot nematode resistance gene. Mol. Breed. 26(2): 357–370.

Pandey, M.K., H.D. Upadhyaya, A. Rathore, V. Vadez, M.S. Sheshshayee, M. Sriswathi, M. Govil, A. Kumar, M.V.C. Gowda, S. Sharma, F. Hamidou, V.A. Kumar, P. Khera, R.S. Bhat, A.W. Khan, S. Singh, H. Li, E. Monyo, H.L. Nadaf, G. Mukri, S.A. Jackson, B. Guo, X. Liang, and R.K. Varshney. 2014. Genomewide association studies for 50 agronomic traits in peanut using the “reference set” comprising 300 genotypes from 48 countries of the semi-arid tropics of the world. PLoS One 9(8).

Peakall, R., and P.E. Smouse. 2012. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research--an update. Bioinformatics 28(19): 2537–9.

Pritchard, J.K., M. Stephens, and P. Donnelly. 2000. Inference of population structure using multilocus genotype data. Genetics 155(2): 945–959.

Tamura, K., Stecher, G., Peterson, D., Filipski, A. and Kumar, S., 2013. MEGA6: molecular evolutionary genetics analysis version 6.0. Molecular biology and evolution, p.mst197.

Tang, R., G. Gao, L. He, Z. Han, S. Shan, R. Zhong, C. Zhou, J. Jiang, Y. Li, and W. Zhuang. 2007. Genetic Diversity in Cultivated Groundnut Based on SSR Markers. J. Genet. Genomics 34(5): 449–459.

Vignal, A., D. Milan, M. SanCristobal, and A. Eggen. A review on SNP and other types of molecular markers and their use in animal genetics. Genet. Sel. Evol. 34(3): 275–305.

Wang, M.L., S. Sukumaran, N. a. Barkley, Z. Chen, C.Y. Chen, B. Guo, R.N. Pittman, H.T. Stalker, C.C. Holbrook, G. a. Pederson, and J. Yu. 2011. Population structure and marker-trait association analysis of the US peanut (Arachis hypogaea L.) mini-core collection. Theor. Appl. Genet. 123(8): 1307–1317.

Weber, J.L. 1990. Informativeness of human (dC-dA)n.(dG-dT)n polymorphisms. Genomics 7(4): 524–30.

Yu, J., G. Pressoir, W.H. Briggs, I. Vroh Bi, M. Yamasaki, J.F. Doebley, M.D. McMullen, B.S. Gaut, D.M. Nielsen, J.B. Holland, S. Kresovich, and E.S. Buckler. 2006. A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. Nat. Genet. 38(2): 203–8.

Table 3.1. The list of 133 SSR markers used in the study.

Marker	Marker name	Repeat motif	Reference
A2	Ad90K4	AT	Leal-Bertioli et al. 2009
A3	Ad90P7	TA	Leal-Bertioli et al. (unpublished)
A4	Ad91O22	AG	Leal-Bertioli et al. 2009
A5	Ad92L5	AT	Leal-Bertioli et al. 2009
A8	Ad95D7	AT	Leal-Bertioli et al. 2009
A9	Ai119F10	TA	Leal-Bertioli et al. 2009
A10	Ai119G12	CAT/TTA	Leal-Bertioli et al. 2009
A12	Ai120L22	AT	Leal-Bertioli et al. (unpublished)
B1	Ai121G16	TTA	Leal-Bertioli et al. 2009
B2	TC4F02	C	Moretzsohn et al. (2005)
B4	TC13E05	TC	Macedo et al. (2012)
B7	TC19B07	TC/CT	Macedo et al. (2012)
B8	TC19B11	TC	Macedo et al. (2012)
B10	TC20B05	GA/TA	Macedo et al. (2012)
B11	TC20E08	GT/GA/TG	Macedo et al. (2012)
B12	TC21C10	GA	Macedo et al. (2012)
C1	TC21D06	CT	Macedo et al. (2012)
C2	TC23C08	GA	Macedo et al. (2012)
C3	TC23E04	GA	Macedo et al. (2012)
C4	TC23F04	GA	Macedo et al. (2012)
C5	TC23H10	GA	Macedo et al. (2012)
C6	TC24B05	TC	Macedo et al. (2012)
C7	TC24C06	TC	Macedo et al. (2012)
C9	TC25G11	CT	Macedo et al. (2012)
C10	TC27H12	AG	Macedo et al. (2012)
C11	TC28B01	AG/GA	Macedo et al. (2012)
D1	TC29H08	CT	Macedo et al. (2012)
D2	TC30D04	GT/GA	Macedo et al. (2012)
D3	TC31E08	CT/CA	Macedo et al. (2012)
D4	TC31G11	AG	Macedo et al. (2012)
D5	TC31H02	GA	Macedo et al. (2012)
D6	TC31H06	CT	Macedo et al. (2012)
D7	TC38D06	AG	Macedo et al. (2012)
D8	TC39B04	CT	Macedo et al. (2012)
D9	TC39F01	AG/GA	Macedo et al. (2012)

Table 3.1. Continued.

Marker	Marker name	Repeat motif	Reference
D10	TC42A02	AG	Macedo et al. (2012)
D11	TC41A10	GA	Macedo et al. (2012)
D12	TC41C11	AG	Macedo et al. (2012)
E2	TC42A05	AG	Macedo et al. (2012)
E3	Ah11.1	TTA	Gimenes et al. (2007)
E4	Ah20	TG	Gimenes et al. (2007)
E6	Ah32	NA	NA
E7	Ah51	AG	Gimenes et al. (2007)
E9	Ah282.1	CCA/AAG	Gimenes et al. (2007)
E11	GM699	AAT	Budiman et al. (2006)
F4	GM1135	TCC	Nagy et al. (2009)
F5	GM1609	CT	Nagy et al. (2009)
F6	GM1733	AT	Nagy et al. (2009)
F9	GM1856	CT	Nagy et al. (2009)
F10	GM1867	AG	Nagy et al. (2009)
G1	GM1907	TTC	Nagy et al. (2009)
G2	GM1979	GA	Nagy et al. (2009)
G3	GM1991	TC	Nagy et al. (2009)
G5	GM2308	CT	Nagy et al. (2009)
G6	GM2350	GA	Nagy et al. (2009)
G7	GM2602	GAA	Nagy et al. (2009)
G8	GM2603	GAA	Nagy et al. (2009)
G11	PM31	CT	He et al. (2003)
G12	PM69	NA	He et al. (2007)
H1	PM85	NA	He et al. (2009)
H2	PM308	CT	He et al. (2003)
H3	PM348	AG	He et al. (2005)
H11	PM671	GGC	He et al. (2006)
H12	PM721	GGC	He et al. (2008)
a1	GM2638	TC	Nagy et al. (2009)
a3	GM2690	AGA/TTG	Nagy et al. (2009)
a5	GM2745	TA	Nagy et al. (2009)
a6	GM2723	GAA	Nagy et al. (2009)
a7	GM2724	TTC	Nagy et al. (2009)
a10	GM2769	CTT	Nagy et al. (2009)
a11	GM2779	AAT	Nagy et al. (2009)

Table 3.1. Continued.

Marker	Marker name	Repeat motif	Reference
a12	GM2767	GAA	Nagy et al. (2009)
b1	GM2774	AT	Nagy et al. (2009)
b4	GM2791	TATGA	Nagy et al. (2009)
b7	GM2788	TCT/GGT	Nagy et al. (2009)
b10	GM2831	CAA	Nagy et al. (2009)
b11	GM2845	CTT	Nagy et al. (2009)
b12	GM2839	CA	Nagy et al. (2009)
cc1	pPGPseq1B9	AG	Ferguson et al. (2004)
cc2	pPGPseq2B9	TTA	Ferguson et al. (2004)
cc3	pPGPseq2G4	TAA	Ferguson et al. (2004)
cc4	pPGPseq3B8	TTA	Ferguson et al. (2004)
cc5	pPGPseq3E10	AAT	Ferguson et al. (2004)
cc6	pPGPseq5D5	GA	Ferguson et al. (2004)
cc7	pPGPseq7G2	ATAG	Ferguson et al. (2004)
cc9	pPGSseq9G5	CT	Ferguson et al. (2004)
c11	pPGSseq10D4	CT	Ferguson et al. (2004)
cc12	pPGSseq11G3	TTC	Ferguson et al. (2004)
d1	pPGSseq13A7	ATA	Ferguson et al. (2004)
d2	pPGSseq13A10	TTA	Ferguson et al. (2004)
d3	pPGSseq13E9	AAT	Ferguson et al. (2004)
d4	pPGSseq14H6	AC	Ferguson et al. (2004)
d5	pPGSseq15C10	AAT	Ferguson et al. (2004)
d6	pPGSseq16C6	TC	Ferguson et al. (2004)
d7	pPGSseq16G8	AT	Ferguson et al. (2004)
d8	pPGSseq17E1	TAT	Ferguson et al. (2004)
d9	pPGSseq18A5	TA	Ferguson et al. (2004)
d10	pPGSseq18C5	ATA	Ferguson et al. (2004)
d12	pPGSseq18G1	TTG	Ferguson et al. (2004)
e2	pPGSseq19A5	ATT	Ferguson et al. (2004)
e3	pPGSseq19B12	TTA	Ferguson et al. (2004)
e4	pPGSseq19D6	AAT	Ferguson et al. (2004)
e5	pPGSseq19D9	TAT	Ferguson et al. (2004)
e8	pPGSseq17E3	TCT	Ferguson et al. (2004)
e9	pPGSseq19B1	AG	Ferguson et al. (2004)
e10	pPGPseq2C11	TTA	Ferguson et al. (2004)
e11	pPGPseq2D12B	AAT	Ferguson et al. (2004)
f1	pPGPseq2F5	TTA	Ferguson et al. (2004)

Table 3.1. Continued.

Marker	Marker name	Repeat motif	Reference
f2	pPGPseq3B5	AG	Ferguson et al. (2004)
f3	TC02D06	AG	Moretzsohn et al. (2005)
f4	TC03A12	TC	Moretzsohn et al. (2005)
f5	TC03E02	CT/CA	Moretzsohn et al. (2005)
f7	TC04F12	CT	Moretzsohn et al. (2005)
f8	TC04G02	TC	Moretzsohn et al. (2005)
f10	TC05A06	TC	Moretzsohn et al. (2005)
f11	TC05D06	AG	Moretzsohn et al. (2005)
f12	TC06E01	GA	Moretzsohn et al. (2005)
g1	TC06H03	AG	Moretzsohn et al. (2005)
g4	TC11B04	GA	Moretzsohn et al. (2005)
g5	TC2A02	CT	Moretzsohn et al. (2005)
g6	TC3E05	GA	Moretzsohn et al. (2005)
g7	gi4925	ATT	Moretzsohn et al. (2005)
g8	RI1F06	ATA/ATT/GA	Moretzsohn et al. (2005)
g9	AC2C05	TG	Moretzsohn et al. (2005)
g10	Ah3	GA/AG/GT	Gimenes et al. (2007)
g11	Ah26	CT	Gimenes et al. (2007)
g12	Ah193	AAC/GA	Moretzsohn et al. (2004)
h2	XIP297	TC	Cuc et al. (2008)
h6	Lec1	AT	Hopkins et al. (1999)
h7	XIP105	CT	Cuc et al. (2008)
h8	XIP108	TC	Cuc et al. (2008)
h9	XIP123	GA	Cuc et al. (2008)
h10	XIP136	CT	Cuc et al. (2008)

Table 3.2. Genetic diversity profile of each SSR markers used in the study.

Marker name	Major allele frequency	Allele number	Gene diversity	Heterozygosity	PIC
Ad90K4	0.24	12	0.85	0.03	0.84
Ad90P7	0.22	8	0.83	0.03	0.81
Ad91O22	0.15	15	0.89	0.93	0.88
Ad92L5	0.30	8	0.79	0.01	0.76
Ad95D7	0.39	4	0.67	0.52	0.60
Ai119F10	0.27	9	0.83	0.02	0.81
Ai119G12	0.30	14	0.84	0.47	0.82
Ai120L22	0.24	8	0.81	0.02	0.78
Ai121G16	0.45	7	0.70	0.00	0.65
TC4F02	0.21	12	0.83	0.91	0.81
TC13E05	0.88	5	0.23	0.06	0.22
TC19B07	0.27	11	0.78	0.00	0.75
TC19B11	0.25	9	0.81	0.08	0.78
TC20B05	0.69	11	0.51	0.38	0.50
TC20E08	0.41	7	0.73	0.93	0.70
TC21C10	0.25	10	0.81	0.29	0.78
TC21D06	0.38	4	0.68	1.00	0.62
TC23C08	0.56	5	0.61	0.45	0.56
TC23E04	0.50	8	0.66	1.00	0.62
TC23F04	0.20	16	0.87	0.93	0.86
TC23H10	0.16	30	0.92	0.93	0.91
TC24B05	0.30	10	0.79	0.00	0.77
TC24C06	0.21	18	0.87	0.18	0.86
TC25G11	0.47	9	0.73	0.01	0.71
TC27H12	0.36	8	0.71	1.00	0.66
TC28B01	0.19	20	0.88	0.22	0.87
TC29H08	0.46	8	0.72	0.06	0.69
TC30D04	0.22	15	0.88	0.00	0.87
TC31E08	0.29	7	0.80	0.37	0.78
TC31G11	0.27	12	0.83	0.02	0.81
TC31H02	0.34	9	0.75	0.98	0.72
TC31H06	0.58	4	0.58	0.82	0.52
TC38D06	0.50	5	0.63	1.00	0.56
TC39B04	0.82	3	0.30	0.37	0.26
TC39F01	0.20	16	0.89	0.07	0.88

Table 3.2. Continued

Marker name	Major allele frequency	Allele number	Gene diversity	Heterozygosity	PIC
TC42A02	0.35	10	0.74	1.00	0.70
TC41A10	0.30	12	0.78	0.06	0.75
TC41C11	0.91	6	0.16	0.04	0.16
TC42A05	0.26	12	0.83	1.00	0.81
Ah11.1	0.50	4	0.52	0.98	0.40
Ah20	0.50	4	0.51	1.00	0.39
Ah32	0.25	15	0.83	1.00	0.81
Ah51	0.43	9	0.73	0.02	0.69
Ah282.1	0.50	4	0.51	0.99	0.39
GM699	0.41	5	0.65	0.00	0.58
GM1135	0.83	2	0.29	0.35	0.25
GM1609	0.47	5	0.56	1.00	0.46
GM1733	0.47	7	0.72	0.95	0.69
GM1856	0.49	5	0.56	1.00	0.46
GM1867	0.47	6	0.57	0.00	0.48
GM1907	0.42	4	0.68	0.96	0.62
GM1979	0.85	8	0.27	0.08	0.26
GM1991	0.55	7	0.61	0.04	0.56
GM2308	0.31	7	0.75	0.97	0.71
GM2350	0.44	7	0.71	0.99	0.66
GM2602	0.50	5	0.64	1.00	0.59
GM2603	0.50	4	0.64	1.00	0.58
PM31	0.46	8	0.68	0.98	0.63
PM69	0.57	11	0.64	0.62	0.62
PM85	0.48	6	0.66	0.99	0.61
PM308	0.31	10	0.79	0.03	0.76
PM348	0.41	3	0.66	0.51	0.58
PM671	0.50	3	0.59	1.00	0.50
PM721	0.74	3	0.40	0.45	0.34
GM2638	0.49	7	0.66	1.00	0.61
GM2690	0.32	6	0.74	0.87	0.69
GM2745	0.48	4	0.54	0.97	0.44
GM2723	0.91	4	0.17	0.16	0.16
GM2724	0.46	5	0.63	0.99	0.55
GM2769	0.49	6	0.57	0.94	0.48
GM2779	0.40	6	0.73	1.00	0.68

Table 3.2. Continued

Marker name	Major allele frequency	Allele number	Gene diversity	Heterozygosity	PIC
GM2767	0.38	6	0.71	0.99	0.66
GM2774	0.49	4	0.63	0.98	0.56
GM2791	0.49	4	0.61	1.00	0.54
GM2788	0.60	3	0.49	0.08	0.38
GM2831	0.52	4	0.52	0.93	0.40
GM2845	0.30	13	0.82	0.02	0.79
GM2839	0.67	4	0.50	0.08	0.45
pPGPseq1B9	0.40	7	0.70	1.00	0.65
pPGPseq2B9	0.38	6	0.74	0.96	0.70
pPGPseq2G4	0.25	12	0.87	0.05	0.85
pPGPseq3B8	0.30	9	0.81	0.01	0.78
pPGPseq3E10	0.34	5	0.76	0.44	0.72
pPGPseq5D5	0.19	15	0.88	0.99	0.86
pPGPseq7G2	0.39	10	0.76	0.02	0.73
pPGSseq9G5	0.44	4	0.61	1.00	0.53
pPGSseq10D4	0.25	13	0.84	0.82	0.82
pPGSseq11G3	0.45	8	0.68	0.02	0.62
pPGSseq13A7	0.56	3	0.53	0.00	0.43
pPGSseq13A10	0.47	5	0.60	0.94	0.51
pPGSseq13E9	0.40	3	0.65	0.98	0.58
pPGSseq14H6	0.49	15	0.72	1.00	0.70
pPGSseq15C10	0.49	8	0.68	1.00	0.64
pPGSseq16C6	0.36	9	0.80	0.09	0.77
pPGSseq16G8	0.18	11	0.88	0.99	0.86
pPGSseq17E1	0.16	22	0.89	1.00	0.89
pPGSseq18A5	0.32	17	0.83	0.08	0.81
pPGSseq18C5	0.27	10	0.81	0.06	0.78
pPGSseq18G1	0.50	7	0.64	0.99	0.58
pPGSseq19A5	0.66	4	0.52	0.04	0.48
pPGSseq19B12	0.93	5	0.13	0.00	0.13
pPGSseq19D6	0.30	15	0.84	0.06	0.83
pPGSseq19D9	0.16	11	0.87	0.02	0.86
pPGSseq17E3	0.42	6	0.72	0.08	0.67
pPGSseq19B1	0.57	3	0.56	0.02	0.49
pPGPseq2C11	0.49	8	0.68	1.00	0.64

Table 3.2. Continued

Marker name	Major allele frequency	Allele number	Gene diversity	Heterozygosity	PIC
pPGPseq2D12B	0.17	27	0.91	1.00	0.91
pPGPseq2F5	0.48	15	0.73	0.51	0.70
pPGPseq3B5	0.50	14	0.71	1.00	0.69
TC02D06	0.34	11	0.77	0.01	0.74
TC03A12	0.22	11	0.84	0.98	0.82
TC03E02	0.50	11	0.70	1.00	0.68
TC04F12	0.47	7	0.71	0.01	0.67
TC04G02	0.50	7	0.69	0.54	0.65
TC05A06	0.35	10	0.76	0.01	0.72
TC05D06	0.50	8	0.68	1.00	0.64
TC06E01	0.43	8	0.74	1.00	0.71
TC06H03	0.22	11	0.84	0.86	0.82
TC11B04	0.21	11	0.87	0.90	0.86
TC2A02	0.52	9	0.68	0.96	0.65
TC3E05	0.34	6	0.77	0.00	0.73
gi4925	0.44	4	0.63	0.02	0.56
RI1F06	0.55	8	0.61	0.50	0.56
AC2C05	0.50	3	0.54	0.00	0.44
Ah3	0.25	12	0.86	0.79	0.84
Ah26	0.58	5	0.53	0.00	0.44
Ah193	0.59	4	0.55	0.01	0.47
XIP297	0.97	2	0.06	0.00	0.05
Lec1	0.20	14	0.87	0.78	0.85
XIP105	0.47	11	0.64	0.99	0.57
XIP108	0.28	10	0.82	0.99	0.79
XIP123	0.30	5	0.75	0.99	0.70
XIP136	0.81	2	0.30	0.38	0.26
Mean	0.42	8.44	0.68	0.54	0.64

Table 3.3. Four subpopulations defined by STRUCTURE analysis for 104 genotypes from the U.S. peanut mini core collection.

G1 (25)	G2 (18)	G3 (25)	G4 (36)
PI259617	PI152146	PI158854	PI290566
PI262038	PI200441	PI240560	PI343398
PI337406	PI259836	PI268586	PI159786
PI356004	PI290620	PI268696	PI162655
PI429420	PI295730	PI268755	PI162857
PI471954	PI313129	PI268806	PI196622
PI482189	PI339960	PI338338	PI196635
PI475918	PI478850	PI155107	PI259658
PI493329	PI502040	PI270998	PI259851
PI493356	PI475863	PI271019	PI157542
PI493547	PI476025	PI288146	PI268868
PI493581	PI502111	PI270786	PI268996
PI493631	PI502120	PI270905	PI274193
PI493693	PI270907	PI337293	PI290536
PI493717	PI494795	PI337399	PI290594
PI493729	PI497639	PI461434	PI292950
PI493880	PI497318	PI481795	PI295250
PI493938	PI497395	PI482120	PI295309
PI325943		PI504614	PI296550
PI331297		PI290560	PI296558
PI343384		PI407667	PI298854
PI471952		PI478819	PI319768
PI403813		PI476432	PI323268
PI497517		PI494018	PI331314
PI461427		PI494034	PI355268
			PI355271
			PI370331
			PI372271
			PI372305
			PI399581
			PI442768
			PI476636
			PI496401
			PI496448
			PI288210
			PI371521

Table 3.4. Summary statistics for the whole panel of peanut genotypes and subpopulations detected by structure analysis based on 133 SSR markers.

Statistics	Overall	G1	G2	G3	G4
Sample size	104	25	18	25	36
Total number of alleles	1130	775	652	715	871
Number of alleles per locus	8.50	5.83	4.90	5.38	6.55
Major allele frequency	0.42	0.52	0.44	0.48	0.53
Genetic diversity	0.68	0.59	0.68	0.62	0.57
PIC	0.64	0.54	0.63	0.57	0.52
F*st*	0.20	0.27	0.04	0.22	0.26

Table 3.5. Genetic distances among four subpopulations defined by STRUCTURE analysis.

Group	G1	G2	G3	G4
G1	0.00	0.19	0.18	0.24
G2	0.37	0.00	0.17	0.16
G3	0.36	0.35	0.00	0.21
G4	0.43	0.34	0.40	0.00

The top diagonal is Nei's minimum distance and the bottom diagonal is pairwise $F_{st.}$

Table 3.6. AMOVA among and within subpopulations detected via STRUCTURE analysis of 133 SSR markers.

Source of variation	Df	Sum of squares	Mean of squares	Variance of variation	Percentage	P-value
Among groups	3	2050.02	683.34	20.50	41.56	<0.0001
Within groups	100	2882.67	28.83	28.83	58.44	<0.0001
Total	103	4932.69		49.33		

Table 3.7. AMOVA among and within the botanical varieties of the U.S. peanut mini core collection based on 133 SSR markers.

Source of variation	Df	Sum of squares	Mean of squares	Variance of variation	Percentage	P-value
Among botanical varieties	3	1046.37	348.79	10.46	21.21	<0.0001
Within botanical varieties	100	3886.32	38.86	38.86	78.79	<0.0001
Total	103	4932.69		49.33		

Table 3.8. Significantly associated markers detected by four models for visual symptoms and ELISA.

	Marker	PCA [a]	PCA+K	Q	Q+K	Marker_R^2 [b]	P-value
Visual symptoms	pPGSseq16C6	√	√			0.106	0.0007
	pPGPseq5D5	√	√	√	√	0.099	0.0011
	GM1135	√	√	√	√	0.088	0.0023
	GM1991	√	√	√	√	0.077	0.0043
	TC23C08	√	√	√	√	0.055	0.0162
	TC24B05	√	√			0.049	0.0239
	pPGSseq17E3	√	√			0.046	0.0286
	TC24C06	√	√	√	√	0.045	0.0304
	pPGSseq10D4	√				0.042	0.0358
	TC30D04	√				0.040	0.0415
	GM2831	√				0.038	0.0459
ELISA result	pPGPseq5D5	√	√	√	√	0.093	0.0019
	GM1991	√	√	√	√	0.062	0.0118
	TC23H10	√	√	√	√	0.053	0.0198
	RI1F06	√				0.050	0.0237
	TC30D04	√		√		0.049	0.0251
	pPGSseq13A7	√				0.045	0.0332
	pPGSseq19D9	√				0.044	0.0349
	pPGSseq16C6	√				0.039	0.0476

a: '√' means the marker is identified in the model.

b: The Marker_R^2 based on PCA model.

Fig. 3.1. Magnitude of Δ K from STRUCTURE analysis of the U.S. peanut mini core collection.

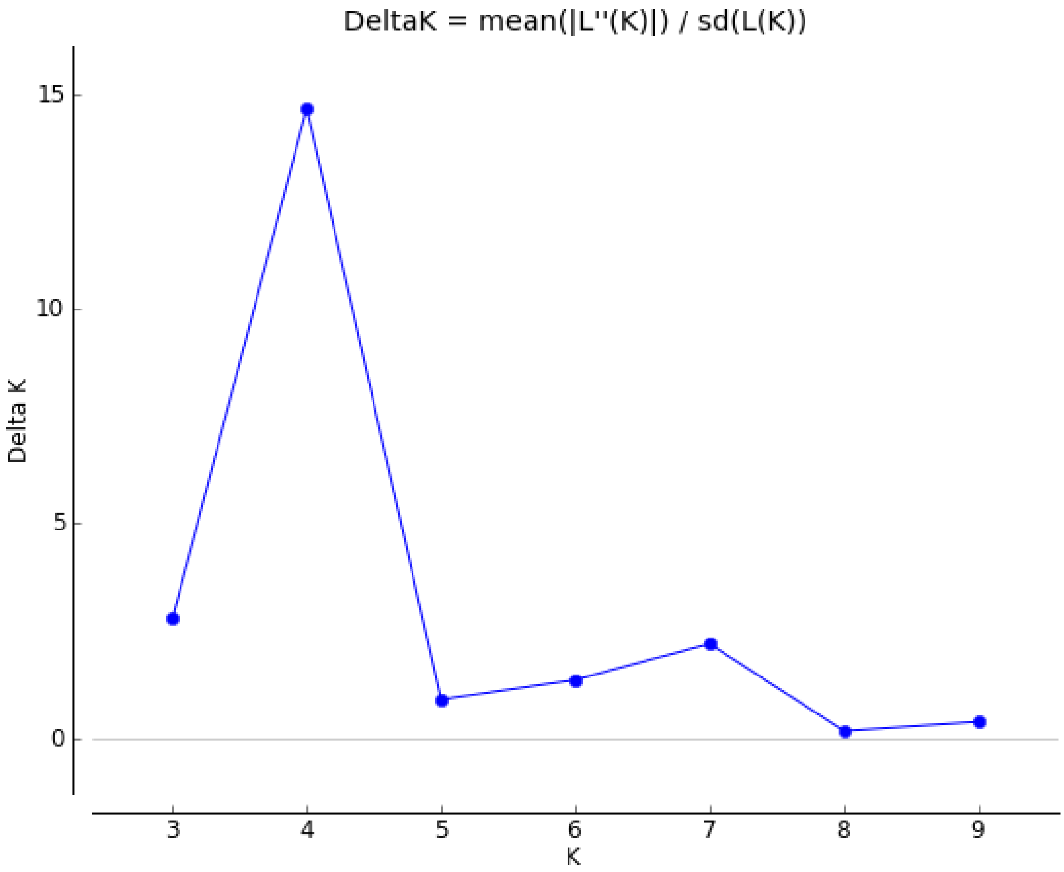


Fig. 3.2. Population structure analysis. The y-axis is the subgroup membership, and x-axis is the genotypes. G1-G4 stands for subpopulations.

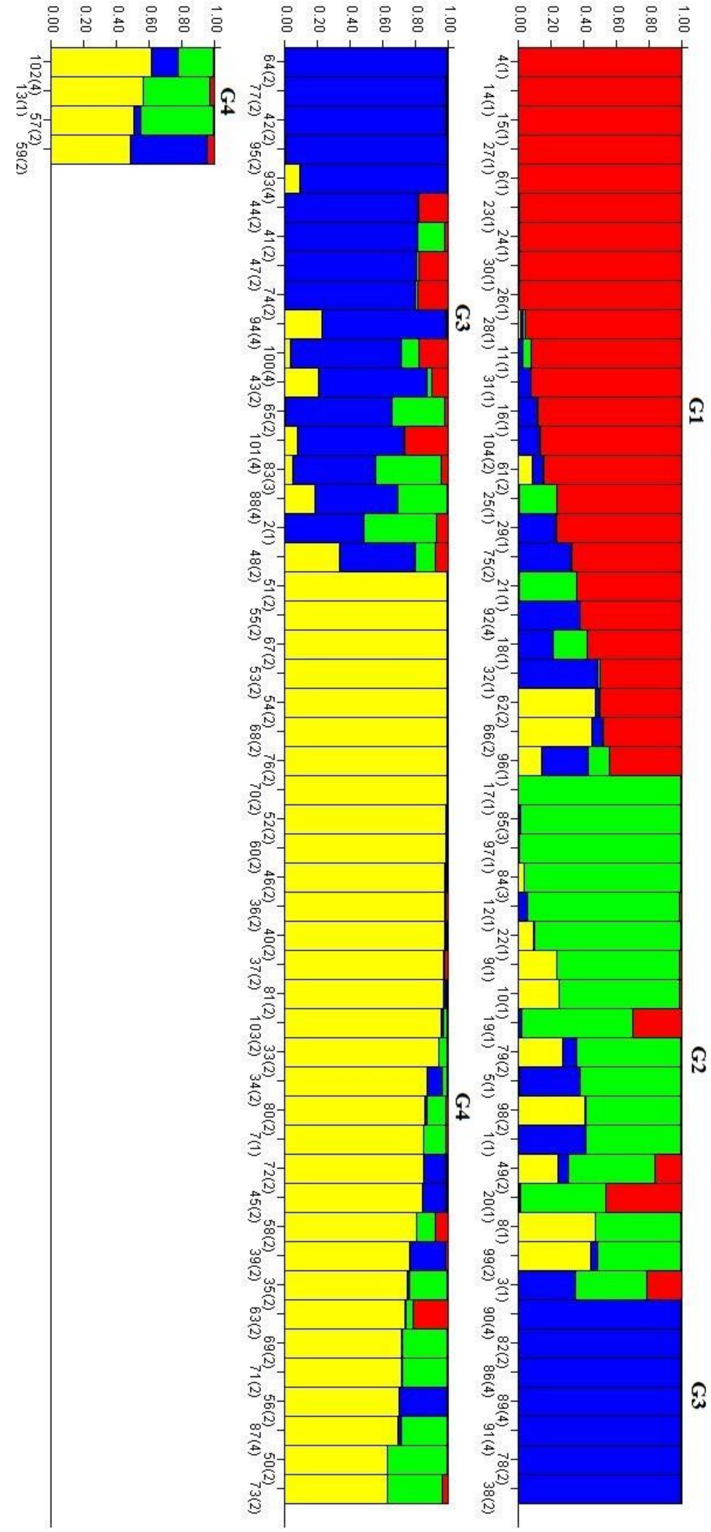


Fig. 3.3. Principal component analysis based on Chord distance for the U.S. peanut mini core collection. The branch colors correspond to the colors of the STRUCTURE clusters from Fig. 3.2, K=4.

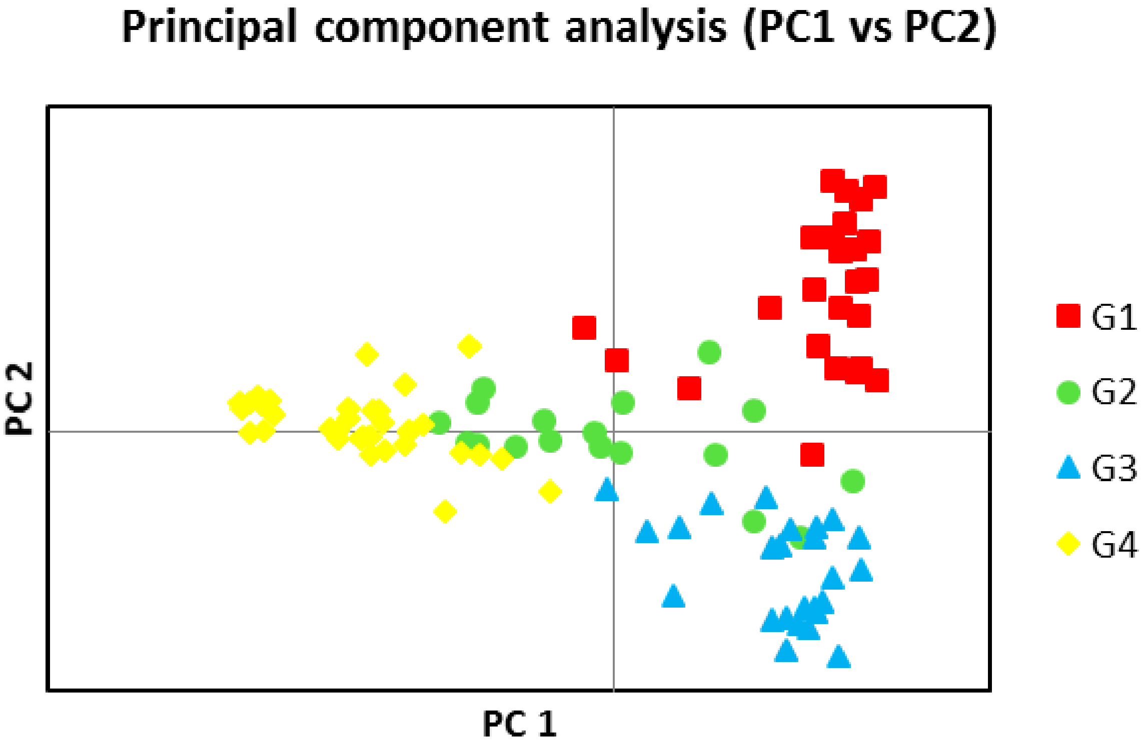


Fig. 3.4. UPGMA tree analysis based on Chord distance for the U.S. peanut mini core collection. The tree colors correspond to the colors of the STRUCTURE clusters from Fig. 3.2, K=4.

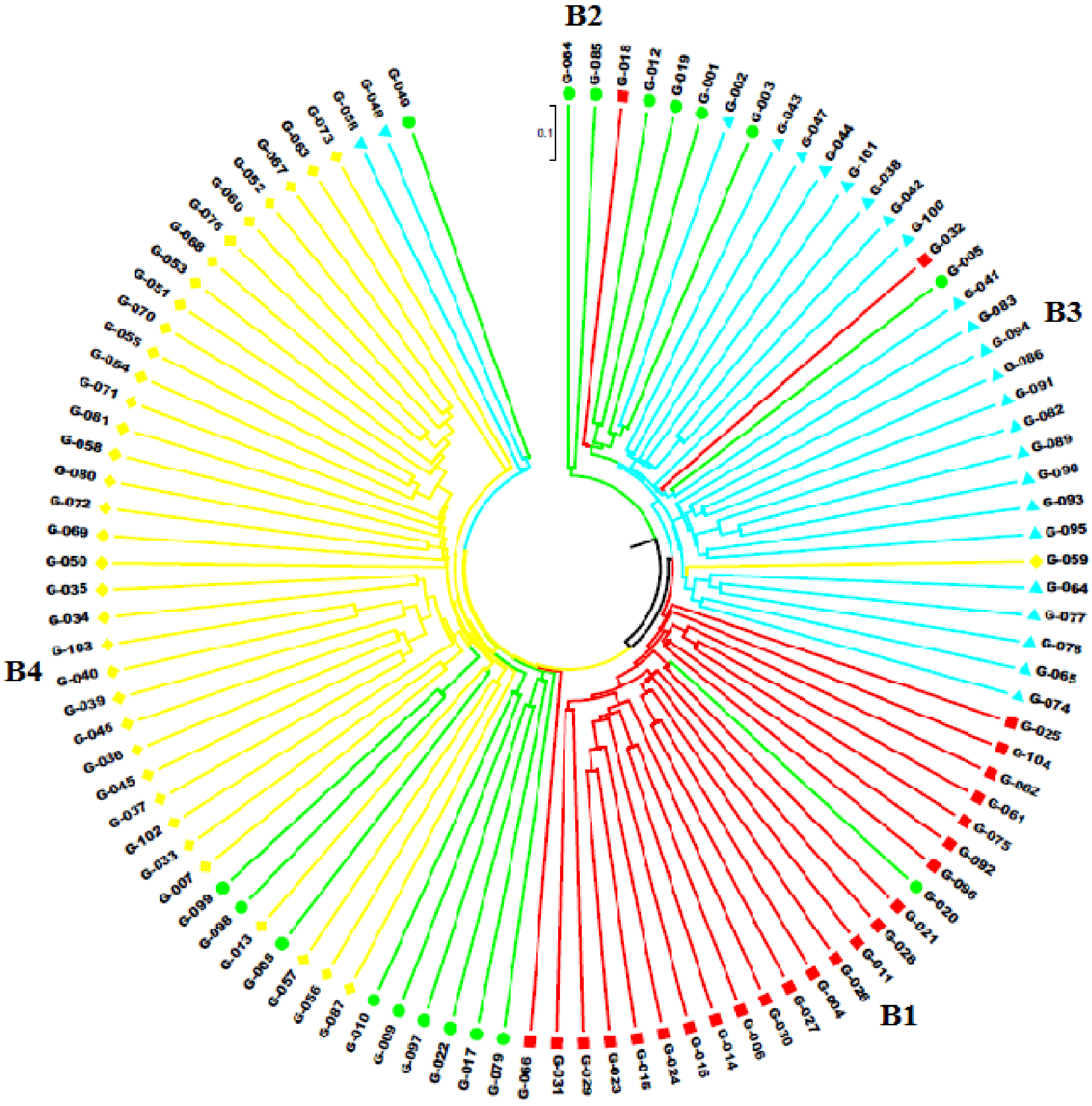
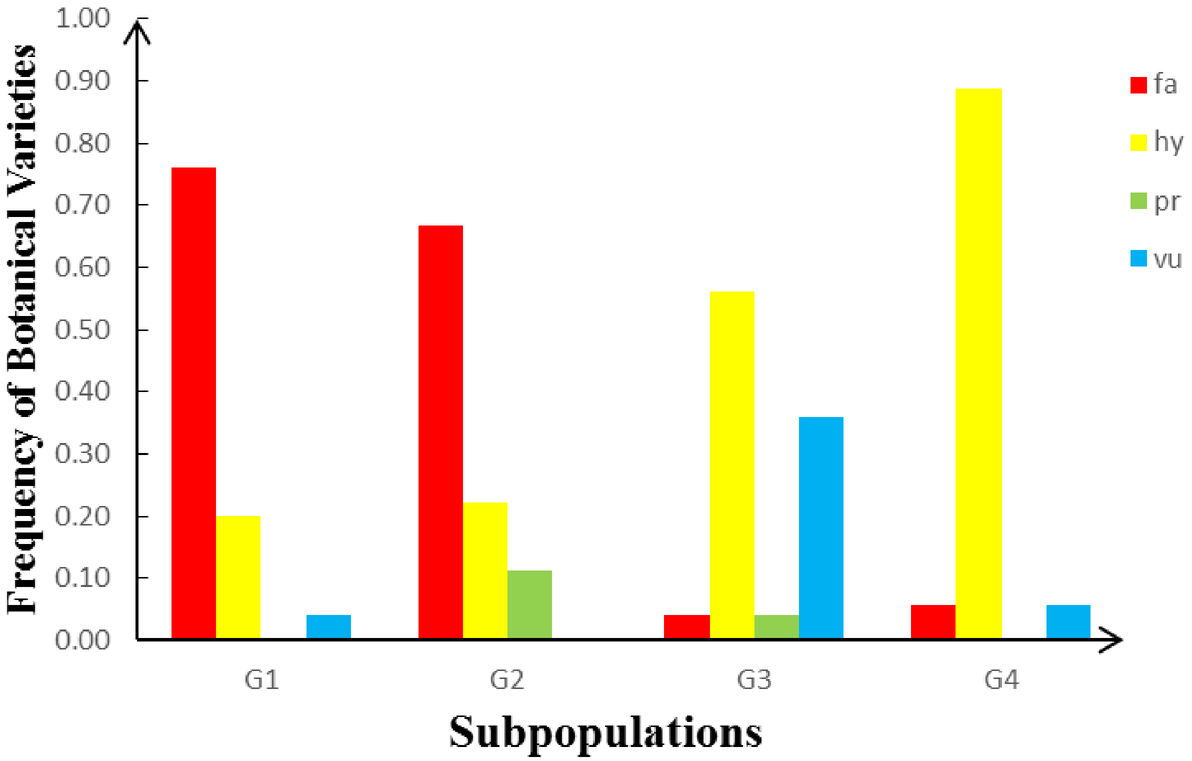


Fig. 3.5. Frequency of botanical variety within each subpopulation.



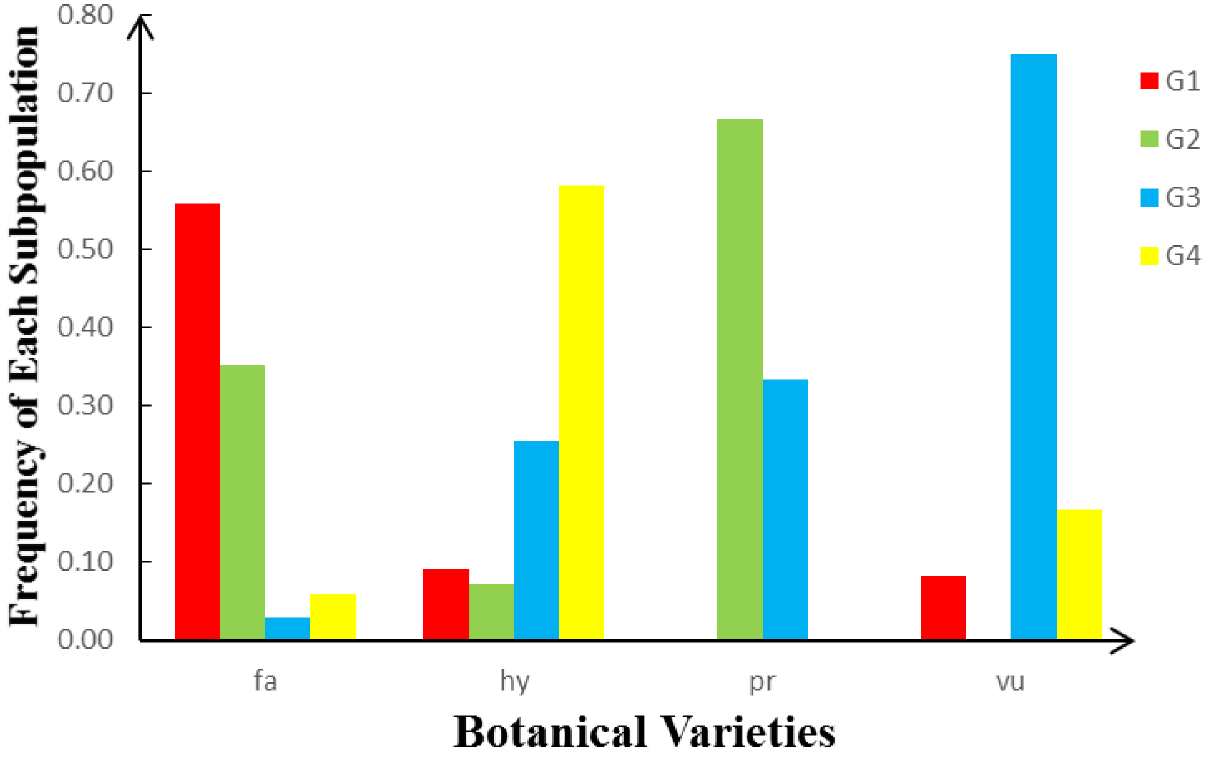
fa: var. *fastigiata*

hy: var. *hypogaea*

pr: var. *peruviana*

vu: var. *vulgaris*

Fig. 3.6. Frequency of each subpopulation within each botanical variety.



Appendix A. Kinship matrix calculated from SSR data for 104 genotypes of the U.S. peanut mini core collection.

Code	Genotype	G-1	G-2	G-3	G-4	G-5	G-6	G-7	G-8	G-9	G-10	G-11	G-12	G-13
G-1	PI152146	2.000	0.898	0.512	0.017	0.233	0.001	0.000	0.000	0.091	0.151	0.212	0.216	0.000
G-2	PI158854	0.898	2.000	0.858	0.012	0.648	0.010	0.000	0.000	0.051	0.119	0.399	0.346	0.000
G-3	PI200441	0.512	0.858	2.000	0.171	0.500	0.051	0.000	0.000	0.000	0.074	0.504	0.315	0.000
G-4	PI259617	0.017	0.012	0.171	2.000	0.000	0.615	0.000	0.000	0.000	0.028	0.669	0.000	0.000
G-5	PI259836	0.233	0.648	0.500	0.000	2.000	0.000	0.000	0.043	0.000	0.000	0.197	0.354	0.000
G-6	PI262038	0.001	0.010	0.051	0.615	0.000	2.000	0.000	0.000	0.000	0.000	0.349	0.000	0.000
G-7	PI290566	0.000	0.000	0.000	0.000	0.000	0.000	2.000	0.709	0.282	0.229	0.000	0.029	0.642
G-8	PI290620	0.000	0.000	0.000	0.000	0.043	0.000	0.709	2.000	0.211	0.287	0.000	0.081	0.469
G-9	PI295730	0.091	0.051	0.000	0.000	0.000	0.000	0.282	0.211	2.000	0.548	0.068	0.091	0.195
G-10	PI313129	0.151	0.119	0.074	0.028	0.000	0.000	0.229	0.287	0.548	2.000	0.000	0.101	0.388
G-11	PI337406	0.212	0.399	0.504	0.669	0.197	0.349	0.000	0.000	0.068	0.000	2.000	0.100	0.000
G-12	PI339960	0.216	0.346	0.315	0.000	0.354	0.000	0.029	0.081	0.091	0.101	0.100	2.000	0.154
G-13	PI343398	0.000	0.000	0.000	0.000	0.000	0.000	0.642	0.469	0.195	0.388	0.000	0.154	2.000
G-14	PI356004	0.000	0.004	0.062	0.820	0.000	1.036	0.000	0.000	0.000	0.000	0.465	0.037	0.000
G-15	PI429420	0.000	0.000	0.066	0.876	0.000	0.798	0.000	0.000	0.000	0.000	0.395	0.000	0.000
G-16	PI471954	0.099	0.086	0.173	0.561	0.000	0.668	0.000	0.000	0.000	0.008	0.249	0.076	0.000
G-17	PI478850	0.169	0.099	0.223	0.000	0.161	0.000	0.000	0.124	0.270	0.324	0.046	0.576	0.130
G-18	PI482189	0.257	0.781	0.586	0.497	0.262	0.260	0.000	0.000	0.000	0.102	0.658	0.046	0.000
G-19	PI502040	0.234	0.444	0.416	0.390	0.122	0.055	0.000	0.024	0.039	0.296	0.382	0.486	0.032
G-20	PI475863	0.000	0.000	0.184	0.282	0.003	0.247	0.000	0.000	0.005	0.074	0.240	0.303	0.000
G-21	PI475918	0.136	0.000	0.065	0.602	0.047	0.580	0.000	0.000	0.000	0.000	0.244	0.101	0.000
G-22	PI476025	0.000	0.000	0.000	0.000	0.040	0.000	0.300	0.270	0.022	0.213	0.000	0.350	0.154
G-23	PI493329	0.000	0.012	0.127	0.587	0.000	0.618	0.000	0.000	0.000	0.000	0.391	0.000	0.000
G-24	PI493356	0.000	0.000	0.021	0.558	0.000	0.665	0.000	0.000	0.000	0.000	0.314	0.000	0.000
G-25	PI493547	0.242	0.227	0.269	0.615	0.041	0.515	0.000	0.000	0.029	0.074	0.380	0.072	0.000
G-26	PI493581	0.123	0.147	0.302	0.851	0.000	0.787	0.000	0.000	0.025	0.065	0.603	0.000	0.000
G-27	PI493631	0.000	0.015	0.098	1.070	0.000	0.618	0.000	0.000	0.000	0.000	0.808	0.000	0.000
G-28	PI493693	0.042	0.092	0.147	0.661	0.212	0.542	0.000	0.000	0.000	0.000	0.636	0.117	0.000
G-29	PI493717	0.026	0.309	0.216	0.331	0.093	0.504	0.000	0.000	0.000	0.000	0.324	0.115	0.000
G-30	PI493729	0.000	0.000	0.002	0.506	0.000	0.544	0.000	0.000	0.000	0.000	0.431	0.072	0.000
G-31	PI493880	0.048	0.052	0.060	0.470	0.000	0.467	0.000	0.000	0.000	0.000	0.306	0.000	0.000
G-32	PI493938	0.158	0.204	0.309	0.017	0.187	0.221	0.000	0.009	0.000	0.000	0.229	0.123	0.000
G-33	PI159786	0.000	0.000	0.000	0.000	0.000	0.000	0.847	0.404	0.179	0.188	0.000	0.000	0.317
G-34	PI162655	0.000	0.000	0.000	0.000	0.011	0.000	0.392	0.147	0.161	0.054	0.000	0.000	0.178
G-35	PI162857	0.000	0.000	0.000	0.000	0.000	0.000	0.383	0.240	0.145	0.000	0.000	0.000	0.216
G-36	PI196622	0.000	0.000	0.000	0.000	0.000	0.000	0.404	0.138	0.014	0.000	0.000	0.000	0.240
G-37	PI196635	0.000	0.000	0.000	0.000	0.000	0.000	0.418	0.109	0.177	0.000	0.000	0.000	0.117
G-38	PI240560	0.083	0.223	0.056	0.000	0.174	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000
G-39	PI259658	0.000	0.000	0.000	0.000	0.000	0.000	0.105	0.000	0.000	0.000	0.000	0.000	0.042
G-40	PI259851	0.000	0.000	0.000	0.000	0.000	0.000	0.324	0.196	0.003	0.101	0.000	0.031	0.255
G-41	PI268586	0.224	0.242	0.151	0.000	0.494	0.000	0.000	0.000	0.000	0.000	0.059	0.037	0.000
G-42	PI268696	0.198	0.129	0.082	0.000	0.149	0.000	0.000	0.000	0.000	0.000	0.000	0.035	0.000
G-43	PI268755	0.070	0.027	0.015	0.000	0.000	0.000	0.000	0.003	0.017	0.000	0.000	0.186	0.000
G-44	PI268806	0.144	0.333	0.179	0.046	0.264	0.027	0.000	0.000	0.000	0.000	0.084	0.061	0.000
G-45	PI268868	0.000	0.000	0.000	0.000	0.000	0.000	0.271	0.106	0.069	0.000	0.000	0.000	0.157
G-46	PI268996	0.000	0.000	0.000	0.000	0.000	0.000	0.385	0.074	0.048	0.025	0.000	0.000	0.171
G-47	PI270786	0.145	0.180	0.103	0.000	0.119	0.168	0.000	0.000	0.000	0.000	0.007	0.121	0.000
G-48	PI270905	0.077	0.000	0.000	0.000	0.000	0.000	0.007	0.087	0.000	0.000	0.000	0.007	0.012
G-49	PI270907	0.104	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.057	0.000	0.000	0.000	0.000
G-50	PI274193	0.000	0.000	0.000	0.000	0.000	0.000	0.274	0.085	0.255	0.064	0.000	0.000	0.101
G-51	PI290536	0.000	0.000	0.000	0.000	0.000	0.000	0.413	0.151	0.321	0.163	0.000	0.000	0.215
G-52	PI290594	0.000	0.000	0.000	0.000	0.000	0.000	0.358	0.193	0.100	0.110	0.000	0.000	0.228

Appendix A. cont.

Code	Genotype	G-1	G-2	G-3	G-4	G-5	G-6	G-7	G-8	G-9	G-10	G-11	G-12	G-13
G-53	PI292950	0.000	0.000	0.000	0.000	0.000	0.000	0.408	0.176	0.160	0.000	0.000	0.000	0.160
G-54	PI295250	0.000	0.000	0.000	0.000	0.000	0.000	0.304	0.228	0.192	0.054	0.000	0.000	0.175
G-55	PI295309	0.000	0.000	0.000	0.000	0.000	0.000	0.400	0.113	0.088	0.013	0.000	0.000	0.212
G-56	PI296550	0.000	0.000	0.000	0.000	0.000	0.000	0.224	0.000	0.000	0.000	0.000	0.000	0.155
G-57	PI296558	0.000	0.000	0.000	0.000	0.000	0.000	0.219	0.036	0.276	0.106	0.000	0.000	0.090
G-58	PI298854	0.000	0.000	0.000	0.000	0.000	0.000	0.404	0.134	0.242	0.186	0.000	0.000	0.209
G-59	PI319768	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-60	PI323268	0.000	0.000	0.000	0.000	0.000	0.000	0.361	0.107	0.056	0.060	0.000	0.000	0.215
G-61	PI325943	0.017	0.000	0.146	0.520	0.000	0.410	0.000	0.000	0.008	0.000	0.282	0.000	0.000
G-62	PI331297	0.000	0.000	0.000	0.164	0.000	0.130	0.000	0.000	0.007	0.062	0.018	0.000	0.000
G-63	PI331314	0.000	0.000	0.000	0.000	0.000	0.000	0.083	0.000	0.000	0.000	0.000	0.000	0.057
G-64	PI337293	0.129	0.302	0.056	0.000	0.135	0.000	0.000	0.000	0.000	0.000	0.000	0.098	0.000
G-65	PI337399	0.398	0.411	0.266	0.000	0.260	0.000	0.000	0.000	0.000	0.000	0.044	0.110	0.000
G-66	PI343384	0.000	0.000	0.078	0.130	0.000	0.042	0.000	0.000	0.105	0.000	0.035	0.000	0.000
G-67	PI355268	0.000	0.000	0.000	0.000	0.000	0.000	0.335	0.150	0.102	0.070	0.000	0.000	0.222
G-68	PI355271	0.000	0.000	0.000	0.000	0.000	0.000	0.292	0.109	0.043	0.132	0.000	0.000	0.281
G-69	PI370331	0.000	0.000	0.000	0.000	0.000	0.000	0.155	0.030	0.123	0.073	0.000	0.000	0.077
G-70	PI372271	0.000	0.000	0.000	0.000	0.000	0.000	0.277	0.163	0.177	0.003	0.000	0.000	0.231
G-71	PI372305	0.000	0.000	0.000	0.000	0.000	0.000	0.197	0.126	0.136	0.004	0.000	0.000	0.134
G-72	PI399581	0.000	0.000	0.000	0.000	0.000	0.000	0.290	0.116	0.000	0.002	0.000	0.000	0.174
G-73	PI442768	0.000	0.000	0.000	0.000	0.000	0.000	0.175	0.117	0.184	0.083	0.000	0.000	0.071
G-74	PI461434	0.322	0.311	0.261	0.000	0.150	0.056	0.000	0.000	0.000	0.000	0.150	0.112	0.000
G-75	PI471952	0.033	0.000	0.105	0.304	0.025	0.373	0.000	0.000	0.000	0.000	0.364	0.000	0.000
G-76	PI476636	0.000	0.000	0.000	0.000	0.000	0.000	0.323	0.075	0.025	0.072	0.000	0.000	0.243
G-77	PI481795	0.262	0.300	0.166	0.000	0.202	0.000	0.000	0.000	0.000	0.000	0.000	0.117	0.000
G-78	PI482120	0.188	0.199	0.151	0.000	0.253	0.000	0.000	0.000	0.000	0.000	0.023	0.000	0.000
G-79	PI494795	0.000	0.000	0.000	0.000	0.000	0.000	0.078	0.016	0.100	0.055	0.000	0.000	0.049
G-80	PI496401	0.000	0.000	0.000	0.000	0.000	0.000	0.143	0.060	0.006	0.046	0.000	0.000	0.092
G-81	PI496448	0.000	0.000	0.000	0.000	0.000	0.000	0.398	0.173	0.161	0.191	0.000	0.000	0.150
G-82	PI504614	0.192	0.308	0.000	0.000	0.198	0.000	0.000	0.000	0.000	0.000	0.000	0.057	0.000
G-83	PI338338	0.081	0.000	0.000	0.000	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.103	0.000
G-84	PI502111	0.011	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.270	0.283	0.000	0.037	0.056
G-85	PI502120	0.000	0.038	0.000	0.000	0.082	0.000	0.000	0.000	0.253	0.075	0.076	0.189	0.000
G-86	PI155107	0.158	0.306	0.139	0.000	0.175	0.089	0.000	0.000	0.000	0.000	0.000	0.021	0.000
G-87	PI157542	0.000	0.000	0.000	0.000	0.000	0.000	0.226	0.101	0.076	0.223	0.000	0.000	0.211
G-88	PI270998	0.331	0.192	0.000	0.000	0.000	0.000	0.000	0.035	0.065	0.008	0.000	0.000	0.000
G-89	PI271019	0.298	0.169	0.023	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.000	0.122	0.000
G-90	PI288146	0.206	0.300	0.034	0.000	0.076	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-91	PI290560	0.161	0.235	0.015	0.000	0.026	0.000	0.000	0.000	0.000	0.000	0.000	0.053	0.000
G-92	PI403813	0.075	0.012	0.087	0.323	0.000	0.377	0.000	0.000	0.000	0.042	0.298	0.000	0.000
G-93	PI407667	0.120	0.250	0.276	0.000	0.053	0.000	0.000	0.000	0.000	0.000	0.000	0.039	0.000
G-94	PI478819	0.104	0.186	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000
G-95	PI476432	0.193	0.316	0.107	0.000	0.260	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-96	PI497517	0.000	0.000	0.191	0.297	0.000	0.258	0.000	0.016	0.000	0.016	0.109	0.000	0.000
G-97	PI497639	0.066	0.058	0.000	0.000	0.098	0.000	0.137	0.088	0.058	0.012	0.000	0.393	0.000
G-98	PI497318	0.000	0.000	0.000	0.000	0.000	0.000	0.319	0.252	0.190	0.000	0.000	0.116	0.122
G-99	PI497395	0.000	0.000	0.000	0.000	0.000	0.000	0.113	0.187	0.062	0.000	0.000	0.041	0.059
G-100	PI494018	0.053	0.164	0.247	0.121	0.207	0.000	0.000	0.000	0.000	0.000	0.102	0.051	0.000
G-101	PI494034	0.182	0.117	0.080	0.000	0.144	0.059	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-102	PI288210	0.000	0.000	0.000	0.000	0.021	0.000	0.006	0.000	0.071	0.000	0.000	0.007	0.059
G-103	PI371521	0.000	0.000	0.000	0.000	0.000	0.000	0.303	0.237	0.000	0.167	0.000	0.000	0.221
G-104	PI461427	0.059	0.019	0.080	0.405	0.000	0.372	0.000	0.000	0.000	0.000	0.309	0.033	0.000

Appendix A. cont.

Code	Genotype	G-14	G-15	G-16	G-17	G-18	G-19	G-20	G-21	G-22	G-23	G-24	G-25	G-26
G-1	PI152146	0.000	0.000	0.099	0.169	0.257	0.234	0.000	0.136	0.000	0.000	0.000	0.242	0.123
G-2	PI158854	0.004	0.000	0.086	0.099	0.781	0.444	0.000	0.000	0.000	0.012	0.000	0.227	0.147
G-3	PI200441	0.062	0.066	0.173	0.223	0.586	0.416	0.184	0.065	0.000	0.127	0.021	0.269	0.302
G-4	PI259617	0.820	0.876	0.561	0.000	0.497	0.390	0.282	0.602	0.000	0.587	0.558	0.615	0.851
G-5	PI259836	0.000	0.000	0.000	0.161	0.262	0.122	0.003	0.047	0.040	0.000	0.000	0.041	0.000
G-6	PI262038	1.036	0.798	0.668	0.000	0.260	0.055	0.247	0.580	0.000	0.618	0.665	0.515	0.787
G-7	PI290566	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.300	0.000	0.000	0.000	0.000
G-8	PI290620	0.000	0.000	0.000	0.124	0.000	0.024	0.000	0.000	0.270	0.000	0.000	0.000	0.000
G-9	PI295730	0.000	0.000	0.000	0.270	0.000	0.039	0.005	0.000	0.022	0.000	0.000	0.029	0.025
G-10	PI313129	0.000	0.000	0.008	0.324	0.102	0.296	0.074	0.000	0.213	0.000	0.000	0.074	0.065
G-11	PI337406	0.465	0.395	0.249	0.046	0.658	0.382	0.240	0.244	0.000	0.391	0.314	0.380	0.603
G-12	PI339960	0.037	0.000	0.076	0.576	0.046	0.486	0.303	0.101	0.350	0.000	0.000	0.072	0.000
G-13	PI343398	0.000	0.000	0.000	0.130	0.000	0.032	0.000	0.000	0.154	0.000	0.000	0.000	0.000
G-14	PI356004	2.000	1.060	0.619	0.032	0.326	0.126	0.267	0.550	0.000	0.788	0.890	0.444	0.615
G-15	PI429420	1.060	2.000	0.726	0.050	0.291	0.091	0.228	0.548	0.000	1.085	0.960	0.351	0.538
G-16	PI471954	0.619	0.726	2.000	0.000	0.246	0.204	0.217	0.519	0.000	0.613	0.712	0.409	0.612
G-17	PI478850	0.032	0.050	0.000	2.000	0.111	0.300	0.094	0.049	0.400	0.041	0.018	0.147	0.071
G-18	PI482189	0.326	0.291	0.246	0.111	2.000	0.446	0.119	0.091	0.000	0.236	0.142	0.554	0.641
G-19	PI502040	0.126	0.091	0.204	0.300	0.446	2.000	0.329	0.165	0.283	0.098	0.007	0.122	0.262
G-20	PI475863	0.267	0.228	0.217	0.094	0.119	0.329	2.000	0.544	0.271	0.217	0.231	0.277	0.378
G-21	PI475918	0.550	0.548	0.519	0.049	0.091	0.165	0.544	2.000	0.088	0.440	0.499	0.276	0.474
G-22	PI476025	0.000	0.000	0.000	0.400	0.000	0.283	0.271	0.088	2.000	0.000	0.000	0.119	0.000
G-23	PI493329	0.788	1.085	0.613	0.041	0.236	0.098	0.217	0.440	0.000	2.000	1.001	0.273	0.375
G-24	PI493356	0.890	0.960	0.712	0.018	0.142	0.007	0.231	0.499	0.000	1.001	2.000	0.371	0.438
G-25	PI493547	0.444	0.351	0.409	0.147	0.554	0.122	0.277	0.276	0.119	0.273	0.371	2.000	0.900
G-26	PI493581	0.615	0.538	0.612	0.071	0.641	0.262	0.378	0.474	0.000	0.375	0.438	0.900	2.000
G-27	PI493631	0.788	0.805	0.564	0.013	0.602	0.319	0.361	0.452	0.000	0.573	0.578	0.560	0.837
G-28	PI493693	0.630	0.656	0.370	0.002	0.427	0.119	0.209	0.422	0.000	0.598	0.539	0.407	0.557
G-29	PI493717	0.593	0.532	0.316	0.000	0.446	0.050	0.189	0.296	0.000	0.423	0.364	0.190	0.300
G-30	PI493729	0.783	0.789	0.525	0.137	0.191	0.000	0.297	0.353	0.000	0.790	0.539	0.367	0.300
G-31	PI493880	0.649	0.773	0.506	0.006	0.149	0.103	0.086	0.337	0.000	0.762	0.622	0.223	0.346
G-32	PI493938	0.187	0.132	0.290	0.000	0.108	0.070	0.112	0.131	0.000	0.263	0.354	0.000	0.127
G-33	PI159786	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.210	0.000	0.000	0.000	0.000
G-34	PI162655	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.174	0.000	0.000	0.000	0.000
G-35	PI162857	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.109	0.000	0.000	0.000	0.000
G-36	PI196622	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-37	PI196635	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000
G-38	PI240560	0.030	0.000	0.159	0.000	0.230	0.000	0.015	0.014	0.000	0.000	0.072	0.104	0.009
G-39	PI259658	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-40	PI259851	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000	0.000
G-41	PI268586	0.000	0.000	0.080	0.011	0.169	0.000	0.027	0.000	0.000	0.000	0.000	0.080	0.002
G-42	PI268696	0.000	0.000	0.151	0.000	0.138	0.021	0.091	0.037	0.000	0.000	0.000	0.079	0.071
G-43	PI268755	0.008	0.000	0.201	0.000	0.000	0.046	0.040	0.007	0.000	0.000	0.046	0.054	0.000
G-44	PI268806	0.000	0.001	0.040	0.000	0.254	0.022	0.041	0.110	0.000	0.000	0.000	0.087	0.028
G-45	PI268868	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-46	PI268996	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.133	0.000	0.000	0.000	0.000
G-47	PI270786	0.101	0.046	0.237	0.000	0.139	0.000	0.000	0.093	0.039	0.036	0.099	0.124	0.108
G-48	PI270905	0.000	0.000	0.000	0.000	0.000	0.000	0.014	0.000	0.110	0.000	0.000	0.000	0.000
G-49	PI270907	0.000	0.000	0.000	0.145	0.000	0.000	0.000	0.000	0.000	0.026	0.000	0.000	0.000
G-50	PI274193	0.000	0.000	0.000	0.019	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000
G-51	PI290536	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-52	PI290594	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Appendix A. cont.

Code	Genotype	G-14	G-15	G-16	G-17	G-18	G-19	G-20	G-21	G-22	G-23	G-24	G-25	G-26
G-53	PI292950	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-54	PI295250	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.032	0.000	0.000	0.000	0.000
G-55	PI295309	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.072	0.000	0.000	0.000	0.000
G-56	PI296550	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000
G-57	PI296558	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-58	PI298854	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.149	0.000	0.000	0.000	0.000
G-59	PI319768	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-60	PI323268	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-61	PI325943	0.412	0.489	0.289	0.000	0.171	0.125	0.069	0.309	0.000	0.413	0.387	0.294	0.275
G-62	PI331297	0.094	0.143	0.013	0.000	0.000	0.000	0.050	0.008	0.000	0.161	0.231	0.118	0.137
G-63	PI331314	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.067	0.000	0.000
G-64	PI337293	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-65	PI337399	0.000	0.000	0.010	0.000	0.243	0.061	0.000	0.000	0.000	0.000	0.000	0.010	0.000
G-66	PI343384	0.042	0.007	0.000	0.000	0.065	0.000	0.001	0.040	0.000	0.000	0.000	0.027	0.173
G-67	PI355268	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.083	0.000	0.000	0.000	0.000
G-68	PI355271	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-69	PI370331	0.000	0.000	0.000	0.026	0.000	0.000	0.000	0.000	0.038	0.000	0.000	0.000	0.000
G-70	PI372271	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000	0.000
G-71	PI372305	0.000	0.000	0.000	0.035	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-72	PI399581	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-73	PI442768	0.000	0.000	0.000	0.107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-74	PI461434	0.000	0.000	0.127	0.000	0.181	0.004	0.017	0.000	0.000	0.000	0.000	0.097	0.004
G-75	PI471952	0.270	0.334	0.357	0.000	0.226	0.076	0.162	0.259	0.000	0.363	0.320	0.332	0.293
G-76	PI476636	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-77	PI481795	0.000	0.000	0.000	0.000	0.118	0.018	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-78	PI482120	0.000	0.000	0.000	0.000	0.189	0.000	0.000	0.000	0.000	0.000	0.013	0.000	0.000
G-79	PI494795	0.000	0.000	0.000	0.052	0.000	0.000	0.000	0.000	0.096	0.000	0.000	0.000	0.000
G-80	PI496401	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-81	PI496448	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-82	PI504614	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-83	PI338338	0.000	0.000	0.000	0.051	0.000	0.029	0.017	0.021	0.022	0.013	0.023	0.071	0.000
G-84	PI502111	0.000	0.000	0.000	0.369	0.000	0.000	0.040	0.000	0.241	0.000	0.000	0.014	0.000
G-85	PI502120	0.000	0.000	0.000	0.482	0.000	0.094	0.000	0.000	0.347	0.000	0.000	0.000	0.000
G-86	PI155107	0.000	0.000	0.098	0.000	0.182	0.032	0.071	0.007	0.000	0.013	0.000	0.000	0.000
G-87	PI157542	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.000	0.116	0.000	0.000	0.000	0.000
G-88	PI270998	0.000	0.000	0.000	0.000	0.005	0.109	0.000	0.000	0.000	0.000	0.000	0.025	0.000
G-89	PI271019	0.000	0.000	0.093	0.000	0.058	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-90	PI288146	0.000	0.000	0.048	0.000	0.153	0.000	0.000	0.021	0.000	0.000	0.000	0.000	0.000
G-91	PI290560	0.000	0.000	0.000	0.000	0.000	0.041	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-92	PI403813	0.328	0.472	0.359	0.000	0.093	0.000	0.000	0.138	0.000	0.414	0.491	0.302	0.336
G-93	PI407667	0.000	0.000	0.010	0.000	0.006	0.007	0.000	0.000	0.000	0.019	0.000	0.000	0.000
G-94	PI478819	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-95	PI476432	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-96	PI497517	0.167	0.252	0.089	0.000	0.055	0.000	0.000	0.061	0.000	0.130	0.195	0.180	0.130
G-97	PI497639	0.000	0.000	0.000	0.516	0.000	0.238	0.091	0.000	0.750	0.000	0.000	0.000	0.000
G-98	PI497318	0.000	0.000	0.000	0.093	0.000	0.000	0.000	0.000	0.236	0.000	0.000	0.000	0.000
G-99	PI497395	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.074	0.000	0.000	0.000	0.000
G-100	PI494018	0.016	0.050	0.042	0.000	0.223	0.116	0.150	0.011	0.000	0.000	0.001	0.204	0.019
G-101	PI494034	0.022	0.016	0.094	0.000	0.198	0.000	0.000	0.000	0.000	0.043	0.057	0.064	0.000
G-102	PI288210	0.000	0.000	0.000	0.016	0.000	0.086	0.026	0.000	0.004	0.000	0.000	0.000	0.000
G-103	PI371521	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-104	PI461427	0.527	0.554	0.407	0.000	0.205	0.103	0.088	0.362	0.000	0.444	0.557	0.376	0.392

Appendix A. cont.

Code	Genotype	G-27	G-28	G-29	G-30	G-31	G-32	G-33	G-34	G-35	G-36	G-37	G-38	G-39
G-1	PI152146	0.000	0.042	0.026	0.000	0.048	0.158	0.000	0.000	0.000	0.000	0.000	0.083	0.000
G-2	PI158854	0.015	0.092	0.309	0.000	0.052	0.204	0.000	0.000	0.000	0.000	0.000	0.223	0.000
G-3	PI200441	0.098	0.147	0.216	0.002	0.060	0.309	0.000	0.000	0.000	0.000	0.000	0.056	0.000
G-4	PI259617	1.070	0.661	0.331	0.506	0.470	0.017	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-5	PI259836	0.000	0.212	0.093	0.000	0.000	0.187	0.000	0.011	0.000	0.000	0.000	0.174	0.000
G-6	PI262038	0.618	0.542	0.504	0.544	0.467	0.221	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-7	PI290566	0.000	0.000	0.000	0.000	0.000	0.000	0.847	0.392	0.383	0.404	0.418	0.000	0.105
G-8	PI290620	0.000	0.000	0.000	0.000	0.000	0.009	0.404	0.147	0.240	0.138	0.109	0.000	0.000
G-9	PI295730	0.000	0.000	0.000	0.000	0.000	0.000	0.179	0.161	0.145	0.014	0.177	0.000	0.000
G-10	PI313129	0.000	0.000	0.000	0.000	0.000	0.000	0.188	0.054	0.000	0.000	0.000	0.000	0.000
G-11	PI337406	0.808	0.636	0.324	0.431	0.306	0.229	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-12	PI339960	0.000	0.117	0.115	0.072	0.000	0.123	0.000	0.000	0.000	0.000	0.000	0.043	0.000
G-13	PI343398	0.000	0.000	0.000	0.000	0.000	0.000	0.317	0.178	0.216	0.240	0.117	0.000	0.042
G-14	PI356004	0.788	0.630	0.593	0.783	0.649	0.187	0.000	0.000	0.000	0.000	0.000	0.030	0.000
G-15	PI429420	0.805	0.656	0.532	0.789	0.773	0.132	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-16	PI471954	0.564	0.370	0.316	0.525	0.506	0.290	0.000	0.000	0.000	0.000	0.000	0.159	0.000
G-17	PI478850	0.013	0.002	0.000	0.137	0.006	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-18	PI482189	0.602	0.427	0.446	0.191	0.149	0.108	0.000	0.000	0.000	0.000	0.000	0.230	0.000
G-19	PI502040	0.319	0.119	0.050	0.000	0.103	0.070	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-20	PI475863	0.361	0.209	0.189	0.297	0.086	0.112	0.000	0.000	0.000	0.000	0.000	0.015	0.000
G-21	PI475918	0.452	0.422	0.296	0.353	0.337	0.131	0.000	0.000	0.000	0.000	0.000	0.014	0.000
G-22	PI476025	0.000	0.000	0.000	0.000	0.000	0.000	0.210	0.174	0.109	0.000	0.012	0.000	0.000
G-23	PI493329	0.573	0.598	0.423	0.790	0.762	0.263	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-24	PI493356	0.578	0.539	0.364	0.539	0.622	0.354	0.000	0.000	0.000	0.000	0.000	0.072	0.000
G-25	PI493547	0.560	0.407	0.190	0.367	0.223	0.000	0.000	0.000	0.000	0.000	0.000	0.104	0.000
G-26	PI493581	0.837	0.557	0.300	0.300	0.346	0.127	0.000	0.000	0.000	0.000	0.000	0.009	0.000
G-27	PI493631	2.000	0.646	0.470	0.654	0.456	0.087	0.000	0.000	0.000	0.000	0.000	0.074	0.000
G-28	PI493693	0.646	2.000	0.430	0.503	0.551	0.257	0.000	0.000	0.000	0.000	0.000	0.080	0.000
G-29	PI493717	0.470	0.430	2.000	0.483	0.633	0.347	0.000	0.000	0.000	0.000	0.000	0.296	0.000
G-30	PI493729	0.654	0.503	0.483	2.000	0.791	0.100	0.000	0.000	0.000	0.000	0.000	0.053	0.000
G-31	PI493880	0.456	0.551	0.633	0.791	2.000	0.264	0.000	0.000	0.000	0.000	0.000	0.081	0.000
G-32	PI493938	0.087	0.257	0.347	0.100	0.264	2.000	0.000	0.000	0.000	0.000	0.000	0.206	0.064
G-33	PI159786	0.000	0.000	0.000	0.000	0.000	0.000	2.000	0.712	0.620	0.626	0.731	0.000	0.338
G-34	PI162655	0.000	0.000	0.000	0.000	0.000	0.000	0.712	2.000	0.813	0.547	0.564	0.000	0.282
G-35	PI162857	0.000	0.000	0.000	0.000	0.000	0.000	0.620	0.813	2.000	0.658	0.637	0.000	0.422
G-36	PI196622	0.000	0.000	0.000	0.000	0.000	0.000	0.626	0.547	0.658	2.000	0.830	0.000	0.445
G-37	PI196635	0.000	0.000	0.000	0.000	0.000	0.000	0.731	0.564	0.637	0.830	2.000	0.000	0.498
G-38	PI240560	0.074	0.080	0.296	0.053	0.081	0.206	0.000	0.000	0.000	0.000	0.000	2.000	0.000
G-39	PI259658	0.000	0.000	0.000	0.000	0.000	0.064	0.338	0.282	0.422	0.445	0.498	0.000	2.000
G-40	PI259851	0.000	0.000	0.000	0.000	0.000	0.000	0.408	0.279	0.487	0.554	0.521	0.000	0.660
G-41	PI268586	0.012	0.066	0.222	0.000	0.104	0.382	0.000	0.075	0.000	0.000	0.000	0.352	0.091
G-42	PI268696	0.049	0.000	0.220	0.012	0.157	0.147	0.000	0.000	0.000	0.000	0.000	0.978	0.000
G-43	PI268755	0.032	0.040	0.138	0.000	0.024	0.130	0.000	0.195	0.116	0.021	0.000	0.471	0.000
G-44	PI268806	0.067	0.070	0.187	0.037	0.063	0.264	0.000	0.000	0.000	0.000	0.000	0.763	0.000
G-45	PI268868	0.000	0.000	0.000	0.000	0.000	0.000	0.583	0.552	0.576	0.685	0.909	0.000	0.536
G-46	PI268996	0.000	0.000	0.000	0.000	0.000	0.000	0.573	0.512	0.452	0.742	0.777	0.000	0.680
G-47	PI270786	0.085	0.107	0.277	0.115	0.211	0.284	0.000	0.000	0.000	0.000	0.000	0.794	0.000
G-48	PI270905	0.000	0.000	0.000	0.000	0.000	0.053	0.053	0.034	0.069	0.029	0.060	0.295	0.209
G-49	PI270907	0.000	0.000	0.000	0.000	0.000	0.000	0.032	0.000	0.000	0.058	0.020	0.017	0.000
G-50	PI274193	0.000	0.000	0.000	0.000	0.000	0.000	0.238	0.252	0.151	0.194	0.269	0.000	0.047
G-51	PI290536	0.000	0.000	0.000	0.000	0.000	0.000	0.434	0.336	0.175	0.438	0.374	0.000	0.220
G-52	PI290594	0.000	0.000	0.000	0.000	0.000	0.000	0.330	0.113	0.264	0.235	0.204	0.000	0.172

Appendix A. cont.

Code	Genotype	G-27	G-28	G-29	G-30	G-31	G-32	G-33	G-34	G-35	G-36	G-37	G-38	G-39
G-53	PI292950	0.000	0.000	0.000	0.000	0.000	0.000	0.355	0.281	0.117	0.309	0.279	0.000	0.112
G-54	PI295250	0.000	0.000	0.000	0.000	0.000	0.000	0.230	0.227	0.319	0.324	0.174	0.000	0.175
G-55	PI295309	0.000	0.000	0.000	0.000	0.000	0.000	0.421	0.267	0.278	0.369	0.322	0.000	0.169
G-56	PI296550	0.000	0.000	0.000	0.000	0.000	0.000	0.096	0.057	0.000	0.125	0.124	0.028	0.000
G-57	PI296558	0.000	0.000	0.000	0.000	0.000	0.000	0.091	0.039	0.021	0.000	0.113	0.000	0.023
G-58	PI298854	0.000	0.000	0.000	0.000	0.000	0.000	0.252	0.142	0.229	0.198	0.215	0.000	0.164
G-59	PI319768	0.000	0.000	0.000	0.000	0.000	0.000	0.087	0.104	0.018	0.041	0.022	0.116	0.186
G-60	PI323268	0.000	0.000	0.000	0.000	0.000	0.000	0.289	0.026	0.220	0.289	0.138	0.000	0.108
G-61	PI325943	0.394	0.451	0.288	0.283	0.292	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-62	PI331297	0.140	0.079	0.000	0.093	0.033	0.000	0.023	0.000	0.000	0.000	0.000	0.000	0.000
G-63	PI331314	0.000	0.000	0.000	0.000	0.000	0.000	0.152	0.006	0.046	0.256	0.174	0.000	0.024
G-64	PI337293	0.000	0.000	0.044	0.000	0.100	0.160	0.000	0.000	0.000	0.000	0.000	0.440	0.000
G-65	PI337399	0.000	0.000	0.111	0.000	0.000	0.228	0.000	0.000	0.000	0.000	0.000	0.294	0.000
G-66	PI343384	0.056	0.099	0.000	0.043	0.033	0.026	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-67	PI355268	0.000	0.000	0.000	0.000	0.000	0.000	0.401	0.056	0.231	0.338	0.240	0.000	0.191
G-68	PI355271	0.000	0.000	0.000	0.000	0.000	0.000	0.271	0.190	0.102	0.304	0.137	0.000	0.088
G-69	PI370331	0.000	0.000	0.000	0.000	0.000	0.000	0.148	0.130	0.132	0.158	0.195	0.000	0.112
G-70	PI372271	0.000	0.000	0.000	0.000	0.000	0.000	0.272	0.184	0.203	0.415	0.250	0.000	0.133
G-71	PI372305	0.000	0.000	0.000	0.000	0.000	0.000	0.174	0.019	0.057	0.132	0.152	0.000	0.154
G-72	PI399581	0.000	0.000	0.000	0.000	0.000	0.000	0.309	0.228	0.078	0.225	0.281	0.000	0.000
G-73	PI442768	0.000	0.000	0.000	0.025	0.000	0.000	0.170	0.094	0.045	0.102	0.134	0.000	0.000
G-74	PI461434	0.001	0.040	0.087	0.000	0.064	0.241	0.000	0.000	0.000	0.000	0.000	0.330	0.000
G-75	PI471952	0.350	0.300	0.222	0.319	0.313	0.033	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-76	PI476636	0.000	0.000	0.000	0.000	0.000	0.000	0.390	0.230	0.082	0.291	0.194	0.000	0.109
G-77	PI481795	0.000	0.000	0.098	0.000	0.000	0.144	0.000	0.000	0.000	0.000	0.000	0.334	0.000
G-78	PI482120	0.000	0.000	0.135	0.000	0.003	0.114	0.000	0.000	0.000	0.000	0.000	0.543	0.000
G-79	PI494795	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.015	0.000	0.000
G-80	PI496401	0.000	0.000	0.000	0.000	0.000	0.000	0.214	0.096	0.021	0.232	0.269	0.000	0.062
G-81	PI496448	0.000	0.000	0.000	0.000	0.000	0.000	0.406	0.158	0.132	0.419	0.250	0.000	0.043
G-82	PI504614	0.000	0.000	0.073	0.000	0.000	0.070	0.000	0.000	0.000	0.000	0.000	0.362	0.000
G-83	PI338338	0.000	0.000	0.000	0.014	0.032	0.048	0.000	0.000	0.000	0.000	0.000	0.084	0.000
G-84	PI502111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000
G-85	PI502120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-86	PI155107	0.000	0.006	0.229	0.000	0.001	0.137	0.000	0.000	0.000	0.000	0.000	0.446	0.000
G-87	PI157542	0.000	0.000	0.000	0.000	0.000	0.000	0.156	0.072	0.217	0.140	0.073	0.000	0.056
G-88	PI270998	0.000	0.000	0.035	0.000	0.000	0.002	0.000	0.000	0.000	0.000	0.000	0.117	0.000
G-89	PI271019	0.000	0.000	0.097	0.000	0.078	0.153	0.000	0.000	0.000	0.000	0.000	0.237	0.000
G-90	PI288146	0.000	0.000	0.150	0.000	0.020	0.151	0.000	0.000	0.000	0.000	0.000	0.524	0.000
G-91	PI290560	0.000	0.000	0.000	0.000	0.000	0.089	0.000	0.000	0.000	0.000	0.000	0.443	0.000
G-92	PI403813	0.403	0.195	0.094	0.271	0.249	0.136	0.000	0.000	0.000	0.000	0.000	0.022	0.000
G-93	PI407667	0.000	0.000	0.197	0.000	0.032	0.134	0.000	0.000	0.000	0.000	0.000	0.197	0.000
G-94	PI478819	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.164	0.000
G-95	PI476432	0.000	0.000	0.107	0.000	0.000	0.073	0.000	0.000	0.000	0.000	0.000	0.209	0.000
G-96	PI497517	0.218	0.096	0.022	0.190	0.027	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-97	PI497639	0.000	0.000	0.000	0.000	0.000	0.000	0.088	0.060	0.095	0.038	0.017	0.000	0.062
G-98	PI497318	0.000	0.000	0.000	0.000	0.000	0.000	0.352	0.412	0.571	0.221	0.370	0.000	0.209
G-99	PI497395	0.000	0.000	0.000	0.000	0.000	0.000	0.125	0.258	0.441	0.284	0.241	0.000	0.230
G-100	PI494018	0.037	0.076	0.124	0.000	0.024	0.072	0.000	0.000	0.000	0.000	0.000	0.317	0.024
G-101	PI494034	0.000	0.030	0.190	0.000	0.166	0.319	0.000	0.000	0.000	0.000	0.000	0.750	0.000
G-102	PI288210	0.000	0.000	0.000	0.000	0.000	0.014	0.206	0.220	0.164	0.353	0.420	0.005	0.512
G-103	PI371521	0.000	0.000	0.000	0.000	0.000	0.000	0.379	0.307	0.443	0.493	0.445	0.000	0.655
G-104	PI461427	0.348	0.414	0.267	0.420	0.363	0.045	0.000	0.000	0.000	0.000	0.000	0.218	0.000

Appendix A. cont.

Code	Genotype	G-40	G-41	G-42	G-43	G-44	G-45	G-46	G-47	G-48	G-49	G-50	G-51	G-52
G-1	PI152146	0.000	0.224	0.198	0.070	0.144	0.000	0.000	0.145	0.077	0.104	0.000	0.000	0.000
G-2	PI158854	0.000	0.242	0.129	0.027	0.333	0.000	0.000	0.180	0.000	0.000	0.000	0.000	0.000
G-3	PI200441	0.000	0.151	0.082	0.015	0.179	0.000	0.000	0.103	0.000	0.000	0.000	0.000	0.000
G-4	PI259617	0.000	0.000	0.000	0.000	0.046	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-5	PI259836	0.000	0.494	0.149	0.000	0.264	0.000	0.000	0.119	0.000	0.000	0.000	0.000	0.000
G-6	PI262038	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.168	0.000	0.000	0.000	0.000	0.000
G-7	PI290566	0.324	0.000	0.000	0.000	0.000	0.271	0.385	0.000	0.007	0.000	0.274	0.413	0.358
G-8	PI290620	0.196	0.000	0.000	0.003	0.000	0.106	0.074	0.000	0.087	0.000	0.085	0.151	0.193
G-9	PI295730	0.003	0.000	0.000	0.017	0.000	0.069	0.048	0.000	0.000	0.057	0.255	0.321	0.100
G-10	PI313129	0.101	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000	0.064	0.163	0.110
G-11	PI337406	0.000	0.059	0.000	0.000	0.084	0.000	0.000	0.007	0.000	0.000	0.000	0.000	0.000
G-12	PI339960	0.031	0.037	0.035	0.186	0.061	0.000	0.000	0.121	0.007	0.000	0.000	0.000	0.000
G-13	PI343398	0.255	0.000	0.000	0.000	0.000	0.157	0.171	0.000	0.012	0.000	0.101	0.215	0.228
G-14	PI356004	0.000	0.000	0.000	0.008	0.000	0.000	0.000	0.101	0.000	0.000	0.000	0.000	0.000
G-15	PI429420	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.046	0.000	0.000	0.000	0.000	0.000
G-16	PI471954	0.000	0.080	0.151	0.201	0.040	0.000	0.000	0.237	0.000	0.000	0.000	0.000	0.000
G-17	PI478850	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.145	0.019	0.000	0.000
G-18	PI482189	0.000	0.169	0.138	0.000	0.254	0.000	0.000	0.139	0.000	0.000	0.000	0.000	0.000
G-19	PI502040	0.000	0.000	0.021	0.046	0.022	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-20	PI475863	0.000	0.027	0.091	0.040	0.041	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000
G-21	PI475918	0.000	0.000	0.037	0.007	0.110	0.000	0.000	0.093	0.000	0.000	0.000	0.000	0.000
G-22	PI476025	0.025	0.000	0.000	0.000	0.000	0.000	0.133	0.039	0.110	0.000	0.014	0.000	0.000
G-23	PI493329	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.026	0.000	0.000	0.000
G-24	PI493356	0.000	0.000	0.000	0.046	0.000	0.000	0.000	0.099	0.000	0.000	0.000	0.000	0.000
G-25	PI493547	0.000	0.080	0.079	0.054	0.087	0.000	0.000	0.124	0.000	0.000	0.000	0.000	0.000
G-26	PI493581	0.000	0.002	0.071	0.000	0.028	0.000	0.000	0.108	0.000	0.000	0.000	0.000	0.000
G-27	PI493631	0.000	0.012	0.049	0.032	0.067	0.000	0.000	0.085	0.000	0.000	0.000	0.000	0.000
G-28	PI493693	0.000	0.066	0.000	0.040	0.070	0.000	0.000	0.107	0.000	0.000	0.000	0.000	0.000
G-29	PI493717	0.000	0.222	0.220	0.138	0.187	0.000	0.000	0.277	0.000	0.000	0.000	0.000	0.000
G-30	PI493729	0.000	0.000	0.012	0.000	0.037	0.000	0.000	0.115	0.000	0.000	0.000	0.000	0.000
G-31	PI493880	0.000	0.104	0.157	0.024	0.063	0.000	0.000	0.211	0.000	0.000	0.000	0.000	0.000
G-32	PI493938	0.000	0.382	0.147	0.130	0.264	0.000	0.000	0.284	0.053	0.000	0.000	0.000	0.000
G-33	PI159786	0.408	0.000	0.000	0.000	0.000	0.583	0.573	0.000	0.053	0.032	0.238	0.434	0.330
G-34	PI162655	0.279	0.075	0.000	0.195	0.000	0.552	0.512	0.000	0.034	0.000	0.252	0.336	0.113
G-35	PI162857	0.487	0.000	0.000	0.116	0.000	0.576	0.452	0.000	0.069	0.000	0.151	0.175	0.264
G-36	PI196622	0.554	0.000	0.000	0.021	0.000	0.685	0.742	0.000	0.029	0.058	0.194	0.438	0.235
G-37	PI196635	0.521	0.000	0.000	0.000	0.000	0.909	0.777	0.000	0.060	0.020	0.269	0.374	0.204
G-38	PI240560	0.000	0.352	0.978	0.471	0.763	0.000	0.000	0.794	0.295	0.017	0.000	0.000	0.000
G-39	PI259658	0.660	0.091	0.000	0.000	0.000	0.536	0.680	0.000	0.209	0.000	0.047	0.220	0.172
G-40	PI259851	2.000	0.000	0.000	0.000	0.000	0.487	0.650	0.000	0.232	0.065	0.100	0.236	0.361
G-41	PI268586	0.000	2.000	0.395	0.191	0.296	0.000	0.000	0.363	0.034	0.000	0.000	0.000	0.000
G-42	PI268696	0.000	0.395	2.000	0.548	0.429	0.000	0.000	0.415	0.168	0.000	0.000	0.000	0.000
G-43	PI268755	0.000	0.191	0.548	2.000	0.267	0.162	0.000	0.296	0.173	0.000	0.000	0.000	0.000
G-44	PI268806	0.000	0.296	0.429	0.267	2.000	0.000	0.000	0.500	0.110	0.000	0.000	0.000	0.000
G-45	PI268868	0.487	0.000	0.000	0.162	0.000	2.000	0.769	0.000	0.047	0.076	0.181	0.282	0.223
G-46	PI268996	0.650	0.000	0.000	0.000	0.000	0.769	2.000	0.000	0.027	0.005	0.107	0.454	0.292
G-47	PI270786	0.000	0.363	0.415	0.296	0.500	0.000	0.000	2.000	0.304	0.000	0.000	0.000	0.000
G-48	PI270905	0.232	0.034	0.168	0.173	0.110	0.047	0.027	0.304	2.000	0.283	0.000	0.000	0.000
G-49	PI270907	0.065	0.000	0.000	0.000	0.000	0.076	0.005	0.000	0.283	2.000	0.104	0.091	0.000
G-50	PI274193	0.100	0.000	0.000	0.000	0.000	0.181	0.107	0.000	0.000	0.104	2.000	0.464	0.383
G-51	PI290536	0.236	0.000	0.000	0.000	0.000	0.282	0.454	0.000	0.000	0.091	0.464	2.000	0.741
G-52	PI290594	0.361	0.000	0.000	0.000	0.000	0.223	0.292	0.000	0.000	0.000	0.383	0.741	2.000

Appendix A. cont.

Code	Genotype	G-40	G-41	G-42	G-43	G-44	G-45	G-46	G-47	G-48	G-49	G-50	G-51	G-52
G-53	PI292950	0.253	0.000	0.000	0.000	0.000	0.280	0.308	0.000	0.000	0.026	0.425	0.777	0.865
G-54	PI295250	0.253	0.000	0.000	0.000	0.000	0.191	0.237	0.000	0.000	0.000	0.475	0.682	0.784
G-55	PI295309	0.230	0.000	0.000	0.000	0.000	0.315	0.299	0.000	0.000	0.000	0.466	0.588	0.589
G-56	PI296550	0.035	0.000	0.000	0.037	0.053	0.155	0.208	0.000	0.000	0.030	0.222	0.317	0.283
G-57	PI296558	0.062	0.000	0.000	0.000	0.000	0.074	0.098	0.000	0.000	0.241	0.389	0.491	0.282
G-58	PI298854	0.298	0.000	0.000	0.000	0.000	0.147	0.266	0.000	0.000	0.198	0.516	0.663	0.706
G-59	PI319768	0.067	0.000	0.056	0.000	0.176	0.028	0.090	0.000	0.003	0.108	0.088	0.406	0.322
G-60	PI323268	0.276	0.000	0.000	0.000	0.000	0.177	0.218	0.000	0.000	0.044	0.395	0.674	0.899
G-61	PI325943	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.000	0.000	0.000
G-62	PI331297	0.006	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000
G-63	PI331314	0.131	0.000	0.000	0.000	0.000	0.197	0.116	0.000	0.084	0.128	0.213	0.278	0.274
G-64	PI337293	0.000	0.339	0.363	0.101	0.307	0.000	0.000	0.364	0.181	0.104	0.000	0.000	0.000
G-65	PI337399	0.000	0.262	0.116	0.000	0.281	0.000	0.000	0.152	0.085	0.432	0.000	0.000	0.000
G-66	PI343384	0.000	0.000	0.039	0.000	0.000	0.000	0.000	0.144	0.000	0.000	0.059	0.267	0.198
G-67	PI355268	0.360	0.000	0.000	0.000	0.000	0.238	0.319	0.000	0.000	0.090	0.350	0.742	0.961
G-68	PI355271	0.355	0.000	0.000	0.000	0.000	0.152	0.217	0.000	0.000	0.000	0.294	0.590	0.828
G-69	PI370331	0.171	0.000	0.000	0.000	0.000	0.212	0.156	0.000	0.133	0.094	0.349	0.366	0.392
G-70	PI372271	0.112	0.000	0.000	0.000	0.000	0.183	0.261	0.000	0.000	0.000	0.407	0.598	0.514
G-71	PI372305	0.109	0.000	0.000	0.000	0.000	0.117	0.199	0.000	0.023	0.067	0.396	0.397	0.470
G-72	PI399581	0.078	0.000	0.000	0.000	0.000	0.245	0.224	0.000	0.035	0.086	0.152	0.349	0.273
G-73	PI442768	0.208	0.000	0.000	0.000	0.000	0.133	0.128	0.000	0.064	0.449	0.444	0.344	0.346
G-74	PI461434	0.000	0.286	0.339	0.203	0.127	0.000	0.000	0.273	0.075	0.121	0.000	0.000	0.000
G-75	PI471952	0.000	0.000	0.080	0.028	0.028	0.000	0.000	0.166	0.000	0.000	0.000	0.000	0.000
G-76	PI476636	0.292	0.000	0.000	0.000	0.000	0.193	0.307	0.000	0.011	0.000	0.333	0.715	0.853
G-77	PI481795	0.000	0.290	0.276	0.106	0.322	0.000	0.000	0.277	0.079	0.074	0.000	0.000	0.000
G-78	PI482120	0.000	0.295	0.518	0.067	0.448	0.000	0.000	0.316	0.056	0.077	0.000	0.000	0.000
G-79	PI494795	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.072	0.000	0.094	0.048	0.153
G-80	PI496401	0.196	0.000	0.000	0.000	0.000	0.161	0.220	0.000	0.000	0.174	0.342	0.381	0.246
G-81	PI496448	0.189	0.000	0.000	0.000	0.000	0.245	0.226	0.000	0.048	0.006	0.320	0.346	0.350
G-82	PI504614	0.000	0.256	0.194	0.278	0.275	0.000	0.000	0.225	0.148	0.022	0.000	0.000	0.000
G-83	PI338338	0.000	0.007	0.006	0.129	0.113	0.000	0.000	0.198	0.000	0.000	0.000	0.000	0.000
G-84	PI502111	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.106	0.000	0.000
G-85	PI502120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.115	0.011	0.000	0.000
G-86	PI155107	0.000	0.233	0.282	0.115	0.420	0.000	0.000	0.303	0.000	0.000	0.000	0.000	0.000
G-87	PI157542	0.141	0.000	0.000	0.000	0.000	0.075	0.069	0.000	0.000	0.000	0.259	0.309	0.264
G-88	PI270998	0.000	0.058	0.283	0.000	0.000	0.000	0.000	0.000	0.114	0.000	0.044	0.000	0.000
G-89	PI271019	0.000	0.176	0.347	0.225	0.337	0.000	0.000	0.301	0.056	0.000	0.000	0.000	0.000
G-90	PI288146	0.000	0.196	0.431	0.317	0.496	0.000	0.000	0.353	0.120	0.000	0.000	0.000	0.000
G-91	PI290560	0.000	0.053	0.469	0.146	0.242	0.000	0.000	0.094	0.078	0.112	0.000	0.000	0.000
G-92	PI403813	0.000	0.067	0.065	0.000	0.000	0.000	0.000	0.168	0.000	0.000	0.000	0.000	0.000
G-93	PI407667	0.000	0.135	0.273	0.171	0.260	0.000	0.000	0.156	0.000	0.011	0.000	0.000	0.000
G-94	PI478819	0.000	0.036	0.000	0.093	0.072	0.000	0.000	0.177	0.080	0.000	0.026	0.000	0.000
G-95	PI476432	0.000	0.217	0.184	0.115	0.260	0.000	0.000	0.203	0.000	0.000	0.000	0.000	0.000
G-96	PI497517	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.097	0.000	0.000	0.000	0.000	0.000
G-97	PI497639	0.067	0.012	0.000	0.000	0.000	0.000	0.053	0.000	0.088	0.014	0.052	0.000	0.000
G-98	PI497318	0.256	0.000	0.022	0.190	0.000	0.444	0.202	0.000	0.204	0.079	0.155	0.071	0.022
G-99	PI497395	0.153	0.000	0.000	0.220	0.000	0.297	0.188	0.000	0.233	0.000	0.055	0.089	0.000
G-100	PI494018	0.000	0.573	0.186	0.323	0.289	0.000	0.000	0.225	0.000	0.000	0.000	0.000	0.000
G-101	PI494034	0.000	0.377	0.440	0.218	0.584	0.000	0.000	0.443	0.183	0.024	0.000	0.000	0.000
G-102	PI288210	0.384	0.000	0.000	0.000	0.000	0.393	0.537	0.000	0.139	0.000	0.059	0.064	0.085
G-103	PI371521	1.099	0.000	0.000	0.000	0.000	0.464	0.666	0.000	0.184	0.077	0.102	0.302	0.363
G-104	PI461427	0.000	0.024	0.074	0.000	0.066	0.000	0.000	0.162	0.100	0.008	0.000	0.000	0.000

Appendix A. cont.

Code	Genotype	G-53	G-54	G-55	G-56	G-57	G-58	G-59	G-60	G-61	G-62	G-63	G-64	G-65
G-1	PI152146	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.000	0.000	0.129	0.398
G-2	PI158854	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.302	0.411
G-3	PI200441	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.146	0.000	0.000	0.056	0.266
G-4	PI259617	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.520	0.164	0.000	0.000	0.000
G-5	PI259836	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.135	0.260
G-6	PI262038	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.410	0.130	0.000	0.000	0.000
G-7	PI290566	0.408	0.304	0.400	0.224	0.219	0.404	0.000	0.361	0.000	0.000	0.083	0.000	0.000
G-8	PI290620	0.176	0.228	0.113	0.000	0.036	0.134	0.000	0.107	0.000	0.000	0.000	0.000	0.000
G-9	PI295730	0.160	0.192	0.088	0.000	0.276	0.242	0.000	0.056	0.008	0.007	0.000	0.000	0.000
G-10	PI313129	0.000	0.054	0.013	0.000	0.106	0.186	0.000	0.060	0.000	0.062	0.000	0.000	0.000
G-11	PI337406	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.282	0.018	0.000	0.000	0.044
G-12	PI339960	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.098	0.110
G-13	PI343398	0.160	0.175	0.212	0.155	0.090	0.209	0.000	0.215	0.000	0.000	0.057	0.000	0.000
G-14	PI356004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.412	0.094	0.000	0.000	0.000
G-15	PI429420	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.489	0.143	0.000	0.000	0.000
G-16	PI471954	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.289	0.013	0.000	0.000	0.010
G-17	PI478850	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-18	PI482189	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.171	0.000	0.000	0.000	0.243
G-19	PI502040	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.125	0.000	0.000	0.000	0.061
G-20	PI475863	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.069	0.050	0.000	0.000	0.000
G-21	PI475918	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.309	0.008	0.000	0.000	0.000
G-22	PI476025	0.000	0.032	0.072	0.017	0.000	0.149	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-23	PI493329	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.413	0.161	0.013	0.000	0.000
G-24	PI493356	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.387	0.231	0.067	0.000	0.000
G-25	PI493547	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.294	0.118	0.000	0.000	0.010
G-26	PI493581	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.275	0.137	0.000	0.000	0.000
G-27	PI493631	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.394	0.140	0.000	0.000	0.000
G-28	PI493693	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.451	0.079	0.000	0.000	0.000
G-29	PI493717	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.288	0.000	0.000	0.044	0.111
G-30	PI493729	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.283	0.093	0.000	0.000	0.000
G-31	PI493880	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.292	0.033	0.000	0.100	0.000
G-32	PI493938	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.160	0.228
G-33	PI159786	0.355	0.230	0.421	0.096	0.091	0.252	0.087	0.289	0.000	0.023	0.152	0.000	0.000
G-34	PI162655	0.281	0.227	0.267	0.057	0.039	0.142	0.104	0.026	0.000	0.000	0.006	0.000	0.000
G-35	PI162857	0.117	0.319	0.278	0.000	0.021	0.229	0.018	0.220	0.000	0.000	0.046	0.000	0.000
G-36	PI196622	0.309	0.324	0.369	0.125	0.000	0.198	0.041	0.289	0.000	0.000	0.256	0.000	0.000
G-37	PI196635	0.279	0.174	0.322	0.124	0.113	0.215	0.022	0.138	0.000	0.000	0.174	0.000	0.000
G-38	PI240560	0.000	0.000	0.000	0.028	0.000	0.000	0.116	0.000	0.000	0.000	0.000	0.440	0.294
G-39	PI259658	0.112	0.175	0.169	0.000	0.023	0.164	0.186	0.108	0.000	0.000	0.024	0.000	0.000
G-40	PI259851	0.253	0.253	0.230	0.035	0.062	0.298	0.067	0.276	0.000	0.006	0.131	0.000	0.000
G-41	PI268586	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.339	0.262
G-42	PI268696	0.000	0.000	0.000	0.000	0.000	0.000	0.056	0.000	0.000	0.000	0.000	0.363	0.116
G-43	PI268755	0.000	0.000	0.000	0.037	0.000	0.000	0.000	0.000	0.000	0.014	0.000	0.101	0.000
G-44	PI268806	0.000	0.000	0.000	0.053	0.000	0.000	0.176	0.000	0.000	0.000	0.000	0.307	0.281
G-45	PI268868	0.280	0.191	0.315	0.155	0.074	0.147	0.028	0.177	0.000	0.000	0.197	0.000	0.000
G-46	PI268996	0.308	0.237	0.299	0.208	0.098	0.266	0.090	0.218	0.000	0.000	0.116	0.000	0.000
G-47	PI270786	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.047	0.000	0.000	0.364	0.152
G-48	PI270905	0.000	0.000	0.000	0.000	0.000	0.000	0.003	0.000	0.000	0.000	0.084	0.181	0.085
G-49	PI270907	0.026	0.000	0.000	0.030	0.241	0.198	0.108	0.044	0.000	0.000	0.128	0.104	0.432
G-50	PI274193	0.425	0.475	0.466	0.222	0.389	0.516	0.088	0.395	0.000	0.047	0.213	0.000	0.000
G-51	PI290536	0.777	0.682	0.588	0.317	0.491	0.663	0.406	0.674	0.000	0.000	0.278	0.000	0.000
G-52	PI290594	0.865	0.784	0.589	0.283	0.282	0.706	0.322	0.899	0.000	0.000	0.274	0.000	0.000

Appendix A. cont.

Code	Genotype	G-53	G-54	G-55	G-56	G-57	G-58	G-59	G-60	G-61	G-62	G-63	G-64	G-65
G-53	PI292950	2.000	0.824	0.715	0.367	0.249	0.535	0.296	0.751	0.000	0.019	0.300	0.000	0.000
G-54	PI295250	0.824	2.000	0.769	0.280	0.280	0.467	0.207	0.633	0.000	0.124	0.302	0.000	0.000
G-55	PI295309	0.715	0.769	2.000	0.534	0.356	0.365	0.100	0.583	0.000	0.084	0.281	0.000	0.000
G-56	PI296550	0.367	0.280	0.534	2.000	0.524	0.152	0.103	0.307	0.000	0.088	0.078	0.171	0.000
G-57	PI296558	0.249	0.280	0.356	0.524	2.000	0.371	0.161	0.242	0.000	0.038	0.062	0.000	0.388
G-58	PI298854	0.535	0.467	0.365	0.152	0.371	2.000	0.191	0.768	0.000	0.000	0.205	0.000	0.000
G-59	PI319768	0.296	0.207	0.100	0.103	0.161	0.191	2.000	0.259	0.000	0.021	0.000	0.186	0.216
G-60	PI323268	0.751	0.633	0.583	0.307	0.242	0.768	0.259	2.000	0.000	0.080	0.311	0.000	0.000
G-61	PI325943	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	2.000	0.543	0.064	0.064	0.018
G-62	PI331297	0.019	0.124	0.084	0.088	0.038	0.000	0.021	0.080	0.543	2.000	0.232	0.000	0.000
G-63	PI331314	0.300	0.302	0.281	0.078	0.062	0.205	0.000	0.311	0.064	0.232	2.000	0.000	0.000
G-64	PI337293	0.000	0.000	0.000	0.171	0.000	0.000	0.186	0.000	0.064	0.000	0.000	2.000	0.355
G-65	PI337399	0.000	0.000	0.000	0.000	0.388	0.000	0.216	0.000	0.018	0.000	0.000	0.355	2.000
G-66	PI343384	0.094	0.158	0.115	0.040	0.154	0.316	0.138	0.124	0.092	0.088	0.000	0.000	0.165
G-67	PI355268	0.730	0.665	0.607	0.277	0.219	0.840	0.370	1.031	0.000	0.144	0.339	0.000	0.000
G-68	PI355271	0.817	0.684	0.610	0.311	0.173	0.582	0.221	0.862	0.000	0.132	0.311	0.000	0.000
G-69	PI370331	0.584	0.517	0.476	0.180	0.268	0.282	0.160	0.512	0.000	0.107	0.319	0.000	0.000
G-70	PI372271	0.655	0.862	0.855	0.457	0.270	0.385	0.146	0.566	0.000	0.075	0.355	0.000	0.000
G-71	PI372305	0.472	0.515	0.573	0.305	0.258	0.226	0.043	0.327	0.000	0.000	0.310	0.000	0.000
G-72	PI399581	0.435	0.330	0.596	0.388	0.079	0.233	0.170	0.234	0.000	0.098	0.160	0.052	0.000
G-73	PI442768	0.350	0.338	0.229	0.102	0.301	0.517	0.128	0.349	0.000	0.000	0.307	0.000	0.037
G-74	PI461434	0.000	0.000	0.000	0.000	0.000	0.000	0.259	0.000	0.100	0.000	0.000	0.419	0.552
G-75	PI471952	0.000	0.000	0.000	0.000	0.000	0.000	0.125	0.000	0.823	0.453	0.000	0.094	0.108
G-76	PI476636	0.943	0.721	0.667	0.351	0.246	0.506	0.297	0.737	0.000	0.052	0.299	0.000	0.000
G-77	PI481795	0.000	0.000	0.000	0.035	0.000	0.000	0.201	0.000	0.076	0.035	0.000	0.755	0.597
G-78	PI482120	0.000	0.000	0.000	0.000	0.000	0.000	0.179	0.000	0.017	0.124	0.028	0.671	0.449
G-79	PI494795	0.118	0.101	0.151	0.116	0.060	0.139	0.022	0.167	0.000	0.114	0.292	0.012	0.000
G-80	PI496401	0.362	0.418	0.449	0.291	0.216	0.235	0.000	0.277	0.000	0.054	0.328	0.000	0.000
G-81	PI496448	0.510	0.437	0.641	0.442	0.084	0.351	0.000	0.399	0.000	0.000	0.167	0.000	0.000
G-82	PI504614	0.000	0.000	0.000	0.081	0.000	0.000	0.059	0.000	0.000	0.000	0.000	0.712	0.264
G-83	PI338338	0.000	0.000	0.000	0.058	0.000	0.000	0.000	0.000	0.019	0.118	0.004	0.058	0.000
G-84	PI502111	0.018	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.090	0.000	0.086	0.000	0.000
G-85	PI502120	0.000	0.000	0.000	0.000	0.000	0.064	0.000	0.051	0.030	0.000	0.000	0.004	0.058
G-86	PI155107	0.000	0.000	0.000	0.000	0.000	0.000	0.036	0.000	0.000	0.000	0.000	0.495	0.197
G-87	PI157542	0.237	0.326	0.430	0.149	0.046	0.349	0.000	0.415	0.000	0.000	0.166	0.000	0.000
G-88	PI270998	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	0.077	0.021
G-89	PI271019	0.000	0.000	0.000	0.130	0.000	0.000	0.042	0.000	0.000	0.000	0.000	0.562	0.222
G-90	PI288146	0.000	0.000	0.000	0.095	0.000	0.000	0.012	0.000	0.000	0.000	0.000	0.623	0.258
G-91	PI290560	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.592	0.123
G-92	PI403813	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.566	0.318	0.000	0.216	0.000
G-93	PI407667	0.000	0.000	0.000	0.039	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.248	0.178
G-94	PI478819	0.000	0.000	0.000	0.088	0.034	0.000	0.059	0.000	0.000	0.000	0.000	0.120	0.006
G-95	PI476432	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.240	0.216
G-96	PI497517	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.505	0.202	0.000	0.055	0.000
G-97	PI497639	0.000	0.000	0.000	0.000	0.000	0.048	0.000	0.000	0.000	0.000	0.037	0.000	0.079
G-98	PI497318	0.005	0.136	0.185	0.044	0.025	0.094	0.000	0.033	0.000	0.000	0.189	0.000	0.000
G-99	PI497395	0.044	0.199	0.116	0.018	0.024	0.000	0.052	0.006	0.000	0.000	0.182	0.000	0.000
G-100	PI494018	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.096	0.000	0.000	0.043	0.126
G-101	PI494034	0.000	0.000	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.000	0.000	0.174	0.248
G-102	PI288210	0.039	0.106	0.067	0.062	0.000	0.000	0.004	0.000	0.000	0.000	0.128	0.000	0.000
G-103	PI371521	0.269	0.216	0.224	0.000	0.052	0.362	0.158	0.293	0.000	0.000	0.061	0.000	0.000
G-104	PI461427	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.375	0.032	0.000	0.050	0.000

Appendix A. cont.

Code	Genotype	G-66	G-67	G-68	G-69	G-70	G-71	G-72	G-73	G-74	G-75	G-76	G-77	G-78
G-1	PI152146	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.322	0.033	0.000	0.262	0.188
G-2	PI158854	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.311	0.000	0.000	0.300	0.199
G-3	PI200441	0.078	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.261	0.105	0.000	0.166	0.151
G-4	PI259617	0.130	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.304	0.000	0.000	0.000
G-5	PI259836	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.150	0.025	0.000	0.202	0.253
G-6	PI262038	0.042	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.056	0.373	0.000	0.000	0.000
G-7	PI290566	0.000	0.335	0.292	0.155	0.277	0.197	0.290	0.175	0.000	0.000	0.323	0.000	0.000
G-8	PI290620	0.000	0.150	0.109	0.030	0.163	0.126	0.116	0.117	0.000	0.000	0.075	0.000	0.000
G-9	PI295730	0.105	0.102	0.043	0.123	0.177	0.136	0.000	0.184	0.000	0.000	0.025	0.000	0.000
G-10	PI313129	0.000	0.070	0.132	0.073	0.003	0.004	0.002	0.083	0.000	0.000	0.072	0.000	0.000
G-11	PI337406	0.035	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.150	0.364	0.000	0.000	0.023
G-12	PI339960	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.112	0.000	0.000	0.117	0.000
G-13	PI343398	0.000	0.222	0.281	0.077	0.231	0.134	0.174	0.071	0.000	0.000	0.243	0.000	0.000
G-14	PI356004	0.042	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.270	0.000	0.000	0.000
G-15	PI429420	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.334	0.000	0.000	0.000
G-16	PI471954	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.127	0.357	0.000	0.000	0.000
G-17	PI478850	0.000	0.000	0.000	0.026	0.000	0.035	0.000	0.107	0.000	0.000	0.000	0.000	0.000
G-18	PI482189	0.065	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.181	0.226	0.000	0.118	0.189
G-19	PI502040	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.076	0.000	0.018	0.000
G-20	PI475863	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.017	0.162	0.000	0.000	0.000
G-21	PI475918	0.040	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.259	0.000	0.000	0.000
G-22	PI476025	0.000	0.083	0.000	0.038	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-23	PI493329	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.363	0.000	0.000	0.000
G-24	PI493356	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.320	0.000	0.000	0.013
G-25	PI493547	0.027	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.097	0.332	0.000	0.000	0.000
G-26	PI493581	0.173	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.293	0.000	0.000	0.000
G-27	PI493631	0.056	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.350	0.000	0.000	0.000
G-28	PI493693	0.099	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.300	0.000	0.000	0.000
G-29	PI493717	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.087	0.222	0.000	0.098	0.135
G-30	PI493729	0.043	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.319	0.000	0.000	0.000
G-31	PI493880	0.033	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.064	0.313	0.000	0.000	0.003
G-32	PI493938	0.026	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.241	0.033	0.000	0.144	0.114
G-33	PI159786	0.000	0.401	0.271	0.148	0.272	0.174	0.309	0.170	0.000	0.000	0.390	0.000	0.000
G-34	PI162655	0.000	0.056	0.190	0.130	0.184	0.019	0.228	0.094	0.000	0.000	0.230	0.000	0.000
G-35	PI162857	0.000	0.231	0.102	0.132	0.203	0.057	0.078	0.045	0.000	0.000	0.082	0.000	0.000
G-36	PI196622	0.000	0.338	0.304	0.158	0.415	0.132	0.225	0.102	0.000	0.000	0.291	0.000	0.000
G-37	PI196635	0.000	0.240	0.137	0.195	0.250	0.152	0.281	0.134	0.000	0.000	0.194	0.000	0.000
G-38	PI240560	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.330	0.000	0.000	0.334	0.543
G-39	PI259658	0.000	0.191	0.088	0.112	0.133	0.154	0.000	0.000	0.000	0.000	0.109	0.000	0.000
G-40	PI259851	0.000	0.360	0.355	0.171	0.112	0.109	0.078	0.208	0.000	0.000	0.292	0.000	0.000
G-41	PI268586	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.286	0.000	0.000	0.290	0.295
G-42	PI268696	0.039	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.339	0.080	0.000	0.276	0.518
G-43	PI268755	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.203	0.028	0.000	0.106	0.067
G-44	PI268806	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.127	0.028	0.000	0.322	0.448
G-45	PI268868	0.000	0.238	0.152	0.212	0.183	0.117	0.245	0.133	0.000	0.000	0.193	0.000	0.000
G-46	PI268996	0.000	0.319	0.217	0.156	0.261	0.199	0.224	0.128	0.000	0.000	0.307	0.000	0.000
G-47	PI270786	0.144	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.273	0.166	0.000	0.277	0.316
G-48	PI270905	0.000	0.000	0.000	0.133	0.000	0.023	0.035	0.064	0.075	0.000	0.011	0.079	0.056
G-49	PI270907	0.000	0.090	0.000	0.094	0.000	0.067	0.086	0.449	0.121	0.000	0.000	0.074	0.077
G-50	PI274193	0.059	0.350	0.294	0.349	0.407	0.396	0.152	0.444	0.000	0.000	0.333	0.000	0.000
G-51	PI290536	0.267	0.742	0.590	0.366	0.598	0.397	0.349	0.344	0.000	0.000	0.715	0.000	0.000
G-52	PI290594	0.198	0.961	0.828	0.392	0.514	0.470	0.273	0.346	0.000	0.000	0.853	0.000	0.000

Appendix A. cont.

Code	Genotype	G-66	G-67	G-68	G-69	G-70	G-71	G-72	G-73	G-74	G-75	G-76	G-77	G-78
G-53	PI292950	0.094	0.730	0.817	0.584	0.655	0.472	0.435	0.350	0.000	0.000	0.943	0.000	0.000
G-54	PI295250	0.158	0.665	0.684	0.517	0.862	0.515	0.330	0.338	0.000	0.000	0.721	0.000	0.000
G-55	PI295309	0.115	0.607	0.610	0.476	0.855	0.573	0.596	0.229	0.000	0.000	0.667	0.000	0.000
G-56	PI296550	0.040	0.277	0.311	0.180	0.457	0.305	0.388	0.102	0.000	0.000	0.351	0.035	0.000
G-57	PI296558	0.154	0.219	0.173	0.268	0.270	0.258	0.079	0.301	0.000	0.000	0.246	0.000	0.000
G-58	PI298854	0.316	0.840	0.582	0.282	0.385	0.226	0.233	0.517	0.000	0.000	0.506	0.000	0.000
G-59	PI319768	0.138	0.370	0.221	0.160	0.146	0.043	0.170	0.128	0.259	0.125	0.297	0.201	0.179
G-60	PI323268	0.124	1.031	0.862	0.512	0.566	0.327	0.234	0.349	0.000	0.000	0.737	0.000	0.000
G-61	PI325943	0.092	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.100	0.823	0.000	0.076	0.017
G-62	PI331297	0.088	0.144	0.132	0.107	0.075	0.000	0.098	0.000	0.000	0.453	0.052	0.035	0.124
G-63	PI331314	0.000	0.339	0.311	0.319	0.355	0.310	0.160	0.307	0.000	0.000	0.299	0.000	0.028
G-64	PI337293	0.000	0.000	0.000	0.000	0.000	0.000	0.052	0.000	0.419	0.094	0.000	0.755	0.671
G-65	PI337399	0.165	0.000	0.000	0.000	0.000	0.000	0.000	0.037	0.552	0.108	0.000	0.597	0.449
G-66	PI343384	2.000	0.200	0.173	0.060	0.047	0.048	0.088	0.217	0.133	0.058	0.107	0.000	0.000
G-67	PI355268	0.200	2.000	0.906	0.460	0.481	0.335	0.310	0.402	0.000	0.000	0.717	0.000	0.000
G-68	PI355271	0.173	0.906	2.000	0.512	0.567	0.382	0.273	0.278	0.000	0.000	0.976	0.000	0.000
G-69	PI370331	0.060	0.460	0.512	2.000	0.571	0.387	0.274	0.375	0.000	0.000	0.497	0.000	0.000
G-70	PI372271	0.047	0.481	0.567	0.571	2.000	0.684	0.435	0.271	0.000	0.000	0.573	0.000	0.000
G-71	PI372305	0.048	0.335	0.382	0.387	0.684	2.000	0.297	0.273	0.000	0.000	0.440	0.000	0.000
G-72	PI399581	0.088	0.310	0.273	0.274	0.435	0.297	2.000	0.071	0.000	0.000	0.349	0.000	0.000
G-73	PI442768	0.217	0.402	0.278	0.375	0.271	0.273	0.071	2.000	0.000	0.000	0.420	0.000	0.000
G-74	PI461434	0.133	0.000	0.000	0.000	0.000	0.000	0.000	0.000	2.000	0.359	0.000	0.521	0.501
G-75	PI471952	0.058	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.359	2.000	0.000	0.246	0.342
G-76	PI476636	0.107	0.717	0.976	0.497	0.573	0.440	0.349	0.420	0.000	0.000	2.000	0.000	0.000
G-77	PI481795	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.521	0.246	0.000	2.000	1.032
G-78	PI482120	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.501	0.342	0.000	1.032	2.000
G-79	PI494795	0.000	0.214	0.094	0.355	0.190	0.314	0.037	0.027	0.000	0.054	0.181	0.000	0.091
G-80	PI496401	0.031	0.434	0.283	0.461	0.496	0.422	0.523	0.445	0.000	0.000	0.254	0.000	0.000
G-81	PI496448	0.001	0.369	0.488	0.285	0.614	0.382	0.444	0.247	0.000	0.000	0.560	0.000	0.000
G-82	PI504614	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.336	0.112	0.000	0.602	0.405
G-83	PI338338	0.000	0.000	0.000	0.000	0.000	0.027	0.000	0.000	0.088	0.074	0.000	0.076	0.086
G-84	PI502111	0.000	0.000	0.002	0.214	0.005	0.092	0.052	0.005	0.000	0.000	0.000	0.000	0.000
G-85	PI502120	0.000	0.048	0.000	0.157	0.058	0.281	0.000	0.000	0.071	0.000	0.000	0.000	0.000
G-86	PI155107	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.160	0.248	0.000	0.523	0.503
G-87	PI157542	0.000	0.442	0.341	0.267	0.345	0.368	0.230	0.097	0.000	0.000	0.335	0.000	0.000
G-88	PI270998	0.000	0.000	0.000	0.003	0.000	0.108	0.000	0.000	0.144	0.000	0.000	0.035	0.112
G-89	PI271019	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.322	0.267	0.000	0.552	0.418
G-90	PI288146	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.260	0.169	0.000	0.638	0.611
G-91	PI290560	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.266	0.047	0.000	0.485	0.490
G-92	PI403813	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.075	0.575	0.000	0.062	0.005
G-93	PI407667	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.140	0.100	0.000	0.297	0.224
G-94	PI478819	0.000	0.000	0.000	0.022	0.000	0.161	0.232	0.000	0.000	0.000	0.000	0.121	0.054
G-95	PI476432	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.000	0.181	0.150	0.000	0.347	0.460
G-96	PI497517	0.166	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.071	0.239	0.000	0.000	0.000
G-97	PI497639	0.018	0.000	0.000	0.042	0.046	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.000
G-98	PI497318	0.000	0.101	0.000	0.107	0.077	0.132	0.003	0.242	0.000	0.000	0.000	0.000	0.000
G-99	PI497395	0.000	0.046	0.000	0.134	0.135	0.069	0.093	0.121	0.000	0.000	0.000	0.000	0.000
G-100	PI494018	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.072	0.151	0.000	0.128	0.088
G-101	PI494034	0.057	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.213	0.075	0.000	0.153	0.239
G-102	PI288210	0.000	0.005	0.020	0.113	0.127	0.035	0.000	0.129	0.000	0.000	0.059	0.000	0.000
G-103	PI371521	0.000	0.379	0.291	0.142	0.134	0.126	0.086	0.212	0.000	0.000	0.242	0.000	0.000
G-104	PI461427	0.150	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.100	0.334	0.000	0.000	0.072

Appendix A. cont.

Code	Genotype	G-79	G-80	G-81	G-82	G-83	G-84	G-85	G-86	G-87	G-88	G-89	G-90	G-91
G-1	PI152146	0.000	0.000	0.000	0.192	0.081	0.011	0.000	0.158	0.000	0.331	0.298	0.206	0.161
G-2	PI158854	0.000	0.000	0.000	0.308	0.000	0.000	0.038	0.306	0.000	0.192	0.169	0.300	0.235
G-3	PI200441	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.139	0.000	0.000	0.023	0.034	0.015
G-4	PI259617	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-5	PI259836	0.000	0.000	0.000	0.198	0.000	0.000	0.082	0.175	0.000	0.000	0.048	0.076	0.026
G-6	PI262038	0.000	0.000	0.000	0.000	0.068	0.000	0.000	0.089	0.000	0.000	0.000	0.000	0.000
G-7	PI290566	0.078	0.143	0.398	0.000	0.000	0.011	0.000	0.000	0.226	0.000	0.000	0.000	0.000
G-8	PI290620	0.016	0.060	0.173	0.000	0.000	0.000	0.000	0.000	0.101	0.035	0.000	0.000	0.000
G-9	PI295730	0.100	0.006	0.161	0.000	0.000	0.270	0.253	0.000	0.076	0.065	0.000	0.000	0.000
G-10	PI313129	0.055	0.046	0.191	0.000	0.000	0.283	0.075	0.000	0.223	0.008	0.000	0.000	0.000
G-11	PI337406	0.000	0.000	0.000	0.000	0.000	0.000	0.076	0.000	0.000	0.000	0.000	0.000	0.000
G-12	PI339960	0.000	0.000	0.000	0.057	0.103	0.037	0.189	0.021	0.000	0.000	0.122	0.000	0.053
G-13	PI343398	0.049	0.092	0.150	0.000	0.000	0.056	0.000	0.000	0.211	0.000	0.000	0.000	0.000
G-14	PI356004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-15	PI429420	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-16	PI471954	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.098	0.000	0.000	0.093	0.048	0.000
G-17	PI478850	0.052	0.000	0.000	0.000	0.051	0.369	0.482	0.000	0.003	0.000	0.000	0.000	0.000
G-18	PI482189	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.182	0.000	0.005	0.058	0.153	0.000
G-19	PI502040	0.000	0.000	0.000	0.000	0.029	0.000	0.094	0.032	0.000	0.109	0.000	0.000	0.041
G-20	PI475863	0.000	0.000	0.000	0.000	0.017	0.040	0.000	0.071	0.000	0.000	0.000	0.000	0.000
G-21	PI475918	0.000	0.000	0.000	0.000	0.021	0.000	0.000	0.007	0.000	0.000	0.000	0.021	0.000
G-22	PI476025	0.096	0.000	0.000	0.000	0.022	0.241	0.347	0.000	0.116	0.000	0.000	0.000	0.000
G-23	PI493329	0.000	0.000	0.000	0.000	0.013	0.000	0.000	0.013	0.000	0.000	0.000	0.000	0.000
G-24	PI493356	0.000	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-25	PI493547	0.000	0.000	0.000	0.000	0.071	0.014	0.000	0.000	0.000	0.025	0.000	0.000	0.000
G-26	PI493581	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-27	PI493631	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-28	PI493693	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000	0.000	0.000	0.000	0.000
G-29	PI493717	0.000	0.000	0.000	0.073	0.000	0.000	0.000	0.229	0.000	0.035	0.097	0.150	0.000
G-30	PI493729	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-31	PI493880	0.000	0.000	0.000	0.000	0.032	0.000	0.000	0.001	0.000	0.000	0.078	0.020	0.000
G-32	PI493938	0.000	0.000	0.000	0.070	0.048	0.000	0.000	0.137	0.000	0.002	0.153	0.151	0.089
G-33	PI159786	0.008	0.214	0.406	0.000	0.000	0.000	0.000	0.000	0.156	0.000	0.000	0.000	0.000
G-34	PI162655	0.000	0.096	0.158	0.000	0.000	0.005	0.000	0.000	0.072	0.000	0.000	0.000	0.000
G-35	PI162857	0.000	0.021	0.132	0.000	0.000	0.000	0.000	0.000	0.217	0.000	0.000	0.000	0.000
G-36	PI196622	0.000	0.232	0.419	0.000	0.000	0.000	0.000	0.000	0.140	0.000	0.000	0.000	0.000
G-37	PI196635	0.015	0.269	0.250	0.000	0.000	0.000	0.000	0.000	0.073	0.000	0.000	0.000	0.000
G-38	PI240560	0.000	0.000	0.000	0.362	0.084	0.000	0.000	0.446	0.000	0.117	0.237	0.524	0.443
G-39	PI259658	0.000	0.062	0.043	0.000	0.000	0.000	0.000	0.000	0.056	0.000	0.000	0.000	0.000
G-40	PI259851	0.000	0.196	0.189	0.000	0.000	0.000	0.000	0.000	0.141	0.000	0.000	0.000	0.000
G-41	PI268586	0.000	0.000	0.000	0.256	0.007	0.000	0.000	0.233	0.000	0.058	0.176	0.196	0.053
G-42	PI268696	0.000	0.000	0.000	0.194	0.006	0.000	0.000	0.282	0.000	0.283	0.347	0.431	0.469
G-43	PI268755	0.000	0.000	0.000	0.278	0.129	0.000	0.000	0.115	0.000	0.000	0.225	0.317	0.146
G-44	PI268806	0.000	0.000	0.000	0.275	0.113	0.000	0.000	0.420	0.000	0.000	0.337	0.496	0.242
G-45	PI268868	0.000	0.161	0.245	0.000	0.000	0.000	0.000	0.000	0.075	0.000	0.000	0.000	0.000
G-46	PI268996	0.000	0.220	0.226	0.000	0.000	0.000	0.000	0.000	0.069	0.000	0.000	0.000	0.000
G-47	PI270786	0.000	0.000	0.000	0.225	0.198	0.000	0.000	0.303	0.000	0.000	0.301	0.353	0.094
G-48	PI270905	0.072	0.000	0.048	0.148	0.000	0.000	0.000	0.000	0.000	0.114	0.056	0.120	0.078
G-49	PI270907	0.000	0.174	0.006	0.022	0.000	0.000	0.115	0.000	0.000	0.000	0.000	0.000	0.112
G-50	PI274193	0.094	0.342	0.320	0.000	0.000	0.106	0.011	0.000	0.259	0.044	0.000	0.000	0.000
G-51	PI290536	0.048	0.381	0.346	0.000	0.000	0.000	0.000	0.000	0.309	0.000	0.000	0.000	0.000
G-52	PI290594	0.153	0.246	0.350	0.000	0.000	0.000	0.000	0.000	0.264	0.000	0.000	0.000	0.000

Appendix A. cont.

Code	Genotype	G-79	G-80	G-81	G-82	G-83	G-84	G-85	G-86	G-87	G-88	G-89	G-90	G-91
G-53	PI292950	0.118	0.362	0.510	0.000	0.000	0.018	0.000	0.000	0.237	0.000	0.000	0.000	0.000
G-54	PI295250	0.101	0.418	0.437	0.000	0.000	0.000	0.000	0.000	0.326	0.000	0.000	0.000	0.000
G-55	PI295309	0.151	0.449	0.641	0.000	0.000	0.000	0.000	0.000	0.430	0.020	0.000	0.000	0.000
G-56	PI296550	0.116	0.291	0.442	0.081	0.058	0.000	0.000	0.000	0.149	0.000	0.130	0.095	0.009
G-57	PI296558	0.060	0.216	0.084	0.000	0.000	0.000	0.000	0.000	0.046	0.000	0.000	0.000	0.000
G-58	PI298854	0.139	0.235	0.351	0.000	0.000	0.000	0.064	0.000	0.349	0.000	0.000	0.000	0.000
G-59	PI319768	0.022	0.000	0.000	0.059	0.000	0.000	0.000	0.036	0.000	0.000	0.042	0.012	0.000
G-60	PI323268	0.167	0.277	0.399	0.000	0.000	0.011	0.051	0.000	0.415	0.000	0.000	0.000	0.000
G-61	PI325943	0.000	0.000	0.000	0.000	0.019	0.090	0.030	0.000	0.000	0.000	0.000	0.000	0.000
G-62	PI331297	0.114	0.054	0.000	0.000	0.118	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-63	PI331314	0.292	0.328	0.167	0.000	0.004	0.086	0.000	0.000	0.166	0.008	0.000	0.000	0.000
G-64	PI337293	0.012	0.000	0.000	0.712	0.058	0.000	0.004	0.495	0.000	0.077	0.562	0.623	0.592
G-65	PI337399	0.000	0.000	0.000	0.264	0.000	0.000	0.058	0.197	0.000	0.021	0.222	0.258	0.123
G-66	PI343384	0.000	0.031	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-67	PI355268	0.214	0.434	0.369	0.000	0.000	0.000	0.048	0.000	0.442	0.000	0.000	0.000	0.000
G-68	PI355271	0.094	0.283	0.488	0.000	0.000	0.002	0.000	0.000	0.341	0.000	0.000	0.000	0.000
G-69	PI370331	0.355	0.461	0.285	0.000	0.000	0.214	0.157	0.000	0.267	0.003	0.000	0.000	0.000
G-70	PI372271	0.190	0.496	0.614	0.000	0.000	0.005	0.058	0.000	0.345	0.000	0.000	0.000	0.000
G-71	PI372305	0.314	0.422	0.382	0.000	0.027	0.092	0.281	0.000	0.368	0.108	0.000	0.000	0.000
G-72	PI399581	0.037	0.523	0.444	0.000	0.000	0.052	0.000	0.000	0.230	0.000	0.000	0.000	0.000
G-73	PI442768	0.027	0.445	0.247	0.000	0.000	0.005	0.000	0.000	0.097	0.000	0.000	0.000	0.000
G-74	PI461434	0.000	0.000	0.000	0.336	0.088	0.000	0.071	0.160	0.000	0.144	0.322	0.260	0.266
G-75	PI471952	0.054	0.000	0.000	0.112	0.074	0.000	0.000	0.248	0.000	0.000	0.267	0.169	0.047
G-76	PI476636	0.181	0.254	0.560	0.000	0.000	0.000	0.000	0.000	0.335	0.000	0.000	0.000	0.000
G-77	PI481795	0.000	0.000	0.000	0.602	0.076	0.000	0.000	0.523	0.000	0.035	0.552	0.638	0.485
G-78	PI482120	0.091	0.000	0.000	0.405	0.086	0.000	0.000	0.503	0.000	0.112	0.418	0.611	0.490
G-79	PI494795	2.000	0.235	0.103	0.000	0.044	0.177	0.266	0.000	0.346	0.054	0.000	0.088	0.000
G-80	PI496401	0.235	2.000	0.369	0.000	0.003	0.127	0.000	0.000	0.365	0.084	0.000	0.000	0.000
G-81	PI496448	0.103	0.369	2.000	0.000	0.000	0.106	0.066	0.000	0.460	0.090	0.000	0.000	0.000
G-82	PI504614	0.000	0.000	0.000	2.000	0.358	0.040	0.022	0.677	0.000	0.163	0.734	0.979	0.604
G-83	PI338338	0.044	0.003	0.000	0.358	2.000	0.114	0.109	0.266	0.103	0.113	0.301	0.419	0.420
G-84	PI502111	0.177	0.127	0.106	0.040	0.114	2.000	0.653	0.012	0.142	0.100	0.000	0.022	0.110
G-85	PI502120	0.266	0.000	0.066	0.022	0.109	0.653	2.000	0.000	0.262	0.234	0.034	0.075	0.187
G-86	PI155107	0.000	0.000	0.000	0.677	0.266	0.012	0.000	2.000	0.000	0.334	0.554	0.769	0.768
G-87	PI157542	0.346	0.365	0.460	0.000	0.103	0.142	0.262	0.000	2.000	0.205	0.000	0.000	0.000
G-88	PI270998	0.054	0.084	0.090	0.163	0.113	0.100	0.234	0.334	0.205	2.000	0.151	0.267	0.510
G-89	PI271019	0.000	0.000	0.000	0.734	0.301	0.000	0.034	0.554	0.000	0.151	2.000	1.002	0.626
G-90	PI288146	0.088	0.000	0.000	0.979	0.419	0.022	0.075	0.769	0.000	0.267	1.002	2.000	0.816
G-91	PI290560	0.000	0.000	0.000	0.604	0.420	0.110	0.187	0.768	0.000	0.510	0.626	0.816	2.000
G-92	PI403813	0.006	0.000	0.000	0.090	0.311	0.179	0.123	0.400	0.000	0.083	0.162	0.099	0.285
G-93	PI407667	0.000	0.000	0.000	0.521	0.404	0.017	0.015	0.733	0.000	0.374	0.755	0.750	0.630
G-94	PI478819	0.060	0.111	0.063	0.429	0.198	0.106	0.135	0.608	0.183	0.517	0.282	0.486	0.464
G-95	PI476432	0.000	0.000	0.000	0.455	0.257	0.000	0.049	0.647	0.057	0.354	0.421	0.738	0.494
G-96	PI497517	0.000	0.007	0.025	0.002	0.014	0.107	0.092	0.004	0.000	0.219	0.074	0.000	0.095
G-97	PI497639	0.261	0.000	0.000	0.106	0.000	0.330	0.431	0.000	0.025	0.000	0.000	0.000	0.000
G-98	PI497318	0.215	0.198	0.054	0.000	0.000	0.058	0.050	0.000	0.092	0.011	0.000	0.000	0.000
G-99	PI497395	0.132	0.169	0.160	0.000	0.000	0.024	0.014	0.000	0.081	0.000	0.000	0.000	0.000
G-100	PI494018	0.000	0.000	0.000	0.214	0.033	0.000	0.000	0.248	0.000	0.000	0.137	0.141	0.015
G-101	PI494034	0.000	0.000	0.000	0.279	0.000	0.000	0.000	0.283	0.000	0.064	0.140	0.284	0.097
G-102	PI288210	0.035	0.079	0.038	0.000	0.000	0.021	0.000	0.000	0.000	0.000	0.000	0.000	0.000
G-103	PI371521	0.052	0.215	0.223	0.000	0.000	0.000	0.000	0.000	0.174	0.000	0.000	0.000	0.000
G-104	PI461427	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.032

Appendix A. cont.

Code	Genotype	G-92	G-93	G-94	G-95	G-96	G-97	G-98	G-99	G-100	G-101	G-102	G-103	G-104
G-1	PI152146	0.075	0.120	0.104	0.193	0.000	0.066	0.000	0.000	0.053	0.182	0.000	0.000	0.059
G-2	PI158854	0.012	0.250	0.186	0.316	0.000	0.058	0.000	0.000	0.164	0.117	0.000	0.000	0.019
G-3	PI200441	0.087	0.276	0.004	0.107	0.191	0.000	0.000	0.000	0.247	0.080	0.000	0.000	0.080
G-4	PI259617	0.323	0.000	0.000	0.000	0.297	0.000	0.000	0.000	0.121	0.000	0.000	0.000	0.405
G-5	PI259836	0.000	0.053	0.000	0.260	0.000	0.098	0.000	0.000	0.207	0.144	0.021	0.000	0.000
G-6	PI262038	0.377	0.000	0.000	0.000	0.258	0.000	0.000	0.000	0.000	0.059	0.000	0.000	0.372
G-7	PI290566	0.000	0.000	0.000	0.000	0.000	0.137	0.319	0.113	0.000	0.000	0.006	0.303	0.000
G-8	PI290620	0.000	0.000	0.000	0.000	0.016	0.088	0.252	0.187	0.000	0.000	0.000	0.237	0.000
G-9	PI295730	0.000	0.000	0.000	0.000	0.000	0.058	0.190	0.062	0.000	0.000	0.071	0.000	0.000
G-10	PI313129	0.042	0.000	0.025	0.000	0.016	0.012	0.000	0.000	0.000	0.000	0.000	0.167	0.000
G-11	PI337406	0.298	0.000	0.000	0.000	0.109	0.000	0.000	0.000	0.102	0.000	0.000	0.000	0.309
G-12	PI339960	0.000	0.039	0.000	0.000	0.000	0.393	0.116	0.041	0.051	0.000	0.007	0.000	0.033
G-13	PI343398	0.000	0.000	0.000	0.000	0.000	0.000	0.122	0.059	0.000	0.000	0.059	0.221	0.000
G-14	PI356004	0.328	0.000	0.000	0.000	0.167	0.000	0.000	0.000	0.016	0.022	0.000	0.000	0.527
G-15	PI429420	0.472	0.000	0.000	0.000	0.252	0.000	0.000	0.000	0.050	0.016	0.000	0.000	0.554
G-16	PI471954	0.359	0.010	0.000	0.000	0.089	0.000	0.000	0.000	0.042	0.094	0.000	0.000	0.407
G-17	PI478850	0.000	0.000	0.000	0.000	0.000	0.516	0.093	0.000	0.000	0.000	0.016	0.008	0.000
G-18	PI482189	0.093	0.006	0.000	0.000	0.055	0.000	0.000	0.000	0.223	0.198	0.000	0.000	0.205
G-19	PI502040	0.000	0.007	0.017	0.000	0.000	0.238	0.000	0.000	0.116	0.000	0.086	0.000	0.103
G-20	PI475863	0.000	0.000	0.000	0.000	0.000	0.091	0.000	0.000	0.150	0.000	0.026	0.000	0.088
G-21	PI475918	0.138	0.000	0.000	0.000	0.061	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.362
G-22	PI476025	0.000	0.000	0.000	0.000	0.000	0.750	0.236	0.074	0.000	0.000	0.004	0.000	0.000
G-23	PI493329	0.414	0.019	0.000	0.000	0.130	0.000	0.000	0.000	0.000	0.043	0.000	0.000	0.444
G-24	PI493356	0.491	0.000	0.000	0.000	0.195	0.000	0.000	0.000	0.001	0.057	0.000	0.000	0.557
G-25	PI493547	0.302	0.000	0.000	0.000	0.180	0.000	0.000	0.000	0.204	0.064	0.000	0.000	0.376
G-26	PI493581	0.336	0.000	0.000	0.000	0.130	0.000	0.000	0.000	0.019	0.000	0.000	0.000	0.392
G-27	PI493631	0.403	0.000	0.000	0.000	0.218	0.000	0.000	0.000	0.037	0.000	0.000	0.000	0.348
G-28	PI493693	0.195	0.000	0.000	0.000	0.096	0.000	0.000	0.000	0.076	0.030	0.000	0.000	0.414
G-29	PI493717	0.094	0.197	0.000	0.107	0.022	0.000	0.000	0.000	0.124	0.190	0.000	0.000	0.267
G-30	PI493729	0.271	0.000	0.000	0.000	0.190	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.420
G-31	PI493880	0.249	0.032	0.000	0.000	0.027	0.000	0.000	0.000	0.024	0.166	0.000	0.000	0.363
G-32	PI493938	0.136	0.134	0.000	0.073	0.013	0.000	0.000	0.000	0.072	0.319	0.014	0.000	0.045
G-33	PI159786	0.000	0.000	0.000	0.000	0.000	0.088	0.352	0.125	0.000	0.000	0.206	0.379	0.000
G-34	PI162655	0.000	0.000	0.000	0.000	0.000	0.060	0.412	0.258	0.000	0.000	0.220	0.307	0.000
G-35	PI162857	0.000	0.000	0.000	0.000	0.000	0.095	0.571	0.441	0.000	0.000	0.164	0.443	0.000
G-36	PI196622	0.000	0.000	0.000	0.000	0.000	0.038	0.221	0.284	0.000	0.000	0.353	0.493	0.000
G-37	PI196635	0.000	0.000	0.000	0.000	0.000	0.017	0.370	0.241	0.000	0.000	0.420	0.445	0.000
G-38	PI240560	0.022	0.197	0.164	0.209	0.000	0.000	0.000	0.000	0.317	0.750	0.005	0.000	0.218
G-39	PI259658	0.000	0.000	0.000	0.000	0.000	0.062	0.209	0.230	0.024	0.000	0.512	0.655	0.000
G-40	PI259851	0.000	0.000	0.000	0.000	0.000	0.067	0.256	0.153	0.000	0.000	0.384	1.099	0.000
G-41	PI268586	0.067	0.135	0.036	0.217	0.000	0.012	0.000	0.000	0.573	0.377	0.000	0.000	0.024
G-42	PI268696	0.065	0.273	0.000	0.184	0.000	0.000	0.022	0.000	0.186	0.440	0.000	0.000	0.074
G-43	PI268755	0.000	0.171	0.093	0.115	0.000	0.000	0.190	0.220	0.323	0.218	0.000	0.000	0.000
G-44	PI268806	0.000	0.260	0.072	0.260	0.000	0.000	0.000	0.000	0.289	0.584	0.000	0.000	0.066
G-45	PI268868	0.000	0.000	0.000	0.000	0.000	0.000	0.444	0.297	0.000	0.000	0.393	0.464	0.000
G-46	PI268996	0.000	0.000	0.000	0.000	0.000	0.053	0.202	0.188	0.000	0.000	0.537	0.666	0.000
G-47	PI270786	0.168	0.156	0.177	0.203	0.097	0.000	0.000	0.000	0.225	0.443	0.000	0.000	0.162
G-48	PI270905	0.000	0.000	0.080	0.000	0.000	0.088	0.204	0.233	0.000	0.183	0.139	0.184	0.100
G-49	PI270907	0.000	0.011	0.000	0.000	0.000	0.014	0.079	0.000	0.000	0.024	0.000	0.077	0.008
G-50	PI274193	0.000	0.000	0.026	0.000	0.000	0.052	0.155	0.055	0.000	0.000	0.059	0.102	0.000
G-51	PI290536	0.000	0.000	0.000	0.000	0.000	0.000	0.071	0.089	0.000	0.000	0.064	0.302	0.000
G-52	PI290594	0.000	0.000	0.000	0.000	0.000	0.000	0.022	0.000	0.000	0.000	0.085	0.363	0.000

Appendix A. cont.

Code	Genotype	G-92	G-93	G-94	G-95	G-96	G-97	G-98	G-99	G-100	G-101	G-102	G-103	G-104
G-53	PI292950	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.044	0.000	0.000	0.039	0.269	0.000
G-54	PI295250	0.000	0.000	0.000	0.000	0.000	0.000	0.136	0.199	0.000	0.000	0.106	0.216	0.000
G-55	PI295309	0.000	0.000	0.000	0.000	0.000	0.000	0.185	0.116	0.000	0.000	0.067	0.224	0.000
G-56	PI296550	0.000	0.039	0.088	0.000	0.000	0.000	0.044	0.018	0.000	0.000	0.062	0.000	0.000
G-57	PI296558	0.000	0.000	0.034	0.000	0.000	0.000	0.025	0.024	0.000	0.000	0.000	0.052	0.000
G-58	PI298854	0.000	0.000	0.000	0.000	0.000	0.048	0.094	0.000	0.000	0.000	0.000	0.362	0.000
G-59	PI319768	0.000	0.000	0.059	0.000	0.000	0.000	0.000	0.052	0.000	0.043	0.004	0.158	0.000
G-60	PI323268	0.000	0.000	0.000	0.000	0.000	0.000	0.033	0.006	0.000	0.000	0.000	0.293	0.000
G-61	PI325943	0.566	0.000	0.000	0.000	0.505	0.000	0.000	0.000	0.096	0.000	0.000	0.000	0.375
G-62	PI331297	0.318	0.000	0.000	0.000	0.202	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.032
G-63	PI331314	0.000	0.000	0.000	0.000	0.000	0.037	0.189	0.182	0.000	0.000	0.128	0.061	0.000
G-64	PI337293	0.216	0.248	0.120	0.240	0.055	0.000	0.000	0.000	0.043	0.174	0.000	0.000	0.050
G-65	PI337399	0.000	0.178	0.006	0.216	0.000	0.079	0.000	0.000	0.126	0.248	0.000	0.000	0.000
G-66	PI343384	0.000	0.000	0.000	0.000	0.166	0.018	0.000	0.000	0.000	0.057	0.000	0.000	0.150
G-67	PI355268	0.000	0.000	0.000	0.000	0.000	0.000	0.101	0.046	0.000	0.000	0.005	0.379	0.000
G-68	PI355271	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.291	0.000
G-69	PI370331	0.000	0.000	0.022	0.000	0.000	0.042	0.107	0.134	0.000	0.000	0.113	0.142	0.000
G-70	PI372271	0.000	0.000	0.000	0.000	0.000	0.046	0.077	0.135	0.000	0.000	0.127	0.134	0.000
G-71	PI372305	0.000	0.000	0.161	0.000	0.000	0.000	0.132	0.069	0.000	0.000	0.035	0.126	0.000
G-72	PI399581	0.000	0.000	0.232	0.041	0.000	0.000	0.003	0.093	0.000	0.000	0.000	0.086	0.000
G-73	PI442768	0.000	0.000	0.000	0.000	0.000	0.000	0.242	0.121	0.000	0.000	0.129	0.212	0.000
G-74	PI461434	0.075	0.140	0.000	0.181	0.071	0.000	0.000	0.000	0.072	0.213	0.000	0.000	0.100
G-75	PI471952	0.575	0.100	0.000	0.150	0.239	0.000	0.000	0.000	0.151	0.075	0.000	0.000	0.334
G-76	PI476636	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.059	0.242	0.000
G-77	PI481795	0.062	0.297	0.121	0.347	0.000	0.041	0.000	0.000	0.128	0.153	0.000	0.000	0.000
G-78	PI482120	0.005	0.224	0.054	0.460	0.000	0.000	0.000	0.000	0.088	0.239	0.000	0.000	0.072
G-79	PI494795	0.006	0.000	0.060	0.000	0.000	0.261	0.215	0.132	0.000	0.000	0.035	0.052	0.000
G-80	PI496401	0.000	0.000	0.111	0.000	0.007	0.000	0.198	0.169	0.000	0.000	0.079	0.215	0.000
G-81	PI496448	0.000	0.000	0.063	0.000	0.025	0.000	0.054	0.160	0.000	0.000	0.038	0.223	0.000
G-82	PI504614	0.090	0.521	0.429	0.455	0.002	0.106	0.000	0.000	0.214	0.279	0.000	0.000	0.000
G-83	PI338338	0.311	0.404	0.198	0.257	0.014	0.000	0.000	0.000	0.033	0.000	0.000	0.000	0.000
G-84	PI502111	0.179	0.017	0.106	0.000	0.107	0.330	0.058	0.024	0.000	0.000	0.021	0.000	0.000
G-85	PI502120	0.123	0.015	0.135	0.049	0.092	0.431	0.050	0.014	0.000	0.000	0.000	0.000	0.000
G-86	PI155107	0.400	0.733	0.608	0.647	0.004	0.000	0.000	0.000	0.248	0.283	0.000	0.000	0.000
G-87	PI157542	0.000	0.000	0.183	0.057	0.000	0.025	0.092	0.081	0.000	0.000	0.000	0.174	0.000
G-88	PI270998	0.083	0.374	0.517	0.354	0.219	0.000	0.011	0.000	0.000	0.064	0.000	0.000	0.000
G-89	PI271019	0.162	0.755	0.282	0.421	0.074	0.000	0.000	0.000	0.137	0.140	0.000	0.000	0.000
G-90	PI288146	0.099	0.750	0.486	0.738	0.000	0.000	0.000	0.000	0.141	0.284	0.000	0.000	0.000
G-91	PI290560	0.285	0.630	0.464	0.494	0.095	0.000	0.000	0.000	0.015	0.097	0.000	0.000	0.032
G-92	PI403813	2.000	0.190	0.160	0.271	0.640	0.000	0.000	0.000	0.157	0.106	0.000	0.000	0.406
G-93	PI407667	0.190	2.000	0.524	0.768	0.048	0.000	0.000	0.000	0.210	0.086	0.000	0.000	0.000
G-94	PI478819	0.160	0.524	2.000	0.541	0.172	0.000	0.000	0.000	0.100	0.000	0.000	0.000	0.000
G-95	PI476432	0.271	0.768	0.541	2.000	0.143	0.000	0.000	0.000	0.264	0.255	0.000	0.000	0.000
G-96	PI497517	0.640	0.048	0.172	0.143	2.000	0.000	0.000	0.000	0.036	0.000	0.000	0.000	0.317
G-97	PI497639	0.000	0.000	0.000	0.000	0.000	2.000	0.282	0.289	0.008	0.000	0.106	0.083	0.026
G-98	PI497318	0.000	0.000	0.000	0.000	0.000	0.282	2.000	0.977	0.028	0.000	0.335	0.266	0.000
G-99	PI497395	0.000	0.000	0.000	0.000	0.000	0.289	0.977	2.000	0.167	0.000	0.334	0.210	0.000
G-100	PI494018	0.157	0.210	0.100	0.264	0.036	0.008	0.028	0.167	2.000	0.483	0.022	0.000	0.025
G-101	PI494034	0.106	0.086	0.000	0.255	0.000	0.000	0.000	0.000	0.483	2.000	0.000	0.000	0.229
G-102	PI288210	0.000	0.000	0.000	0.000	0.000	0.106	0.335	0.334	0.022	0.000	2.000	0.375	0.000
G-103	PI371521	0.000	0.000	0.000	0.000	0.000	0.083	0.266	0.210	0.000	0.000	0.375	2.000	0.000
G-104	PI461427	0.406	0.000	0.000	0.000	0.317	0.026	0.000	0.000	0.025	0.229	0.000	0.000	2.000