RFLP markers and genetic linkage of oil content and hypodermis color in sunflower seed (*Helianthus annuus L.*)

by

Alberto Javier Leon

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GENERAL INTRODUCTION

Thesis Format

This thesis is written as three manuscripts with a general introduction and general conclusions. The first manuscript reports the creation of an RFLP map in sunflower. The second manuscript reports the genetic linkage analysis for seed oil percentage and its components. The third manuscript reports the genetic linkage analysis for seed hypodermis color and the relation between this and seed oil percentage. References cited in the general introduction are listed following the general conclusions.

Literature Review

Taxonomy and origin

Sunflower (*Helianthus annuus L.*) belongs to the *Asteraceae* family which contains more than 50 species related to the cultivated sunflower. In the genus *Helianthus* there are species with different ploidies (diploid, tetraploid, and hexaploid). The cultivated sunflower is a diploid (2n=2x=34).

Sunflowers are native species of western North America and Mexico. They were used for different purposes by the Indians of that area. Seeds were used as a source of food, to produce flour and cakes, while heads and roots were used for medicinal purposes (Skoric, 1988).

The single-head sunflower type used for commercial production was selected by the Indians from the multiplebranched wild-type (Skoric, 1988). Open-pollinated populations were used at the beginning of commercial sunflower cultivation during the 17th century (Fick, 1978). Leclercq reported the discovery of a source of cytoplasmic male sterility (CMS) in the wild specie *Helianthus petiolaris*, in 1969. One year later Kinman, in the U.S.A., found genes for restoration of Leclercq's cytoplasm. Currently, most cultivated sunflower in Argentina, Australia, the U.S.A., and western Europe are single-cross and three-way-cross hybrids with a common cytoplasm.

Cultivation

More than 14 millon hectares of sunflower are grown each year in the world. Some of the most important countries that grow sunflower are Argentina, Russia, Yugoslavia, United States, Turkey, Australia, France, Spain, Hungary, Rumania, and China. Most of the cultivated sunflower is grown as a source of oil (salad oil, cooking oil, margarine industries). Low-oil sunflower cultivars (confectionery) are also grown but total production and market demand are relatively insignificant.

Breeding objectives and commodity value

One of the principal goals of sunflower breeding programs is development of cultivars with high oil yield. In addition, oil quality has become a more important breeding objective in some breeding programs.

Sunflower oil yield per unit area is determined by the seed yield per unit area and oil percentage (%) in the seed

Oil Yield (Kg/ha)=Seed Yield (Kg/ha) x Oil (%)/100

Usually farmers are paid according to the weight of seed harvested, with a bonus related to the oil percentage. Normally, there is a base value and a bonus, in the seed price, per point above the base value. If the oil percentage is lower than the base value farmers get a discount in the price. In Argentina, for example, the sunflower price increases 2% for each 1% increase of oil percentage over 44% (base value) and has the same discount per point lower than the base value.

In the example in Table 1, comparing hybrids 1 and 2 we can see that a farmer can get the same income despite a lower

Table 1. Comparison of farmers income with different bonus according with the seed oil percentage

HYBRID	SEED YIELD	OIL %	OIL YIELD	PRICE	BONUS %	INCOME
1	100	44.0	44	10	0.00	1000
2	90	49.5	44	10	11.0	1000
3	90	49.5	44	10	16.5	1048

Income=Yield x Price x (1+Bonus)

seed yield with hybrid 2. The lower yield was compensated by the 11% of bonification (2% per point over the base; 44%). If we compare hybrids 2 and 3 in a country with a different pricing system (3% per point over the base) the component of oil percentage would be more important. Notice that the oil yield is the same for all the hybrids.

As a summary, both components of oil yield per unit area are important when breeding for oil percentage. In addition, as the premium for oil percentage increases the oil percentage has higher importance. In other words, a lower seed yield can be accepted when oil bonus is higher.

Seed morphology

Sunflower achene (botanic term) is a fruit consisting of a kernel (real seed) and a pericarp (hull). The word 'seed' is used as a synonym of 'achene' in the sunflower research community, and will be used so in this paper. The seed size varies from 7 to 25 mm in length and from 4 to 13 mm in width (Fick, 1978), and the kernel percentage varies from 48 to 84% (Vranceanu, 1977).

The kernel consists of an embryo, endosperm, and a seed coat. The pericarp consists of different layers: cuticle (external layer), epidermis, hypodermis, armor layer, fibrose tissue, and finally the parenchymal layers (Nassanov, 1940; cited by Vranceanu, 1977). The color of the pericarp of the seed could be considered as a complex trait since it is determined by the epidermis, hypodermis, and armor layer pigments (Putt, 1940; Mosjidis, 1982). The epidermis layer can be free of pigments or have black or dark brown stripes (Putt, 1944). These stripes can be thin or so thick that they can cover the whole seed, thus giving the main color of the seed. Below the epidermis is the hypodermis layer, which can also be either pigmented or unpigmented (Mosjidis, 1982). If pigmented, it can have white or colored (purple anthocyanin) pigments. It then gives the main color of the seed, provided the epidermis is not completely pigmented. The third layer (armor layer) can have dark brownish-black or white pigments (Putt, 1944). This layer contributes to the color of the seed only if the two first layers are free of pigments.

For example, white seed with black stripes is the consequence of the presence of a white pigmented hypodermis with black pigments in the stripes of the epidermis. Gray seed with black stripes is the result of a black armor layer, an unpigmented hypodermis (Putt, 1940) and black stripes of the epidermis.

Sunflower oil

Oil percentage

The oil percentage in the seed can be partitioned into kernel oil percentage, kernel weight percentage, and the hull components:

Seed Oil %=[Kernel % x Kernel oil % + Hull % x Hull Oil %]/100

The components are defined as follows:

Kernel %=[Kernel weight / total seed weight] x 100
Hull %=[Hull weight / total seed weight] x 100=100 - Kernel %
Kernel oil %=[Kernel oil weight / total kernel weight] x 100
Hull oil %=[hull oil weight / total hull weight] x 100

Most of the oil in the sunflower seed is located in the kernel. The kernel weight percentage, kernel oil percentage, and hull oil percentage vary from 48 to 84%, 40 to 70%, and 1.6 to 6% respectively (Vranceanu, 1977). The seed oil percentage in commercial sunflower hybrids varies from 35% to 56%.

In early studies oil percentage was measured by chemical methods (Soxhlet). Nuclear Magnetic Resonance (NMR) analyzers are now being used for this purpose. The principle of nuclear magnetic resonance consists of the capacity of a material to absorb energy of a certain frequency when located in a magnetic field (Vranceanu, 1977). The analyzer is calibrated with 10 grams of pure oil and then 10 gram samples of seed are put into the magnetic field for oil percentage determination. The oil value (percentage) is directly read in the analyzer. NMR allows breeders to determine quickly oil quantity with high precision (±0.1 points of oil percentage; Fick, 1974) without destroying the seed.

Oil composition

Sunflower oil is characterized, as compared with other crops, by its high concentration (90%) of polyunsaturated fatty acids (Table 2). Linoleic acid (18:2) is more abundant than oleic acid (18:1) in the normal cultivated sunflower. Saturated fatty acids are present in a lower proportion and consist basically of palmitic (16:0) and stearic (18:0) acids. Skoric (1988) reported that linoleic acid percentage in the seed varies from 55% to 65% while oleic ranges from 20% to 30%. Oil with a high concentration of linoleic acid is

Table 2. Fatty acid composition of selected oilseeds (Dorrel G.D. 1978)

	FATTY ACID									
CROP	12:0	14:0	16:0	18:0	20:0	18:1	18:2	18:3	20:1	22:1	Other
	%										
Sunflower			7	4		17	72				
Coconut	44	18	11	6		7	2				12
Corn			12	2		29	56	1			
Cottonseed		1	29	4		24	40				2
Olive			14	2		64	16	2			2
Palm		1	48	4		38	9				
Peanut			6	5	2	61	22				4
Rapeseed			4	2		17	13	9	15	41	
Safflower			7	2		13	78				
Soybean			11	4		25	51	9			

desired for salad oil and margarine industries. High oleic types are preferred for cooking and frying because the higher degree of saturation minimizes oxidative changes during frying. Also high oleic types can be heated to a higher temperature(Miller, 1987). The ratio of these two components (linoleic and oleic) of the oil depends on the genotype and the environmental conditions during crop production. In warmer environments, the percentage of oleic acid increases and the percentage of linoleic acid decreases (Miller, 1987).

Oil accumulation and synthesis

Oil accumulation in the seed begins when the embryo starts growing and finishes at physiological maturity. Oil percentage in the seed reaches its maximum value before physiological maturity (Gambhir *et al.*, 1981; Pozzi, 1986; Vranceanu, 1977). Despite the lower oil percentage at physiological maturity, the total amount of oil is higher due to the increase in the seed weight (Ruskovskii, 1935; Popov, 1955; Dubleanskaia, 1957, 1960, 1966; cited by Vranceanu, 1977).

The oil percentage in the seed not only depends on the cultivar but also on the production environment. Skoric (1988) reported that mean daily temperature, soil moisture at seed filling, and the duration of seed filling influence oil percentage. On the other hand, when studying the dynamics of oil accumulation in 8 hybrids Pozzi (1986) found little difference in the duration of the filling stage. However, he reported high differences in the oil accumulation rate. The accumulation followed a square regression function. Vranceanu (1977) also reported a high influence of temperature and water during oil synthesis.

Fatty acids are synthesized from simple sugars. The pathway has acetic aldehyde as an intermediate product. Two molecules of acetic aldehyde are needed to produce crotonic aldehyde.

$$2\ CH_3.CHO \xrightarrow{\hspace{4em}} CH_3CHOH.CH_3CHO + H_2O$$

acetic aldehyde crotonic aldehyde

The reaction of acetic aldehyde with water released by the reaction above forms sorbinic aldehyde.

$$\text{acetic aldehyde} + H_2O \xrightarrow{\hspace{3em}} \text{Sorbinic aldehyde}$$

The union of 3 molecules of the latter produces the aldehydes responsible for the synthesis of the stearic, oleic and linoleic acids.

This model is supported by the presence of acetic aldehyde both in sunflower leaves and flower parts. Furthermore, it is thought that oil synthesis can already start in the leaves, as acetic aldehyde is quickly transformed in those organs into small fatty acids, which are volatile and soluble both in water and in the cytoplasm. These small molecules are transported to the seeds, where they are converted into longer fatty acids by the action of enzyme complexes, especially lipase (Sarapov 1959; cited by Vranceanu, 1977).

Genetics

Seed hypodermis color

Genetic studies in pigmented hypodermis showed that purple anthocyanin pigments seem to be dominant over white pigments. A dominant gene *T* (Sazyperow, 1944; cited by Leclercq, 1966) or a major dominant gene and two modifiers (Mosjidis, 1982) seem to control the genetics of color in pigmented hypodermis. Leclercq (1979) reported a single dominant gene (*Gb*) controlling the seed color but it was not specified in his report which layer was being studied. It is generally accepted among sunflower breeders that white seed has lower oil percentage than black/gray seed (Stoenescu, personal communication). However reports showing relation between seed color and oil percentage could not be located.

Oil percentage

Because sunflower seed oil percentage is considered a quantitative trait, knowledge of the *heritability, genetic effects, heterosis, maternal effects, as well as understanding the relationships with other traits of agronomic interest* are very useful tools to define the breeding strategy for improving this trait.

Heritability

Basically, two methods have been used to measure the heritability of seed oil percentage in sunflower. One method uses F2 populations, F1, both parents and backcrosses of the F1 to both parents (Martinez, 1979; Fick, 1975). The second method used to estimate *narrow sense heritability* (portion of the genetic variance that can be transmitted to the next generation) was through the parent-offspring regression of the F3 families and their F2 plants. A relatively high heritability for oil percentage in the whole seed was found by Fick (1975). Broad sense heritability was 0.72, and narrow sense was 0.61 when the F2 population and backcrosses were used. Based on parent-offspring regression, the value was 0.52 for narrow sense heritability. Martinez *et al.* (1974), working with F2 populations and backcrosses of the F1 to the recurrent parents, found a value of 0.63 for broad sense heritability and 0.52 for narrow sense heritability. These results are similar to those obtained by Fick (1975). Due to the relatively high heritability of this trait, selection in early generations of the breeding process can effectively improve oil percentage in sunflower seed.

Gene action

Gupta *et al.* (1982) working with two F2 populations and the reciprocal backcrosses indicated the presence of highly significant additive effects, significant dominant effects for one cross, and highly significant interactions for both populations. In this case the genetic effects were estimated by the method of Hayman (1958). Estimates of General Combining Ability (GCA) and Specific Combining Ability (SCA) were compared by Bedov (1985) and Areco (1985) to determine the importance of additive effects for oil percentage. GCA represents the importance of additive effects and additive x additive interaction. On the other hand, SCA is an estimator of non-additive effects (Falconer, 1981). When studying combining ability for oil and protein percentage in sunflower seed, Bedov (1985) found high heterotic effects for oil percentage in the seed, by means of a diallel cross of 11 parents showing a wide range in oil percentage (from 25.55% to 50.57%). The ratio of General Combining ability (GCA) to Specific Combining Ability (SCA), 19.09, indicated additive effects were primarily involved in the control of oil percentage. Areco *et al.* (1985) evaluated diallel of six varieties and reported a GCA/SCA ratio of 3.77. This suggests additive effects are more important than non-additive effects in the expression of oil percentage.

Refoyo *et al.* (1986) studied oil percentage in seed and the partition of oil percentage in kernel and kernel percentage in the seed, using 35 single cross hybrids (7 Cms lines x 5 restorer lines) in 2 experiments (with and without irrigation). Significant additive effects were reported for the three traits in both environments. Dominant effects for oil percentage in seed and in the kernel only in the experiment with irrigation.

These results strongly indicated that large additive effects control oil percentage in the whole seed. However, some non-additive effects have been reported for this trait. Russell (1953) reported different results saying that "dominant and or complementary effects could determine oil percentage". As usual, these types of genetic estimates depend upon population, parents, and possibly the environment.

Heterosis

Since most sunflower cultivars are hybrids, it is important to evaluate the genetic control of seed oil percentage in hybrids, as well as the relationship between oil percentage in the inbred progeny and hybrid progeny. Many researchers have studied oil percentage in F1 hybrids (F2 seed) and their parents. Their results vary considerably depending on the parents used and the testing environment.

Fick (1975) reported dominant effects for oil percentage (i.e., higher than the mean of the parents) in F1 plants of the cross P-21 (39.5%) x Mena RR-18-1 (27.7%). Reciprocal crosses showed different values for oil percentage: 38.2%

when P-21 was used as female and 34.7% when Mena was used as female. Comparing the mean of 6 hybrids (F1) with the mean of their 12 parents, Dedio (1982) found heterotic effects for seed oil percentage (+9%), kernel oil percentage (+6%) and kernel percentage in the seed (+3%). In Bedov (1985), the oil percentage of the F1 was superior to the oil percentage of the best parent (overdominance) in most cases. However, when one of the parents had high oil percentage the number of crosses exhibiting overdominance decreased. For example, overdominance was not observed for any crosses involving the parent with the highest oil percentage (L-11; 50.57%). On the other hand, in all the crosses involving the parents with the lowest oil percentage (25.55%) overdominant effects were present except in the cross with L-11.

In summary, a wide range of results have been reported by many authors. Gene action for oil percentage in F1 hybrids goes from dominance for low oil percentage to overdominance for high oil percentage.

When studying the relationship of different traits between F3, F4, F5, F6 lines and the expression of those traits in hybrids, Miller *et al.* (1982) found a high correlation between F4, F5, and F6 generations for oil percentage, and a high correlation between oil percentage in F4 families and oil percentage in the hybrids of those families with a tester. These results suggest again a relatively high heritability for this trait, and the effectiveness of improving the trait during inbreeding.

Oil percentage and other traits

Since the oil percentage in hybrid progeny depends on the oil percentage in the inbred parents understanding the relationships between seed oil percentage with other seed characteristics in the inbred progeny (kernel %, kernel oil percentage, etc.) is very useful for determining a strategy for modifying these traits.

Putt (1943) found a significant positive correlation between oil percentage in the whole seed and kernel percentage in the seed. Also a negative correlation was found between kernel percentage and seed size. Russell (1953) working with 62 inbreds from 12 different populations found a positive correlation between oil percentage with kernel percentage and seed weight per bushel. However, a negative correlation between oil percentage and weight of 1000 seeds was found. The tendency of higher oil percentage in smaller seed found by Putt (1943) and Russell (1953) was also reported by Fick (1974).

Marinkovic (1992) studying oil yield in hybrids and lines reported positive correlations among oil percentage in seed with number of seeds per head, weight of 1000 seeds, test weight, kernel percentage, and seed yield per plant. In addition, path-coefficient analysis determined that weight of

1000 seeds and number of flowers per head were the most important traits for determining hybrid seed yield. Marinkovic's results suggested that both components of yield (number of seeds and seed weight) could be important in the seed yield per area unit. Since seed weight has been negatively correlated with oil percentage in previous reports, selection only for oil percentage in early generations of the inbreeding process could reduce seed size and seed yield. Therefore no increase in oil yield per area unit (principal goal) may be obtained.

Maternal effect

Maternal effects in the oil percentage of seed have been studied by two authors (Pawlowski, 1964; and Thompson *et al.* (1979). Reciprocal crosses between high and low oil percentage genotypes were done by Pawlowski (1964). The oil percentage in the F1 kernel (produced on the female parent plant) largely depended on the oil percentage of the female *per se*. Thompson *et al.* (1979) conducted a diallel cross of two oilseed lines and two non-oilseed (Confectionery) and did not detect pollen effects for oil percentage or kernel percentage.

The available data suggest pollen source has little or no effect on oil percentage, but a high maternal effect is evident. Oil percentage seems to be determined largely by the genotype of the female plant producing the seed rather than the genotype of the embryo.

Molecular markers

Further understanding of correlations between quantitative traits, as well as the quantitative traits *per se* may depend upon additional knowledge of gene number, location, gene effects, and gene action. These kind of issues, and many others, have focused the attention of many researchers on the uses of molecular markers. Molecular markers have started being used in plant breeding programs to detect Quantitative Trait Loci (QTL) linked to them.

Working with isozyme markers, Edwards *et al.* (1987) found several significant associations between those markers and QTL in maize. Two F2 populations represented by 1700-1900 individuals and 15 to 18 marker loci were used in this experiment. A different number of genes were correlated (single-factor ANOVA) with the expression of one or more of each of the 82 quantitative traits. Different types of gene action were found for QTLs controlling one or more traits. The proportion of phenotypic variation was explained by individual and cumulative markers. The correlation between the variance of a trait and the level of homozygosity or heterozygosity at each marker locus, as well as the effect of percentage of heterozygosity in individual plants and the expression of a trait were also reported.

The advent of restriction fragment length polymorphisms (RFLPs) as genetic markers has seen the rapid development of linkage maps for a number of important crop species including maize (Helentjaris, 1987), rice (McCouch *et al.*, 1988), common beans (Vallejos *et al.*, 1992), tomato and potato (Tanksley *et al.*, 1992). The ubiquity of these markers in plant genomes has enabled the construction of highly saturated maps allowing the analysis of complex quantitative traits.

The first report of using an RFLP linkage map to investigate quantitative traits was done in tomato by Paterson *et al.* (1988). They used a population of 237 BC1F1 plants to measure the traits (fruit mass, Ph, and solubles solids concentration) and to score 68 marker loci (63 RFLP+5 isozyme) to map the QTLs. Using interval mapping (maximum likelihood method) it was found 4 and 6 QTLs controlling each of the quantitative traits. In later studies, with the same species and traits, Paterson *et al.* (1991) again found different numbers of QTL measured on F2 plants and their F3 families in different environments. The number of QTL and the gene effects varied and depended on the population (F2 or F3) and the environment. The high frequency of closely located QTL affecting different traits, suggested the possibility of pleiotropic effects for some linkages. Few cases of epistasis were reported. Genetic linkage analysis was done by Edwards *et al.* (1992) using RFLP and isozyme markers with one of the two maize populations previously used in the study with isozyme markers. Despite the smaller population size, the higher number of marker loci allowed identification of the same genomic factors for the traits. Due to the smaller distance between marker loci the amounts of phenotypic variation explained by the marker loci (R^2) were higher.

Research to localize QTL for oil percentage linked to RFLP markers have been conducted by Diers *et al.* (1992). The study was done using 252 markers (243 of which were RFLP markers) in a F2:3 population (60 families) derived from a cross of high oil (*G. max*) and low oil (*G. soja*) percentage lines. One major genetic factor explaining 43% of the variation was located in one of the 31 linkage groups. Alleles coming from *G. max* at significant loci were always increasing the mean value of the trait.

Contrary to the crops mentioned before, cultivated sunflower does not posses a classical linkage map and only few studies have been conducted using molecular markers. Crouzillat *et al.* (1991) studied the relation between the restoration of 16 sunflower cytoplasm and RFLPs of mitochondrial DNA. Studying the mitochondrial DNA with 12 probes and three restriction enzymes they found 12 patterns of restoration and 13 cytotypes. Different degrees of restoration corresponded to specific restriction fragment patterns. Choumane and Heizmann (1988) reported that repeat length heterogeneity and restriction polymorphism of rDNA were characteristic the 61 ecotypes and 39 species of Helianthus.

Using an rDNA probe Kauter *et al.* (1991) demonstrated the utility of RFLPs for identifying interspecific crosses between cultivated sunflower and *Helianthus resinosus*. Recently Berry *et al.* (in review), using low copy genomic probes to fingerprint inbred lines, has revealed the presence of RFLPs among inbred lines of cultivated sunflower. Due to this fact and that sunflower is a diploid crop species (2n=2x=34) with inbred lines and suitable segregating populations he suggested that it should be extremely amenable to RFLP analysis.

Research Objectives

Although some research was done using molecular markers in sunflower, no RFLP linkage map has been published and no work has been reported using RFLPs for analysis of quantitative traits. The primary objective of this project was to identify RFLP markers linked to genes affecting oil percentage in the seed and in its components (Paper II of this thesis) and seed hypodermis color (Paper III of this thesis). To achieve these objectives an RFLP linkage map was constructed (Paper I of this thesis).

The results of this research may be useful not only as a source of basic information but also for practical breeding. Basic information about gene number, gene action, and correlations among seed components and oil percentage would be useful in conventional breeding programs. Knowledge of markers linked with oil percentage would be useful in backcross programs to introduce genes for high oil percentage into lines with low oil percentage but high seed yield in specific hybrid combinations.

PAPER I. CONSTRUCTION OF AN RFLP MAP FOR CULTIVATED SUNFLOWER

ABSTRACT

A detailed linkage map of *Helianthus annuus* was constructed based on the segregation of 234 RFLP loci, detected by 213 probes, in an F_2 population of 289 individuals (derived from a cross between the inbred lines HA89 and ZENB8). The genetic markers covered 1380 centiMorgans (cM) of the sunflower genome and were arranged in 17 linkage groups, corresponding to the haploid number of chromosomes in this species. One locus was found to be unlinked. Although the average interval size was 5.9 cM, there were a number of regions larger than 20 cM that were devoid of markers. Genotypic classes at twenty-three loci deviated significantly from the expected ratios (1:2:1 or 3:1) all showing a reduction in the ZENB8 homozygous class. The majority of these loci were found to map to four regions on linkage groups G, L and P.

INTRODUCTION

The advent of restriction fragment length polymorphisms (RFLPs) as genetic markers (Botstein *et al.*, 1980) has enabled the rapid development of linkage maps for a number of important crop species including maize (Helentjaris 1987), rice (McCouch *et al.*, 1988), wheat (Liu and Tsunewaki 1991), barley (Heun *et al.*, 1991), potato (Gebhardt *et al.*, 1989), soybean (Shoemaker *et al.*, 1992), *Phaseolus vulgaris* (Vallejos *et al.*, 1992) and *Brassica napus* (Landry *et al.*, 1991). The ubiquitous distribution of these markers in plant genomes has enabled the construction of highly saturated maps allowing the analysis of complex quantitative traits in species such as tomato (Paterson *et al.*, 1988), maize (Edwards *et al.*, 1987) and soybean (Diers *et al.*, 1992).

Cultivated sunflower is a diploid species (2n=2x=34) and is second only to soybean in its importance as an annual oilseed crop. However the genetics of only a small number of traits have been studied in detail (Miller 1992). As a consequence of this sunflower does not possess a classical genetic map. The only linkage reported to date is that between the nuclear genetic male sterility (GMS) gene and the *T* gene coding for anthocyanin pigmentation in the plant (Leclerq 1966). In addition the use of molecular markers in sunflower has only focused on the identification of interspecific crosses (Krauter *et al.*, 1991) and the taxonomy of the genus *Helianthus* (Choumane and Heizmann 1988;

Gentzbittel *et al.*, 1992). A recent fingerprinting study of elite inbred lines has shown that there are high levels of restriction fragment length polymorphism in cultivated sunflower (Berry *et al.*, in review). This and the fact that sunflower is a diploid with developed inbred lines and suitable segregating populations suggests that it should be extremely amenable to RFLP mapping.

In this paper we describe the construction of an RFLP map for sunflower which will be used to identify QTL affecting seed oil content and other agronomic traits.

MATERIALS AND METHODS

The general molecular biology methods followed are those described by Sambrook *et al.* (1989).

Plant Material

An F2 population (289 individuals) was made by selfing a single F_1 of the proprietary inbred line ZENB8 crossed to the public line HA89 (USDA). The F_2 population thus produced was also segregating for traits such as seed color, seed oil content, seed length, days to flowering and head and stem diameter.

RFLP Probes

In total 361 cDNAs isolated from etiolated seedlings (coded with the prefix C) and 29 PstI genomic clones (coded with the prefix H) had been selected as low copy RFLP probes from the libraries described by Berry *et al.* (in review). These were screened against the two parental lines digested with one of five restriction enzymes (*Dra*I, *Eco*RI, *Eco*RV, *Hin*dIII and *Xba*I) to identify the polymorphic markers. Twenty-four of the RFLP probes mapped were obtained through GIE Cartisol, France.

DNA Isolation, Digestion and Southern Blotting

Three fully expanded leaves were cut from each F_2 plant and frozen on dry ice for transportation to the laboratory.

The leaf tissue was then lyophilized, ground to a fine powder in a mill and DNA extracted using a modified version of the protocol described by Rogers and Bendich (1985). The DNA was quantified fluorimetrically and digested to completion using 4 units of enzyme/microgramme according to the manufacturers instructions (Northumbria Biologicals Ltd.). Ten microgrammes of DNA/lane were loaded onto 1.0% TBE-agarose (Seakem) slab gels and electrophoresis performed overnight at 3 Volts/cm. The DNA was transferred onto Hybond-N membrane (Amersham) via Southern blotting with 20x SSC and fixed by baking for 2 hours at 80°C, followed by UV cross-linking at 60 mJ in a Stratalinker (Stratagene).

Hybridizations

Probe fragments were generated from recombinant plasmids using PCR and the products gel-purified prior to labelling with [α-^{32}P] dCTP (Amersham) via random priming (Feinberg and Vogelstein 1983). The unincorporated radioactivity was removed by spin-column chromatography using Sephadex G50 (Sigma). Hybridizations were performed at 60°C overnight using standard conditions and the excess probe removed by two, 30 minute washes in 0.5x SSC, 0.1% SDS at 60°C. Filters were exposed to XOMAT-AR X-ray film (Kodak) with two intensifying screens at -80°C. After autoradiography the radioactive probes were removed from the filters by two 20 minute washes in 0.1x SSC, 0.5% SDS at 80°C.

Linkage Analysis

Autoradiographs were independently scored twice and if conflicts in scoring arose and could not be resolved, the data were excluded from the analysis. If more than 5% of the RFLP scores for a given locus were missing, the hybridization was repeated. The segregation of the alleles at each locus was checked against the expected ratios for codominant (1:2:1) and dominant (3:1) markers using the Chi-squared test, with a significance level of 5%.

The genetic map was constructed using the MAPMAKER computer program version 3.0 (Lander *et al.*, 1987). Initially a two point linkage analysis was conducted to determine the maximum likelihood recombination fraction and the LOD score for each of the possible pairs of loci. Linkage groups were formed using the "group" command on the two point data with recombination values less than 0.35 and a constant LOD score of 3.0.

Three point linkage analyses were conducted for the loci within each group and these data used in conjunction with the "order" command. The "order" function tries to find a subset of five informative loci to start building the linkage group; however this starting point is random and different orderings of loci can be found for the same group. Therefore the "order" function was repeated several times for each group to try and find the one containing the largest number of loci. These orders were then tested using the multipoint function "ripple" and the loci whose positions were ambiguous (*i.e.* those placed automatically at a LOD of 2.0) were noted.

Loci which had been excluded on the basis of the three point linkage data were placed using the "try" command and initially unlinked loci were mapped using the "near" command by increasing the recombination default to 0.50. The Kosambi function was used to obtain the centiMorgan (cM) values (Kosambi 1944).

Multiple loci detected by a single probe were coded with the probe number plus the suffix A, B, C or D etc. to indicate each duplicate locus.

RESULTS

Probe Selection and Segregation

From the three hundred and ninety RFLP clones screened against the parental inbred lines, two hundred and thirteen (55%) detected polymorphism. The majority of these were revealed in digestions with the restriction enzymes *Eco*RI or *Eco*RV (Table 1). In general, probe/enzyme combinations were chosen on the basis of their ability to reveal clear and simple polymorphism in order to make the interpretation of the RFLP data more reliable. In total the 213 polymorphic probes detected 235 loci, with only 25 of these scored as dominant markers (3:1).

Twenty-three loci (indicated by an asterisk (*) in Figure 1) showed distorted segregation ratios ($P<0.05$) all with a reduction in the ZENB8 homozygous class (Table 2). Eighteen of these loci mapped to four regions on linkage groups G, L and P. Taking into account only the codominant markers within these regions, the HA89 and ZENB8 allele frequencies were 54% and 45%, respectively. In comparison, the allele frequency across the genome as a whole was 51% and 49% for HA89 and ZENB8, respectively.

Description of the Map

Analysis of the segregation data using MAPMAKER revealed that 234 loci were arranged in 17 linkage groups (Figure 1), covering 1380 cM of the sunflower genome (Table 3). One locus

(C0592) segregated independently. The distribution of marker loci between the different linkage groups is shown in Table 3. Linkage groups F and Q have the lowest number of mapped loci. The average map interval was 5.9 cM, however there were 11 regions on 10 linkage groups which were greater than 20 cM. In general the probes that detected duplicated regions hybridized to two unlinked loci (Table 4); however two probes H2045 and C0463 revealed loci on six different linkage groups.

The best order of markers on each linkage group (*i.e.* the one which gave the highest LOD score) is given in Figure 1; however these orders are not unequivocal. Loci whose positions are uncertain are shown in square brackets on the map because they were either placed at a LOD score of less than 3.0 or were excluded by the three-point linkage data.

DISCUSSION

We report here a genetic linkage map for *H. annuus*, comprising 234 loci organized into 17 linkage groups (Figure 1) which probably correspond to the 17 haploid chromosomes of cultivated sunflower. The letter identifying each linkage group is completely arbitrary as no classical genetic map exists for sunflower. The coverage of 1380 cM probably represents 60-80% of the sunflower genome, based on comparisons with a RAPD map constructed for *H. anomalus* (an interspecific hybrid between *H. annuus* and *H. petiolaris*) which covers 2338 cM (Reisberg *et al.*, 1993) and our other maps (unpublished data). The distribution of markers between the 17 groups is fairly uniform (Table 3) with, in general, the largest groups containing the most markers. The differences between the overall lengths of the linkage groups (*e.g.* group G is 2.5 times bigger than group D) may be related to chromosome size differences as is the case in tomato (Bernatzky and Tanksley 1986) or be a factor of the incomplete sampling of the genome. Although the majority of loci are well dispersed (average interval of 5.9 cM), there are 11 regions where the distance between pairs of adjacent markers exceeds 20 cM. Similar "gaps" have been reported in most plant RFLP maps *e.g. Brassica rapa* (Song *et al.*, 1991) and barley (Graner *et al.*, 1991) and they probably represent highly recombinogenic regions of the genome or reflect an under-representation of clones from these areas in the libraries, used as probe sources.

The majority of mapped loci were scored as codominant markers and followed the expected 1:2:1 segregation ratio in the F_2 population. However there were a number of loci that showed distorted segregation (Table 2) and these were found to be localized to 4 chromosomal regions on linkage groups G, L and P (Figure 1). Similar findings have also been reported in the RFLP maps of *Brassica napus* (Landry *et al.*, 1991), lettuce (Landry *et al.*, 1987), rice (McCouch *et al.*, 1988) and *Phaseolus vulgaris* (Nodari *et al.*, 1993) among others and this distortion is thought to be due to the presence of deleterious alleles in these regions. In this study the distorted segregation was always due to a reduction in the ZENB8 homozygous class, but in the F_2 populations cited above there were genomic regions showing reductions in both homozygous classes. This suggests that there was selection against the ZENB8 genome between the selfing of the F_1 and the flowering of the F_2, when the leaf tissue was harvested. Skewed distributions largely towards one homozygote have only been reported in interspecific crosses of tomato (Bernatzky and Tanksley 1986) and lentil (Havey and Muehlbauer 1989) and in barley double haploids due to variation in tissue culture response (Graner *et al.*, 1991).

The sunflower RFLP map reported here is being supplemented using mapping data from other F_2 populations, but there is still a continuing need for more RFLP markers. The use of cDNA clones as the primary source of probes will enable the saturation of the most important areas of the sunflower genome (*i.e.* genic regions) and allow the dissection of quantitative traits into their component Mendelian factors.

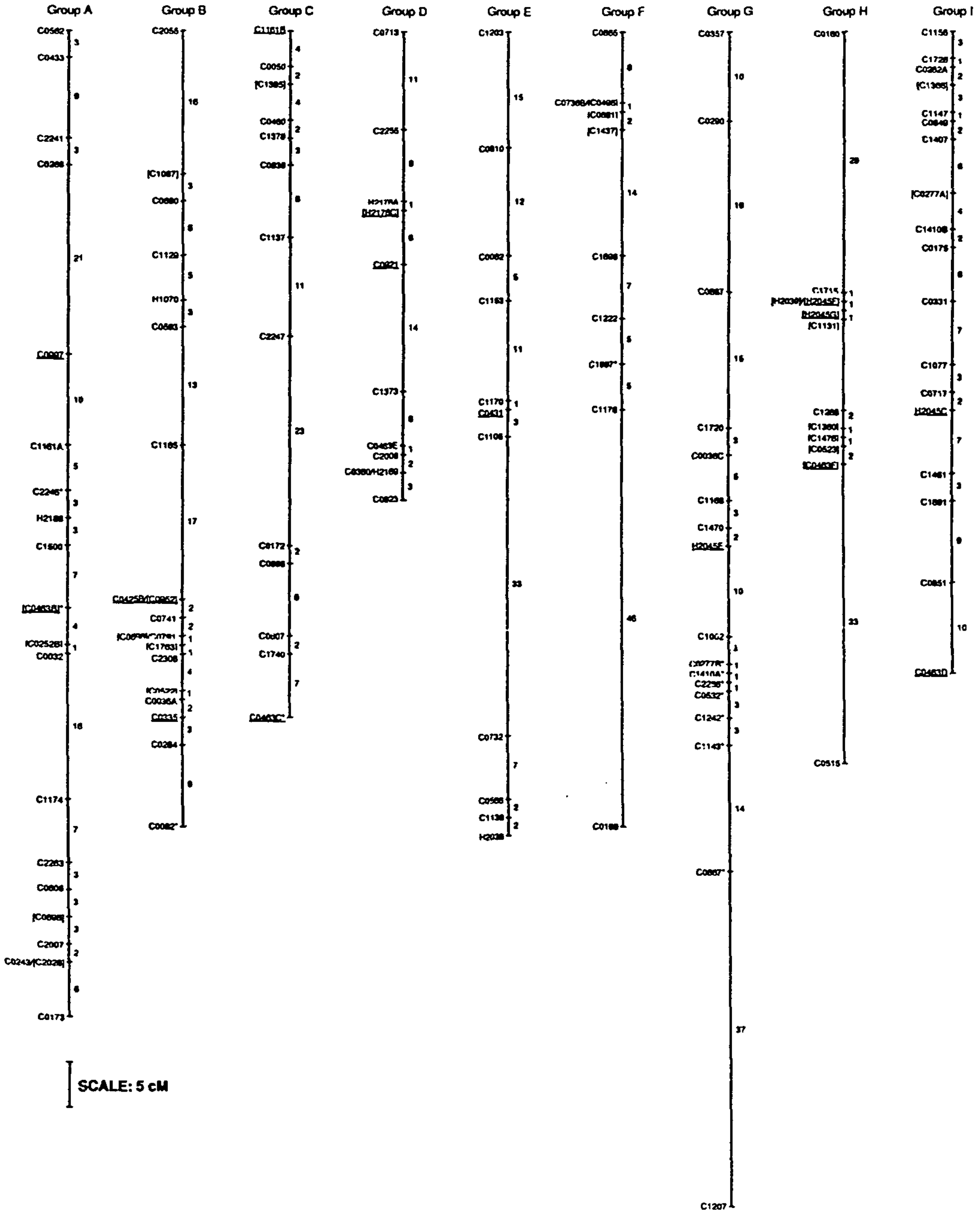

Figure 1. Sunflower RFLP linkage map of 234 loci identified by 213 probes. The seventeen linkage groups are listed at the top, the loci listed on the left and the map distances in centiMorgans (cM) on the right. The nomenclature of the RFLP loci is described in "Materials and Methods". Loci mapped as dominant markers are underlined and those deviating from the expected Mendelian segregation ratios (P<0.05) are indicated with *. The loci with uncertain map positions are indicated by square brackets.

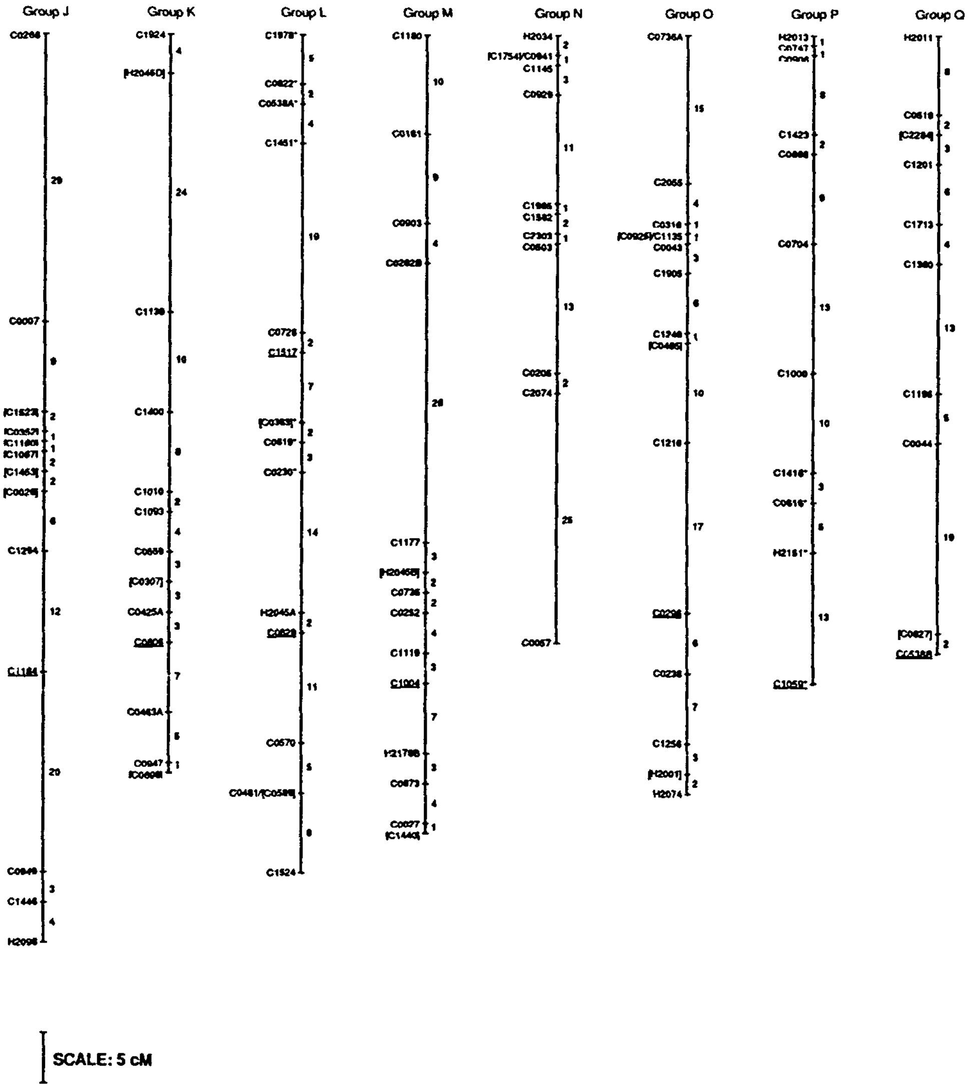

Figure 1. Continued

Table 1. Numbers of probes mapped in conjunction with the five restriction enzymes

Enzyme	*Eco*RV	*Eco*RI	*Hin*dIII	*Dra*I	*Xba*I	Total
No. of probes	92	89	22	8	2	213

Table 2. Loci showing distorted segregation ($p<0.05$) from the expected ratios of 1:2:1 or 3:1 (A=HA89 homozygous class, H=heterozygous class, and B=ZENB8 homozygous class)

Locus	Group	A	H	B	χ^2
C0277B	G	81	147	52	6.71
C1410A		80	155	50	8.51
C2286		82	152	51	8.01
C0532		80	155	52	7.31
C1242		75	161	49	9.55
C1143		82	150	49	9.04
C0667		74	157	48	9.24
C1978	L(1)	72	159	48	9.58
C0822		72	153	48	8.21
C0538A		73	157	51	7.32
C1451		65	161	52	8.18
C0383	(2)	88	141	50	10.38
C0619		88	145	51	9.77
C0230		86	139	55	6.88
C1418	P	70	159	46	10.91
C0616		71	161	51	8.20
H2151		67	164	54	7.67
C1059		61	172	53	12.21
C2246	A	67	153	53	6.12
C0463B		..	226	51	6.41
C0082	B	65	161	56	6.25
C0463C	C	97	181	..	14.51
C1997	F	63	152	50	7.02

Table 3. Size in centiMorgans and number of loci in each of the 17 linkage groups

Group	No. of loci	Size (cM)
A	20	109
B	19	88
C	13	76
D	11	52
E	11	90
F	10	88
G	17	129
H	12	83
I	18	71
J	13	90
K	13	74
L	15	81
N	12	62
O	15	76
P	11	65
Q	10	62
Total	234	1380

Table 4. Sunflower RFLP probes detecting multiple loci

Probe	No. of loci	Groups
C0036	2	B,G
C0252	2	A,M
C0277	2	G,I
C0282	2	I,M
C0425	2	B,K
C0463	6	A,C,D,I,H,K
C0538	2	L,Q
C0736	2	F,O
C1161	2	A,C
C1410	2	G,I
H2045	7	G,H,I,K,L,M
H2178	3	D,M

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PAPER II. USE OF RFLP MARKERS FOR GENETIC LINKAGE ANALYSIS OF OIL PERCENTAGE IN SUNFLOWER

ABSTRACT

Increased seed oil percentage is an important objective when breeding for high oil yield in sunflower. Although some researchers have investigated the genetics and heritability of sunflower oil percentage, most analyses were conducted on the oil percentage in the whole seed through conventional breeding and biometric procedures. The primary objective of this research was to identify restriction fragment length polymorphisms (RFLPs) linked to quantitative trait loci (QTL) affecting oil percentage in the whole seed, kernel oil percentage and kernel percentage. An F_2 population consisting of 289 individuals was produced by crossing two inbred lines that differ for the traits. RFLP and trait data were obtained directly from self-pollinated F_2 plants. RFLP markers (identifying 201 loci) located six regions representing 57% of the genetic variation of seed oil percentage. Two of these regions were associated with kernel oil percentage, two with kernel percentage and two with both components. Additive gene action was predominant for seed oil percentage and its components.

INTRODUCTION

Sunflower Oil

Most cultivated sunflower is grown as a source of oil. Thus, one of the principal goals of sunflower breeding programs is the development of F_1 hybrid cultivars with high oil yield (Skoric, 1988). Sunflower oil yield per unit area is determined by the product of seed yield per unit area and oil percentage in the seed. Thus, consideration of both components of oil yield per unit area is important when breeding for oil percentage.

The oil percentage in the seed is a function of kernel oil percentage, kernel weight percentage, and the hull components (Seed Oil %= [Kernel % x Kernel oil % + Hull % x Hull Oil %] / 100). Kernel oil percentage, kernel weight percentage and hull oil percentage vary from 40 to 70%, 48 to 78%, and 1.6 to 6% respectively (Vranceanu, 1977). Seed oil percentage is largely determined by the genotype of the maternal parent (Pawlowski, 1964; and Thompson *et al.*, 1979). Kernel oil percentage seems to have more influence on the expression of seed oil percentage than does kernel percentage, and there appears to be no genetic linkage between these two components (Dedio, 1982). Improvement of seed oil percentage in the hybrid progeny has been achieved by increasing seed oil percentage in the inbred progeny (Miller, 1982). This improvement from previous breeding has been accomplished by a reduction of the hull percentage (or increase of kernel percentage) and to a lesser extent by an increase of the kernel oil percentage (Gundaev, 1971; cited by Fick, 1978).

Biometric and Quantitative Genetic Studies of Seed Oil Percentage

Seed oil percentage has relatively high broad sense heritability (0.6-0.7) and high narrow sense heritability (0.5-0.6) on a single plant basis (Martinez *et al.*, 1979; Fick, 1975). The number of factors controlling seed oil percentage or its components has not been reported, however some research has been done to study gene action involved in the expression of the traits. Highly significant additive, dominant, and epistatic effects were determined for seed oil percentage using two F_2 populations and their reciprocal backcrosses (Gupta *et al.*, 1982). Estimates of General (GCA) and Specific Combining Ability (SCA) (Bedov, 1985; Areco *et al.*, 1985) indicated additive effects were more important for seed oil percentage. Significant additive effects were also reported for seed oil, kernel oil, and kernel percentages, although significant dominant effects for seed oil percentage and kernel percentage were detected in irrigated conditions (Refoyo *et al.*, 1986). Additive effects have been reported for hull percentage (Vranceanu and Stoenescu, 1969; cited by Fick, 1978). Dominant and complementary effects for seed oil percentage were suggested by Russell (1953), and dominant effects for kernel oil percentage by Vranceanu and Stoenescu

(1969; cited by Fick, 1978). These results indicate that additive effects predominantly influence oil percentage in the whole seed and its components; however, some non-additive effects also seem to affect these traits.

Molecular Markers

The difficulty in understanding the genetic basis of traits may be due to the lack of knowledge about gene number, location, gene action and effects. This situation has focused the attention on the use of molecular markers to detect linkage with quantitative trait loci (QTL). Restriction fragment length polymorphisms (RFLPs) have been used for developing genetic maps and the detection of QTL in tomato (Paterson *et al.*, 1988), corn (Edwards *et al.*, 1992), and soybean (Diers *et al.*, 1992), among others.

Few studies have been conducted using molecular markers in sunflower. RFLPs have been used to study the relation between the restoration of sunflower male sterile cytoplasms and RFLPs of mitochondrial DNA (Crouzillat *et al.*, 1991), for taxonomic studies of the genus *Helianthus* (Choumane and Heizmann, 1988), and to identify interspecific crosses between cultivated sunflower and *Helianthus resinosus* (Krauter *et al.*, 1991). Recently, nuclear RFLPs have been reported among elite inbred lines of *Helianthus annuus* (Berry *et al.*, in review a).

Linkage between genetic factors and RFLPs have not been reported in sunflower. The primary objective of this project is to identify RFLPs linked to QTL affecting oil percentage in the seed and its components, kernel oil percentage and kernel percentage. The results of this research may be useful not only as a source of basic information but also for practical breeding. Basic information about gene number, gene action, and genetic correlations between seed components and oil percentage would be useful in conventional breeding programs. Knowledge of RFLPs linked to oil percentage genes would be useful in backcross programs to introduce DNA regions for high oil percentage into lines with low oil percentage but high seed yield in specific hybrid combinations.

MATERIALS AND METHODS

Germplasm and Field Design

An F_2 population was used to carry out the experiment. A cross between inbred lines ZENB8 and HA89 was made in 1990 at Venado Tuerto (Argentina) and a single F_1 plant was self-pollinated the following year in the same location. ZENB8 is a proprietary inbred line derived from a cross between two Argentine populations and maintained through more than 10 generations of self-pollination. HA89 is a line released by the USDA in Fargo, N.D. ZENB8 has 33, 43, and 59% of seed oil, kernel oil, and kernel percentage, respectively. HA89 has 49, 56, and 77% of seed oil, kernel oil, and kernel percentage, respectively. Both parents have normal cytoplasm and nonrestorer genes (B lines) for Leclercq's cytoplasm.

Three hundred and forty F_2 plants were planted in rows at Fargo,ND on May 14th 1992. Two seeds per hill were sown with a hand planter and thinned to one plant per hill. The space between rows was 75 cm and the distance between hills was 30 cm. Five rows of each parent and the F_1 were planted at different periods (-10, -5, 0, +5, +12 days relative to the F_2 planting date), to estimate the within row error variance. Before anthesis, heads were covered with pollination bags to ensure self-pollination.

RFLP Data Collection

Three leaves of each of 289 F_2 plants were collected in containers with dry ice and frozen at -70 °C. Samples were lyophilized, and ground to a fine powder with a cyclone mill. DNA was extracted, quantified and digested with a restriction enzyme (*Eco*RI, *Eco*RV, *Hind*III, *Dra*I, or *Xba*I). Electrophoresis was conducted with TBE-agarose (Seakem) slab gels. DNA was transferred onto Hybond-N membrane (Amershan) via Southern blotting. Blots were briefly exposed to ultraviolet light. Low copy probes were prepared from cDNA (coded with the prefix C) and *Pst*I genomic clones (coded with the prefix H) as described in Berry *et al.* (in review b). Hybridizations were conducted using the conditions described in Sambrook *et al.* (1989). Filters were exposed to XOMAT-AR X-ray film (Kodak). Autoradiographs were independently scored twice. If conflicts in scoring arose and could not be resolved, the data were excluded from the analysis. A total of 198 probes (identifying 201 codominant loci) were used to locate QTL.

Evaluation of Seed oil and Its Components

The sunflower achene is a fruit consisting of a kernel (true seed) and a pericarp (hull). The kernel consists of an embryo, endosperm and a seed coat. The pericarp (maternal tissue) consists of several layers, cuticle (external layer), epidermis, hypodermis, phytomelanin layer, fibrose tissue, and finally parenchymal layers adjacent to the kernel (Nassanov, 1940; cited by Vranceanu, 1977). In the sunflower research community the word 'seed' is used synonymously with 'achene' and will be used so in this paper.

Three seed traits were evaluated. Seed oil percentage, and its partition in kernel oil and kernel percentage components were measured in a 10 g sample of F_3 seed of each F_2 plant. The partition and components are described as follows:

Seed Oil %=[Kernel % x Kernel oil % + Hull % x Hull Oil %]/100

where,
Kernel %=[Kernel weight / total seed weight] 100
Hull %=[Hull weight / total seed weight] 100=100 - Kernel %
Kernel oil %=[Kernel oil weight / total kernel weight] 100
Hull oil %=[hull oil weight / total hull weight] 100

The seed samples were dried at 35 °C for 8 hours to approximately 4% moisture before analyzing the seed oil percentage in a Nuclear Magnetic Resonance Analyzer (NMR). Then, samples were manually dehulled to measure the hull and kernel weight percentages. A five-gram sample of kernel was taken to measure kernel oil percentage.

Statistical Analysis

The analysis was divided in three major parts, analysis of phenotypic data, analysis of RFLP data, and combined analysis for the detection of QTL. Analyses were done with programs written in version 6.04 of SAS (SAS Institute Inc. 1982).

Phenotypic data

Row effects were tested with analyses of variance (ANOVA), considering rows as a source of variation (estimating phenotypic and within row variance plus among row variance), and plants within a row as an estimator of the phenotypic and within row variance. Significant row effects were not detected ($P>0.05$) for any trait in this trial.

Simple-Pearson phenotypic correlations between seed oil percentage and its components were calculated to estimate the relationship between traits (appendix 1). To estimate the total phenotypic variability due to genetic effects, broad sense heritabilities (h^2) were calculated according to Allard (1966). The within-row variance was estimated by pooling within-row variances of the parent and F_1 rows. The error variance among rows was estimated in the F_2 population. The genetic variation was then estimated subtracting the within and among variances from the phenotypic variance (appendix 2).

RFLP data analysis

The genetic map was constructed (Berry *et al.*, in review b) using the MAPMAKER computer program version 3.0 (Lander *et al.*, 1987). The genetic markers covered 1380 centiMorgans (cM; Kosambi function) and were arranged in 17 linkage groups, corresponding to the haploid number of chromosomes in this species. The average interval size was 5.9 cM. There were a number of regions larger than 20 cM that were devoid of markers. The segregation of alleles at each locus was checked against the expected ratios for an F_2 population (1:2:1 and 3:1; for codominant and dominant markers, respectively) using the Chi-square test with a significance level of 5%. Results showed that genotypic classes at 23 loci deviated significantly from the expected ratios. Those loci exhibited a reduction in the ZENB8 homozygous class. The majority of the loci (18/23) were found to map to four regions, representing linkage groups 'G', 'L' and 'P' (Berry *et al.*, in review b).

The genomic composition of each F_2 plant was determined from the frequencies of each genotypic class (homozygous ZENB8, heterozygous, homozygous HA89) across all loci. Frequencies of each class were the number of loci having each genotypic class divided by the total number of loci scored for each plant. The average genomic composition of the F_2 population was determined as the average value for each class across the population (appendix 3).

Detection of QTL

For each trait, single factor analyses of variance were conducted within marker-loci for the genotypic classes and their trait value (Edwards *et al.*, 1987). F-tests were used to determine if significant variation in trait expression was associated with the marker-locus genotypic classes. Significant F-values provide evidence of linkage between a QTL and a marker locus. For this research, evidence of linkage was declared when the F-test at any locus for any trait gave a probability lower than 1%. In addition, whenever the probability for seed oil percentage was lower than 5%, and any of its components at the same region was also lower than 5%, evidence of linkage was considered. This criterion was established because the probability of having two false positives (at the 5 % level) located in the same genomic region is lower than 5% when the two traits are not completely correlated (r=1). At the stated per locus error rate (1%) the probability of having at least one false positive across the genome (type I error) is 87%. Since this the first investigation designed to detect linkage between RFLP loci and factors affecting oil percentage, a more liberal test for linkage may be appropriate.

For those loci where F-tests were statistically significant, additive and dominant effects were calculated according to Edwards *et al.* (1987). Those loci with highest significant F-tests within regions of closely linked RFLP loci were selected as flanking markers. Additive effects for the interval between flanking markers were determined as the sum of the two partial regression coefficients for the regression of trait values on flanking markers (appendix 4). The sum of the regression coefficients for the two flanking markers estimates the additive effect of a QTL located in the interval (Wright and Mowers, in review). The expected additive effect for seed oil percentage was estimated by multiplying the additive effect of the component affecting seed oil percentage in that region times the mean of the other component. The d/a ratio scale described by Edwards *et al.* (1987) was used to classify gene action. The d/a ratio was calculated by dividing the dominant(d) to additive(a) effects of the marker(s) significantly linked to the QTL.

Multiple regression analysis was conducted to estimate phenotypic variation explained by additive effects. An independent variable (Q_i) was created based on the weight of each partial regression coefficient on marker classes (AA, Aa, aa; coded 1 0 -1, respectively). The dependant variables were the seed trait values (appendix 5). The coefficient of determination (R^2) for multiple regression estimates the proportion of variation accounted by the model. This regression model estimates the sum total of additive effects. This R^2 was compared with the estimated broad sense heritability to calculate the amount of genetic variation accounted by the regression.

For detection of epistatic effects, two-way Analyses of Variance were conducted for those loci with significant F-tests for seed oil percentage. Pairs of markers were taken and the interlocus interaction variance was partitioned into additive x additive, additive x dominance, dominance x additive and dominance x dominance interactions (Edwards *et al.*, 1987).

RESULTS

Phenotypic Data

Trait means for the parents, F_1 and F_2 progeny are presented in Table 1. Inbred HA89 seed oil percentage exceed that of ZENB8 by 19 percentage points. This difference is reflected by the higher kernel oil and kernel percentages of HA89. In the F_2 progeny, the distribution of all traits (appendix 6) did not fit a normal distribution (α:0.05). Coefficients of Skewness (γ_1) for seed oil percentage, kernel oil percentage, and kernel percentage, were -0.54, -0.42, and -0.54, respectively. In all cases the skewness was towards high values. Transgressive segregants were not detected for seed oil percentage. The seed oil percentage of the F_2 plants was within the range of the parents' mean values. Broad sense heritabilities were 0.47, 0.29, and 0.41, for seed oil percentage, kernel oil percentage, and kernel percentage, respectively (Table 1).

Kernel oil percentage and kernel percentage were positively correlated with seed oil percentage (0.82 and 0.47, respectively). The correlation between these two components was 0.33.

RFLP Data Analysis

The RFLP linkage map used for this study (Fig. 1) has been reported in a separate manuscript (Berry *et al.*, in review b). The average genomic composition of the F_2

population is shown in Fig. 2. The composition of individual F_2 plants homozygous for HA89 or ZENB8 alleles ranged from 5.1 to 57.4%, or 5.4 to 47.5%, respectively. The allele frequency across the genome was 51% and 49% for HA89 and ZENB8, respectively.

The seed oil percentage mean for the ten percent (i = 1.76) of plants having the highest (>49.5%) and lowest (<38.0%) seed oil percentage was 50.7 and 35.5%, respectively. ZENB8 allele frequency across the overall genome ranged from 25 to 57% and 36 to 66% for the selection with highest and lowest oil percentage, respectively. The ZENB8 allele frequency across regions unlinked to QTL associated with seed oil content ranged from 31 to 57% and 32 to 64% for the selection for high and low seed oil percentage, respectively.

Detection of QTL

Overall, seven regions were significantly associated with seed oil percentage or one of its components; however most regions were significantly associated with more than one trait (Table 2). In the majority of these regions, additive effects were more important than non-additive.

For kernel percentage, nineteen percent of the phenotypic variation (Table 3) was explained by four QTL (Fig. 1). Individually, QTL accounted for three to seven percent of the phenotypic variation. Additive effects in all regions, and additive gene action in two of the four regions seems to control the expression of the trait. Dominance or partial dominance gene action was present in the other two genomic regions.

For kernel oil percentage five unlinked regions (Fig. 1) explained twenty percent of the phenotypic variation (Table 3). A region with major effects was located to linkage group 'B' that accounted for 10% of the variation. Other significant regions explained less than five percent. Additive gene effects were present in almost all regions except in linkage group 'N'. The ratio d/a indicated that kernel oil percentage was mainly controlled by additive gene action; although, the region in linkage group 'N' exhibited overdominance for lower kernel oil percentage.

Alleles at six genomic regions were significantly associated with seed oil percentage. QTL were located in regions affecting kernel oil percentage and/or kernel percentage (Fig. 1). These regions accounted for 27% of the phenotypic variation, with regions in linkage groups 'B' and 'G' having the largest contributions, 13% and 12% respectively (Table 3). When only these two regions were included in the multilocus analysis, they accounted for 23% of the phenotypic variation. Other significant regions explained between 3 and 1%. Intralocus interaction was present in three regions with overdominace gene action for higher or lower seed oil percentage. Epistatic effects between pairs of marker loci were not statistically significant.

Additive effects for higher values of seed oil percentage, kernel oil percentage, and kernel percentage were usually derived from the alleles of the parent with highest oil percentage (HA89) (Table 3). In one region (linkage group 'J') alleles coming from ZENB8 increased the seed oil percentage.

In most cases, the observed additive effects of the regions controlling oil percentage in the whole seed matched their expected values estimated from the additive effects of the seed oil component(s) in those same regions (Table 4). Although, in linkage group 'G' the observed additive value (-2.53) was higher than the expected one (-0.92). The region associated with kernel oil percentage in linkage group 'Q' ($P<0.01$) was not detected ($P>0.05$) when the analysis was done with oil percentage in the whole seed.

DISCUSSION

Phenotypic Results and QTL Detection

Significant QTL were found in this experiment for all traits. Six genomic regions controlling seed oil percentage and at least one of the seed oil components were identified.

Heritability and genetic variance explained by QTL

Heritability of seed oil percentage (Table 1) was lower than previously reported values (0.6-0.7) for individual F_2 plants (Martinez *et al.*, 1979; Fick, 1975). Possibly, a larger genetic distance between the parents used by Martinez (high oil *H. annuus* inbred x low oil *H. annuus* wild type) and Fick (oil variety 'Peredovik' x confectionery variety 'Mennonite') and the environmental effects may account for some of the difference in the estimations.

Broad-sense heritability estimates the phenotypic variation due to genetic sources. Thus, the maximum phenotypic variation that multiple loci analysis can explain is the estimate of heritability. The coefficient of determination (R^2) in the multiple loci analysis of regions associated with seed oil, kernel oil and kernel percentages explained 27%, 20%, and 19% of the phenotypic variation, respectively. When comparing these values with the heritability of the traits, the QTL explain 57%, 69% and 46% of the genetic variation for seed oil, kernel oil and kernel percentage, respectively. Dominance and genotypic by environment interaction are included in the estimation of the genetic variance (Hallauer and Miranda,1988), while only additive effects are included in the sum of the regression coefficients of the flanking markers. Thus, it is expected that the genetic variation explained by the model probably underestimates the real importance of the six regions, since the model does not account for dominant or interaction effects. Since the RFLP map probably represents 60-80% of the sunflower genome (Berry *et al.*, in review b), it is expected that these values may be an upper limit for the genetic variation explained by the QTL.

The higher standard error of the mean for kernel percentage in HA89 than that for ZENB8 (Table 1) could be related to the different hull (or kernel) percentage between the lines. It is more difficult to dehull seed with low hull percentage (high kernel percentage) than that with high hull percentage, as part of the kernel may be left with the hull. This circumstance could have increased the kernel percentage error variance and affect the heritability value and the genetic variation explained by the QTL. Variability in dehulling lines with different hull percentage was also reported by Dedio (1982).

Phenotypic correlation and QTL localization

Consistent with prior observations (Dedio, 1982) the seed oil components kernel oil and kernel percentage were positively correlated with oil percentage in the whole seed. The higher correlation of seed oil percentage with kernel oil percentage than with kernel percentage suggests that kernel oil percentage has more influence in the determination of seed oil percentage.

Phenotypic correlations between traits are determined by genetic or environmental correlation. The sources of genetic correlations are pleiotropy or linkage (Falconer, 1981). For the six regions controlling seed oil percentage (Fig. 1) two were only associated with kernel oil percentage (linkage groups 'C' and 'I'), two with kernel percentage (linkage groups 'G' and 'J') and the other two with both traits (linkage groups 'B' and 'N'). As kernel oil and kernel percentage are components of the oil percentage in the whole seed, the coincidence in QTL localization suggests showing pleiotropic effects. This effect could be responsible for the degree of correlation reported between both kernel oil and kernel percentages with seed oil percentage. It is impossible to discern if the positive correlation (0.33) between kernel oil and kernel percentages was due to linkage or pleiotropic effects (linkage groups 'B' and 'N'). Contrary to a previous report (Dedio, 1982), in this population regions controlling both traits were genetically associated. This discrepancy can be explained by the fact that the presence of genetic linkage between traits depends on the localization of the QTL that are segregating for the traits and this is function of the population used in the study.

Gene action and effects

Additive effects mainly control the expression of seed oil percentage and its components (Table 3). Although three regions showed overdominance for seed oil percentage, the means of the homozygous HA89 and heterozygous classes are not statistically significant at the 5% level, at two regions (linkage groups 'C' and 'I'). Thus, in these two regions it is more likely that gene action is dominance rather than overdominance. Also, gene action for kernel oil percentage in these regions is additive or partially dominant. The fact that dominant or overdominant gene action was associated with the regions with lowest additive effects also suggests that additive effects are much more important than non-additive effects. This is supported by the small difference in seed oil percentage mean between the F_1 and F_2 progeny. Moreover, the success obtained in increasing the oil percentage in hybrid progeny by selecting for this trait in inbred progeny could probably be explained by the relative importance of additive effects in the expression of seed oil percentage, since dominant effects are not transmitted from inbreds to hybrids. This type of gene action agrees with results based on conventional breeding and biometric methodologies (Gupta and Khanna, 1982; Bedov, 1985; Areco *et al.*, 1985; Martinez *et al.*, 1979; Fick, 1975).

The observed seed-oil-percentage additive effect in linkage group 'G' is higher (+1.61) than expected from the kernel percentage effect (Table 4). The experimental error incurred when dehulling the seed may have contributed to this discrepancy. The mean kernel percentage of the HA89/HA89 genotypic class could have been lowered if some kernel pieces remained with the hull in some samples. Thus, it is likely that the observed additive effect of kernel percentage in this HA89 region was underestimated.

Level of significance for QTL detection

If only a 1% level of significance had been taken into account in this experiment then regions for seed oil percentage in linkage groups 'I' and 'J' (Table 2) would not have been declared significant when in fact QTL for its components kernel oil percentage in linkage 'I' and kernel percentage in linkage 'J' were declared significant at the 1% level. Moreover, both kernel oil and seed oil percentages are significantly associated, at the 5% level in region(s) in linkage group 'C'. The probability of having two false positives located in the same region is lower than 5% if the two traits are not completely correlated. The region in linkage group 'Q' declared linked with kernel oil percentage at the 1% level of significance was not declared linked at the

5% level with seed oil percentage. Either a type I error for kernel oil percentage or a type II error for seed oil percentage could have occurred. The simultaneous study of seed oil percentage with its components seems to help in the detection and understanding of the traits.

Genomic Composition and Breeding Utility

If one wanted to conduct a backcross program to improve the seed oil percentage in ZENB8 by improving only one of its components without affecting the other, then the backcrosses should not include regions in linkage groups where both components are genetically associated (i.e., groups 'B' and 'N'). Because region 'B' is controlling almost half of the genetic variability, then the potential genetic gain would be reduced; assuming components are genetically associated due to pleiotropic effects.

The resources spent determining genomic composition of individuals or families for mapping QTL can be utilized by using the data to help conventional breeding in the selection among families. The information could be useful to select for diversity across families to initiate testcrosses, to select for level of homozygosity, to select for degree of relationship with one of the parents after selecting for the trait of interest based on the phenotypic values. Among the ten percent (i = 1.76) of plants having the highest oil percentage, there is enough variation in ZENB8 allele frequency across overall genome (0.25-0.57) or across regions unlinked to oil QTL (0.31-0.57) to use the RFLP genotype for background selection.

Although in most regions higher trait values are coming from the parent with higher mean trait value (HA89) there are some regions where ZENB8 contributes to increase values. Although, transgressive segregants could not be located.

In summary, Six genomic regions explaining 57% of the genetic variation of seed oil percentage were found. Of these, two were associated with kernel oil percentage, two with kernel percentage and two with both components. Additive effects were found to be more important than non-additive effects in the expression of seed oil percentage and its components. The study of seed oil percentage together with its components seems to help in localizing QTL and getting a better understanding of the seed oil percentage. $F_{2:3}$ families have been planted in four locations in Argentina to study the repeatability of the results reported here and to define the DNA regions of HA89 that will be transferred, through a backcross program, to the high yielding (in specific hybrid combination) but low oil percentage ZENB8 line.

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APPENDIX 1

$$r_{XY} = \sigma_{XY} / \sqrt{(\sigma^2_X \sigma^2_Y)}$$

r_{XY} = Correlation coefficient between trait X and Y

σ_{XY} = Phenotypic covariance between traits X and Y

σ^2_X & σ^2_Y = Phenotypic variances for traits X and Y, respectively

APPENDIX 2

$$h^2 = \sigma^2_g / \sigma^2_{ph}$$

h^2 = Broad sense heritability

σ^2_g = Genetic variance

σ^2_{ph} = Phenotypic variance

$$\sigma^2_g = \sigma^2_{ph} - \sigma^2_e$$

σ^2_e = Environmental variance

$$\sigma^2_e = \sigma^2_w + \sigma^2_b$$

σ^2_w = Average within row variance estimated in P_1, P_2 and F_1 rows.

σ^2_b = Between row variance estimated in F_2 population.

APPENDIX 3

$$X_{..k} = (\textstyle\sum_j X_{.jk}) \ / \ r$$

$X_{..k}$ = Average frequency of each marker class (k= 1 to 3; AA, Aa, aa) across the *i*th plant.

r = Number of F_2 plants.

$X_{.jk}$ = Frequency of each marker class in each *i*th plant across the *j*th marker.

$$X_{.jk} = (\textstyle\sum_i X_{ijk}) \ / \ n$$

X_{ijk} = Number of markers having the k^{th} class in each *i*th plant across the *j*th marker loci.

n = number of molecular markers for the *i*th plant.

APPENDIX 4

$$Y_i = b_1X_{1i} + b_2\ X_{2i}$$

Y_i = Phenotypic value of the *i*th plant

X_{1i} and X_{2i} = Marker loci classes (coded -1, 0, 1; for AA, Aa, aa) for loci 1 and loci 2, respectively.

$b_1$and b_2 = Partial regression coefficients of flanking markers.

Wright and Mowers (in review) have shown that for large F_2 populations and complete interference between flanking markers $(M_1 \text{ -}^{c1}\text{- } Q \text{ -}^{c2}\text{- } M_2)$ the sum of the two regression coefficients estimates the factor additive effect:

$$\begin{bmatrix} b1 \\ b2 \end{bmatrix} \rightarrow \alpha \begin{bmatrix} c1/c \\ c2/c \end{bmatrix}\ ,\ so\ \ b_1+b_2 \rightarrow \alpha$$

$\boldsymbol{\alpha}$ = Additive effect

M_1 and M_2 = Loci 1 and 2, respectively.

Q = Quantitative trait loci

c1 and c2 = Recombination fractions between loci 1 and Q and loci 2 and Q, respectively.

c = c1 + c2 (complete interference)

APPENDIX 5

$$Y_i = \boldsymbol{\beta}_0 + \boldsymbol{\beta}_1 Q_1 + \boldsymbol{\beta}_2 Q_2 \ldots. + \boldsymbol{\beta}_n Q_n$$

Y_i = Phenotypic value of the *i*th plant.

$\boldsymbol{\beta}_0$ = Intercept coefficient.

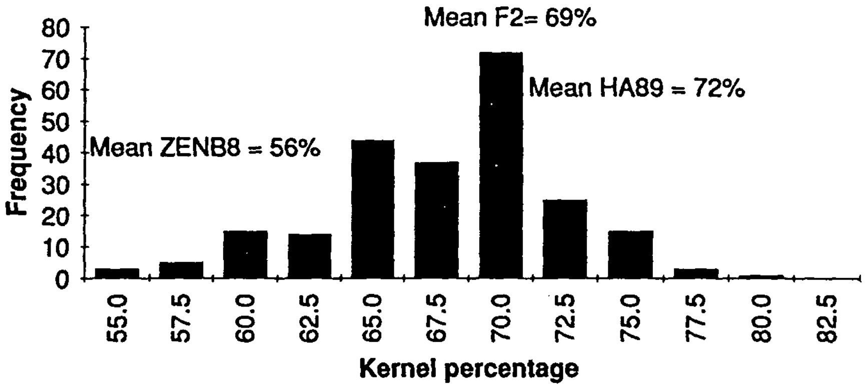
$\boldsymbol{\beta}_1 \ldots \boldsymbol{\beta}_n$ = Partial regression coefficients for the $Q_1 \ldots Q_n$th variable

$$Q_n = [b_{1n} / (b_{1n}+b_{2n})]X_{1n} + [b_{2n} / (b_{1n}+b_{2n})]X_{2n}$$

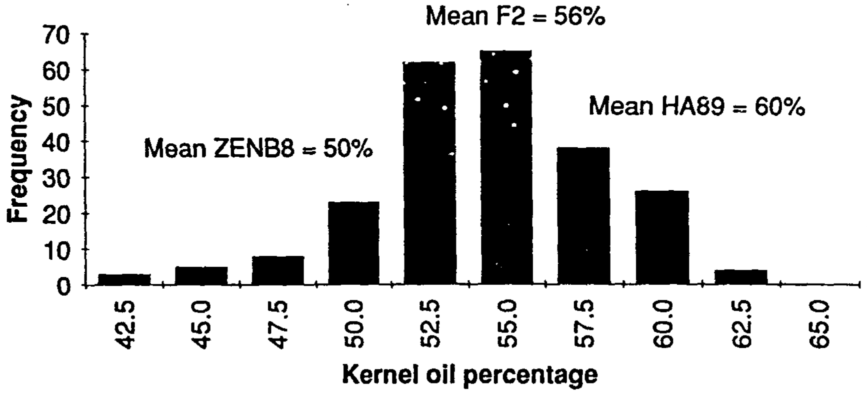
Where b_{1n} and b_{2n} are the partial regression coefficients of the two-variable flanking marker regression, with X_{1n} and X_{2n} the marker classes AA, Aa, aa (coded 1 0 -1, respectively) for the flanking markers at the *n*th QTL.

APPENDIX 6

Distribution of kernel percentage



Distribution of Kernel oil percentage



Distribution of Seed oil percentage

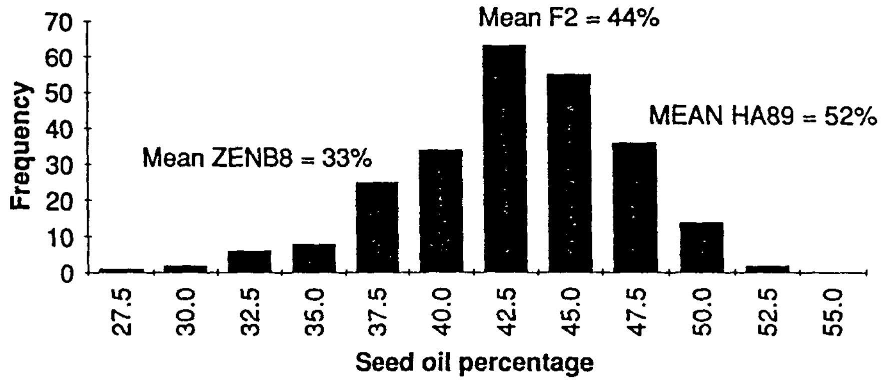


Table 1. Trait means, variance components and broad sense heritabilities.

Material	Seed oil %	Kernel oil %	Kernel %
ZENB8	33 ± 1.4†	50 ± 2.0	56 ± 1.4
HA89	52 ± 2.7	60 ± 2.2	72 ± 2.7
F_1	46 ± 2.8	57 ± 2.1	70 ± 2.8
F_2	44 ± 0.5	56 ± 0.5	69 ± 0.6
Estimates			
σ^2p‡	18.31	13.52	20.28
σ^2g§	8.66	3.94	8.26
σ^2¶	9.65	9.58	12.02
h^2#	0.47	0.29	0.41

† Mean ± 2 Standard errors of mean (day 0, relative to F_2 planting)

‡ Phenotypic variance

§ Genotypic variance

¶ Experimental error variance

Broad sense heritability

Table 2. Loci detecting significant variation for seed oil, kernel oil and kernel percentages.

Linkage group	Marker	Seed oil %		Kernel oil %		Kernel %	
		P>F	R^2†	P>F	R^2†	P>F	R^2†
B	C0952	****	0.10	****	0.09	*	0.03
B	C0741	****	0.13	****	0.13	**	0.05
B	C0696	****	0.13	****	0.12	**	0.06
B	C0791	****	0.13	****	0.13	**	0.05
B	C1763	****	0.14	****	0.13	**	0.05
B	C2308	****	0.15	****	0.13	**	0.05
B	C0522	****	0.12	****	0.13	*	0.03
B	C0036A	****	0.11	****	0.10	**	0.05
B	C0284	****	0.13	****	0.11	**	0.04
B	C0082	****	0.09	****	0.08	***	0.07
C	C1395		0.01	*	0.03		0.01
C	C1137	*	0.03	*	0.03		0.01
G	C0357	*	0.03		0.01		0.01
G	C0290	****	0.08		0.01	**	0.05
G	C0887	****	0.11		0.01	**	0.05
G	C1720	**	0.04		0.01		0.01
I	C1156	*	0.03	*	0.04		0.00
I	C1728	*	0.03	*	0.04		0.00
I	C1366	*	0.03	**	0.05		0.00
I	C1147	*	0.03	*	0.04		0.00
I	C0649		0.01	*	0.03		0.01
I	C1407		0.02	*	0.03		0.01
I	C0277A		0.01	*	0.03		0.01
I	C1410B		0.01	**	0.04		0.02
I	C0175		0.01	*	0.03		0.02

Table 2. Continued

		Seed oil %		Kernel oil %		Kernel %	
Group	Marker	Prob.	R^2†	Prob.	R^2†	Prob.	R^2†
J	C0007		0.02		0.00	*	0.03
J	C1523		0.02		0.00	*	0.03
J	C1160	*	0.03		0.01	**	0.04
J	C1067	*	0.03		0.00	*	0.04
J	C1453	*	0.03		0.00	**	0.04
J	C0026		0.02		0.00	*	0.03
J	C1294		0.01		0.01	**	0.05
N	C1965	***	0.07	*	0.04		0.02
N	C1562	**	0.05		0.02	*	0.03
N	C2303	***	0.07	*	0.04	*	0.03
N	C0503	*	0.04		0.02		0.02
Q	C1713		0.01	*	0.03		0.01
Q	C1380		0.01	*	0.03		0.01
Q	C1195		0.01	**	0.05		0.00
Q	C0044		0.01	*	0.04		0.00

*, **, ***, ****: Significance level of 0.05, 0.01, 0.001 and 0.0001 respectively.

† Coefficient of determination (R^2). Amount of variation explained by each marker.

Table 3. Location, genetic effects and contribution of the regions controlling oil percentage

Trait	Linkage group	R^2	R^2†	Additive‡ effect	High parent	d/a§	Gene¶ action
				oil %			
Kernel %	B	0.07	0.19	-2.25	HA89	+0.15	A
	G	0.05		-1.67	HA89	-0.68	D
	J	0.04		1.57	ZENB8	+0.68	D
	N	0.03		-1.09	HA89	+0.10	A
Kernel oil %	B	0.10	0.20	-2.20	HA89	+0.42	A
	C	0.02		-0.86	HA89	+0.34	A
	I	0.05		-1.17	HA89	-0.06	A
	N	0.03		0.00	-	-4.50	OD
	Q	0.04		1.21	ZENB8	+0.19	A
Seed oil %	B	0.13	0.27	-2.98	HA89	+0.39	A
	C	0.01		-0.65	HA89	+1.49	OD
	G	0.12		-2.53	HA89	-0.24	A
	I	0.01		-0.59	HA89	+1.64	OD
	J	0.03		1.14	ZENB8	-0.28	A
	N	0.02		-0.81	HA89	-2.47	OD

† Amount of variation explained by all DNA regions with significant F test.

‡ Negative sign means an increase of the mean value of the trait due to HA89 alleles. A positive sign means due to ZENB8 alleles.

§ Ratio of the average dominant and additive effects of the markers located within a significant region. A positive sign means dominance for higher value of the trait. A negative sign means dominance for lower value of the trait.

¶ A=additive or partial dominance, D=partial dominance or dominance, OD=overdominance. Based on the scale of the ratio d/a reported by Edwards *et al.* (1987.).

Table 4. Expected additive effects of the different regions controlling seed oil percentage

Linkage group	Seed oil %		
	Expected	Observed	Difference
B	-2.76	-2.98	+0.22
C	-0.59	-0.65	+0.06
G	-0.92	-2.53	+1.61*
I	-0.80	-0.60	-0.20
J	0.87	1.14	+0.23
N	0.60	-0.80	+0.20
Q	1.21	-	-1.21*

* Significant at 0.05 probability level

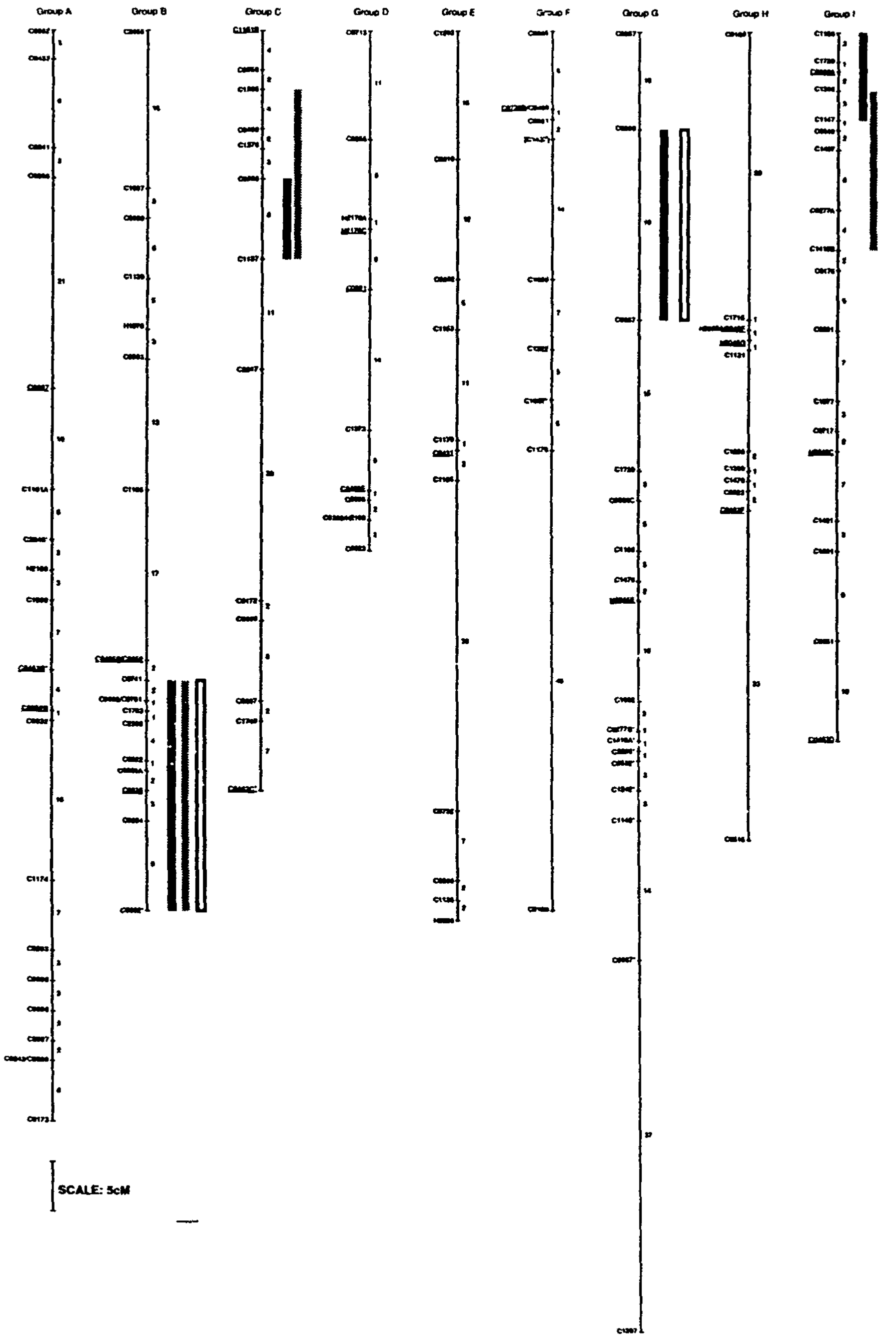


Figure 1. RFLP map and distribution of QTL affecting seed oil percentage (black blocks), kernel oil percentage (shaded blocks) and kernel percentage (white blocks). The seventeen linkage groups are listed at the top, loci on the left and map distances (cM) on the right. Loci mapped as dominant markers are underlined and those deviating from the expected segregation ratios (P<0.05) are indicated with *. The loci with uncertain map positions are indicated by square brackets.

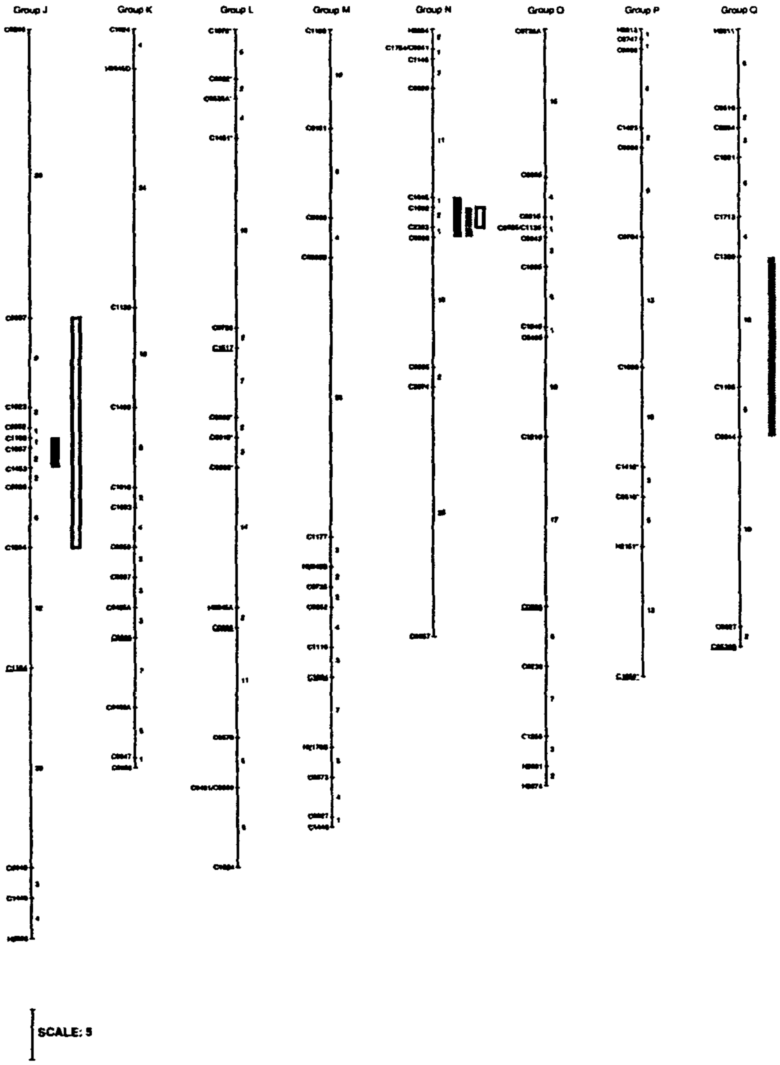


Figure 1. Continued

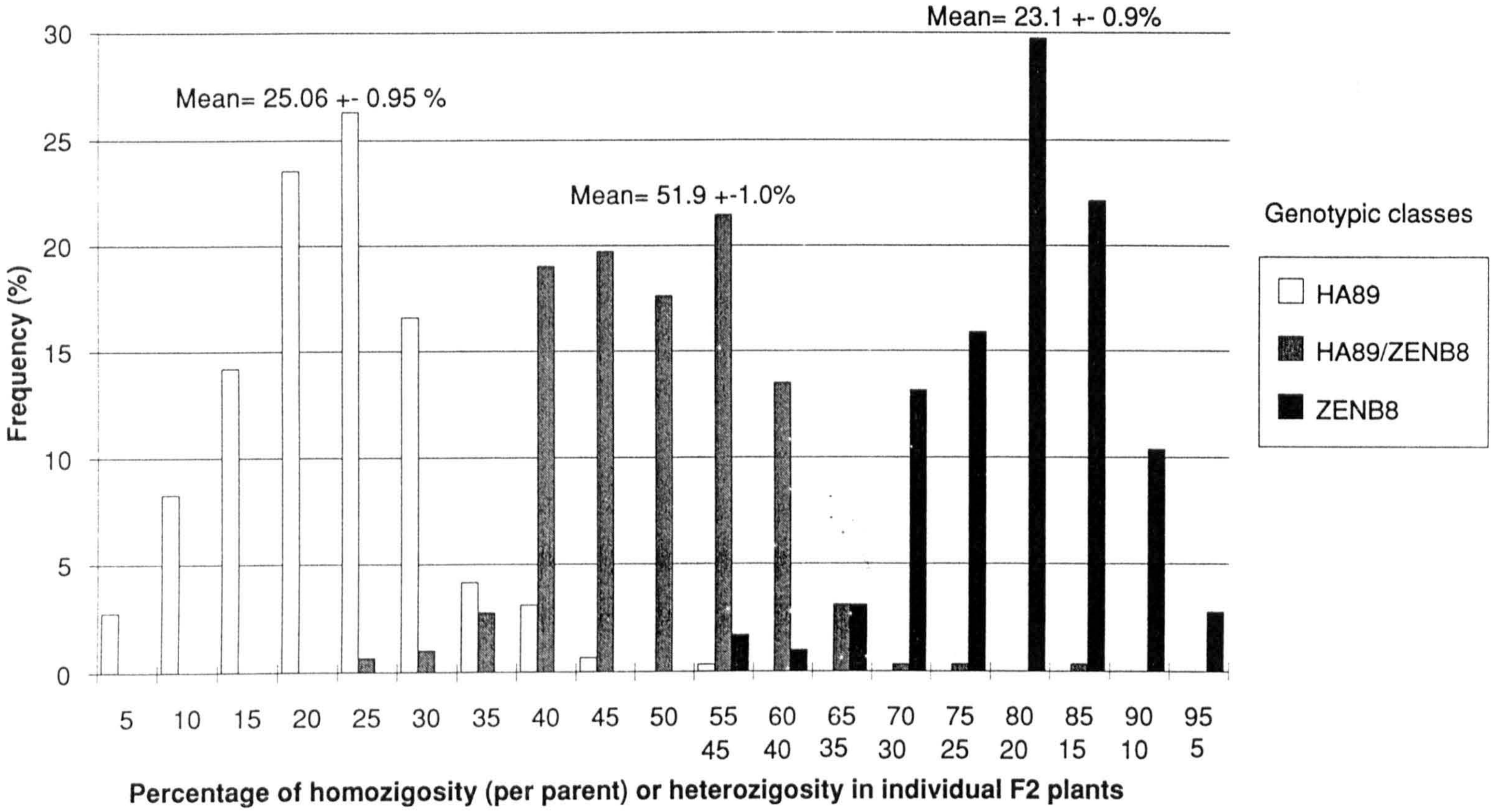


Figure 2. Average genomic composition of F_2 plants

PAPER III. GENETIC MAPPING OF SEED HYPODERMIS COLOR AND ITS RELATION WITH SEED OIL CONTENT

ABSTRACT

Sunflower seed color is determined by pigmentation of three layers of the sunflower pericarp (hull), epidermis, hypodermis, and phytomelanin layer. Although a major gene was reported controlling the inheritance of color in pigmented hypodermis, the inheritance of pigmented versus unpigmented hypodermis was not reported. The objectives of this research were to identify RFLP markers linked to factor(s) affecting seed hypodermis pigmentation and to assess the relation between this trait and oil percentage in the sunflower seed. An F_2 single-cross population was produced from inbred parents that differed for the traits. Two hundred sixty seven F_2 plants and their F_3 families were evaluated. A dominant factor (*Hyp*) controlling the presence of white pigments in the hypodermis was located to linkage group 'G'. Seeds with white hypodermis had lower oil percentage than those with unpigmented hypodermis. The *Hyp* factor was found located in the same map interval region as one QTL with major effects on with seed oil percentage.

INTRODUCTION

Seed Color

The sunflower achene is a fruit consisting of a kernel (true seed) and a pericarp (hull). The kernel consists of an embryo, endosperm and a seed coat. The pericarp (maternal tissue) consists of several layers, cuticle (external layer), epidermis, hypodermis, phytomelanin layer, fibrose tissue, and finally parenchymal layers adjacent to the kernel (Nassanov, 1940; cited by Vranceanu, 1977). In the sunflower research community the word 'seed' is used synonymously with 'achene' and will be used so in this paper.

The pericarp color is determined by the pigmentation of the epidermis, hypodermis, and phytomelanin layer (Putt, 1940; Mosjidis, 1982). The epidermis layer can be uniformly unpigmented or have black or dark brown pigmented stripes of varying thickness. Below the epidermis, the hypodermis can also be either completely unpigmented or pigmented (white or purple). If the third layer (phytomelanin layer) is present it has uniform dark brown-black pigments (Putt, 1944).

Genetic studies have identified factors with qualitative effects on pigment development in the hypodermis. A dominant gene *T* was reported controlling the presence of anthocyanin pigments in the hypodermis (Sazyperow, 1914; cited by Leclercq, 1966). Mosjidis (1982) reported that a major dominant gene (*C*) must be present to have purple color in that layer, and two complementary genes (*Y* and *P*) gave different intensity of purple pigmentation. Leclercq (1979) reported a single dominant gene (*Gb*) controlling seed color but it was not specified in his report which layer was being studied.

Relation between Seed Color and Oil Content

It is generally assumed among sunflower breeders that white seed with black stripes has lower oil percentage than either black or gray seed (Stoenescu, personal communication). If this assumption is true then seed color could be used as a genetic marker for selecting high oil seeds when the parents of a population differ in seed hypodermis color. However, reports showing relation between seed color and oil percentage could not be located.

The oil percentage in the sunflower seed is function of the kernel oil percentage, kernel (or hull) percentage and hull oil percentage (Seed Oil %= [Kernel % x Kernel oil % + Hull % x Hull Oil %] / 100). Kernel oil percentage, kernel weight percentage and hull oil percentage vary from 40 to 70%, 48 to 78%, and 1 to 6%, respectively (Vranceanu, 1977). In a recent study (Leon *et al.*, in preparation) six genomic regions controlling the expression of seed oil percentage have been located with RFLPs. All these regions were also significantly associated with at least one of the seed oil components.

Molecular Markers

Few studies have been conducted using molecular markers in sunflower. In general, the published nuclear DNA RFLP analyses have been focused on studies of interspecific crosses (Krauter *et al.*, 1991) and the taxonomy of the genus *Helianthus* (Choumane and Heizmann, 1983; Gentzbittel *et al.*, 1992). Berry *et al.* (in review a), using low copy genomic probes to fingerprint inbred lines, has revealed RFLPs among inbred lines of cultivated sunflower. Recently, an RFLP map of sunflower was reported by Berry *et al.* (in review, b). This was used to identify RFLP markers linked to QTL affecting oil percentage in the seed (Leon *et al.*, in preparation).

Although some research was done in the study of the inheritance of color in pigmented hypodermis, reports of the genetics of pigmented versus unpigmented hypodermis and linkage between seed color and oil content have not been located. The primary objective of this research was to identify RFLP markers linked to region(s) controlling the expression of pigmentation in the hypodermis, and to compare their location with those QTL reported for seed oil percentage.

MATERIALS AND METHODS

Germplasm and Field Designs

The population used in this study was created by crossing inbred lines ZENB8 and HA89. One F1 plant was self pollinated to produce the F_2 generation. Three hundred and forty F_2 plants were grown in Fargo, ND in the 1992 growing season (Leon et al., in preparation) and self pollinated to produce F_3 families. Two hundred sixty seven F_3 families were evaluated in one replication of a completely randomized design at Balcarce, Argentina, during the period November 92 through March 93. Families were grown in single row plots 3 m long and 0.70 m wide. Rows were planted and thinned to 10 pl/row (47000 plants/ha).

ZENB8 is a proprietary inbred line derived from a cross between two Argentine populations and maintained through more than 10 generations of self-pollination. It has low seed oil percentage (33%) and white seed color (white hypodermis with black phytomelanin layer) with black stripes. HA89 is a line released by the USDA in Fargo, N.D and has high seed oil percentage (49%) and gray seed color (unpigmented hypodermis with black phytomelanin layer) with black stripes in the epidermis layer. Both parents have normal cytoplasm and nonrestorer genes (B lines) for Leclercq's cytoplasm.

Trait Characterization

Characterization of hypodermis color and oil percentage were accomplished using the seed harvested form each F_2 plant. F_3 generation data were collected from a bulk of seed (equal volume from each plant) harvested from the ten F_3 plants. F_2 plants and F_3 families were placed into classes according with the presence or absence of white pigments in the hypodermis. Classes of F_2 plants were 'white pigmented' and 'unpigmented hypodermis'. For F_3 families, classes were 'white pigmented', 'unpigmented' and 'segregating'. In accordance with a previous classification scheme (Putt, 1940) unpigmented hypodermis was declared when gray color was observed between the black stripes of the epidermis. The 'segregating' class consist of seeds with white and unpigmented hypodermis in the bulked sample of the F_3 plants. This classification differs from that used by Mosjidis (1982). He called 'no pigmented hypodermis' the one that had white pigments, and pigmented the one with purple pigments. It is also different from the one used by the Plant Introduction Station (Ames,IA) since the main seed color is the one which covers the biggest percentage surface of the seed. Thus, HA89 was classified as black seed with gray stripes since the predominant color of the seed was attributed to the thick black stripes of the epidermis layer. It was clearly stated by Putt (1940, 1944) and Mosjidis (1982) that the stripes of the seed are present in the epidermis layer.

Seed oil percentage was determined with a Nuclear Magnetic Resonance Analyzer (NMR). A twelve gram sample of seed was taken from each F_2 plant or the bulk of F_3 plants. Samples were dried to 35 °C for 8 hours to approximately 4% moisture, then 10 g samples were used for the seed oil percentage determination.

RFLP Map and QTL Controlling Seed oil Percentage

The RFLP data collection and linkage map used for this study was reported in a separate manuscript (Berry et al., in review). The genetic markers covered 1380 centiMorgans (cM) and were arranged in 17 linkage groups, corresponding to the haploid number of chromosomes in this species. The average interval size was 5.9 cM.

Six genomic regions controlling the expression of seed oil content in the whole seed were located (Leon *et al.*, in preparation) in the same population used for this study. Of these, two were associated with kernel oil percentage (linkage groups ‘C’ and ‘I’), two with kernel percentage (linkage groups ‘G’ and ‘J’) and two with both components (linkage groups ‘B’ and ‘N’).

Statistical Analysis

Number of factor(s) and localization

For the hypothesis of one dominant factor model Chi-square tests were used to determine the goodness of fit of the observed numbers of each hypodermis class and the expected ratio 3 (white pigmented) : 1 (unpigmented) ratio an F_2 generation (appendix 1). The observed number of each class in F_3 families was tested to the expected ratio 1 (white) : 2 (segregating) : 1 (unpigmented). Since there is only one degree of freedom for the Chi-square tests in the F_2 generation a correction factor (-0.5) was applied (Gomez and Gomez, 1984).

The possible number of factors controlling the presence of white pigments was also estimated using ANOVA. Single factor analyses of variance (Edwards *et al.*, 1987) were conducted within marker loci for the genotypic classes and hypodermis color (coded 0, 0.75, and 1; for unpigmented, segregating, and white pigmented, respectively). Evidence of linkage between an RFLP locus and a factor controlling pigmentation in the hypodermis was indicated when the F test gave a probability lower than 0.01. Coefficient of determination (R^2) for each marker locus was calculated as the ratio of the sum of squares accounted for by the RFLP classes and the total sum of squares.

At RFLP loci exhibiting significant association, additive and dominant effects were determined from differences between mean trait values of marker locus genotypic classes, according to Edwards *et al.* (1987). Within groups of closely linked RFLP loci, those showing the highest significant F-tests were selected as flanking markers for the factor locus. Additive and dominant effects of the factor were estimated correcting the effects at the RFLP locus by the recombination fraction distance (r) between the marker and factor loci (Edwards *et al.*, 1987) (appendix 2). In the F_3 generation, families that have heterozygous genotypic class in the F_2 for a given marker loci express half of the dominant effects in the F_3 families (Hallauer and Miranda, 1988), so dominant effects were multiplied by a factor of two.

The *d/a* scale described by Edwards *et al.*(1987) was used to classify gene action of the factor(s). The *d/a* ratio was calculated dividing the estimated dominant(*d*) to additive(*a*) effects of the factor.

MAPMAKER computer program (Lander *et al.*,1987) was used to estimate the distance (r) between the flanking markers and the factor(s) affecting hypodermis pigmentation. Hypodermis pigmentation classes of F_3 families were used as morphological marker classes (codominant marker) and placed with a LOD score of 3.0 and a recombination value of 0.35 cM (Kosambi).

Relation between seed hypodermis color and oil percentage

Single factor analyses of variance (ANOVA) were conducted for the hypodermis pigmentation classes and their seed oil percentage. F-test were used to determine if significant variation in seed oil content was associated with the hypodermis pigmentation classes. Among F_2 plants, the difference between the two classes (white pigments vs. unpigmented hypodermis) was tested with F test (**α**: 0.05). In F_3 families, differences among the three classes (uniformly white pigments, segregating, and uniformly unpigmented hypodermis) were tested with F-test, and differences between pair of classes were tested with the Least Significant Difference (LSD; **α**:0.05).

RESULTS AND DISCUSSION

Linkage analysis for hypodermis color

Characterization of the trait for the different progenies is presented in Table 1. Segregation of hypodermis pigmentation among F_2 plants and F_3 families fit the expected ratios for a single dominant factor. White pigmented hypodermis showed dominance over unpigmented. Concordant with this results, single factor analyses of variance identified one highly significant ($P<0.0001$) region associated with inheritance of hypodermis pigmentation (Table 2). Results from both progenies showed that C0290 is probably the closest RFLP locus to the factor since it has the highest coefficient of determination (0.70), additive and dominant effects. It is also possible to predict that the most likely position of the factor is within the interval C0290-C0887 than in C0357-C0290. Since C0357 and C0887 have R^2 of similar magnitude, with similar additive and dominant effects, it is expected that the location of the factor is midway between these two markers and this position is in the interval C0290-C0887.

Since this phenotype seems to be controlled by one factor, it was used as a codominant morphological marker to locate its position. Three point linkage analysis (MAPMAKER) placed the *Hyp* factor loci at 7.4 cM from C0290 and at 15.5 cM from C0887 (Fig. 1). In the RFLP map (Berry *et al.*, in review) the interval between these two markers was 19 cM. With the placement of the *Hyp* marker loci the distance changes to 22.9 cM. This kind of difference is expected due to the lack of possibility to measure double crossovers between C0290 and C0887 without having a marker in the interval.

Additive and dominant effects of the *Hyp* factor estimated from the RFLP genotypic class means at locus C0290 gave an estimated additive and dominant effect of 0.49 and 0.51, respectively. Since the phenotypic classes 'white pigments', 'segregating' and 'no-pigments' were arbitrary coded with values of '1', '0.75' and '0', respectively, the true additive and dominant effects of the factor is '0.5' if there is only one factor with dominant gene action controlling the trait. This expected values matched with the observed ones when corrected by the distance to the factor locus.

A *d/a* ratio of 1.04 also indicated that dominant gene action controls the expression of white pigments. Effects for the presence of white pigments in the hypodermis are coming from the parent with white hypodermis color (ZENB8). In other words unpigmented hypodermis is a recessive trait, and alleles are coming from HA89.

Based on this experiment, it is not possible to discern whether the *Hyp* factor is the same major gene reported by Mosjidis (1982) or Sazyperow (1914; cited by Leclercq, 1966) since they worked with white and anthocyanin pigmented hypodermis, and in this experiment, the presence or absence of a white pigment in the hypodermis of the sunflower seed was evaluated. At least two models can be developed from these observations. First, the presence or absence of pigments in the hypodermis is controlled by one factor and in this experiment both lines carry alleles for white pigments at another locus. A second model is that this factor is the same reported previously and there is an allelic series at this locus that produces anthocyanin pigments, white pigments or unpigmented hypodermis.

Relation between seed hypodermis color and oil percentage

Differences in seed oil percentage among hypodermis pigmentation phenotypes was highly significant when evaluated in F_2 plants and their F_3 progeny (Table 3). Seed with unpigmented hypodermis (HA89 type) had ten percent (3-4 percentage points) higher seed oil percentage than white pigmented hypodermis seed (ZENB8 type) in both types of progeny. In F_3 families segregating for hypodermis pigmentation the mean oil percentage is closer to the white class than to the unpigmented one.

The *Hyp* locus is located in the same genomic region (linkage group 'G') where a QTL with a major effect for seed oil percentage has been located (Leon *et al.*, in preparation) in this population (Fig. 1). Gene action at this region was dominance for low oil percentage. ZENB8 alleles contributed the low oil percentage. The higher oil percentage effect at this region was explained by the higher kernel (or lower hull) percentage effect of alleles coming from the line with higher seed oil and kernel percentages (HA89). It was impossible to determine if the *Hyp* locus that controls the hypodermis color in the hull is linked or has pleiotropic effects with that controlling the seed oil percentage. But this similar map position probably explains the relation between seed hypodermis color and oil percentage in this population.

In summary, a major dominant factor (*Hyp*) controlling hypodermis pigmentation was identified in linkage group 'G'. Phenotypic studies showed that seeds with white hypodermis color had lower oil percentage than those with unpigmented hypodermis. This *Hyp* factor was located in the same genomic region as one QTL with major effect controlling seed oil percentage. This coincidence in localization is probably responsible for the relation between hypodermis pigmentation and oil percentage in this population.

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APPENDIX 1

$$\chi^2 = \sum (O_i - E_i - 0.5)^2 \;/\; E_i$$

where O_i and E_i are the observed and expected number of plants or families having the *i*th phenotype (pigmented, segregating, and unpigmented, respectively). The E_i value was estimated multiplying the total number of plants or families times the probability of having the *i*th phenotype for one dominant factor model.

APPENDIX 2

$$a = (\mathrm{MM} - \mathrm{mm}/2)\ /\ (1 - 2\mathrm{r})$$

$$d = [\mathrm{Mm} - (\mathrm{MM}+\mathrm{mm})/2]\ /\ (1 - 2\mathrm{r})^2$$

where *a* and *d* are the additive and dominant effects of the factors, respectively; MM, Mm, mm the mean trait value of the genotypic marker classes, and 'r' is the recombination fraction between one RFLP marker and the factor loci.

Table 1. Summary and analysis of segregation for hypodermis pigmentation among F_2 plants and F_3 families.

	Hypodermis pigmentation			Expected	
Generation	White	Segregating	Unpigmented	ratio	$\chi 2$†
F_2	212	-	55	3:1	2.53
F_3	74	131	50	1:2:1	4.72

† $\chi 2$ (0.05) tabular is 3.84 for F_2, and 5.99 for F3.

Table 2. Summary of single factor analysis of variance in a region in linkage group 'G'.

Progeny	Locus	P > F	R^2†	*a*‡	*d*§
				units	
F_2 plants	C0357	0.0001	0.40	0.33	0.30
	C0290	0.0001	0.65	0.42	0.37
	C0887	0.0001	0.37	0.30	0.24
	C1720	0.0001	0.16	0.20	0.14
F_3 families	C0357	0.0001	0.48	0.33	0.35
	C0290	0.0001	0.70	0.42	0.38
	C0887	0.0001	0.42	0.32	0.24
	C1720	0.0001	0.19	0.21	0.17

† Coefficient of determination.

‡ Additive effect. A positive sign means an increase of the mean value of the trait due to ZENB8 alleles.

§ Dominant effect. A positive sign means dominance for white pigmented hypodermis.

Table 3. Seed oil percentage in seed with different hypodermis pigmentation.

Progeny	Hypodermis pigmentation	Oil %†	LSD‡
F_2 plants	Unpigmented	46.5 ± 1.0	
	White	43.4 ± 1.0	
	Unpigmented	43.3 ± 0.6	a
F_3 families	Segregating	40.6 ± 0.6	b
	White	39.4 ± 0.6	c

† Mean ± 2 standards error of the mean.

‡ LSD(0.05)= 0.70. Different letters indicate that means are statistically different.

F-test were significant at the 0.001 level of probability for both progenies.

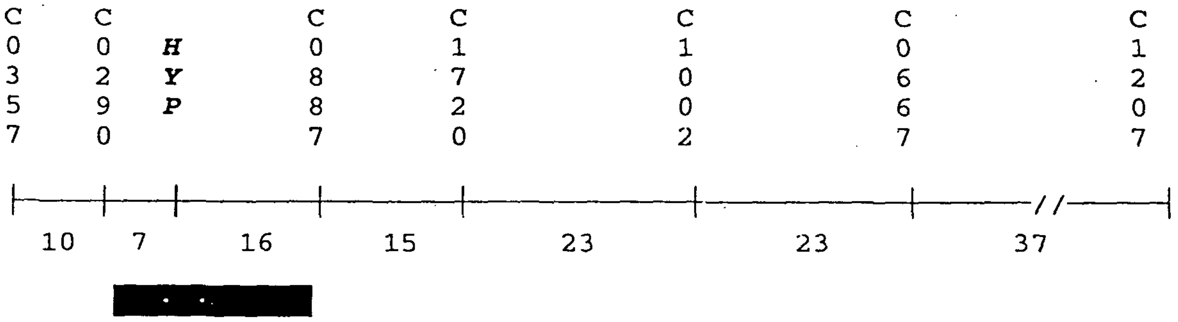

Fig. 1. Localization of the ***Hyp*** locus in linkage group ‘G’. Numbers represent distances (cM) between markers. Black block shows the localization of a QTL controlling seed oil percentage according with a previous research (Leon et al.,in preparation).

GENERAL CONCLUSIONS

A linkage map of *H.annuus* was constructed based on the segregation of 234 RFLP loci detected by 213 probes, in an F_2 population of 289 individuals. The genetic markers covered 1380 centiMorgans (cM) of the sunflower genome and were arranged in 17 linkage groups, corresponding to the haploid number of chromosomes in this species. One locus was found to be unlinked. Although the average interval size was 5.9 cM, there were a number regions larger than 20 cM that were devoid of markers. Twenty-three loci deviated significantly from the expected Mendelian ratios for an F2 population (1:2:1 or 3:1); all showing a reduction in the same homozygous class. The majority of these loci were found to map to the same four regions on linkage groups G, L, and P.

This sunflower RFLP map was then used for the genetic linkage analyses. Significant associations were reported for all traits studied in this research. RFLP markers located six regions that explained at least 57% of the genetic variation for seed oil percentage. Two of these regions were associated with kernel oil percentage, two with kernel percentage and two with both components. Additive gene action was predominant for seed oil content and its components. The simultaneous study of seed oil content and its components seems to help in localizing QTL and provide a better understanding of seed oil content trait.

Biometric studies showed that seeds with white hypodermis color had lower oil content than those with unpigmented hypodermis. A dominant genetic factor (*Hyp*) controlling the presence of white pigments in the hypodermis of the seed was located to linkage group 'G'. This genomic region is located in the same region as one QTL with mayor effects on seed oil percentage.

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APPENDIX

TABLE A1. Distances between RFLP markers (Mapmaker output)

LINKAGE GROUP A

```
 Markers          Distance
  67  C0562         3.0 cM
  46  C0433         8.6 cM
 182  C2241         3.2 cM
  26  C0266        20.5 cM
 117  C0997        10.0 cM
 226  C1161         5.0 cM
 183  C2246         2.8 cM
 211  H2188         3.2 cM
 157  C1500         7.2 cM
  50  C0463B        4.0 cM
  25  C0252B        0.8 cM
   4  C0032        15.7 cM
 232  C1174         6.9 cM
 186  C2263         3.4 cM
  73  C0606         2.9 cM
  82  C0689         2.8 cM
 177  C2007         2.0 cM
  23  C0243         0.4 cM
 179  C2028         6.4 cM
  16  C0173      ----------
                  108.8 cM   20 markers   log-likelihood=-898.87
```

LINKAGE GROUP B

```
 Markers          Distance
 176  C2005        15.5 cM
 125  C1087         3.1 cM
  80  C0680         5.6 cM
 215  C1129         5.2 cM
 198  H1070         3.1 cM
  72  C0593        13.4 cM
 229  C1165        16.8 cM
  44  C0425B        0.3 cM
 116  C0952         2.0 cM
  93  C0741         1.6 cM
  83  C0696         0.4 cM
  95  C0791         0.7 cM
 169  C1763         0.8 cM
 190  C2308         3.7 cM
  61  C0522         1.4 cM
   5  C0036A        1.8 cM
  38  C0335         3.0 cM
  32  C0284         9.3 cM
  13  C0082      ----------
                   87.8 cM   19 markers   log-likelihood=-776.02
```

TABLE A1. Continued

LINKAGE GROUP C

```
Markers            Distance
227  C1161B          4.2 cM
  9  C0050           2.1 cM
142  C1395           3.7 cM
 47  C0460           2.0 cM
140  C1378           3.4 cM
101  C0838           7.7 cM
217  C1137          10.9 cM
184  C2247          23.3 cM
 15  C0172           1.5 cM
107  C0896           8.2 cM
 74  C0607           1.7 cM
167  C1740           7.1 cM
 51  C0463C       ----------
                    75.8 cM   13 markers   log-likelihood=-634.19
```

LINKAGE GROUP D

```
Markers            Distance
 86  C0713          10.6 cM
185  C2255           8.4 cM
208  H2178A          0.6 cM
210  H2178C          5.8 cM
110  C0921          14.4 cM
139  C1373           6.4 cM
 53  C0463E          1.0 cM
178  C2008           1.7 cM
 41  C0360           0.3 cM
207  H2169           2.8 cM
 99  C0823        ----------
                    52.2 cM   11 markers   log-likelihood=-495.41
```

TABLE A1. Continued

LINKAGE GROUP E

```
 Markers            Distance
 129   C1203         14.8 cM
  97   C0810         12.0 cM
  12   C0062          4.5 cM
 127   C1153         10.5 cM
 231   C1170          0.9 cM
  45   C0431          2.6 cM
 213   C1105         32.7 cM
  89   C0732          7.3 cM
  68   C0566          1.9 cM
 220   C1138          2.4 cM
 195   H2038        ----------
                     89.5 cM    11 markers   log-likelihood=-661.62
```

LINKAGE GROUP F

```
 Markers            Distance
 103   C0865          8.4 cM
  92   C0736B         0.0 cM
  57   C0496          0.9 cM
  81   C0681          2.1 cM
 149   C1437         13.9 cM
 162   C1696          6.5 cM
 131   C1222          5.0 cM
 175   C1997          5.1 cM
 233   C1176         45.9 cM
  14   C0169        ----------
                     87.9 cM    10 markers   log-likelihood=-570.11
```

TABLE A1. Continued

LINKAGE GROUP G

```
  Markers              Distance
   40  C0357              9.5 cM
   33  C0290             19.0 cM
  106  C0887             14.6 cM
  165  C1720              3.2 cM
    6  C0036C             4.7 cM
  230  C1168              3.2 cM
  155  C1470              1.9 cM
  203  H2045E            10.2 cM
  119  C1002              3.3 cM
   29  C0277B             1.2 cM
  145  C1410A             0.5 cM
  188  C2286              0.7 cM
   63  C0532              3.2 cM
  132  C1242              3.1 cM
  222  C1143             13.7 cM
   79  C0667             37.0 cM
  238  C1207           ----------
                        129.1 cM   17 markers   log-likelihood=-885.51
```

LINKAGE GROUP H

```
  Markers              Distance
   18  C0180             28.7 cM
  164  C1715              1.3 cM
  193  H0230              1.3 cM
  204  H2045F             0.0 cM
  205  H2045G             1.0 cM
  219  C1131             10.4 cM
  135  C1288              2.1 cM
  137  C1360              1.2 cM
  156  C1476              1.2 cM
   62  C0523              2.2 cM
   54  C0463F            33.1 cM
   59  C0515           ----------
                          82.5 cM   12 markers   log-likelihood=-538.34
```

TABLE A1. Continued

LINKAGE GROUP I

Markers		Distance
224	C1156	2.7 cM
166	C1728	1.2 cM
30	C0282A	1.7 cM
138	C1366	3.2 cM
223	C1147	1.1 cM
78	C0649	1.6 cM
144	C1407	6.3 cM
28	C0277A	4.0 cM
146	C1410B	2.4 cM
17	C0175	6.0 cM
37	C0331	7.1 cM
124	C1077	3.3 cM
87	C0717A	2.3 cM
201	H2045C	6.7 cM
154	C1461	3.0 cM
170	C1891	8.8 cM
102	C0851	10.0 cM
52	C0463D	----------
		71.1 cM

71.1 cM 18 markers log-likelihood=-708.32

LINKAGE GROUP J

Markers		Distance
27	C0268	29.2 cM
1	C0007	8.8 cM
159	C1523	2.1 cM
39	C0352	0.7 cM
225	C1160	0.9 cM
123	C1067	1.6 cM
153	C1453	1.8 cM
2	C0026	6.2 cM
136	C1294	11.5 cM
236	C1184	20.0 cM
115	C0949	3.3 cM
151	C1446	3.9 cM
197	H2098	----------
		90.0 cM

90.0 cM 13 markers log-likelihood=-680.09

TABLE A1. Continued

LINKAGE GROUP K

```
  Markers          Distance
  172  C1924         3.8 cM
  202  H2045D       24.1 cM
  221  C1139         9.6 cM
  143  C1400         8.4 cM
  121  C1010         1.9 cM
  126  C1093         3.5 cM
   66  C0559         3.4 cM
   35  C0307         3.0 cM
   43  C0425A        3.0 cM
   96  C0806         6.9 cM
   49  C0463A        5.2 cM
  114  C0947         1.3 cM
   84  C0698       ----------
                    74.0 cM   13 markers   log-likelihood=-634.31
```

LINKAGE GROUP L

```
  Markers          Distance
  174  C1978         5.0 cM
   98  C0822         2.4 cM
   64  C0538A        4.3 cM
  152  C1451        18.9 cM
   88  C0728         1.6 cM
  158  C1517         7.4 cM
   42  C0383         1.6 cM
   76  C0619         3.3 cM
   21  C0230        13.7 cM
  199  H2045A        2.1 cM
   77  C0628        10.6 cM
   69  C0570         4.7 cM
   55  C0481         0.2 cM
   70  C0589         7.7 cM
  160  C1524       ----------
                    83.4 cM   15 markers   log-likelihood=-716.69
```

TABLE A1. Continued

LINKAGE GROUP M

```
  Markers           Distance
  235   C1180        10.4 cM
   19   C0181         9.1 cM
  108   C0903         3.9 cM
   31   C0282B       27.5 cM
  234   C1177         3.3 cM
  200   H2045B        2.1 cM
   90   C0735         1.6 cM
   24   C0252         4.1 cM
  214   C1119         2.6 cM
  120   C1004         7.3 cM
  209   H2178B        3.4 cM
  105   C0873         4.2 cM
    3   C0027         1.4 cM
  150   C1440       ----------
                     80.9 cM   14 markers   log-likelihood=-674.27
```

LINKAGE GROUP N

```
  Markers           Distance
  194   H2034         2.2 cM
  168   C1754         0.0 cM
  113   C0941         1.4 cM
  218   C1145         3.1 cM
  112   C0929        10.9 cM
  173   C1965         1.3 cM
  161   C1562         2.1 cM
  189   C2303         1.4 cM
   58   C0503        12.7 cM
   20   C0205         2.4 cM
  181   C2074        24.5 cM
   10   C0057       ----------
                     62.1 cM   12 markers   log-likelihood=-486.32
```

TABLE A1. Continued

LINKAGE GROUP O

```
  Markers           Distance
   91  C0736        15.2 cM
  180  C2055         3.5 cM
   36  C0316         0.6 cM
  111  C0925         0.2 cM
  216  C1135         1.4 cM
    7  C0043         3.4 cM
  171  C1905         6.2 cM
  133  C1249         0.9 cM
   56  C0485        10.3 cM
  130  C1210        16.6 cM
   34  C0296         5.6 cM
   22  C0238         6.9 cM
  134  C1256         2.7 cM
  212  H2001         2.3 cM
  196  H2074      ----------
                    75.9 cM   15 markers   log-likelihood=-692.41
```

LINKAGE GROUP P

```
  Markers           Distance
  192  H2013         1.4 cM
   94  C0747         1.0 cM
  109  C0906         8.2 cM
  148  C1423         1.6 cM
  104  C0866         8.8 cM
   85  C0704        13.3 cM
  118  C1000        10.3 cM
  147  C1418         2.7 cM
   75  C0616         5.3 cM
  206  H2151        12.6 cM
  122  C1059      ----------
                    65.3 cM   11 markers   log-likelihood=-603.38
```

TABLE A1. Continued

LINKAGE GROUP Q

```
Markers          Distance
191  H2011          8.3 cM
 60  C0519          2.3 cM
187  C2284          2.8 cM
128  C1201          5.9 cM
163  C1713          4.2 cM
141  C1380         13.3 cM
237  C1195          4.6 cM
  8  C0044         18.7 cM
100  C0827          1.5 cM
 65  C0538B      ----------
                   61.7 cM   10 markers   log-likelihood=-554.61
```

TABLE A2. Chi-square analysis of segregation of marker classes for a 1 AA : 2 AB : 1BB or 3 A_ : 1 BB ratio

Group	Probe	P<0.05	Prob	Chi-sq	# AA	# AB	# BB	Total
A	C0562		0.37908	1.94	65	132	79	276
A	C0433		0.55711	1.17	69	130	76	275
A	C2241		0.44264	1.63	69	132	79	280
A	C0266		0.50158	1.38	63	129	75	267
A	C0997		0.27117	2.61	223		59	282
A	C1161A		0.08804	4.86	61	151	55	267
A	C2246	*	0.04689	6.12	67	156	53	276
A	H2188		0.62189	0.95	71	152	66	289
A	C1500		0.40052	1.83	66	143	58	267
A	C0463B	*	0.03707	6.59	226		51	277
A	C0252B		0.38868	1.89	222		61	283
A	C0032		0.27665	2.57	75	152	60	287
A	C1174		0.17377	3.50	67	160	62	289
A	C2263		0.35701	2.06	64	152	64	280
A	C0606		0.60957	0.99	64	147	67	278
A	C0689		0.52205	1.30	62	146	66	274
A	C2007		0.62814	0.93	68	150	66	284
A	C0243		0.77492	0.51	68	148	68	284
A	C2028		0.95123	0.10	70	134	67	271
A	C0173		0.95123	0.10	67	140	70	277
B	C2005		0.87372	0.27	67	142	73	282
B	C1087		0.1549	3.73	57	145	79	281
B	C0680		0.39259	1.87	61	141	77	279
B	C1129		0.70117	0.71	67	137	76	280
B	H1070		0.16122	3.65	67	156	59	282
B	C0593		0.65705	0.84	67	144	78	289
B	C1165		0.41066	1.78	60	147	68	275

TABLE A2. Continued

Group	Probe	P<0.05	Prob	Chi-sq	# AA	# AB	# BB	Total
B	C0425B		0.99501	0.01	212		72	284
B	C0952		0.38868	1.89	60	148	69	277
B	C0741		0.70822	0.69	65	147	70	282
B	C0696		0.3588	2.05	60	149	72	281
B	C0791		0.42956	1.69	60	146	71	277
B	C1763		0.56836	1.13	64	150	71	285
B	C2308		0.34301	2.14	60	150	70	280
B	C0522		0.30882	2.35	60	147	62	269
B	C0036A		0.31822	2.29	62	155	70	287
B	C0335		0.2466	2.80	218		57	275
B	C0284		0.0773	5.12	61	160	61	282
B	C0082	*	0.04394	6.25	65	161	56	282
C	C1161B		1	0.00	208		70	278
C	C0050		0.10435	4.52	71	158	57	286
C	C1395		0.11824	4.27	72	159	58	289
C	C0460		0.40861	1.79	69	145	59	273
C	C1378		0.28365	2.52	72	155	61	288
C	C0838		0.74082	0.60	73	136	64	273
C	C1137		0.81465	0.41	71	149	68	288
C	C2247		0.69073	0.74	75	143	65	283
C	C0172		0.16696	3.58	83	132	63	278
C	C0896		0.16122	3.65	82	132	61	275
C	C0607		0.36788	2.00	81	144	64	289
C	C1740		0.57695	1.10	77	133	68	278
C	C0463C	***	0.0008	14.25	181		97	278
D	C0713		0.50662	1.36	72	150	63	285
D	C2255		0.91851	0.17	67	142	71	280
D	H2178A		0.2265	2.97	69	149	57	275

TABLE A2. Continued

Group	Probe	P<0.05	Prob	Chi-sq	# AA	# AB	# BB	Total
D	H2178		0.35169	2.09	69	155	63	287
D	C0921		0.95123	0.10	212		68	280
D	C1373		0.41895	1.74	65	155	68	288
D	C0463E		0.87372	0.27	68	140	74	282
D	C2008		0.55433	1.18	67	150	65	282
D	C0360		0.82696	0.38	69	146	67	282
D	H2169		0.67032	0.80	74	130	69	273
D	C0823		0.63128	0.92	69	152	67	288
E	C1203		0.19691	3.25	72	153	58	283
E	C0810		0.26185	2.68	68	153	60	281
E	C0062		0.75957	0.55	71	132	73	276
E	C1153		0.84366	0.34	68	144	75	287
E	C1170		1	0.00	71	142	71	284
E	C0431		0.67706	0.78	69	146	64	279
E	C1105		0.98511	0.03	70	143	70	283
E	C0732		0.67706	0.78	76	137	76	289
E	C0566		0.91851	0.17	74	140	70	284
E	C1138		0.35169	2.09	59	142	75	276
E	H2038		0.79852	0.45	207		63	270
F	C0865		0.58567	1.07	69	152	66	287
F	C0736B		0.77492	0.51	221		67	288
F	C0496		0.72253	0.65	70	150	67	287
F	C0681		0.91851	0.17	66	140	70	276
F	C1437		0.44264	1.63	69	150	62	281
F	C1696		0.17119	3.53	60	152	61	273
F	C1222		0.10593	4.49	68	157	57	282
F	C1997	*	0.0299	7.02	63	152	50	265
F	C1176		0.06081	5.60	62	163	61	286

TABLE A2. Continued

Group	Probe	P<0.05	Prob	Chi-sq	# AA	# AB	# BB	Total
F	C0169		0.91393	0.18	70	148	71	289
G	C0357		0.27665	2.57	56	144	66	266
G	C0290		0.16948	3.55	58	154	75	287
G	C0887		0.24537	2.81	65	152	60	277
G	C1720		0.33287	2.20	64	143	57	264
G	C0036C		0.32303	2.26	81	143	63	287
G	C1168		0.21871	3.04	75	153	59	287
G	C1470		0.23224	2.92	73	153	59	285
G	H2045G		0.94176	0.12	216		69	285
G	C1002		0.1764	3.47	81	139	59	279
G	C0277B	*	0.03491	6.71	81	147	52	280
G	C1410A	*	0.01419	8.51	80	155	50	285
G	C2286	*	0.01822	8.01	82	152	51	285
G	C0532	*	0.02586	7.31	80	155	52	287
G	C1242	**	0.00844	9.55	75	161	49	285
G	C1143	*	0.01089	9.04	82	150	49	281
G	C0667	**	0.00985	9.24	74	157	48	279
G	C1207		0.37908	1.94	63	154	69	286
H	C0180		0.72615	0.64	64	141	73	278
H	C1715		0.7788	0.50	65	144	68	277
H	H2030		0.94176	0.12	69	135	71	275
H	H2045E		0.69073	0.74	74	137	77	288
H	H2045G		0.07353	5.22	77	155	55	287
H	C1131		0.74082	0.60	72	148	66	286
H	C1288		0.95123	0.10	71	136	70	277
H	C1360		0.46767	1.52	70	142	59	271
H	C1476		0.90937	0.19	73	143	68	284
H	C0523		0.88692	0.24	70	142	66	278

TABLE A2. Continued

Group	Probe	P<0.05	Prob	Chi-sq	# AA	# AB	# BB	Total
H	C0463F		0.82696	0.38	209		76	285
H	C0515		0.81058	0.42	75	137	72	284
I	C1156		0.63128	0.92	73	138	62	273
I	C1728		0.96561	0.07	71	138	68	277
I	C0282A		1	0.00	207		69	276
I	C1366		0.94176	0.12	73	139	71	283
I	C1147		0.99501	0.01	68	134	67	269
I	C0649		0.96561	0.07	71	144	74	289
I	C1407		0.96561	0.07	69	142	72	283
I	C0277A		0.76721	0.53	71	149	67	287
I	C1410B		0.8781	0.26	68	143	74	285
I	C0175		0.85214	0.32	73	135	71	279
I	C0331		0.25158	2.76	58	147	75	280
I	C1077		0.20291	3.19	59	151	78	288
I	C0717		0.11192	4.38	53	148	68	269
I	H2045C		0.89137	0.23	210		75	285
I	C1461		0.12556	4.15	58	146	82	286
I	C1891		0.2658	2.65	51	130	67	248
I	C0851		0.19691	3.25	58	147	78	283
I	C0463D		0.51944	1.31	200		78	278
J	C0268		0.48919	1.43	74	150	63	287
J	C0007		0.08543	4.92	71	160	57	288
J	C1523		0.59156	1.05	73	142	62	277
J	C0352		0.65051	0.86	76	142	65	283
J	C1160		0.44933	1.60	79	141	64	284
J	C1067		0.39852	1.84	82	140	67	289
J	C1453		0.3588	2.05	79	142	62	283
J	C0026		0.39653	1.85	79	139	63	281

TABLE A2. Continued

Group	Probe	P<0.05	Prob	Chi-sq	# AA	# AB	# BB	Total
J	C1294		0.09255	4.76	78	132	53	263
J	C1184		0.19691	3.25	78	147	58	283
J	C0949		0.48191	1.46	75	139	61	275
J	C1446		0.29083	2.47	72	144	57	273
J	H2074	*	0.0216	7.67	67	164	54	285
K	C1924		0.77105	0.52	67	147	68	282
K	H2045D		0.93239	0.14	217		69	286
K	C1139		0.44486	1.62	62	149	67	278
K	C1400		0.90937	0.19	69	147	72	288
K	C1010		0.39653	1.85	75	133	80	288
K	C1093		0.6005	1.02	75	133	75	283
K	C0559		0.82283	0.39	74	136	68	278
K	C0307		0.10915	4.43	74	145	53	272
K	C0425A		0.80654	0.43	208		76	284
K	C0806		0.76338	0.54	71	145	65	281
K	C0463A		0.78663	0.48	204		75	279
K	C0947		0.16864	3.56	75	122	78	275
K	C0698		0.20291	3.19	81	129	78	288
L	C1978	**	0.00831	9.58	72	159	48	279
L	C0822	*	0.01649	8.21	72	153	48	273
L	C0538A	*	0.02573	7.32	73	157	51	281
L	C1451	*	0.01674	8.18	65	161	52	278
L	C0728		0.17291	3.51	78	145	57	280
L	C1517		0.13199	4.05	83	145	59	287
L	C0383	**	0.00557	10.38	88	141	50	279
L	C0619	**	0.00756	9.77	88	145	51	284
L	C0230	*	0.03206	6.88	86	139	55	280
L	H2045A		0.06298	5.53	226		53	279

TABLE A2. Continued

Group	Probe	P<0.05	Prob	Chi-sq	# AA	# AB	# BB	Total
L	C0628		0.62814	0.93	76	146	65	287
L	C0570		0.54607	1.21	220		63	283
L	C0481		0.8825	0.25	75	140	73	288
L	C0589		0.84366	0.34	76	140	73	289
L	C1524		0.59452	1.04	77	136	66	279
M	C1180		0.98511	0.03	73	145	71	289
M	C0181		0.50409	1.37	65	153	69	287
M	C0903		0.17204	3.52	76	153	58	287
M	C0282B		0.91393	0.18	203		72	275
M	C1177		0.46767	1.52	59	134	56	249
M	H2045B		0.80654	0.43	205		75	280
M	C0735		0.1979	3.24	62	154	62	278
M	C0252A		0.12185	4.21	60	158	64	282
M	C1109		0.67706	0.78	68	151	68	287
M	C1004		0.16447	3.61	63	158	63	284
M	H2178B		0.80252	0.44	210		64	274
M	C0873		0.76338	0.54	72	147	66	285
M	C0027		0.74082	0.60	72	148	66	286
M	C1440		0.68386	0.76	68	133	59	260
N	H2034		0.78663	0.48	204		75	279
N	C1754		0.3396	2.16	69	150	60	279
N	C0941		0.24051	2.85	72	155	60	287
N	C1145		0.1764	3.47	68	159	61	288
N	C0929		0.20909	3.13	67	155	60	282
N	C1965		0.11192	4.38	76	140	53	269
N	C1562		0.07353	5.22	77	155	55	287
N	C2303		0.25538	2.73	75	142	57	274
N	C0503		0.14734	3.83	75	146	55	276

TABLE A2. Continued

Group	Probe	P<0.05	Prob	Chi-sq	# AA	# AB	# BB	Total
N	C0205		0.83946	0.35	72	146	67	285
N	C2074		0.80252	0.44	66	144	67	277
N	C0057		0.85642	0.31	66	143	71	280
O	C0736A		0.27253	2.60	80	130	77	287
O	C2055		0.54881	1.20	78	137	66	281
O	C0316		0.96561	0.07	73	142	70	285
O	C0925		0.90937	0.19	75	143	70	288
O	C1135		0.90484	0.20	75	141	71	287
O	C0043		0.72979	0.63	75	134	71	280
O	C1905		0.60351	1.01	65	143	62	270
O	C1249		0.48191	1.46	68	153	65	286
O	C0485		0.75957	0.55	67	144	65	276
O	C1210		0.25795	2.71	68	145	56	269
O	C0296		0.76338	0.54	73	136	75	284
O	C0238		0.15961	3.67	59	119	77	255
O	C1256		0.32628	2.24	76	129	78	283
O	H2001		0.68729	0.75	73	135	76	284
O	H2074		0.89137	0.23	69	139	74	282
P	H2013		0.35169	2.09	73	154	62	289
P	C0747		0.53794	1.24	71	151	64	286
P	C0906		0.2982	2.42	74	154	61	289
P	C1423		0.22537	2.98	68	151	58	277
P	C0866		0.0696	5.33	75	157	55	287
P	C0704		0.12556	4.15	73	156	57	286
P	C1000		0.51944	1.31	72	147	62	281
P	C1418	**	0.00427	10.91	70	159	46	275
P	C0616	*	0.01657	8.20	71	161	51	283
P	H2151		0.89137	0.23	70	147	69	286

TABLE A2. Continued

Group	Probe	P<0.05	Prob	Chi-sq	# AA	# AB	# BB	Total
P	C1059	**	0.00223	12.21	61	172	53	286
Q	H2011		0.48191	1.46	79	134	68	281
Q	C0519		0.31506	2.31	81	133	66	280
Q	C2284		0.54064	1.23	75	138	62	275
Q	C1201		0.42105	1.73	79	133	66	278
Q	C1713		0.21331	3.09	72	143	55	270
Q	C1380		0.66698	0.81	72	146	64	282
Q	C1195		0.37344	1.97	68	152	62	282
Q	C0044		0.2982	2.42	64	153	63	280
Q	C0827		0.31037	2.34	66	153	62	281
Q	C0538B		0.92774	0.15	214		68	282
	C0592		0.25032	2.77	55	143	65	263

TABLE A3. Genetic linkage for seed oil percentage

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
A	C0562		0.7816	0.00	0.25	0.51	-0.11	0.84	43.75	43.89	44.25	0.55	0.40	0.52	58	110	67
A	C0433		0.7548	0.00	0.29	0.45	0.00	1.00	43.68	43.97	44.26	0.56	0.42	0.54	61	108	65
A	C2241		0.7172	0.00	0.07	0.85	0.44	0.43	43.77	44.28	43.92	0.55	0.40	0.53	60	115	65
A	C0266		0.8615	0.00	-0.01	0.99	0.31	0.59	43.83	44.13	43.82	0.58	0.41	0.54	55	113	63
A	C1161A		0.7423	0.00	-0.32	0.45	-0.10	0.86	44.29	43.87	43.64	0.61	0.37	0.62	49	130	47
A	C2246		0.8288	0.00	-0.24	0.58	-0.14	0.81	44.26	43.89	43.79	0.59	0.37	0.63	54	134	47
A	H2188		0.7941	0.00	-0.22	0.59	-0.23	0.68	44.33	43.88	43.89	0.57	0.37	0.58	56	133	55
A	C1500		0.7128	0.00	-0.30	0.46	-0.20	0.72	44.41	43.91	43.81	0.58	0.38	0.58	54	122	54
A	C0032		0.52	0.01	0.23	0.55	-0.56	0.31	44.03	43.71	44.50	0.53	0.38	0.58	65	125	54
A	C1174		0.169	0.01	0.26	0.53	-0.98	0.07	44.29	43.57	44.80	0.56	0.37	0.58	57	135	54
A	C2263		0.2739	0.01	0.46	0.26	-0.65	0.24	43.92	43.73	44.84	0.57	0.38	0.58	58	127	55
A	C0606		0.9143	0.00	0.17	0.68	0.03	0.95	43.77	43.97	44.10	0.56	0.39	0.56	58	122	58
A	C0689		0.6172	0.00	0.32	0.42	-0.31	0.58	43.86	43.87	44.51	0.57	0.38	0.56	55	123	57
A	C2007		0.9423	0.00	0.07	0.86	0.16	0.77	43.84	44.08	43.98	0.55	0.38	0.56	60	125	58
A	C0243		0.8621	0.00	0.21	0.60	0.08	0.89	43.72	44.01	44.14	0.55	0.39	0.56	60	124	58
A	C2028		0.9831	0.00	0.07	0.85	0.01	0.99	43.82	43.90	43.97	0.55	0.41	0.57	62	112	57
A	C0173		0.9571	0.00	0.11	0.77	0.03	0.95	43.90	44.05	44.13	0.56	0.40	0.55	59	117	61
B	C2005		0.3817	0.01	-0.32	0.42	0.61	0.27	43.97	44.26	43.34	0.56	0.39	0.54	58	121	62
B	C1087	***	0.0004	0.06	-1.53	0.00	0.04	0.95	45.59	44.10	42.53	0.58	0.37	0.50	51	121	67

TABLE A3. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
B	C0680	**	0.0092	0.04	-1.18	0.00	0.07	0.90	45.16	44.05	42.80	0.56	0.39	0.52	56	119	65
B	C1129	***	0.0002	0.07	-1.45	0.00	0.82	0.13	45.07	44.43	42.17	0.54	0.39	0.53	61	116	63
B	C0593	***	0.001	0.06	-1.42	0.00	0.31	0.57	45.29	44.18	42.45	0.55	0.37	0.53	58	126	62
B	C1165	****	0	0.11	-1.78	0.00	1.49	0.01	44.90	44.62	41.35	0.57	0.36	0.56	51	129	53
B	C0952	****	0.0000	0.10	-1.91	0.00	0.97	0.07	45.34	44.40	41.52	0.55	0.35	0.56	54	130	53
B	C0741	****	0.0000	0.13	-2.23	0.00	0.88	0.09	45.68	44.33	41.22	0.53	0.35	0.55	56	130	53
B	C0696	****	0.0000	0.13	-2.11	0.00	1.07	0.04	45.45	44.41	41.23	0.56	0.35	0.54	52	132	55
B	C0791	****	0.0000	0.13	-2.14	0.00	1.05	0.04	45.47	44.38	41.19	0.55	0.35	0.53	52	129	55
B	C1763	****	0.0000	0.14	-2.25	0.00	0.88	0.09	45.73	44.36	41.24	0.54	0.35	0.53	55	132	56
B	C2308	****	0.0000	0.15	-2.42	0.00	0.80	0.12	45.96	44.35	41.13	0.55	0.35	0.54	52	133	55
B	C0522	****	0.0000	0.12	-2.15	0.00	0.88	0.09	45.75	44.49	41.46	0.56	0.35	0.57	51	131	49
B	C0036A	****	0.0000	0.11	-2.03	0.00	0.80	0.12	45.59	44.37	41.53	0.55	0.35	0.55	54	136	55
B	C0284	****	0.0000	0.13	-2.35	0.00	0.65	0.21	45.88	44.18	41.18	0.56	0.34	0.56	50	140	50
B	C0082	****	0.0000	0.09	-2.01	0.00	0.44	0.41	45.57	44.00	41.54	0.55	0.34	0.61	55	140	45
C	C0050		0.0898	0.02	-0.74	0.08	0.79	0.16	44.27	44.32	42.79	0.59	0.36	0.62	53	142	48
C	C1395		0.2758	0.01	-0.63	0.13	0.35	0.52	44.42	44.14	43.16	0.58	0.36	0.61	55	142	49
C	C0460		0.0572	0.02	-0.50	0.23	1.19	0.04	43.86	44.55	42.85	0.59	0.38	0.60	53	131	51
C	C1378		0.0592	0.02	-0.70	0.09	0.95	0.08	44.16	44.41	42.77	0.56	0.36	0.59	57	136	52
C	C0838		0.1238	0.02	-0.57	0.16	0.84	0.13	43.94	44.21	42.79	0.57	0.39	0.58	56	121	54

TABLE A3. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
C	C1137	*	0.0286	0.03	-0.71	0.07	1.07	0.05	44.15	44.51	42.73	0.57	0.37	0.56	56	132	58
C	C2247		0.2914	0.01	-0.50	0.22	0.57	0.30	44.18	44.26	43.19	0.55	0.38	0.59	60	130	53
C	C0172		0.5954	0.00	0.39	0.31	-0.04	0.94	43.66	44.01	44.44	0.53	0.40	0.56	65	114	58
C	C0896		0.5339	0.01	0.41	0.31	-0.29	0.61	43.70	43.81	44.51	0.54	0.41	0.58	65	113	55
C	C0607		0.1271	0.02	0.76	0.05	-0.29	0.60	43.42	43.89	44.95	0.52	0.39	0.56	68	121	57
C	C1740		0.14	0.02	0.75	0.05	-0.26	0.64	43.44	43.93	44.93	0.53	0.41	0.56	67	112	60
D	C0713		0.671	0.00	-0.26	0.50	0.33	0.55	44.02	44.09	43.49	0.55	0.39	0.56	61	123	58
D	C2255		0.6653	0.00	-0.35	0.37	-0.07	0.90	44.41	44.00	43.72	0.56	0.39	0.52	57	119	65
D	C1373		0.4536	0.01	-0.47	0.24	0.25	0.65	44.34	44.12	43.40	0.58	0.37	0.57	55	134	57
D	C0463E		0.5097	0.01	-0.45	0.25	-0.03	0.96	44.38	43.90	43.47	0.57	0.39	0.54	57	119	63
D	C2008		0.6598	0.00	-0.35	0.39	-0.15	0.79	44.44	43.93	43.73	0.57	0.38	0.59	57	131	54
D	C0360		0.4008	0.01	-0.48	0.23	-0.33	0.55	44.62	43.81	43.67	0.55	0.38	0.57	59	127	56
D	H2169		0.4579	0.01	-0.43	0.28	-0.33	0.55	44.58	43.82	43.71	0.56	0.38	0.57	59	128	57
D	C0823		0.4133	0.01	-0.53	0.19	-0.13	0.82	44.59	43.94	43.54	0.56	0.37	0.57	58	131	56
E	C1203		0.5022	0.01	0.48	0.24	-0.07	0.89	43.55	43.96	44.51	0.54	0.37	0.62	63	133	47
E	C0810		0.8825	0.00	0.09	0.82	0.24	0.66	43.81	44.14	43.99	0.56	0.38	0.59	58	129	52
E	C0062		0.7841	0.00	0.23	0.56	-0.21	0.71	43.81	43.83	44.27	0.55	0.41	0.54	61	110	62
E	C1153		0.4974	0.01	0.37	0.34	0.39	0.48	43.39	44.15	44.13	0.55	0.39	0.53	60	120	64
E	C1170		0.5831	0.00	0.40	0.30	0.05	0.93	43.60	44.05	44.40	0.53	0.39	0.57	64	121	57

TABLE A3. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
E	C0431		0.8121	0.00	0.25	0.53	0.07	0.90	43.68	44.00	44.19	0.55	0.39	0.60	62	123	52
E	C1105		0.4471	0.01	0.49	0.21	-0.10	0.85	43.58	43.97	44.56	0.53	0.39	0.56	65	119	58
E	C0732		0.104	0.02	0.70	0.06	0.55	0.32	43.06	44.31	44.46	0.52	0.39	0.54	67	117	62
E	C0566		0.2656	0.01	0.49	0.21	0.53	0.33	43.19	44.22	44.17	0.53	0.38	0.57	64	123	56
E	C1138		0.4804	0.01	0.44	0.28	0.34	0.55	43.38	44.16	44.26	0.59	0.39	0.56	53	122	60
E	H2038		0.2532	0.01	0.61	0.12	0.26	0.64	43.24	44.11	44.47	0.54	0.39	0.56	62	118	57
F	C0865		0.469	0.01	-0.48	0.23	-0.08	0.88	44.52	43.95	43.55	0.55	0.38	0.58	62	128	55
F	C0496		0.3241	0.01	-0.43	0.27	-0.55	0.32	44.69	43.72	43.84	0.54	0.39	0.55	63	121	60
F	C0681		0.5369	0.01	-0.21	0.59	-0.55	0.32	44.37	43.61	43.95	0.56	0.40	0.54	59	115	63
F	C1437		0.291	0.01	-0.36	0.36	-0.69	0.21	44.64	43.59	43.92	0.54	0.39	0.57	62	120	56
F	C1696		0.0588	0.02	-0.98	0.02	-0.28	0.63	45.08	43.82	43.12	0.59	0.38	0.59	53	127	53
F	C1222		0.1696	0.01	-0.77	0.07	-0.14	0.81	44.79	43.89	43.25	0.56	0.37	0.62	59	134	48
F	C1997		0.138	0.02	-0.56	0.20	-0.81	0.16	45.03	43.65	43.90	0.58	0.37	0.66	54	130	42
F	C1176	*	0.0496	0.02	-0.93	0.03	-0.58	0.29	45.23	43.71	43.36	0.59	0.36	0.61	52	142	49
F	C0169		0.5065	0.01	-0.18	0.65	-0.59	0.28	44.49	43.72	44.13	0.56	0.38	0.54	58	125	63
G	C0357	*	0.0275	0.03	-1.01	0.02	-0.75	0.19	45.49	43.74	43.47	0.61	0.38	0.57	48	124	56
G	C0290	****	0	0.08	-1.82	0.00	-0.30	0.57	46.11	43.99	42.47	0.59	0.35	0.52	48	135	62
G	C0887	****	0	0.11	-2.13	0.00	-0.66	0.22	46.45	43.66	42.19	0.56	0.36	0.57	53	133	51
G	C1720	**	0.0074	0.04	-1.22	0.00	-0.70	0.22	45.50	43.58	43.06	0.58	0.39	0.61	54	121	49

TABLE A3. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
G	C0036C	**	0.0089	0.04	-1.06	0.01	-0.63	0.25	45.31	43.62	43.19	0.51	0.38	0.57	69	122	54
G	C1168	*	0.034	0.03	-1.02	0.01	-0.09	0.88	44.99	43.89	42.96	0.51	0.38	0.59	68	126	51
G	C1470		0.0676	0.02	-0.93	0.02	-0.02	0.98	44.85	43.91	43.00	0.52	0.38	0.60	66	126	50
G	C1002		0.1938	0.01	-0.65	0.11	-0.33	0.55	44.73	43.75	43.44	0.51	0.39	0.61	70	122	48
G	C0277B		0.2712	0.01	-0.65	0.14	-0.16	0.78	44.62	43.81	43.33	0.51	0.38	0.69	70	128	39
G	C1410A		0.1504	0.02	-0.84	0.06	0.05	0.93	44.65	43.87	42.98	0.51	0.37	0.71	70	136	36
G	C2286		0.1501	0.02	-0.79	0.07	-0.13	0.82	44.72	43.81	43.15	0.50	0.37	0.69	72	133	38
G	C0532		0.1512	0.02	-0.78	0.07	-0.13	0.82	44.70	43.79	43.14	0.50	0.36	0.69	71	135	38
G	C1242		0.3951	0.01	-0.22	0.62	-0.64	0.26	44.60	43.73	44.16	0.53	0.36	0.70	66	141	37
G	C1143		0.3311	0.01	-0.24	0.58	-0.69	0.23	44.50	43.58	44.02	0.50	0.37	0.71	72	132	36
G	C0667		0.3753	0.01	-0.26	0.57	-0.65	0.27	44.57	43.67	44.06	0.53	0.37	0.73	65	137	35
H	C0180		0.5978	0.00	-0.23	0.57	-0.48	0.40	44.34	43.63	43.88	0.58	0.39	0.56	55	121	59
H	C1715		0.2004	0.01	-0.42	0.31	-0.83	0.14	44.94	43.70	44.11	0.58	0.38	0.58	55	127	55
H	H2030		0.2191	0.01	-0.24	0.55	-0.89	0.11	44.71	43.59	44.23	0.55	0.37	0.58	60	131	55
H	C1131		0.1799	0.01	-0.24	0.54	-0.95	0.08	44.79	43.60	44.31	0.55	0.38	0.57	59	128	56
H	C1288		0.6988	0.00	0.31	0.43	-0.18	0.76	43.79	43.93	44.42	0.57	0.40	0.56	58	116	61
H	C1360		0.9908	0.00	0.06	0.89	-0.02	0.97	43.92	43.95	44.03	0.56	0.39	0.61	59	122	49
H	C1476		0.9429	0.00	0.04	0.93	-0.18	0.74	44.09	43.94	44.16	0.55	0.39	0.57	61	124	58
H	C0523		0.9724	0.00	0.09	0.83	0.05	0.93	43.73	43.87	43.91	0.56	0.39	0.57	59	121	56

TABLE A3. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
H	C0515		0.9327	0.00	0.03	0.94	-0.20	0.71	44.10	43.92	44.16	0.53	0.41	0.54	66	113	63
I	C1156	*	0.0247	0.03	-0.61	0.12	1.23	0.02	44.02	44.64	42.80	0.54	0.38	0.55	60	122	57
I	C1728	*	0.0322	0.03	-0.70	0.07	1.10	0.05	44.06	44.46	42.66	0.54	0.38	0.57	61	122	55
I	C1366	*	0.0262	0.03	-0.76	0.05	1.05	0.06	44.24	44.53	42.72	0.55	0.38	0.56	60	123	58
I	C1147	*	0.0306	0.03	-0.66	0.10	1.22	0.03	43.99	44.54	42.66	0.56	0.39	0.59	59	122	53
I	C0649		0.1933	0.01	-0.59	0.13	0.54	0.32	44.32	44.28	43.14	0.56	0.38	0.55	58	127	61
I	C1407		0.1471	0.02	-0.61	0.12	0.64	0.24	44.31	44.34	43.08	0.56	0.38	0.55	57	125	60
I	C0277A		0.3526	0.01	-0.52	0.19	0.31	0.57	44.35	44.13	43.30	0.56	0.38	0.56	58	127	59
I	C1410B		0.2808	0.01	-0.62	0.11	0.00	0.99	44.57	43.95	43.33	0.57	0.38	0.53	55	123	64
I	C0175		0.4505	0.01	-0.48	0.21	-0.09	0.86	44.52	43.95	43.57	0.54	0.39	0.53	59	117	63
I	C0331		0.36	0.01	-0.47	0.25	0.41	0.47	44.29	44.22	43.34	0.62	0.38	0.53	49	126	65
I	C1077		0.4733	0.01	-0.49	0.22	-0.15	0.79	44.62	43.98	43.63	0.62	0.38	0.52	47	130	69
I	C0717		0.3947	0.01	-0.44	0.30	-0.58	0.31	44.72	43.71	43.85	0.65	0.37	0.54	43	129	62
I	C1461		0.4637	0.01	-0.45	0.26	0.21	0.71	44.39	44.15	43.49	0.61	0.39	0.51	50	123	71
I	C1891		0.5838	0.01	-0.36	0.42	0.33	0.58	44.02	44.00	43.31	0.68	0.41	0.57	41	113	59
I	C0851		0.2199	0.01	-0.65	0.10	0.23	0.67	44.62	44.20	43.32	0.60	0.38	0.52	50	123	67
J	C0268		0.4841	0.01	-0.20	0.63	-0.58	0.30	44.49	43.72	44.10	0.52	0.38	0.62	68	128	48
J	C0007		0.0783	0.02	0.86	0.04	-0.62	0.26	43.55	43.78	45.26	0.55	0.36	0.62	60	138	47
J	C1523		0.161	0.02	0.77	0.06	-0.28	0.61	43.38	43.87	44.92	0.56	0.38	0.60	59	128	51

TABLE A3. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
J	C1160	*	0.0237	0.03	1.06	0.01	-0.48	0.38	43.21	43.79	45.32	0.53	0.37	0.59	63	127	52
J	C1067	*	0.0458	0.03	0.93	0.02	-0.50	0.36	43.38	43.81	45.23	0.52	0.38	0.58	66	126	54
J	C1453	*	0.0359	0.03	1.02	0.01	-0.11	0.83	43.02	43.93	45.06	0.53	0.37	0.59	63	126	51
J	C0026		0.0912	0.02	0.86	0.03	-0.33	0.55	43.33	43.85	45.04	0.53	0.38	0.59	64	124	52
J	C1294		0.2575	0.01	0.46	0.27	0.61	0.28	43.22	44.29	44.14	0.54	0.39	0.64	63	120	44
J	C1184		0.3292	0.01	0.44	0.28	0.50	0.37	43.31	44.25	44.20	0.53	0.38	0.63	65	130	47
J	C0949		0.5011	0.01	0.40	0.30	-0.33	0.54	43.81	43.87	44.60	0.51	0.38	0.57	66	115	53
J	C1446		0.4564	0.01	0.48	0.24	-0.29	0.60	43.71	43.90	44.68	0.55	0.39	0.61	61	122	49
J	H2074		0.2519	0.01	0.67	0.10	0.02	0.98	43.38	44.06	44.71	0.52	0.38	0.62	67	129	48
K	C1924		0.4436	0.01	-0.24	0.55	0.62	0.27	43.98	44.36	43.51	0.57	0.38	0.55	56	125	60
K	C1139	*	0.0476	0.03	-1.01	0.01	-0.02	0.96	45.02	43.98	43.00	0.59	0.37	0.56	51	129	56
K	C1400		0.1423	0.02	-0.71	0.07	0.37	0.50	44.55	44.21	43.14	0.57	0.38	0.53	56	125	65
K	C1010		0.2775	0.01	-0.60	0.11	-0.06	0.91	44.66	44.00	43.47	0.55	0.40	0.50	61	113	72
K	C1093		0.2385	0.01	-0.63	0.10	0.13	0.81	44.55	44.05	43.28	0.54	0.40	0.52	62	112	67
K	C0559		0.2129	0.01	-0.63	0.10	0.33	0.54	44.52	44.22	43.25	0.54	0.39	0.54	61	117	60
K	C0307		0.1787	0.02	-0.76	0.07	-0.17	0.77	44.85	43.91	43.32	0.56	0.38	0.64	58	126	45
K	C0806		0.288	0.01	-0.58	0.15	0.35	0.53	44.36	44.13	43.19	0.57	0.38	0.57	56	125	57
K	C0947	*	0.0304	0.03	-0.66	0.08	1.05	0.06	44.21	44.61	42.89	0.55	0.41	0.51	59	108	70
K	C0698		0.0647	0.02	-0.59	0.12	0.91	0.10	44.19	44.52	43.02	0.55	0.40	0.51	61	114	70

TABLE A3. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
L	C1978		0.4336	0.01	0.38	0.38	-0.61	0.29	44.03	43.80	44.79	0.56	0.37	0.67	60	136	42
L	C0822		0.7869	0.00	0.24	0.59	-0.28	0.62	43.95	43.90	44.42	0.57	0.37	0.66	56	135	42
L	C1451		0.7592	0.00	0.23	0.60	-0.31	0.59	43.86	43.78	44.33	0.61	0.36	0.64	49	143	45
L	C0728		0.6628	0.00	0.25	0.53	0.35	0.53	43.53	44.14	44.04	0.56	0.38	0.59	59	128	53
L	C1517		0.6961	0.00	0.32	0.42	0.13	0.81	43.61	44.06	44.25	0.54	0.38	0.59	63	127	54
L	C0383		0.6962	0.00	-0.08	0.84	0.48	0.40	43.83	44.23	43.66	0.53	0.39	0.64	66	126	46
L	C0619		0.8152	0.00	0.10	0.81	0.31	0.58	43.66	44.07	43.86	0.52	0.38	0.62	67	127	47
L	C0230		0.9776	0.00	-0.04	0.93	0.11	0.84	43.90	43.97	43.82	0.52	0.40	0.60	68	118	52
L	C0628	*	0.0263	0.03	-0.54	0.16	1.28	0.02	43.86	44.60	42.78	0.54	0.38	0.56	61	125	58
L	C0481		0.3685	0.01	-0.40	0.28	0.48	0.38	44.17	44.25	43.36	0.55	0.40	0.52	61	116	68
L	C0589		0.3394	0.01	-0.40	0.29	0.54	0.33	44.16	44.30	43.36	0.54	0.40	0.52	62	116	68
L	C1524		0.135	0.02	-0.58	0.14	0.75	0.18	44.25	44.41	43.08	0.56	0.40	0.55	60	116	61
M	C1180		0.7594	0.00	0.06	0.88	0.40	0.47	43.75	44.21	43.87	0.54	0.39	0.54	64	120	62
M	C0181		0.4315	0.01	0.22	0.59	0.66	0.24	43.41	44.29	43.85	0.58	0.37	0.56	55	131	58
M	C0903		0.3733	0.01	-0.23	0.58	0.74	0.18	43.80	44.31	43.34	0.53	0.37	0.61	64	132	49
M	C1177		0.3458	0.01	-0.61	0.16	-0.24	0.68	44.81	43.96	43.59	0.62	0.39	0.61	46	118	47
M	C0735		0.0838	0.02	-0.90	0.03	-0.33	0.56	44.99	43.76	43.18	0.59	0.37	0.60	52	134	51
M	C0252A		0.0802	0.02	-0.90	0.03	-0.35	0.52	45.06	43.81	43.26	0.59	0.36	0.58	51	137	54
M	C1109		0.08	0.02	-0.65	0.10	-0.85	0.12	45.08	43.58	43.78	0.56	0.38	0.56	58	128	58

TABLE A3. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
M	C1004		0.1176	0.02	-0.75	0.07	-0.55	0.32	44.99	43.69	43.49	0.58	0.37	0.58	53	134	54
M	C0873		0.3936	0.01	-0.42	0.28	-0.45	0.41	44.66	43.78	43.81	0.55	0.39	0.56	62	123	58
M	C0027		0.5539	0.00	-0.40	0.31	-0.22	0.69	44.52	43.90	43.72	0.56	0.38	0.56	59	127	58
M	C1440		0.6429	0.00	-0.38	0.36	0.11	0.84	44.38	44.11	43.62	0.57	0.40	0.59	56	115	52
N	H2034		0.2431	0.01	-0.14	0.74	-0.91	0.10	44.62	43.57	44.35	0.57	0.37	0.61	57	135	50
N	C1754		0.1003	0.02	-0.39	0.35	-1.08	0.06	44.98	43.52	44.21	0.58	0.38	0.60	56	131	51
N	C0941		0.115	0.02	-0.44	0.28	-0.94	0.09	44.90	43.52	44.02	0.55	0.37	0.59	59	134	51
N	C1145		0.2075	0.01	-0.30	0.46	-0.88	0.11	44.80	43.62	44.20	0.58	0.36	0.59	55	138	52
N	C0929		0.0896	0.02	-0.31	0.46	-1.16	0.04	44.97	43.50	44.35	0.58	0.37	0.60	54	134	51
N	C1965	***	0.0004	0.07	-0.58	0.15	-1.96	0.00	45.58	43.04	44.42	0.52	0.39	0.62	66	117	46
N	C1562	**	0.0018	0.05	-0.66	0.09	-1.59	0.00	45.44	43.18	44.11	0.50	0.37	0.61	69	128	48
N	C2303	***	0.0003	0.07	-0.74	0.06	-1.86	0.00	45.61	43.02	44.14	0.51	0.38	0.59	67	117	50
N	C0503	*	0.0126	0.04	-0.57	0.16	-1.37	0.02	45.24	43.29	44.10	0.52	0.39	0.61	68	119	49
N	C2074		0.1134	0.02	-0.75	0.06	-0.52	0.35	45.02	43.75	43.52	0.56	0.38	0.57	57	124	56
N	C0057		0.6583	0.00	-0.11	0.78	0.48	0.39	43.87	44.24	43.64	0.58	0.38	0.56	55	128	58
O	C0736A		0.8955	0.00	0.00	1.00	-0.26	0.64	44.12	43.86	44.11	0.52	0.40	0.55	68	115	62
O	C2055		0.4931	0.01	-0.46	0.25	-0.12	0.83	44.51	43.93	43.58	0.54	0.39	0.60	64	123	52
O	C0316		0.2227	0.01	-0.67	0.09	0.24	0.66	44.46	44.03	43.12	0.55	0.38	0.57	60	127	55
O	C0925		0.2045	0.01	-0.69	0.08	0.27	0.62	44.53	44.11	43.16	0.54	0.38	0.58	62	129	55

TABLE A3. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
O	C1135		0.1958	0.01	-0.69	0.08	0.28	0.61	44.53	44.12	43.15	0.54	0.38	0.57	62	127	56
O	C0043		0.3277	0.01	-0.58	0.14	-0.03	0.96	44.51	43.90	43.34	0.54	0.39	0.56	63	119	58
O	C1905		0.0982	0.02	-0.90	0.03	0.19	0.74	44.70	43.99	42.90	0.59	0.38	0.60	54	126	51
O	C1249		0.1371	0.02	-0.72	0.07	0.49	0.37	44.40	44.17	42.96	0.56	0.37	0.57	57	131	55
O	C1210		0.2384	0.01	-0.53	0.22	0.73	0.20	44.10	44.31	43.05	0.57	0.38	0.64	56	130	45
O	C0296		0.1209	0.02	-0.45	0.24	0.91	0.10	44.05	44.51	43.15	0.56	0.39	0.53	59	119	65
O	C0238		0.4087	0.01	-0.26	0.52	0.66	0.27	43.92	44.31	43.39	0.62	0.43	0.54	49	103	64
O	C1256	*	0.029	0.03	-0.40	0.28	1.32	0.02	43.85	44.77	43.05	0.54	0.40	0.51	61	110	70
O	H2001		0.0524	0.02	-0.43	0.26	1.16	0.04	43.81	44.54	42.95	0.55	0.40	0.52	60	114	67
O	H2074		0.136	0.02	-0.47	0.21	0.83	0.13	44.10	44.46	43.16	0.55	0.40	0.51	60	116	69
P	H2013		0.7158	0.00	0.32	0.43	0.10	0.85	43.63	44.06	44.27	0.56	0.37	0.57	58	132	56
P	C0747		0.3863	0.01	0.51	0.20	0.31	0.58	43.27	44.09	44.29	0.57	0.38	0.56	56	129	58
P	C0906		0.4555	0.01	0.42	0.29	0.36	0.51	43.40	44.18	44.24	0.56	0.37	0.58	59	132	55
P	C1423		0.1657	0.02	0.54	0.19	0.76	0.18	43.03	44.32	44.11	0.57	0.38	0.60	57	128	52
P	C0866		0.1465	0.02	0.42	0.30	0.88	0.11	43.12	44.42	43.97	0.55	0.37	0.60	61	133	50
P	C0704		0.5582	0.00	0.03	0.94	0.59	0.28	43.63	44.26	43.70	0.57	0.37	0.60	57	135	51
P	C1000		0.8838	0.00	0.16	0.69	-0.17	0.76	43.84	43.83	44.16	0.57	0.38	0.59	57	127	54
P	C1418		0.3042	0.01	0.50	0.26	-0.69	0.22	43.88	43.68	44.87	0.56	0.36	0.68	58	139	39
P	C0616		0.7778	0.00	0.16	0.70	-0.36	0.52	44.06	43.86	44.39	0.56	0.36	0.66	59	141	43

TABLE A3. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
P	H2151		0.4669	0.01	0.48	0.25	-0.30	0.59	43.70	43.88	44.67	0.57	0.36	0.63	57	139	47
P	C1059		0.4856	0.01	0.34	0.43	-0.53	0.34	44.01	43.81	44.68	0.58	0.35	0.63	53	144	46
Q	H2011		0.9169	0.00	-0.06	0.88	-0.21	0.70	44.15	43.88	44.03	0.51	0.39	0.56	68	114	56
Q	C0519		0.8396	0.00	0.21	0.59	-0.16	0.78	43.90	43.96	44.33	0.53	0.40	0.58	67	116	56
Q	C2284		0.4053	0.01	0.52	0.19	-0.18	0.75	43.58	43.92	44.61	0.53	0.39	0.57	64	118	54
Q	C1201		0.9199	0.00	0.15	0.69	-0.06	0.91	43.88	43.97	44.18	0.52	0.40	0.57	67	114	56
Q	C1713		0.3488	0.01	0.38	0.35	-0.67	0.24	43.89	43.60	44.66	0.55	0.40	0.61	61	119	51
Q	C1380		0.4822	0.01	0.35	0.38	-0.48	0.39	43.89	43.76	44.60	0.55	0.38	0.58	60	125	54
Q	C1195		0.216	0.01	0.64	0.12	0.42	0.45	43.09	44.15	44.37	0.57	0.37	0.60	57	132	51
Q	C0044		0.3102	0.01	0.63	0.13	0.12	0.83	43.34	44.08	44.59	0.58	0.36	0.59	53	136	52
Q	C0827		0.7138	0.00	0.24	0.56	0.31	0.58	43.59	44.15	44.08	0.58	0.37	0.60	55	134	51

*, **, ***, ****: Significance level of 0.05, 0.01, 0.001, and 0.0001, respectivelly.

RSQ: Coefficient of determination (R-square)

ADDIT and DOM: Additive and dominant effects, respectivelly.

ADPROB and DOPROB: Probability of significance for additive and dominant effects, respectively

MTAA, MTAB, and MTBB: Marker classes means for the trait

STAA, STAB, and STBB: Standard error of the marker class means.

NAA, NAB and NBB: Number of plants having each marker class.

TABLE A4. Genetic linkage for kernel oil percentage

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
A	C0562		0.6857	0.00	-0.15	0.66	-0.38	0.44	55.84	55.32	55.55	0.49	0.35	0.45	54	106	64
A	C0433		0.9598	0.00	0.06	0.87	-0.11	0.82	55.45	55.40	55.57	0.49	0.36	0.47	56	103	63
A	C2241		0.5911	0.00	-0.32	0.35	0.18	0.71	55.82	55.68	55.18	0.49	0.35	0.46	55	111	62
A	C0266		0.4211	0.01	-0.45	0.19	0.05	0.92	55.90	55.49	54.99	0.51	0.35	0.47	50	110	60
A	C1161A		0.294	0.01	-0.55	0.15	0.35	0.49	55.85	55.65	54.76	0.52	0.33	0.55	49	122	44
A	C2246		0.2586	0.01	-0.57	0.12	0.34	0.49	55.85	55.62	54.71	0.50	0.33	0.55	54	124	45
A	H2188		0.3909	0.01	-0.46	0.19	0.22	0.66	55.83	55.59	54.91	0.49	0.33	0.50	56	124	53
A	C1500		0.1217	0.02	-0.66	0.06	0.40	0.41	55.94	55.68	54.61	0.49	0.34	0.50	54	112	53
A	C0032		0.785	0.00	-0.21	0.55	0.19	0.70	55.58	55.56	55.17	0.46	0.34	0.51	63	117	52
A	C1174		0.7888	0.00	-0.17	0.64	0.25	0.61	55.55	55.63	55.21	0.50	0.33	0.51	54	128	52
A	C2263		0.6018	0.00	-0.09	0.80	0.48	0.33	55.39	55.78	55.21	0.50	0.34	0.51	56	119	53
A	C0606		0.2414	0.01	-0.12	0.74	0.81	0.10	55.18	55.87	54.94	0.48	0.34	0.50	57	115	54
A	C0689		0.7224	0.00	0.14	0.68	0.33	0.49	55.28	55.75	55.57	0.48	0.33	0.49	54	116	53
A	C2007		0.1713	0.02	-0.11	0.75	0.90	0.06	55.15	55.94	54.93	0.48	0.34	0.50	59	118	54
A	C0243		0.5184	0.01	-0.21	0.54	0.48	0.32	55.45	55.72	55.03	0.48	0.34	0.50	58	118	54
A	C2028		0.5429	0.01	-0.22	0.52	0.46	0.36	55.44	55.68	54.99	0.48	0.36	0.51	60	107	53
A	C0173		0.5675	0.01	-0.29	0.40	0.32	0.51	55.69	55.73	55.11	0.49	0.35	0.49	57	112	56
B	C2005		0.6232	0.00	-0.24	0.49	0.31	0.52	55.57	55.65	55.10	0.50	0.34	0.47	54	114	61
B	C1087	**	0.0074	0.04	-1.06	0.00	-0.15	0.74	56.72	55.51	54.60	0.51	0.33	0.44	48	113	66

TABLE A4. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
B	C0680		0.066	0.02	-0.79	0.02	-0.01	0.98	56.33	55.52	54.74	0.50	0.34	0.45	52	112	64
B	C1129	**	0.0022	0.05	-1.12	0.00	0.47	0.32	56.42	55.78	54.19	0.48	0.34	0.46	57	109	62
B	C0593	*	0.0244	0.03	-0.93	0.01	-0.10	0.83	56.53	55.49	54.67	0.49	0.33	0.47	54	119	61
B	C1165	***	0.0003	0.07	-1.24	0.00	1.05	0.03	56.21	56.02	53.73	0.53	0.33	0.50	47	123	52
B	C0952	****	0.0001	0.09	-1.45	0.00	0.82	0.08	56.49	55.86	53.59	0.49	0.31	0.49	51	124	50
B	C0741	****	0.0000	0.13	-1.85	0.00	0.91	0.05	56.79	55.85	53.10	0.47	0.31	0.48	53	124	50
B	C0696	****	0.0000	0.12	-1.69	0.00	0.98	0.03	56.58	55.87	53.20	0.49	0.31	0.48	49	126	52
B	C0791	****	0.0000	0.13	-1.80	0.00	0.88	0.06	56.75	55.84	53.16	0.49	0.31	0.48	49	123	52
B	C1763	****	0.0000	0.13	-1.87	0.00	0.72	0.12	56.97	55.82	53.22	0.48	0.31	0.47	52	126	53
B	C2308	****	0.0000	0.13	-1.92	0.00	0.70	0.13	57.04	55.81	53.19	0.49	0.31	0.48	50	126	52
B	C0522	****	0.0000	0.13	-1.91	0.00	0.81	0.08	57.03	55.93	53.21	0.49	0.30	0.51	48	126	45
B	C0036A	****	0.0000	0.10	-1.61	0.00	0.93	0.05	56.61	55.92	53.38	0.49	0.31	0.49	51	131	51
B	C0284	****	0.0000	0.11	-1.81	0.00	0.74	0.11	56.81	55.75	53.20	0.51	0.30	0.50	46	135	47
B	C0082	****	0.0000	0.08	-1.64	0.00	0.55	0.25	56.64	55.55	53.35	0.49	0.30	0.55	52	135	41
C	C0050		0.1336	0.02	-0.71	0.06	0.41	0.40	55.95	55.66	54.53	0.52	0.31	0.55	50	138	44
C	C1395	*	0.0466	0.03	-0.92	0.01	0.11	0.82	56.35	55.55	54.52	0.51	0.31	0.53	51	136	47
C	C0460		0.3339	0.01	-0.48	0.20	0.39	0.44	55.75	55.66	54.79	0.53	0.33	0.54	49	127	48
C	C1378		0.1587	0.02	-0.70	0.06	0.14	0.77	56.12	55.56	54.72	0.50	0.32	0.52	53	131	49
C	C0838		0.1765	0.02	-0.64	0.08	-0.29	0.56	56.16	55.23	54.88	0.51	0.34	0.51	52	116	51

TABLE A4. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
C	C1137	*	0.0392	0.03	-0.80	0.02	0.55	0.25	56.03	55.78	54.43	0.51	0.32	0.49	51	128	55
C	C2247		0.1328	0.02	-0.60	0.09	0.53	0.27	55.86	55.79	54.65	0.50	0.33	0.50	54	124	53
C	C0172		0.6105	0.00	0.29	0.39	0.24	0.62	55.07	55.60	55.65	0.48	0.35	0.48	58	110	58
C	C0896		0.7497	0.00	0.26	0.45	0.05	0.91	55.14	55.45	55.66	0.48	0.35	0.49	58	108	55
C	C0607		0.2634	0.01	0.52	0.13	-0.30	0.53	55.16	55.37	56.19	0.47	0.34	0.49	61	116	57
C	C1740		0.2831	0.01	0.52	0.13	-0.24	0.63	55.14	55.41	56.17	0.48	0.36	0.48	60	107	60
D	C0713		0.5943	0.00	-0.34	0.32	-0.12	0.80	55.84	55.38	55.16	0.48	0.34	0.49	57	118	55
D	C2255		0.9201	0.00	0.00	0.99	0.20	0.68	55.44	55.63	55.43	0.50	0.34	0.47	53	115	61
D	C1373		0.6281	0.00	-0.27	0.46	0.29	0.54	55.62	55.65	55.09	0.51	0.33	0.50	52	128	54
D	C0463E		0.649	0.00	-0.32	0.36	0.04	0.94	55.73	55.45	55.09	0.50	0.34	0.48	53	115	59
D	C2008		0.8902	0.00	-0.16	0.67	-0.10	0.83	55.72	55.46	55.41	0.51	0.33	0.52	53	127	50
D	C0360		0.6846	0.00	-0.23	0.52	-0.28	0.56	55.88	55.37	55.42	0.49	0.33	0.51	55	123	52
D	H2169		0.6269	0.00	-0.21	0.55	-0.36	0.46	55.92	55.34	55.49	0.49	0.33	0.51	56	124	53
D	C0823		0.7648	0.00	-0.26	0.47	-0.04	0.93	55.79	55.49	55.27	0.50	0.33	0.51	54	127	52
E	C1203		0.2519	0.01	0.60	0.10	-0.10	0.83	54.99	55.48	56.18	0.47	0.33	0.54	61	125	45
E	C0810		0.6833	0.00	0.31	0.38	-0.06	0.91	55.27	55.53	55.89	0.48	0.33	0.53	58	122	47
E	C0062		0.1603	0.02	0.54	0.11	-0.56	0.26	55.24	55.22	56.33	0.47	0.36	0.49	61	104	56
E	C1153		0.1517	0.02	0.65	0.05	-0.11	0.82	54.87	55.41	56.17	0.47	0.34	0.48	60	114	58
E	C1170		0.3706	0.01	0.49	0.16	-0.11	0.82	55.13	55.50	56.10	0.47	0.34	0.51	63	115	52

TABLE A4. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
E	C0431		0.5919	0.00	0.37	0.31	-0.04	0.94	55.16	55.49	55.89	0.47	0.34	0.54	61	117	47
E	C1105		0.2164	0.01	0.59	0.09	-0.21	0.67	55.08	55.46	56.26	0.46	0.35	0.51	64	113	53
E	C0732		0.2908	0.01	0.43	0.20	0.42	0.38	54.90	55.75	55.75	0.46	0.35	0.47	64	110	60
E	C0566		0.3349	0.01	0.39	0.25	0.43	0.37	54.84	55.66	55.62	0.47	0.34	0.50	59	118	54
E	C1138		0.6318	0.00	0.25	0.49	0.36	0.47	55.07	55.67	55.57	0.54	0.34	0.49	48	117	58
E	H2038		0.2921	0.01	0.50	0.15	0.30	0.53	54.80	55.60	55.79	0.49	0.35	0.49	57	113	55
F	C0865		0.3632	0.01	-0.01	0.98	0.69	0.16	55.17	55.85	55.15	0.47	0.34	0.50	61	118	54
F	C0496		0.9735	0.00	-0.06	0.85	0.07	0.89	55.53	55.54	55.41	0.47	0.35	0.48	62	111	59
F	C0681		0.9692	0.00	0.08	0.80	-0.01	0.99	55.32	55.39	55.48	0.48	0.36	0.46	58	105	62
F	C1437		0.9896	0.00	0.00	0.99	-0.07	0.89	55.48	55.41	55.49	0.47	0.35	0.49	61	110	56
F	C1696		0.6183	0.00	-0.36	0.33	0.06	0.90	55.78	55.48	55.06	0.51	0.34	0.52	52	118	51
F	C1222		0.3376	0.01	-0.32	0.38	0.62	0.21	55.45	55.75	54.82	0.48	0.33	0.54	58	125	46
F	C1997		0.6484	0.00	-0.32	0.40	-0.15	0.76	55.89	55.41	55.24	0.50	0.33	0.58	53	121	40
F	C1176		0.2403	0.01	-0.63	0.09	0.01	0.98	56.13	55.51	54.87	0.52	0.32	0.53	50	134	48
F	C0169		0.3351	0.01	-0.32	0.35	-0.57	0.23	56.14	55.24	55.50	0.50	0.34	0.47	54	119	61
G	C0357		0.3376	0.01	-0.26	0.48	-0.66	0.19	56.16	55.24	55.65	0.53	0.34	0.50	48	115	54
G	C0290		0.2809	0.01	-0.57	0.11	-0.01	0.99	56.13	55.55	54.98	0.53	0.33	0.48	48	126	59
G	C0887		0.2498	0.01	-0.51	0.17	-0.45	0.36	56.24	55.28	55.22	0.52	0.33	0.55	51	128	46
G	C1720		0.3689	0.01	-0.02	0.96	-0.73	0.16	55.89	55.14	55.85	0.51	0.35	0.57	54	116	44

TABLE A4. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
G	C0036C		0.5911	0.00	-0.02	0.96	-0.49	0.31	55.78	55.27	55.74	0.45	0.34	0.53	68	116	49
G	C1168		0.4461	0.01	0.11	0.76	-0.62	0.21	55.74	55.23	55.96	0.45	0.33	0.56	66	123	44
G	C1470		0.7125	0.00	0.12	0.75	-0.39	0.43	55.60	55.32	55.84	0.46	0.33	0.57	64	124	43
G	C1002		0.5714	0.00	0.26	0.47	-0.43	0.38	55.48	55.30	55.99	0.44	0.34	0.55	69	115	44
G	C0277B		0.7338	0.00	0.25	0.52	-0.31	0.55	55.45	55.38	55.94	0.45	0.34	0.63	69	121	35
G	C1410A		0.8824	0.00	0.07	0.87	-0.25	0.62	55.58	55.39	55.71	0.44	0.32	0.65	70	129	32
G	C2286		0.7367	0.00	0.14	0.72	-0.39	0.44	55.61	55.36	55.88	0.44	0.33	0.63	71	126	34
G	C0532		0.7902	0.00	0.08	0.84	-0.34	0.49	55.59	55.32	55.74	0.44	0.32	0.63	70	128	34
G	C1242		0.2887	0.01	0.46	0.24	-0.66	0.19	55.52	55.32	56.44	0.46	0.32	0.63	65	133	34
G	C1143		0.3746	0.01	0.24	0.55	-0.71	0.17	55.67	55.19	56.14	0.44	0.33	0.64	71	124	33
G	C0667		0.183	0.02	-0.01	0.97	-0.92	0.08	56.06	55.12	56.03	0.46	0.33	0.65	64	128	33
H	C0180		0.2011	0.01	0.30	0.40	-0.78	0.12	55.50	55.02	56.09	0.50	0.34	0.49	53	115	55
H	C1715		0.9524	0.00	0.00	1.00	-0.15	0.76	55.66	55.50	55.65	0.51	0.34	0.51	53	119	53
H	H2030		0.624	0.00	0.08	0.83	-0.46	0.34	55.69	55.30	55.84	0.49	0.33	0.51	57	124	53
H	C1131		0.5107	0.01	0.14	0.69	-0.53	0.27	55.66	55.27	55.94	0.48	0.33	0.50	57	121	54
H	C1288		0.4818	0.01	0.42	0.23	0.03	0.96	55.08	55.53	55.93	0.50	0.36	0.49	55	110	59
H	C1360		0.8912	0.00	0.15	0.67	0.10	0.84	55.23	55.48	55.53	0.49	0.34	0.53	56	115	47
H	C1476		0.789	0.00	0.24	0.49	-0.02	0.97	55.32	55.54	55.79	0.49	0.34	0.49	58	117	56
H	C0523		0.7749	0.00	0.24	0.49	0.08	0.88	55.10	55.42	55.59	0.49	0.34	0.50	56	115	53

TABLE A4. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
H	C0515		0.9242	0.00	0.05	0.89	0.18	0.71	55.42	55.65	55.51	0.47	0.36	0.47	63	106	61
I	C1156	*	0.0125	0.04	-0.98	0.01	0.50	0.30	56.29	55.80	54.33	0.48	0.33	0.50	56	118	53
I	C1728	*	0.0128	0.04	-1.01	0.00	0.35	0.47	56.25	55.59	54.24	0.48	0.33	0.50	57	119	51
I	C1366	**	0.004	0.05	-1.16	0.00	0.06	0.89	56.61	55.51	54.29	0.48	0.33	0.49	56	119	54
I	C1147	*	0.0144	0.04	-1.04	0.00	0.37	0.46	56.33	55.66	54.25	0.50	0.34	0.53	55	118	49
I	C0649	*	0.0325	0.03	-0.90	0.01	-0.23	0.63	56.55	55.42	54.75	0.50	0.33	0.48	54	123	57
I	C1407	*	0.0338	0.03	-0.91	0.01	-0.12	0.80	56.49	55.46	54.67	0.50	0.33	0.49	53	121	56
I	C0277A	*	0.0459	0.03	-0.86	0.01	-0.19	0.69	56.49	55.43	54.76	0.50	0.33	0.49	54	122	56
I	C1410B	**	0.0079	0.04	-1.03	0.00	-0.48	0.31	56.76	55.25	54.70	0.50	0.33	0.46	51	118	61
I	C0175	*	0.0463	0.03	-0.77	0.02	-0.45	0.34	56.53	55.31	54.99	0.48	0.33	0.46	55	112	60
I	C0331	*	0.031	0.03	-0.95	0.01	-0.08	0.87	56.57	55.54	54.67	0.54	0.33	0.47	45	122	61
I	C1077	*	0.0167	0.03	-0.97	0.01	-0.62	0.20	56.90	55.32	54.96	0.55	0.32	0.45	44	125	65
I	C0717		0.0503	0.03	-0.73	0.05	-0.80	0.10	56.64	55.11	55.19	0.55	0.32	0.47	41	123	58
I	C1461		0.0554	0.02	-0.83	0.02	-0.24	0.62	56.54	55.47	54.87	0.52	0.34	0.45	49	118	65
I	C1891		0.1665	0.02	-0.70	0.07	0.12	0.81	56.03	55.45	54.63	0.58	0.36	0.49	40	105	56
I	C0851		0.0509	0.03	-0.84	0.02	-0.20	0.67	56.55	55.51	54.88	0.51	0.34	0.45	49	115	64
J	C0268	*	0.0178	0.03	-0.39	0.27	-1.18	0.01	56.48	54.91	55.70	0.45	0.33	0.54	66	122	45
J	C0007		0.8258	0.00	0.02	0.96	-0.30	0.54	55.67	55.38	55.71	0.49	0.32	0.56	56	134	43
J	C1523		0.7846	0.00	-0.01	0.98	-0.34	0.49	55.69	55.34	55.67	0.50	0.33	0.54	54	126	46

TABLE A4. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
J	C1160		0.4738	0.01	0.30	0.40	-0.47	0.34	55.47	55.30	56.07	0.48	0.33	0.54	58	125	47
J	C1067		0.7049	0.00	0.15	0.68	-0.37	0.45	55.57	55.35	55.87	0.47	0.33	0.53	61	124	49
J	C1453		0.6425	0.00	0.32	0.37	-0.17	0.72	55.22	55.37	55.87	0.48	0.33	0.53	58	124	46
J	C0026		0.7704	0.00	0.15	0.67	-0.30	0.53	55.50	55.34	55.80	0.48	0.33	0.54	60	122	47
J	C1294		0.3276	0.01	-0.14	0.71	0.74	0.14	55.23	55.84	54.96	0.47	0.33	0.57	59	116	40
J	C1184		0.4734	0.01	0.01	0.97	0.60	0.23	55.16	55.77	55.19	0.47	0.33	0.56	61	125	44
J	C0949		0.5948	0.00	0.11	0.74	-0.48	0.33	55.63	55.26	55.85	0.47	0.35	0.51	61	110	52
J	C1446		0.6817	0.00	0.25	0.49	-0.29	0.56	55.43	55.39	55.93	0.49	0.35	0.53	57	114	49
J	H2074		0.7756	0.00	0.12	0.74	-0.32	0.51	55.57	55.37	55.81	0.47	0.33	0.53	61	123	48
K	C1924		0.8026	0.00	0.22	0.53	0.11	0.82	55.31	55.64	55.75	0.51	0.34	0.48	53	118	58
K	C1139		0.4128	0.01	-0.37	0.29	-0.41	0.40	56.08	55.29	55.33	0.51	0.32	0.49	49	123	53
K	C1400		0.6363	0.00	-0.27	0.44	-0.28	0.56	55.94	55.39	55.40	0.50	0.34	0.47	54	118	62
K	C1010		0.1768	0.01	-0.42	0.20	-0.68	0.16	56.27	55.17	55.43	0.48	0.35	0.44	58	107	69
K	C1093		0.3489	0.01	-0.38	0.25	-0.46	0.35	56.10	55.26	55.34	0.48	0.36	0.46	59	105	65
K	C0559		0.1266	0.02	-0.60	0.07	-0.47	0.33	56.38	55.30	55.18	0.48	0.35	0.48	58	110	58
K	C0307		0.0549	0.03	-0.76	0.04	-0.54	0.28	56.56	55.26	55.04	0.49	0.34	0.54	55	117	45
K	C0806		0.1819	0.02	-0.59	0.09	-0.39	0.43	56.29	55.31	55.11	0.50	0.34	0.49	53	118	55
K	C0947		0.0769	0.02	-0.69	0.04	0.37	0.44	56.07	55.75	54.68	0.49	0.36	0.45	55	104	66
K	C0698		0.2375	0.01	-0.51	0.12	0.31	0.52	55.90	55.69	54.87	0.49	0.35	0.45	57	110	66

TABLE A4. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
L	C1978		0.0945	0.02	0.82	0.03	-0.24	0.63	54.91	55.49	56.56	0.49	0.33	0.58	58	127	41
L	C0822		0.2226	0.01	0.64	0.09	-0.26	0.60	55.07	55.45	56.34	0.50	0.32	0.56	53	127	42
L	C1451		0.3988	0.01	0.45	0.24	-0.34	0.49	55.14	55.25	56.04	0.54	0.32	0.55	46	134	45
L	C0728		0.9678	0.00	0.03	0.94	-0.12	0.81	55.53	55.43	55.58	0.50	0.33	0.51	54	123	51
L	C1517		0.9235	0.00	0.04	0.92	-0.19	0.70	55.57	55.41	55.64	0.49	0.34	0.51	58	122	52
L	C0383		0.7649	0.00	-0.16	0.66	0.31	0.53	55.48	55.63	55.16	0.48	0.34	0.55	61	120	45
L	C0619		0.9652	0.00	-0.08	0.83	0.09	0.86	55.45	55.46	55.30	0.47	0.33	0.54	62	121	46
L	C0230		0.6992	0.00	-0.23	0.52	-0.24	0.62	55.83	55.36	55.37	0.47	0.35	0.52	63	113	51
L	C0628		0.3446	0.01	-0.37	0.28	0.47	0.33	55.61	55.71	54.86	0.49	0.33	0.49	55	121	56
L	C0481		0.2473	0.01	-0.30	0.37	0.65	0.18	55.50	55.84	54.89	0.50	0.34	0.45	54	113	66
L	C0589		0.208	0.01	-0.29	0.38	0.71	0.14	55.48	55.90	54.89	0.49	0.34	0.45	55	113	66
L	C1524		0.3746	0.01	-0.32	0.37	0.52	0.30	55.58	55.78	54.94	0.51	0.35	0.48	54	113	59
M	C1180		0.993	0.00	-0.03	0.93	-0.04	0.93	55.57	55.50	55.51	0.48	0.34	0.49	60	118	56
M	C0181		0.9781	0.00	0.07	0.86	-0.05	0.92	55.45	55.46	55.58	0.52	0.32	0.51	50	130	52
M	C0903		0.8898	0.00	-0.18	0.63	0.06	0.91	55.62	55.51	55.27	0.48	0.32	0.56	60	130	43
M	C1177		0.3684	0.01	-0.46	0.24	-0.41	0.42	56.10	55.23	55.19	0.55	0.34	0.54	44	113	46
M	C0735		0.3132	0.01	-0.54	0.14	-0.21	0.67	56.07	55.32	54.99	0.52	0.33	0.52	50	126	49
M	C0252A		0.2009	0.01	-0.59	0.10	-0.38	0.43	56.29	55.31	55.11	0.52	0.32	0.51	49	129	52
M	C1109		0.0633	0.02	-0.43	0.22	-0.97	0.05	56.43	55.03	55.57	0.49	0.33	0.49	56	120	56

TABLE A4. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
M	C1004		0.1296	0.02	-0.50	0.16	-0.72	0.14	56.34	55.12	55.34	0.51	0.32	0.50	51	127	52
M	C0873		0.4853	0.01	-0.36	0.30	-0.28	0.56	56.02	55.37	55.30	0.48	0.35	0.49	60	114	57
M	C0027		0.4799	0.01	-0.41	0.23	-0.11	0.82	55.98	55.46	55.16	0.49	0.34	0.49	57	118	57
M	C1440		0.4657	0.01	-0.43	0.22	-0.10	0.84	56.00	55.48	55.15	0.49	0.35	0.50	54	108	51
N	H2034		0.4146	0.01	0.42	0.25	-0.35	0.48	55.27	55.34	56.11	0.51	0.33	0.53	53	128	49
N	C1754		0.4914	0.01	0.26	0.48	-0.48	0.34	55.55	55.33	56.07	0.52	0.34	0.52	52	123	51
N	C0941		0.5824	0.00	0.22	0.54	-0.41	0.39	55.47	55.28	55.91	0.49	0.33	0.51	55	126	51
N	C1145		0.4329	0.01	0.33	0.37	-0.45	0.36	55.43	55.31	56.09	0.52	0.32	0.51	51	130	52
N	C0929		0.256	0.01	0.53	0.15	-0.40	0.42	55.21	55.35	56.28	0.52	0.33	0.52	51	128	50
N	C1965	*	0.0193	0.04	0.44	0.22	-1.33	0.01	55.82	54.93	56.70	0.46	0.34	0.55	61	112	44
N	C1562		0.074	0.02	0.34	0.34	-1.06	0.03	55.76	55.04	56.44	0.46	0.33	0.54	64	123	46
N	C2303	*	0.0106	0.04	0.18	0.61	-1.49	0.00	56.14	54.83	56.50	0.46	0.34	0.53	62	113	48
N	C0503		0.0824	0.02	0.38	0.29	-1.03	0.04	55.70	55.05	56.46	0.46	0.34	0.54	63	115	47
N	C2074		0.4198	0.01	0.24	0.50	-0.55	0.26	55.54	55.22	56.01	0.50	0.34	0.50	54	118	54
N	C0057		0.8969	0.00	-0.06	0.87	0.21	0.67	55.48	55.63	55.36	0.51	0.33	0.49	52	122	55
O	C0736A		0.8746	0.00	-0.06	0.86	0.24	0.62	55.45	55.64	55.34	0.46	0.35	0.49	66	110	57
O	C2055		0.8632	0.00	-0.17	0.63	0.14	0.78	55.64	55.61	55.30	0.47	0.35	0.53	62	116	50
O	C0316		0.4411	0.01	-0.18	0.60	0.57	0.23	55.32	55.71	54.95	0.48	0.33	0.51	58	121	51
O	C0925		0.3051	0.01	-0.26	0.46	0.67	0.16	55.41	55.83	54.89	0.47	0.33	0.51	60	123	51

TABLE A4. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
O	C1135		0.2875	0.01	-0.26	0.46	0.69	0.15	55.41	55.84	54.89	0.48	0.33	0.51	60	121	52
O	C0043		0.7174	0.00	-0.11	0.75	0.37	0.44	55.38	55.64	55.16	0.47	0.35	0.50	61	113	54
O	C1905		0.3312	0.01	-0.31	0.40	0.64	0.21	55.42	55.74	54.79	0.51	0.34	0.54	52	120	47
O	C1249		0.3686	0.01	-0.11	0.77	0.67	0.17	55.19	55.76	54.98	0.49	0.33	0.51	55	125	51
O	C1210		0.1092	0.02	-0.39	0.30	0.98	0.05	55.30	55.89	54.51	0.51	0.33	0.57	53	125	42
O	C0296		0.2059	0.01	-0.29	0.39	0.75	0.12	55.45	55.91	54.87	0.49	0.34	0.47	56	115	60
O	C0238		0.7994	0.00	-0.20	0.58	0.17	0.74	55.61	55.58	55.21	0.54	0.37	0.48	47	99	58
O	C1256		0.1743	0.02	-0.34	0.31	0.75	0.13	55.55	55.96	54.88	0.48	0.36	0.45	59	105	66
O	H2001		0.2764	0.01	-0.31	0.36	0.62	0.20	55.45	55.77	54.84	0.48	0.35	0.46	57	109	63
O	H2074		0.4376	0.01	-0.28	0.40	0.45	0.35	55.60	55.77	55.03	0.48	0.35	0.46	58	110	65
P	H2013		0.9417	0.00	0.09	0.80	0.11	0.82	55.36	55.57	55.55	0.50	0.33	0.50	54	125	55
P	C0747		0.677	0.00	0.26	0.46	0.24	0.61	55.06	55.57	55.58	0.51	0.33	0.49	51	123	57
P	C0906		0.7237	0.00	0.09	0.81	0.37	0.44	55.23	55.69	55.40	0.50	0.33	0.50	54	126	54
P	C1423		0.5963	0.00	0.21	0.58	0.43	0.40	55.06	55.70	55.48	0.52	0.34	0.52	51	123	51
P	C0866		0.3886	0.01	0.12	0.74	0.65	0.19	55.05	55.81	55.28	0.50	0.33	0.53	55	128	49
P	C0704		0.5662	0.00	0.00	1.00	0.52	0.29	55.22	55.74	55.22	0.51	0.33	0.52	53	128	50
P	C1000		0.2532	0.01	0.02	0.96	0.81	0.10	54.98	55.81	55.01	0.50	0.34	0.50	53	119	54
P	C1418		0.9975	0.00	0.03	0.94	-0.01	0.98	55.46	55.47	55.51	0.50	0.32	0.59	53	133	38
P	C0616		0.7356	0.00	-0.17	0.66	0.34	0.49	55.50	55.67	55.16	0.50	0.32	0.57	54	135	42

TABLE A4. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
P	H2151		0.5154	0.01	0.22	0.55	0.47	0.34	55.02	55.70	55.46	0.51	0.32	0.54	52	133	46
P	C1059		0.9343	0.00	0.11	0.77	-0.12	0.81	55.49	55.48	55.71	0.52	0.31	0.55	49	138	44
Q	H2011		0.2618	0.01	0.52	0.12	0.16	0.73	54.94	55.61	55.97	0.43	0.34	0.49	67	107	52
Q	C0519		0.0903	0.02	0.72	0.03	0.20	0.69	54.75	55.67	56.20	0.45	0.35	0.51	66	109	53
Q	C2284	*	0.0211	0.03	0.92	0.01	0.24	0.62	54.54	55.70	56.38	0.45	0.34	0.50	63	110	51
Q	C1201		0.1291	0.02	0.62	0.06	0.31	0.52	54.76	55.69	56.00	0.44	0.35	0.50	66	107	52
Q	C1713	*	0.0363	0.03	0.87	0.01	-0.50	0.32	54.87	55.24	56.62	0.47	0.35	0.53	60	111	48
Q	C1380	*	0.0404	0.03	0.88	0.01	-0.35	0.47	54.88	55.41	56.64	0.48	0.34	0.52	59	119	49
Q	C1195	**	0.0029	0.05	1.10	0.00	0.64	0.18	54.12	55.87	56.33	0.48	0.32	0.53	57	125	47
Q	C0044	*	0.0109	0.04	1.05	0.00	0.28	0.56	54.35	55.68	56.45	0.49	0.31	0.52	53	130	47
Q	C0827		0.0793	0.02	0.71	0.05	0.47	0.32	54.56	55.75	55.99	0.49	0.32	0.52	54	127	47

*, **, ***, ****: Significance level of 0.05, 0.01, 0.001, and 0.0001, respectivelly.

RSQ: Coefficient of determination (R-square)

ADDIT and DOM: Additive and dominant effects, respectivelly.

ADPROB and DOPROB: Probability of significance for additive and dominant effects, respectively

MTAA, MTAB, and MTBB: Marker classes means for the trait

STAA, STAB, and STBB: Standard error of the marker class means.

NAA, NAB and NBB: Number of plants having each marker class.

TABLE A5. Genetic linkage for kernel percentage

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
A	C0562		0.9782	0.00	-0.02	0.97	0.12	0.84	68.93	69.03	68.89	0.60	0.43	0.55	54	106	64
A	C0433		0.8707	0.00	-0.14	0.74	0.24	0.69	68.89	69.00	68.62	0.61	0.45	0.57	56	103	63
A	C2241		0.7455	0.00	-0.31	0.46	-0.13	0.83	69.35	68.91	68.73	0.61	0.43	0.57	55	111	62
A	C0266		0.8069	0.00	-0.15	0.73	-0.36	0.56	69.18	68.67	68.88	0.65	0.44	0.59	50	110	60
A	C1161A		0.7895	0.00	-0.11	0.81	0.39	0.51	68.71	69.00	68.50	0.62	0.39	0.66	49	122	44
A	C2246		0.8357	0.00	0.27	0.55	0.01	0.98	68.52	68.81	69.07	0.62	0.41	0.68	54	124	45
A	H2188		0.7141	0.00	0.34	0.44	-0.16	0.79	68.64	68.82	69.32	0.60	0.41	0.62	56	124	53
A	C1500		0.5687	0.01	0.46	0.29	0.03	0.96	68.41	68.89	69.32	0.60	0.42	0.61	54	112	53
A	C0032		0.0505	0.03	1.02	0.02	-0.34	0.57	68.08	68.76	70.12	0.56	0.41	0.62	63	117	52
A	C1174		0.3439	0.01	0.61	0.16	-0.26	0.66	68.43	68.78	69.65	0.61	0.40	0.62	54	128	52
A	C2263		0.0889	0.02	0.90	0.04	-0.44	0.46	68.25	68.71	70.06	0.60	0.41	0.62	56	119	53
A	C0606		0.2066	0.01	0.62	0.15	0.62	0.31	67.93	69.17	69.17	0.60	0.42	0.62	57	115	54
A	C0689		0.6367	0.00	0.38	0.38	0.22	0.71	68.46	69.07	69.23	0.62	0.42	0.62	54	116	53
A	C2007		0.433	0.01	0.49	0.25	0.33	0.58	68.24	69.06	69.22	0.59	0.42	0.62	59	118	54
A	C0243		0.4591	0.01	0.50	0.24	0.25	0.68	68.24	68.99	69.24	0.59	0.42	0.62	58	118	54
A	C2028		0.439	0.01	0.55	0.20	0.05	0.94	68.25	68.85	69.36	0.59	0.44	0.63	60	107	53
A	C0173		0.3971	0.01	0.57	0.17	0.00	1.00	68.37	68.95	69.52	0.59	0.42	0.60	57	112	56
B	C2005		0.1242	0.02	-0.68	0.11	-0.78	0.19	69.96	68.50	68.61	0.61	0.42	0.57	54	114	61
B	C1087	*	0.0402	0.03	-1.02	0.02	-0.67	0.26	70.33	68.65	68.30	0.64	0.42	0.55	48	113	66

TABLE A5. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
B	C0680		0.0758	0.02	-0.87	0.04	-0.66	0.27	70.12	68.58	68.37	0.62	0.43	0.56	52	112	64
B	C1129		0.0655	0.02	-0.95	0.02	-0.33	0.59	69.96	68.69	68.06	0.60	0.43	0.57	57	109	62
B	C0593		0.0954	0.02	-0.86	0.04	-0.47	0.43	70.02	68.69	68.30	0.61	0.41	0.57	54	119	61
B	C1165	**	0.0013	0.06	-1.64	0.00	0.01	0.99	70.43	68.80	67.15	0.64	0.40	0.61	47	123	52
B	C0952	*	0.0204	0.03	-1.24	0.01	0.23	0.70	69.98	68.97	67.50	0.63	0.40	0.63	51	124	50
B	C0741	**	0.0026	0.05	-1.50	0.00	0.46	0.44	70.13	69.10	67.14	0.61	0.40	0.63	53	124	50
B	C0696	**	0.0014	0.06	-1.60	0.00	0.12	0.83	70.47	68.99	67.27	0.63	0.39	0.61	49	126	52
B	C0791	**	0.0021	0.05	-1.53	0.00	0.33	0.58	70.27	69.07	67.21	0.62	0.39	0.61	49	123	52
B	C1763	**	0.0042	0.05	-1.42	0.00	0.29	0.62	70.10	68.97	67.26	0.61	0.39	0.60	52	126	53
B	C2308	**	0.0037	0.05	-1.44	0.00	0.40	0.50	70.02	68.98	67.13	0.62	0.39	0.61	50	126	52
B	C0522	*	0.0232	0.03	-1.26	0.01	0.31	0.61	69.90	58.94	67.38	0.64	0.40	0.66	48	126	45
B	C0036A	**	0.0045	0.05	-1.45	0.00	0.16	0.78	70.24	68.95	67.33	0.62	0.39	0.62	51	131	51
B	C0284	**	0.0099	0.04	-1.38	0.00	0.32	0.59	70.00	68.94	67.23	0.65	0.38	0.64	46	135	47
B	C0082	***	0.0003	0.07	-1.89	0.00	0.12	0.84	70.63	68.87	66.85	0.61	0.38	0.68	52	135	41
C	C0050		0.6312	0.00	-0.43	0.36	0.19	0.75	69.18	68.94	68.32	0.64	0.39	0.68	50	138	44
C	C1395		0.447	0.01	-0.44	0.34	0.52	0.39	69.02	69.10	68.15	0.63	0.39	0.66	51	136	47
C	C0460		0.3478	0.01	-0.49	0.29	0.62	0.31	68.98	69.11	68.00	0.65	0.40	0.66	49	127	48
C	C1378		0.2806	0.01	-0.60	0.18	0.53	0.37	69.19	69.11	67.98	0.62	0.39	0.64	53	131	49
C	C0838		0.1418	0.02	-0.71	0.10	0.68	0.26	69.19	69.16	67.76	0.61	0.41	0.62	52	116	51

TABLE A5. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
C	C1137		0.1809	0.01	-0.41	0.35	0.93	0.12	68.80	69.32	67.98	0.63	0.40	0.61	51	128	55
C	C2247		0.1284	0.02	-0.69	0.11	0.76	0.20	69.17	69.24	67.79	0.61	0.40	0.62	54	124	53
C	C0172		0.5956	0.00	-0.41	0.33	-0.19	0.75	69.38	68.78	68.57	0.59	0.43	0.59	58	110	58
C	C0896		0.4246	0.01	-0.49	0.25	-0.37	0.54	69.52	68.65	68.53	0.60	0.44	0.62	58	108	55
C	C0607		0.6911	0.00	0.03	0.94	-0.51	0.39	69.11	68.64	69.18	0.58	0.42	0.60	61	116	57
C	C1740		0.6049	0.00	-0.01	0.98	-0.60	0.32	69.18	68.57	69.17	0.59	0.44	0.59	60	107	60
D	C0713		0.7574	0.00	-0.17	0.70	0.38	0.52	68.88	69.09	68.55	0.60	0.42	0.61	57	118	55
D	C2255		0.436	0.01	-0.42	0.32	0.46	0.44	69.15	69.19	68.31	0.62	0.42	0.58	53	115	61
D	C1373		0.5851	0.00	-0.18	0.68	0.56	0.35	68.77	69.15	68.41	0.63	0.40	0.61	52	128	54
D	C0463E		0.7638	0.00	-0.27	0.53	0.22	0.72	69.06	69.01	68.53	0.62	0.42	0.59	53	115	59
D	C2008		0.8799	0.00	-0.13	0.78	-0.25	0.68	69.13	68.76	68.88	0.62	0.40	0.64	53	127	50
D	C0360		0.9354	0.00	-0.15	0.73	-0.07	0.91	69.09	68.87	68.79	0.61	0.41	0.63	55	123	52
D	H2169		0.8939	0.00	-0.17	0.70	-0.16	0.79	69.12	68.80	68.79	0.60	0.41	0.62	56	124	53
D	C0823		0.8891	0.00	-0.21	0.64	-0.05	0.93	69.13	68.87	68.71	0.62	0.40	0.63	54	127	52
E	C1203		0.8861	0.00	-0.21	0.63	-0.04	0.95	69.11	68.86	68.69	0.58	0.41	0.68	61	125	45
E	C0810		0.6545	0.00	-0.23	0.60	0.48	0.42	68.84	69.10	68.38	0.60	0.41	0.66	58	122	47
E	C0062		0.6538	0.00	-0.11	0.79	0.55	0.37	68.74	69.17	68.52	0.58	0.44	0.61	61	104	56
E	C1153		0.7541	0.00	0.19	0.65	0.35	0.56	68.57	69.11	68.95	0.58	0.42	0.59	60	114	58
E	C1170		0.9209	0.00	-0.06	0.90	0.23	0.70	68.84	69.02	68.73	0.56	0.42	0.62	63	115	52

TABLE A5. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
E	C0431		0.955	0.00	-0.10	0.82	0.14	0.82	68.92	68.96	68.72	0.58	0.42	0.66	61	117	47
E	C1105		0.8946	0.00	-0.17	0.69	0.16	0.79	68.98	68.97	68.64	0.57	0.43	0.62	64	113	53
E	C0732		0.5718	0.00	0.23	0.57	0.52	0.38	68.42	69.17	68.88	0.56	0.43	0.58	64	110	60
E	C0566		0.8826	0.00	0.16	0.71	0.19	0.75	68.66	69.01	68.98	0.59	0.41	0.61	59	118	54
E	C1138		0.809	0.00	0.14	0.75	-0.33	0.59	68.96	68.77	69.24	0.65	0.42	0.59	48	117	58
E	H2038		0.7003	0.00	0.36	0.40	-0.05	0.94	68.49	68.81	69.22	0.61	0.43	0.62	57	113	55
F	C0865		0.7777	0.00	-0.11	0.79	0.40	0.51	68.80	69.08	68.57	0.58	0.42	0.62	61	118	54
F	C0496		0.2429	0.01	-0.25	0.55	0.94	0.11	68.69	69.39	68.20	0.57	0.43	0.59	62	111	59
F	C0681		0.5934	0.00	-0.09	0.84	0.61	0.32	68.64	69.16	68.47	0.60	0.45	0.58	58	105	62
F	C1437		0.3791	0.01	-0.31	0.46	0.72	0.23	68.89	69.30	68.27	0.58	0.43	0.60	61	110	56
F	C1696		0.5483	0.01	-0.36	0.41	0.44	0.46	69.04	69.12	68.31	0.62	0.41	0.63	52	118	51
F	C1222		0.3579	0.01	-0.62	0.17	-0.18	0.76	69.53	68.74	68.30	0.60	0.41	0.67	58	125	46
F	C1997		0.4887	0.01	-0.13	0.78	-0.72	0.26	69.34	68.49	69.07	0.63	0.42	0.73	53	121	40
F	C1176		0.2725	0.01	-0.61	0.18	-0.53	0.37	69.80	68.66	68.58	0.64	0.39	0.65	50	134	48
F	C0169		0.4306	0.01	-0.46	0.28	-0.44	0.45	69.59	68.69	68.67	0.61	0.41	0.58	54	119	61
G	C0357		0.2461	0.01	-0.74	0.10	0.04	0.95	69.67	68.97	68.19	0.64	0.42	0.61	48	115	54
G	C0290	**	0.0031	0.05	-1.38	0.00	-0.84	0.15	70.81	68.60	68.05	0.64	0.39	0.57	48	126	59
G	C0887	**	0.0032	0.05	-1.32	0.00	-1.00	0.10	70.67	68.34	68.02	0.62	0.39	0.65	51	128	46
G	C1720		0.2141	0.01	-0.57	0.22	-0.74	0.24	69.80	68.49	68.66	0.62	0.42	0.69	54	116	44

TABLE A5. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
G	C0036C		0.1806	0.01	-0.33	0.43	-0.93	0.12	69.65	68.38	68.98	0.54	0.42	0.64	68	116	49
G	C1168		0.5658	0.00	-0.44	0.32	-0.15	0.80	69.35	68.76	68.48	0.56	0.41	0.68	66	123	44
G	C1470		0.7263	0.00	-0.35	0.43	0.01	0.99	69.22	68.87	68.51	0.57	0.41	0.69	64	124	43
G	C1002		0.4522	0.01	-0.54	0.21	0.25	0.69	69.20	68.90	68.11	0.55	0.42	0.68	69	115	44
G	C0277B		0.6658	0.00	-0.41	0.38	0.28	0.66	69.03	68.89	68.20	0.55	0.42	0.77	69	121	35
G	C1410A		0.3208	0.01	-0.62	0.20	0.69	0.26	68.99	69.06	67.75	0.54	0.39	0.79	70	129	32
G	C2286		0.4236	0.01	-0.56	0.23	0.51	0.40	69.00	68.95	67.88	0.53	0.40	0.77	71	126	34
G	C0532		0.2586	0.01	-0.57	0.22	0.85	0.17	68.94	69.22	67.79	0.54	0.40	0.77	70	128	34
G	C1242		0.5782	0.00	-0.42	0.38	0.48	0.44	68.98	69.05	68.15	0.56	0.39	0.78	65	133	34
G	C1143		0.9736	0.00	-0.09	0.85	0.12	0.85	68.87	68.90	68.70	0.54	0.41	0.80	71	124	33
G	C0667		0.8059	0.00	-0.26	0.58	0.30	0.63	68.98	69.02	68.45	0.56	0.40	0.78	64	128	33
H	C0180		0.5716	0.01	0.44	0.32	-0.20	0.75	68.47	68.71	69.35	0.62	0.42	0.61	53	115	55
H	C1715		0.6105	0.00	-0.27	0.53	-0.47	0.44	69.42	68.67	68.87	0.62	0.42	0.62	53	119	53
H	H2030		0.4307	0.01	-0.12	0.79	-0.75	0.21	69.40	68.54	69.17	0.60	0.40	0.62	57	124	53
H	C1131		0.8079	0.00	-0.02	0.97	-0.39	0.52	69.12	68.72	69.09	0.60	0.41	0.62	57	121	54
H	C1288		0.4946	0.01	0.19	0.66	-0.66	0.28	69.00	68.53	69.37	0.61	0.43	0.59	55	110	59
H	C1360		0.6802	0.00	0.19	0.67	-0.48	0.43	68.96	68.67	69.34	0.60	0.42	0.65	56	115	47
H	C1476		0.4856	0.01	-0.03	0.94	-0.72	0.23	69.29	68.55	69.23	0.59	0.42	0.61	58	117	56
H	C0523		0.8322	0.00	0.00	1.00	-0.37	0.54	69.05	68.69	69.06	0.61	0.42	0.62	56	115	53

TABLE A5. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
H	C0515		0.9807	0.00	-0.07	0.86	0.05	0.94	68.95	68.92	68.80	0.57	0.44	0.58	63	106	61
I	C1156		0.8194	0.00	-0.01	0.97	0.37	0.53	68.82	69.18	68.79	0.59	0.41	0.61	56	118	53
I	C1728		0.7461	0.00	-0.10	0.82	0.45	0.46	68.77	69.12	68.57	0.60	0.42	0.64	57	119	51
I	C1366		0.9065	0.00	-0.03	0.94	0.26	0.66	68.82	69.05	68.76	0.60	0.41	0.61	56	119	54
I	C1147		0.6789	0.00	-0.01	0.98	0.53	0.38	68.64	69.15	68.61	0.60	0.41	0.64	55	118	49
I	C0649		0.5521	0.01	0.09	0.83	-0.63	0.29	69.13	68.59	69.32	0.61	0.41	0.60	54	123	57
I	C1407		0.3697	0.01	0.19	0.65	-0.79	0.18	69.13	68.54	69.52	0.62	0.41	0.60	53	121	56
I	C0277A		0.1783	0.01	-0.11	0.80	-1.10	0.07	69.57	68.37	69.36	0.61	0.41	0.60	54	122	56
I	C1410B		0.1231	0.02	-0.11	0.80	-1.21	0.04	69.65	68.32	69.43	0.63	0.41	0.57	51	118	61
I	C0175		0.0778	0.02	0.04	0.93	-1.34	0.02	69.55	68.24	69.62	0.60	0.42	0.57	55	112	60
I	C0331		0.4281	0.01	-0.15	0.74	-0.78	0.20	69.42	68.49	69.13	0.68	0.41	0.58	45	122	61
I	C1077		0.2872	0.01	0.11	0.80	-0.90	0.13	69.25	68.46	69.48	0.68	0.40	0.56	44	125	65
I	C0717		0.2479	0.01	0.10	0.82	-0.99	0.11	69.37	68.48	69.57	0.70	0.40	0.59	41	123	58
I	C1461		0.4446	0.01	0.54	0.20	0.04	0.95	68.27	68.85	69.35	0.65	0.42	0.56	49	118	65
I	C1891		0.5603	0.01	0.48	0.31	0.28	0.66	68.17	68.93	69.12	0.71	0.44	0.60	40	105	56
I	C0851		0.6092	0.00	0.13	0.76	0.59	0.33	68.45	69.17	68.72	0.65	0.43	0.57	49	115	64
J	C0268		0.4707	0.01	0.16	0.71	-0.73	0.23	69.12	68.56	69.44	0.56	0.41	0.67	66	122	45
J	C0007	*	0.0384	0.03	1.08	0.02	0.42	0.48	67.62	69.13	69.79	0.60	0.39	0.68	56	134	43
J	C1523	*	0.0353	0.03	1.04	0.02	0.63	0.29	67.56	69.22	69.63	0.61	0.40	0.66	54	126	46

TABLE A5. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
J	C1160	**	0.0098	0.04	1.15	0.01	0.78	0.19	67.31	69.24	69.62	0.58	0.39	0.64	58	125	47
J	C1067	*	0.0148	0.04	1.11	0.01	0.66	0.26	67.49	69.26	69.71	0.57	0.40	0.63	61	124	49
J	C1453	**	0.0087	0.04	1.19	0.01	0.70	0.23	67.40	69.29	69.78	0.58	0.39	0.65	58	124	46
J	C0026	*	0.0286	0.03	0.98	0.03	0.76	0.21	67.55	69.29	69.51	0.58	0.41	0.65	60	122	47
J	C1294	**	0.0038	0.05	1.10	0.02	1.22	0.05	67.22	69.54	69.42	0.58	0.41	0.70	59	116	40
J	C1184		0.1425	0.02	0.77	0.09	0.47	0.44	67.92	69.15	69.45	0.58	0.40	0.68	61	125	44
J	C0949		0.246	0.01	0.71	0.09	-0.08	0.90	68.30	68.93	69.71	0.57	0.43	0.62	61	110	52
J	C1446		0.4802	0.01	0.54	0.23	0.00	1.00	68.44	68.97	69.51	0.60	0.43	0.65	57	114	49
J	H2074		0.3412	0.01	0.60	0.16	0.20	0.73	68.20	69.00	69.40	0.57	0.40	0.64	61	123	48
K	C1924		0.2851	0.01	-0.44	0.31	-0.75	0.21	69.70	68.52	68.83	0.62	0.41	0.59	53	118	58
K	C1139		0.3776	0.01	-0.53	0.23	0.42	0.49	69.27	69.15	68.21	0.64	0.40	0.62	49	123	53
K	C1400		0.5055	0.01	-0.18	0.67	0.63	0.29	68.76	69.21	68.40	0.61	0.42	0.57	54	118	62
K	C1010		0.8428	0.00	0.06	0.88	0.34	0.57	68.67	69.07	68.80	0.59	0.44	0.54	58	107	69
K	C1093		0.619	0.00	0.09	0.82	0.57	0.34	68.53	69.19	68.71	0.59	0.44	0.56	59	105	65
K	C0559		0.4415	0.01	0.13	0.76	0.75	0.21	68.36	69.25	68.62	0.60	0.43	0.60	58	110	58
K	C0307		0.2101	0.01	-0.23	0.61	1.07	0.08	68.51	69.35	68.04	0.61	0.42	0.68	55	117	45
K	C0806		0.3622	0.01	0.19	0.67	0.82	0.17	68.30	69.31	68.67	0.62	0.41	0.61	53	118	55
K	C0947		0.3401	0.01	-0.06	0.88	0.88	0.15	68.55	69.37	68.42	0.61	0.44	0.56	55	104	66
K	C0698		0.3373	0.01	-0.01	0.98	0.87	0.14	68.49	69.35	68.47	0.60	0.43	0.56	57	110	66

TABLE A5. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
L	C1978		0.0612	0.02	1.09	0.02	-0.18	0.76	67.97	68.87	70.15	0.59	0.40	0.70	58	127	41
L	C0822		0.2349	0.01	0.73	0.12	0.31	0.61	68.02	69.06	69.48	0.61	0.40	0.69	53	127	42
L	C1451		0.6367	0.00	0.35	0.46	-0.37	0.55	68.78	68.77	69.49	0.67	0.39	0.67	46	134	45
L	C0728		0.9106	0.00	0.05	0.91	-0.25	0.67	68.96	68.76	69.06	0.62	0.41	0.64	54	123	51
L	C1517		0.5965	0.00	-0.03	0.94	-0.60	0.31	69.26	68.62	69.19	0.59	0.41	0.63	58	122	52
L	C0383		0.2767	0.01	-0.23	0.61	-0.89	0.15	69.52	68.41	69.07	0.58	0.41	0.68	61	120	45
L	C0619		0.2826	0.01	-0.24	0.58	-0.85	0.16	69.61	68.52	69.13	0.57	0.41	0.66	62	121	46
L	C0230		0.247	0.01	-0.28	0.51	-0.89	0.14	69.70	68.53	69.14	0.56	0.42	0.63	63	113	51
L	C0628		0.2881	0.01	-0.43	0.32	0.72	0.22	68.93	69.22	68.07	0.61	0.41	0.60	55	121	56
L	C0481		0.1282	0.02	-0.83	0.05	-0.25	0.67	69.89	68.81	68.23	0.61	0.42	0.55	54	113	66
L	C0589		0.1365	0.02	-0.81	0.05	-0.23	0.70	69.85	68.81	68.23	0.60	0.42	0.55	55	113	66
L	C1524		0.1843	0.02	-0.76	0.07	0.23	0.70	69.57	69.04	68.05	0.61	0.42	0.59	54	113	59
M	C1180		0.9161	0.00	0.13	0.75	0.16	0.79	68.68	68.97	68.95	0.58	0.42	0.60	60	118	56
M	C0181		0.8076	0.00	-0.18	0.69	-0.32	0.60	69.24	68.75	68.88	0.64	0.40	0.63	50	130	52
M	C0903		0.3179	0.01	-0.56	0.22	-0.43	0.47	69.65	68.66	68.53	0.58	0.40	0.69	60	130	43
M	C1177		0.677	0.00	-0.38	0.44	0.27	0.69	69.00	68.88	68.24	0.70	0.44	0.68	44	113	46
M	C0735		0.5025	0.01	-0.54	0.24	0.00	1.00	69.46	68.92	68.39	0.64	0.40	0.65	50	126	49
M	C0252A		0.3125	0.01	-0.66	0.15	-0.30	0.62	69.71	68.76	68.40	0.65	0.40	0.63	49	129	52
M	C1109		0.5466	0.01	-0.25	0.56	-0.55	0.35	69.45	68.64	68.95	0.61	0.41	0.61	56	120	56

TABLE A5. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
M	C1004		0.5387	0.01	-0.21	0.64	-0.61	0.31	69.45	68.64	69.04	0.63	0.40	0.62	51	127	52
M	C0873		0.9744	0.00	-0.03	0.94	0.13	0.83	68.90	69.00	68.84	0.58	0.42	0.60	60	114	57
M	C0027		0.8939	0.00	0.02	0.97	0.28	0.64	68.72	69.02	68.75	0.60	0.42	0.60	57	118	57
M	C1440		0.4372	0.01	0.27	0.53	0.66	0.27	68.41	69.33	68.94	0.59	0.42	0.61	54	108	51
N	H2034		0.0591	0.02	-0.84	0.06	0.91	0.13	69.17	69.24	67.49	0.62	0.40	0.64	53	128	49
N	C1754		0.0964	0.02	-0.83	0.06	0.67	0.26	69.29	69.13	67.63	0.62	0.41	0.63	52	123	51
N	C0941		0.1938	0.01	-0.66	0.13	0.62	0.29	69.24	69.20	67.92	0.60	0.40	0.63	55	126	51
N	C1145		0.0641	0.02	-0.73	0.10	0.98	0.10	69.08	69.33	67.62	0.63	0.39	0.62	51	130	52
N	C0929		0.3189	0.01	-0.67	0.14	0.21	0.72	69.45	69.00	68.12	0.63	0.40	0.64	51	128	50
N	C1965		0.0759	0.02	-0.96	0.03	-0.30	0.63	69.90	68.64	67.98	0.58	0.43	0.68	61	112	44
N	C1562	*	0.0446	0.03	-1.08	0.01	0.15	0.80	69.80	68.86	67.63	0.56	0.40	0.66	64	123	46
N	C2303	*	0.0412	0.03	-1.08	0.01	0.06	0.92	69.85	68.83	67.69	0.56	0.42	0.64	62	113	48
N	C0503		0.0821	0.02	-0.98	0.03	0.18	0.76	69.70	68.90	67.74	0.57	0.42	0.66	63	115	47
N	C2074		0.2119	0.01	-0.74	0.09	0.24	0.68	69.57	69.08	68.09	0.61	0.41	0.61	54	118	54
N	C0057		0.5123	0.01	-0.50	0.26	0.13	0.83	69.29	68.92	68.29	0.63	0.41	0.61	52	122	55
O	C0736A		0.7283	0.00	0.15	0.71	-0.43	0.47	68.94	68.66	69.25	0.56	0.43	0.60	66	110	57
O	C2055		0.8225	0.00	0.12	0.78	0.33	0.59	68.58	69.03	68.82	0.58	0.42	0.64	62	116	50
O	C0316		0.378	0.01	-0.22	0.61	0.78	0.19	68.62	69.18	68.18	0.59	0.41	0.63	58	121	51
O	C0925		0.4083	0.01	-0.17	0.70	0.77	0.19	68.65	69.25	68.31	0.58	0.41	0.63	60	123	51

TABLE A5. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
O	C1135		0.4544	0.01	-0.15	0.72	0.73	0.22	68.65	69.22	68.35	0.58	0.41	0.63	60	121	52
O	C0043		0.6424	0.00	-0.13	0.75	0.54	0.37	68.66	69.06	68.39	0.58	0.43	0.62	61	113	54
O	C1905		0.2421	0.01	0.03	0.94	1.01	0.09	68.25	69.29	68.32	0.61	0.40	0.64	52	120	47
O	C1249		0.4623	0.01	-0.33	0.45	0.60	0.31	68.91	69.18	68.25	0.61	0.40	0.63	55	125	51
O	C1210		0.179	0.02	0.23	0.61	1.05	0.08	68.06	69.34	68.52	0.61	0.40	0.68	53	125	42
O	C0296		0.186	0.01	-0.18	0.67	1.06	0.08	68.57	69.45	68.22	0.60	0.42	0.58	56	115	60
O	C0238		0.3712	0.01	-0.03	0.95	0.90	0.16	68.32	69.19	68.26	0.67	0.46	0.60	47	99	58
O	C1256		0.2822	0.01	-0.12	0.77	0.93	0.12	68.54	69.35	68.30	0.59	0.44	0.56	59	105	66
O	H2001		0.3922	0.01	-0.42	0.31	0.53	0.38	69.05	69.17	68.22	0.59	0.43	0.57	57	109	63
O	H2074		0.6309	0.00	-0.09	0.84	0.55	0.35	68.72	69.19	68.55	0.59	0.43	0.56	58	110	65
P	H2013		0.9283	0.00	0.14	0.75	0.13	0.83	68.69	68.95	68.96	0.62	0.40	0.61	54	125	55
P	C0747		0.7522	0.00	0.16	0.71	0.40	0.50	68.47	69.03	68.79	0.63	0.41	0.60	51	123	57
P	C0906		0.7828	0.00	0.11	0.80	0.39	0.52	68.57	69.07	68.80	0.61	0.40	0.61	54	126	54
P	C1423		0.634	0.00	0.07	0.88	0.58	0.35	68.45	69.10	68.59	0.64	0.41	0.64	51	123	51
P	C0866		0.4774	0.01	-0.08	0.86	0.72	0.23	68.55	69.19	68.39	0.61	0.40	0.64	55	128	49
P	C0704		0.8309	0.00	0.27	0.55	0.03	0.95	68.64	68.95	69.18	0.62	0.40	0.64	53	128	50
P	C1000		0.5096	0.01	0.48	0.28	-0.24	0.69	68.42	68.66	69.37	0.62	0.41	0.62	53	119	54
P	C1418		0.4156	0.01	0.60	0.21	-0.38	0.54	68.53	68.75	69.74	0.63	0.40	0.74	53	133	38
P	C0616		0.8592	0.00	0.24	0.61	0.09	0.88	68.59	68.93	69.07	0.62	0.39	0.70	54	135	42

TABLE A5. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
P	H2151		0.4005	0.01	0.59	0.20	0.23	0.70	68.17	68.99	69.35	0.63	0.39	0.67	52	133	46
P	C1059		0.2869	0.01	0.66	0.16	0.38	0.52	68.06	69.11	69.39	0.64	0.38	0.68	49	138	44
Q	H2011		0.2903	0.01	-0.30	0.47	-0.79	0.19	69.66	68.57	69.06	0.54	0.43	0.61	67	107	52
Q	C0519		0.3319	0.01	-0.10	0.81	-0.87	0.15	69.42	68.46	69.23	0.55	0.43	0.62	66	109	53
Q	C2284		0.3602	0.01	-0.11	0.80	-0.84	0.17	69.43	68.48	69.22	0.57	0.43	0.63	63	110	51
Q	C1201		0.3962	0.01	-0.09	0.83	-0.79	0.19	69.35	68.47	69.17	0.55	0.43	0.62	66	107	52
Q	C1713		0.3926	0.01	-0.32	0.45	-0.65	0.28	69.50	68.52	68.85	0.57	0.42	0.64	60	111	48
Q	C1380		0.521	0.01	-0.18	0.67	-0.63	0.30	69.39	68.58	69.02	0.59	0.42	0.65	59	119	49
Q	C1195		0.7409	0.00	0.25	0.58	-0.34	0.57	68.81	68.71	69.30	0.59	0.40	0.65	57	125	47
Q	C0044		0.7202	0.00	0.23	0.61	-0.39	0.51	68.89	68.72	69.34	0.61	0.39	0.65	53	130	47
Q	C0827		0.8343	0.00	0.23	0.61	-0.21	0.73	68.80	68.82	69.26	0.61	0.40	0.66	54	127	47

*, **, ***, ****: Significance level of 0.05, 0.01, 0.001, and 0.0001, respectivelly.

RSQ: Coefficient of determination (R-square)

ADDIT and DOM: Additive and dominant effects, respectivelly.

ADPROB and DOPROB: Probability of significance for additive and dominant effects, respectively

MTAA, MTAB, and MTBB: Marker classes means for the trait

STAA, STAB, and STBB: Standard error of the marker class means.

NAA, NAB and NBB: Number of plants having each marker class.

TABLE A6. Genetic linkage for hypodermis color (F2 population)

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
A	C0562		0.64	0.00	-0.02	0.55	-0.04	0.45	0.23	0.17	0.18	0.05	0.04	0.05	58	115	66
A	C0433		0.41	0.01	-0.02	0.58	-0.07	0.22	0.24	0.16	0.21	0.05	0.04	0.05	62	113	64
A	C2241		0.41	0.01	-0.02	0.60	-0.07	0.21	0.23	0.15	0.20	0.05	0.04	0.045	61	114	67
A	C0266		0.31	0.01	-0.03	0.52	-0.07	0.16	0.25	0.15	0.20	0.05	0.04	0.05	57	113	65
A	C1161A	*	0.02	0.03	-0.05	0.21	-0.12	0.01	0.28	0.11	0.19	0.05	0.03	0.05	51	130	49
A	C2246		0.09	0.02	-0.07	0.08	-0.06	0.25	0.28	0.16	0.15	0.05	0.04	0.055	57	135	48
A	H2188		0.13	0.02	-0.06	0.11	-0.06	0.21	0.28	0.16	0.16	0.05	0.04	0.05	58	134	56
A	C1500		0.11	0.02	-0.05	0.18	-0.08	0.11	0.27	0.14	0.17	0.05	0.04	0.05	56	123	53
A	C0032		0.10	0.02	-0.06	0.09	-0.06	0.25	0.28	0.16	0.15	0.05	0.04	0.055	66	129	53
A	C1174		0.15	0.02	-0.04	0.29	-0.08	0.11	0.27	0.15	0.19	0.05	0.04	0.055	56	141	53
A	C2263		0.39	0.01	-0.01	0.89	-0.07	0.17	0.23	0.16	0.22	0.05	0.04	0.055	56	133	54
A	C0606		0.79	0.00	-0.01	0.77	-0.03	0.53	0.22	0.17	0.20	0.05	0.04	0.05	56	128	57
A	C0689		0.80	0.00	-0.02	0.66	-0.03	0.62	0.22	0.18	0.18	0.05	0.04	0.055	56	127	55
A	C2007		0.92	0.00	-0.02	0.70	-0.01	0.92	0.21	0.19	0.18	0.05	0.04	0.05	59	130	57
A	C0243		0.99	0.00	-0.01	0.91	0.00	0.96	0.19	0.18	0.18	0.05	0.04	0.05	60	130	57
A	C2028		0.81	0.00	-0.02	0.62	0.03	0.66	0.20	0.20	0.16	0.05	0.04	0.055	61	119	56
A	C0173		0.72	0.00	0.02	0.57	-0.03	0.58	0.17	0.17	0.22	0.05	0.04	0.05	58	121	61
B	C2005		0.85	0.00	-0.02	0.71	-0.02	0.65	0.20	0.17	0.18	0.05	0.04	0.05	60	121	63
B	C1087		0.37	0.01	-0.05	0.22	0.03	0.55	0.21	0.20	0.12	0.06	0.04	0.045	53	124	66

TABLE A6. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
B	C0680		0.44	0.01	-0.05	0.23	0.02	0.71	0.23	0.20	0.14	0.05	0.04	0.05	58	120	65
B	C1129		0.29	0.01	-0.04	0.31	0.06	0.25	0.19	0.21	0.12	0.06	0.04	0.05	53	114	61
B	C0593		0.22	0.01	-0.06	0.13	0.04	0.41	0.22	0.21	0.11	0.05	0.04	0.05	60	127	63
B	C1165		0.30	0.01	-0.03	0.36	0.07	0.21	0.19	0.22	0.13	0.05	0.04	0.05	63	117	63
B	C0952		0.58	0.00	0.00	0.97	-0.06	0.30	0.22	0.17	0.22	0.06	0.04	0.055	55	134	51
B	C0741		0.42	0.01	-0.01	0.82	-0.07	0.20	0.23	0.15	0.21	0.05	0.04	0.055	58	132	53
B	C0696		0.35	0.01	-0.03	0.55	-0.07	0.18	0.25	0.16	0.20	0.06	0.04	0.05	53	135	55
B	C0791		0.68	0.00	-0.01	0.92	-0.05	0.39	0.21	0.16	0.20	0.06	0.04	0.05	53	131	55
B	C1763		0.46	0.01	-0.02	0.70	-0.06	0.24	0.23	0.16	0.20	0.05	0.04	0.05	57	135	55
B	C2308		0.57	0.00	-0.03	0.42	-0.04	0.48	0.23	0.16	0.17	0.06	0.04	0.05	53	136	54
B	C0522		0.34	0.01	-0.04	0.33	-0.06	0.29	0.24	0.15	0.17	0.05	0.04	0.055	54	133	48
B	C0036A		0.33	0.01	-0.05	0.24	-0.05	0.37	0.26	0.17	0.17	0.05	0.04	0.055	55	139	54
B	C0284		0.26	0.01	-0.06	0.11	-0.02	0.73	0.25	0.17	0.13	0.05	0.03	0.055	53	143	48
B	C0082		0.13	0.02	-0.08	0.05	-0.02	0.74	0.27	0.18	0.12	0.05	0.03	0.06	56	144	44
C	C0050	*	0.01	0.03	0.11	0.00	-0.04	0.41	0.11	0.17	0.32	0.05	0.04	0.055	57	140	50
C	C1395	**	0.01	0.04	0.12	0.00	-0.06	0.26	0.11	0.17	0.34	0.05	0.03	0.055	58	141	51
C	C0460	*	0.04	0.03	0.10	0.01	0.01	0.82	0.09	0.19	0.28	0.05	0.04	0.055	57	130	51
C	C1378		0.12	0.02	0.08	0.04	-0.01	0.83	0.12	0.18	0.27	0.05	0.04	0.055	60	137	52
C	C0838		0.13	0.02	0.07	0.06	-0.04	0.44	0.14	0.17	0.28	0.05	0.04	0.05	59	121	55

TABLE A6. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
C	C1137		0.35	0.01	0.05	0.16	-0.02	0.70	0.14	0.17	0.24	0.05	0.04	0.05	57	134	58
C	C2247		0.30	0.01	0.06	0.13	-0.01	0.80	0.14	0.18	0.25	0.05	0.04	0.05	59	129	57
C	C0172		0.39	0.01	0.03	0.48	-0.06	0.23	0.19	0.16	0.24	0.05	0.04	0.05	64	118	59
C	C0896		0.23	0.01	0.03	0.51	-0.08	0.11	0.21	0.15	0.25	0.05	0.04	0.05	64	117	56
C	C0607		0.86	0.00	0.01	0.86	-0.03	0.59	0.19	0.17	0.21	0.05	0.04	0.05	68	123	59
C	C1740		0.94	0.00	0.00	0.99	-0.02	0.72	0.20	0.18	0.20	0.05	0.04	0.05	67	114	62
D	C0713		0.23	0.01	-0.06	0.09	-0.02	0.79	0.25	0.18	0.13	0.05	0.04	0.05	60	131	55
D	C2255		0.79	0.00	-0.01	0.81	-0.04	0.52	0.21	0.17	0.20	0.05	0.04	0.05	57	124	62
D	C1373		0.25	0.01	0.06	0.13	0.04	0.48	0.11	0.20	0.22	0.05	0.04	0.05	55	135	59
D	C0463E		0.26	0.01	0.05	0.13	0.04	0.46	0.11	0.20	0.21	0.05	0.04	0.045	57	119	67
D	C2008		0.24	0.01	0.06	0.09	0.01	0.89	0.13	0.19	0.25	0.05	0.04	0.05	57	131	57
D	C0360		0.64	0.00	0.04	0.35	0.01	0.96	0.16	0.19	0.22	0.05	0.04	0.05	59	127	59
D	H2169		0.49	0.01	0.04	0.24	-0.02	0.79	0.15	0.18	0.24	0.05	0.04	0.05	60	129	60
D	C0823		0.66	0.00	0.04	0.37	-0.01	0.90	0.16	0.18	0.22	0.05	0.04	0.05	58	132	59
E	C1203		0.74	0.00	-0.03	0.45	0.01	0.81	0.21	0.19	0.15	0.05	0.04	0.055	63	137	47
E	C0810		0.26	0.01	0.02	0.72	-0.08	0.11	0.21	0.15	0.24	0.05	0.04	0.05	57	132	55
E	C0062		0.54	0.01	0.02	0.71	-0.06	0.29	0.20	0.16	0.22	0.05	0.04	0.05	62	111	64
E	C1153		0.93	0.00	0.01	0.73	-0.01	0.88	0.17	0.18	0.20	0.05	0.04	0.05	58	124	66
E	C1170		0.89	0.00	-0.01	0.74	-0.02	0.73	0.21	0.18	0.19	0.05	0.04	0.05	63	124	60

TABLE A6. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
E	C0431		0.78	0.00	-0.02	0.67	-0.03	0.58	0.22	0.18	0.19	0.05	0.04	0.055	60	127	54
E	C1105		0.59	0.00	-0.01	0.75	-0.05	0.33	0.22	0.17	0.20	0.05	0.04	0.05	63	123	60
E	C0732		0.34	0.01	-0.05	0.17	-0.03	0.61	0.24	0.17	0.15	0.05	0.04	0.045	66	117	67
E	C0566		0.12	0.02	-0.07	0.05	-0.04	0.50	0.27	0.17	0.13	0.05	0.04	0.05	64	121	61
E	C1138		0.09	0.02	-0.07	0.06	-0.07	0.21	0.29	0.16	0.15	0.06	0.04	0.05	52	121	66
E	H2038		0.07	0.02	-0.07	0.06	-0.07	0.19	0.28	0.15	0.15	0.05	0.04	0.05	62	117	62
F	C0865		0.99	0.00	0.01	0.90	0.00	0.99	0.18	0.19	0.19	0.05	0.04	0.05	61	130	58
F	C0496		0.83	0.00	0.01	0.76	0.03	0.60	0.16	0.20	0.19	0.05	0.04	0.05	62	126	60
F	C0681		0.77	0.00	0.02	0.62	0.03	0.59	0.16	0.20	0.19	0.05	0.04	0.05	58	120	63
F	C1437		0.67	0.00	0.03	0.53	0.03	0.53	0.15	0.20	0.20	0.05	0.04	0.05	61	124	57
F	C1696		0.06	0.02	-0.03	0.43	0.12	0.03	0.16	0.24	0.10	0.06	0.04	0.055	52	131	53
F	C1222		0.30	0.01	-0.05	0.24	0.06	0.28	0.20	0.21	0.11	0.05	0.04	0.055	57	138	48
F	C1997		0.63	0.00	-0.03	0.57	0.05	0.41	0.19	0.21	0.14	0.06	0.04	0.06	54	131	43
F	C1176		0.76	0.00	-0.01	0.83	0.04	0.47	0.18	0.20	0.16	0.06	0.04	0.055	52	144	51
F	C0169		0.35	0.01	-0.05	0.17	0.03	0.62	0.22	0.20	0.13	0.05	0.04	0.05	59	127	64
G	C0357	****	0.00	0.46	-0.33	0.00	-0.29	0.00	0.68	0.06	0.02	0.04	0.03	0.035	50	124	58
G	C0290	****	0.00	0.66	-0.42	0.00	-0.37	0.00	0.83	0.05	0.00	0.04	0.02	0.03	47	136	65
G	C0887	****	0.00	0.36	-0.30	0.00	-0.24	0.00	0.61	0.08	0.02	0.04	0.03	0.04	54	132	54
G	C1720	****	0.00	0.16	-0.20	0.00	-0.14	0.00	0.46	0.12	0.06	0.05	0.04	0.05	55	121	52

TABLE A6. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
G	C0036C	****	0.00	0.14	-0.18	0.00	-0.14	0.00	0.42	0.11	0.07	0.05	0.04	0.05	69	121	58
G	C1168	****	0.00	0.10	-0.17	0.00	-0.09	0.07	0.38	0.14	0.06	0.05	0.04	0.05	68	127	54
G	C1470	****	0.00	0.09	-0.15	0.00	-0.12	0.02	0.38	0.12	0.09	0.05	0.04	0.05	66	125	55
G	C1002	**	0.01	0.04	-0.11	0.00	-0.02	0.78	0.29	0.17	0.08	0.05	0.04	0.05	70	120	53
G	C0277B	*	0.03	0.03	-0.09	0.02	-0.05	0.39	0.29	0.16	0.11	0.05	0.04	0.06	69	127	45
G	C1410A	*	0.04	0.03	-0.09	0.02	-0.02	0.66	0.28	0.17	0.10	0.05	0.04	0.06	69	135	42
G	C2286	*	0.03	0.03	-0.09	0.01	-0.03	0.60	0.28	0.16	0.10	0.05	0.04	0.06	72	132	43
G	C0532	*	0.04	0.03	-0.09	0.02	-0.02	0.78	0.27	0.17	0.09	0.05	0.04	0.06	71	133	44
G	C1242		0.19	0.01	-0.07	0.07	0.02	0.71	0.24	0.19	0.10	0.05	0.04	0.06	67	139	41
G	C1143		0.43	0.01	-0.05	0.20	0.01	0.88	0.22	0.18	0.12	0.05	0.04	0.06	73	129	41
G	C0667	*	0.03	0.03	-0.11	0.01	0.02	0.72	0.26	0.18	0.06	0.05	0.03	0.06	65	137	38
H	C0180		0.41	0.01	-0.04	0.33	-0.05	0.35	0.24	0.16	0.17	0.05	0.04	0.05	54	126	59
H	C1715		0.44	0.01	-0.05	0.20	-0.01	0.88	0.23	0.17	0.13	0.05	0.04	0.05	53	134	53
H	H2030		0.46	0.01	-0.05	0.21	0.01	0.86	0.23	0.19	0.13	0.05	0.04	0.055	58	139	53
H	C1131		0.62	0.00	-0.04	0.33	0.00	0.96	0.22	0.19	0.15	0.05	0.04	0.055	59	134	54
H	C1288		0.39	0.01	-0.05	0.21	-0.03	0.61	0.25	0.18	0.16	0.05	0.04	0.05	61	120	58
H	C1360		0.71	0.00	-0.03	0.44	-0.01	0.84	0.23	0.19	0.17	0.05	0.04	0.055	62	124	48
H	C1476		0.38	0.01	-0.05	0.18	-0.02	0.73	0.24	0.18	0.15	0.05	0.04	0.05	63	127	56
H	C0523		0.66	0.00	-0.03	0.37	-0.01	0.95	0.22	0.18	0.15	0.05	0.04	0.055	61	124	54

TABLE A6. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
H	C0515		0.16	0.01	-0.04	0.26	-0.08	0.13	0.26	0.15	0.19	0.05	0.04	0.05	65	116	65
I	C1156		0.36	0.01	-0.02	0.67	0.07	0.17	0.15	0.20	0.12	0.05	0.04	0.05	60	124	58
I	C1728		0.58	0.00	-0.01	0.87	0.05	0.30	0.17	0.22	0.16	0.05	0.04	0.05	60	122	58
I	C1366		0.32	0.01	-0.01	0.94	0.08	0.13	0.16	0.23	0.15	0.05	0.04	0.05	59	124	61
I	C1147		0.26	0.01	0.01	0.92	0.08	0.10	0.14	0.22	0.15	0.05	0.04	0.05	59	122	56
I	C0649		0.57	0.00	0.00	0.98	0.05	0.29	0.16	0.21	0.16	0.05	0.04	0.05	57	129	64
I	C1407		0.68	0.00	0.00	0.99	0.05	0.38	0.16	0.21	0.16	0.05	0.04	0.05	56	127	62
I	C0277A		0.76	0.00	0.00	0.96	0.04	0.46	0.16	0.20	0.17	0.05	0.04	0.05	56	131	61
I	C1410B		0.92	0.00	-0.01	0.80	0.02	0.77	0.19	0.19	0.17	0.06	0.04	0.05	54	126	66
I	C0175		0.68	0.00	-0.01	0.82	0.04	0.40	0.17	0.21	0.16	0.05	0.04	0.05	58	121	64
I	C0331		0.63	0.00	0.02	0.62	0.05	0.39	0.15	0.21	0.18	0.06	0.04	0.05	49	127	67
I	C1077		0.40	0.01	0.05	0.18	0.00	0.98	0.13	0.18	0.23	0.06	0.04	0.045	47	131	71
I	C0717		0.27	0.01	0.05	0.22	-0.05	0.38	0.16	0.16	0.26	0.06	0.04	0.05	44	130	63
I	C1461		0.12	0.02	0.06	0.08	-0.05	0.39	0.14	0.16	0.27	0.06	0.04	0.045	50	126	72
I	C1891		0.18	0.02	0.05	0.22	-0.07	0.23	0.17	0.15	0.26	0.06	0.04	0.05	42	113	61
I	C0851		0.40	0.01	0.05	0.19	-0.01	0.89	0.14	0.18	0.23	0.06	0.04	0.045	51	124	69
J	C0268		0.26	0.01	0.05	0.17	0.04	0.47	0.12	0.21	0.22	0.05	0.04	0.055	67	131	50
J	C0007	*	0.04	0.03	0.10	0.01	-0.03	0.53	0.12	0.18	0.30	0.05	0.04	0.055	62	137	50
J	C1523		0.07	0.02	0.08	0.05	-0.07	0.18	0.16	0.16	0.30	0.05	0.04	0.055	64	124	53

TABLE A6. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
J	C1160	*	0.02	0.03	0.09	0.01	-0.07	0.15	0.13	0.16	0.32	0.05	0.04	0.05	68	124	54
J	C1067	**	0.00	0.04	0.11	0.00	-0.09	0.09	0.13	0.15	0.34	0.05	0.04	0.05	71	122	57
J	C1453	**	0.01	0.04	0.10	0.00	-0.07	0.16	0.12	0.15	0.32	0.05	0.04	0.05	68	122	54
J	C0026	*	0.03	0.03	0.09	0.02	-0.08	0.14	0.15	0.16	0.32	0.05	0.04	0.055	69	121	54
J	C1294	*	0.04	0.03	0.09	0.02	-0.08	0.15	0.15	0.16	0.33	0.05	0.04	0.06	68	118	43
J	C1184		0.17	0.01	0.06	0.10	-0.06	0.26	0.16	0.17	0.28	0.05	0.04	0.055	68	128	50
J	C0949		0.32	0.01	0.02	0.70	-0.08	0.14	0.20	0.14	0.23	0.05	0.04	0.05	70	115	53
J	C1446		0.68	0.00	0.01	0.81	-0.05	0.39	0.21	0.17	0.23	0.05	0.04	0.055	63	123	49
J	H2074		0.34	0.01	0.04	0.25	-0.06	0.29	0.17	0.16	0.26	0.05	0.04	0.055	70	131	47
K	C1924		0.54	0.01	-0.02	0.66	-0.05	0.30	0.22	0.15	0.19	0.05	0.04	0.05	56	128	60
K	C1139		0.89	0.00	0.00	0.96	0.03	0.64	0.18	0.20	0.17	0.06	0.04	0.05	51	131	58
K	C1400		0.74	0.00	-0.01	0.79	0.04	0.47	0.17	0.20	0.16	0.05	0.04	0.05	58	126	65
K	C1010		0.73	0.00	-0.02	0.55	0.03	0.63	0.19	0.20	0.15	0.05	0.04	0.045	63	113	73
K	C1093		0.75	0.00	-0.01	0.88	0.04	0.46	0.17	0.21	0.16	0.05	0.04	0.045	64	113	68
K	C0559		0.70	0.00	0.00	0.97	0.05	0.40	0.16	0.21	0.17	0.05	0.04	0.05	62	117	61
K	C0307		0.94	0.00	0.00	0.97	0.02	0.73	0.18	0.20	0.18	0.05	0.04	0.06	61	127	45
K	C0806		0.70	0.00	0.01	0.81	0.04	0.41	0.16	0.21	0.17	0.05	0.04	0.05	58	127	58
K	C0947		0.61	0.00	0.01	0.85	0.05	0.33	0.16	0.22	0.17	0.05	0.04	0.045	63	107	70
K	C0698		0.63	0.00	-0.01	0.91	0.05	0.34	0.17	0.21	0.16	0.05	0.04	0.045	66	114	69

TABLE A6. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
L	C1978		0.93	0.00	0.02	0.71	0.00	0.97	0.17	0.19	0.20	0.05	0.04	0.06	64	133	45
L	C0822		0.99	0.00	0.00	0.98	-0.01	0.91	0.18	0.18	0.18	0.05	0.04	0.06	61	131	44
L	C1451		0.75	0.00	0.02	0.61	0.03	0.59	0.15	0.20	0.19	0.06	0.04	0.055	53	141	47
L	C0728		0.33	0.01	0.01	0.80	0.08	0.14	0.15	0.23	0.16	0.05	0.04	0.05	63	124	56
L	C1517		0.40	0.01	0.03	0.39	0.05	0.33	0.13	0.21	0.20	0.05	0.04	0.05	68	123	57
L	C0383		0.49	0.01	0.01	0.91	0.06	0.25	0.16	0.22	0.17	0.05	0.04	0.055	71	124	49
L	C0619		0.26	0.01	0.03	0.44	0.07	0.18	0.13	0.22	0.18	0.05	0.04	0.055	72	123	50
L	C0230		0.60	0.00	0.01	0.84	0.05	0.33	0.16	0.21	0.17	0.05	0.04	0.055	72	115	54
L	C0628		0.84	0.00	-0.01	0.91	0.03	0.55	0.18	0.20	0.17	0.05	0.04	0.05	63	125	60
L	C0481		0.92	0.00	-0.01	0.84	0.02	0.73	0.19	0.20	0.17	0.05	0.04	0.05	60	124	65
L	C0589		0.92	0.00	-0.02	0.69	0.01	0.96	0.20	0.19	0.17	0.05	0.04	0.05	61	124	65
L	C1524		0.82	0.00	-0.02	0.68	-0.03	0.63	0.22	0.18	0.19	0.05	0.04	0.05	60	124	59
M	C1180		0.30	0.01	-0.05	0.14	-0.03	0.61	0.25	0.17	0.15	0.05	0.04	0.05	65	123	62
M	C0181		0.33	0.01	-0.06	0.15	0.02	0.71	0.23	0.20	0.13	0.05	0.04	0.05	57	134	57
M	C0903		0.15	0.02	-0.06	0.11	0.07	0.18	0.20	0.21	0.09	0.05	0.04	0.055	65	135	48
M	C1177		0.98	0.00	-0.01	0.88	0.01	0.88	0.20	0.20	0.19	0.06	0.04	0.06	50	119	48
M	C0735		0.68	0.00	-0.03	0.39	-0.01	0.87	0.22	0.18	0.16	0.05	0.04	0.055	55	135	52
M	C0252A		0.66	0.00	-0.03	0.41	0.02	0.70	0.21	0.20	0.15	0.06	0.04	0.055	53	138	55
M	C1109		0.94	0.00	0.00	0.96	-0.02	0.72	0.20	0.18	0.20	0.05	0.04	0.05	61	130	57

TABLE A6. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
M	C1004		0.79	0.00	-0.02	0.57	0.02	0.68	0.20	0.20	0.15	0.05	0.04	0.055	57	135	53
M	C0873		0.93	0.00	0.00	0.96	0.02	0.71	0.17	0.19	0.18	0.05	0.04	0.05	64	125	57
M	C0027		0.86	0.00	0.01	0.84	0.03	0.61	0.16	0.20	0.18	0.05	0.04	0.05	62	129	57
M	C1440		0.54	0.01	0.02	0.72	0.06	0.30	0.15	0.22	0.18	0.05	0.04	0.055	60	115	51
N	H2034		0.97	0.00	-0.01	0.86	0.01	0.87	0.19	0.19	0.18	0.05	0.04	0.055	58	136	51
N	C1754		0.57	0.00	-0.04	0.31	0.02	0.74	0.21	0.19	0.14	0.05	0.04	0.055	57	132	52
N	C0941		0.61	0.00	-0.04	0.37	0.03	0.63	0.20	0.19	0.14	0.05	0.04	0.055	60	136	52
N	C1145		0.73	0.00	-0.02	0.71	0.04	0.48	0.18	0.20	0.15	0.05	0.04	0.055	56	140	53
N	C0929		0.70	0.00	-0.04	0.40	0.00	0.98	0.22	0.19	0.16	0.06	0.04	0.055	54	138	51
N	C1965		0.98	0.00	0.00	0.95	0.01	0.85	0.18	0.18	0.17	0.05	0.04	0.055	63	121	47
N	C1562		0.89	0.00	0.01	0.82	0.02	0.69	0.17	0.20	0.19	0.05	0.04	0.055	66	133	49
N	C2303		0.95	0.00	0.01	0.77	0.01	0.93	0.16	0.17	0.18	0.05	0.04	0.055	64	123	51
N	C0503		0.78	0.00	0.01	0.89	0.04	0.50	0.17	0.21	0.18	0.05	0.04	0.055	65	124	50
N	C2074		0.93	0.00	-0.01	0.80	0.02	0.77	0.19	0.19	0.17	0.06	0.04	0.05	54	126	60
N	C0057		0.92	0.00	0.00	0.99	-0.02	0.68	0.20	0.18	0.20	0.06	0.04	0.05	51	131	61
O	C0736A		0.70	0.00	-0.01	0.71	0.04	0.44	0.18	0.20	0.15	0.05	0.04	0.05	68	114	66
O	C2055		0.88	0.00	0.01	0.93	0.03	0.63	0.17	0.20	0.18	0.05	0.04	0.05	65	122	57
O	C0316		0.86	0.00	-0.02	0.72	0.02	0.67	0.18	0.19	0.16	0.05	0.04	0.05	61	127	58
O	C0925		0.85	0.00	-0.02	0.62	0.02	0.77	0.19	0.19	0.16	0.05	0.04	0.05	63	128	58

TABLE A6. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
O	C1135		0.81	0.00	-0.02	0.59	0.02	0.72	0.19	0.19	0.16	0.05	0.04	0.05	63	127	59
O	C0043		0.97	0.00	-0.01	0.88	-0.01	0.83	0.19	0.18	0.18	0.05	0.04	0.05	63	120	61
O	C1905		0.62	0.00	-0.03	0.54	-0.04	0.45	0.22	0.16	0.18	0.05	0.04	0.055	55	127	52
O	C1249		0.97	0.00	-0.01	0.81	0.00	0.97	0.19	0.19	0.17	0.05	0.04	0.05	58	131	58
O	C1210		0.92	0.00	0.02	0.71	-0.01	0.84	0.18	0.18	0.21	0.05	0.04	0.055	57	128	49
O	C0296		0.95	0.00	0.00	0.99	0.02	0.76	0.18	0.20	0.18	0.05	0.04	0.05	61	118	67
O	C0238		0.75	0.00	0.00	0.97	0.04	0.44	0.16	0.20	0.16	0.06	0.04	0.045	51	101	69
O	C1256		0.92	0.00	0.00	0.95	-0.02	0.69	0.19	0.18	0.20	0.05	0.04	0.045	63	110	72
O	H2001		0.92	0.00	0.01	0.74	-0.01	0.81	0.18	0.18	0.20	0.05	0.04	0.045	62	113	70
O	H2074		0.73	0.00	0.02	0.58	-0.03	0.57	0.18	0.17	0.21	0.05	0.04	0.045	63	115	71
P	H2013		0.23	0.01	0.04	0.32	-0.07	0.15	0.19	0.15	0.26	0.05	0.04	0.055	64	132	54
P	C0747		0.15	0.02	0.05	0.20	-0.08	0.13	0.18	0.15	0.27	0.05	0.04	0.05	62	129	56
P	C0906		0.27	0.01	0.05	0.21	-0.06	0.27	0.17	0.16	0.26	0.05	0.04	0.055	65	131	54
P	C1423		0.66	0.00	0.02	0.55	0.04	0.51	0.15	0.21	0.19	0.05	0.04	0.055	61	128	52
P	C0866		0.55	0.00	0.02	0.57	0.05	0.38	0.14	0.21	0.18	0.05	0.04	0.055	65	133	50
P	C0704		0.59	0.00	0.01	0.83	0.05	0.33	0.15	0.21	0.17	0.05	0.04	0.055	61	137	49
P	C1000		0.58	0.00	-0.01	0.78	0.05	0.31	0.17	0.21	0.15	0.05	0.04	0.055	61	132	49
P	C1418		0.58	0.00	0.01	0.91	0.05	0.32	0.16	0.21	0.16	0.05	0.04	0.065	59	143	37
P	C0616		0.71	0.00	0.02	0.61	0.03	0.56	0.15	0.20	0.19	0.05	0.03	0.06	60	145	42

TABLE A6. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
P	H2151		0.23	0.01	0.02	0.67	0.08	0.11	0.13	0.22	0.16	0.05	0.03	0.06	57	145	45
P	C1059		0.15	0.02	0.05	0.20	0.07	0.16	0.10	0.22	0.20	0.06	0.03	0.055	53	148	46
Q	H2011		0.65	0.00	-0.02	0.62	-0.04	0.45	0.22	0.17	0.19	0.05	0.04	0.05	68	115	59
Q	C0519		0.93	0.00	-0.01	0.72	-0.01	0.89	0.20	0.18	0.18	0.05	0.04	0.05	70	116	57
Q	C2284		0.97	0.00	0.01	0.80	-0.01	0.93	0.18	0.19	0.20	0.05	0.04	0.055	66	118	55
Q	C1201		0.99	0.00	0.00	0.99	0.01	0.91	0.19	0.20	0.19	0.05	0.04	0.05	69	113	58
Q	C1713		0.78	0.00	0.00	0.99	0.04	0.48	0.16	0.20	0.16	0.05	0.04	0.055	62	122	50
Q	C1380		0.83	0.00	0.00	0.97	0.03	0.55	0.17	0.20	0.17	0.05	0.04	0.055	61	128	54
Q	C1195		0.68	0.00	0.03	0.45	0.02	0.66	0.14	0.19	0.20	0.05	0.04	0.055	57	137	51
Q	C0044		0.27	0.01	0.04	0.30	0.07	0.21	0.12	0.22	0.19	0.06	0.04	0.055	53	139	52
Q	C0827		0.13	0.02	0.08	0.05	0.02	0.79	0.11	0.20	0.26	0.05	0.04	0.055	56	137	50

*, **, ***, ****: Significance level of 0.05, 0.01, 0.001, and 0.0001, respectivelly.

RSQ: Coefficient of determination (R-square)

ADDIT and DOM: Additive and dominant effects, respectivelly.

ADPROB and DOPROB: Probability of significance for additive and dominant effects, respectively

MTAA, MTAB, and MTBB: Marker classes means for the trait

STAA, STAB, and STBB: Standard error of the marker class means.

NAA, NAB and NBB: Number of plants having each marker class.

TABLE A7. Genetic linkage for hypodermis color (F2:3 population)

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
A	C0562		0.58	0.00	-0.03	0.45	-0.07	0.44	0.36	0.30	0.31	0.05	0.03	0.045	58	115	66
A	C0433		0.34	0.01	-0.02	0.49	-0.12	0.19	0.37	0.29	0.33	0.05	0.04	0.045	62	113	64
A	C2241		0.38	0.01	-0.02	0.47	-0.11	0.22	0.36	0.29	0.32	0.05	0.03	0.04	61	114	67
A	C0266		0.28	0.01	-0.03	0.36	-0.12	0.18	0.38	0.29	0.32	0.05	0.03	0.045	57	113	65
A	C1161A	*	0.01	0.04	-0.05	0.19	-0.23	0.01	0.40	0.25	0.32	0.05	0.03	0.045	51	130	49
A	C2246		0.14	0.02	-0.06	0.11	-0.10	0.28	0.40	0.30	0.29	0.05	0.03	0.05	57	135	48
A	H2188		0.15	0.02	-0.05	0.17	-0.12	0.17	0.39	0.29	0.31	0.05	0.03	0.045	58	134	56
A	C1500		0.13	0.02	-0.04	0.26	-0.15	0.10	0.39	0.28	0.31	0.05	0.03	0.045	56	123	53
A	C0032		0.15	0.02	-0.05	0.10	-0.08	0.36	0.39	0.30	0.29	0.04	0.03	0.045	66	129	53
A	C1174		0.37	0.01	-0.03	0.37	-0.10	0.29	0.37	0.30	0.31	0.05	0.03	0.045	56	141	53
A	C2263		0.80	0.00	0.01	0.80	-0.06	0.54	0.33	0.31	0.35	0.05	0.03	0.045	56	133	54
A	C0606		1.00	0.00	-0.01	0.93	0.01	0.96	0.32	0.32	0.31	0.05	0.03	0.045	56	128	57
A	C0689		0.96	0.00	-0.01	0.80	0.01	0.93	0.32	0.32	0.31	0.05	0.03	0.045	56	127	55
A	C2007		0.89	0.00	-0.01	0.81	0.04	0.67	0.32	0.33	0.30	0.05	0.03	0.045	59	130	57
A	C0243		0.85	0.00	-0.01	0.92	0.05	0.58	0.30	0.32	0.30	0.05	0.03	0.045	60	130	57
A	C2028		0.47	0.01	-0.02	0.64	0.11	0.25	0.31	0.35	0.28	0.05	0.03	0.045	61	119	56
A	C0173		0.85	0.00	0.02	0.58	-0.02	0.88	0.30	0.31	0.33	0.05	0.03	0.045	58	121	61
B	C2005		0.60	0.00	-0.03	0.40	-0.05	0.58	0.35	0.30	0.30	0.05	0.03	0.045	60	121	63
B	C1087		0.14	0.02	-0.05	0.11	0.09	0.32	0.34	0.34	0.24	0.05	0.03	0.04	53	124	66

TABLE A7. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
B	C0680		0.25	0.01	-0.05	0.13	0.06	0.53	0.36	0.34	0.26	0.05	0.03	0.045	58	120	65
B	C1129		0.09	0.02	-0.05	0.13	0.14	0.13	0.33	0.35	0.23	0.05	0.03	0.045	53	114	61
B	C0593		0.06	0.02	-0.06	0.05	0.12	0.18	0.35	0.35	0.23	0.05	0.03	0.045	60	127	63
B	C1165		0.14	0.02	-0.04	0.20	0.14	0.13	0.33	0.36	0.25	0.05	0.03	0.045	63	117	63
B	C0952		1.00	0.00	0.00	0.95	-0.01	0.96	0.32	0.32	0.32	0.05	0.03	0.05	55	134	51
B	C0741		0.80	0.00	-0.01	0.92	-0.06	0.51	0.33	0.30	0.33	0.05	0.03	0.045	58	132	53
B	C0696		0.88	0.00	-0.02	0.70	-0.03	0.74	0.34	0.31	0.31	0.05	0.03	0.045	53	135	55
B	C0791		0.99	0.00	0.00	0.97	0.02	0.87	0.31	0.32	0.31	0.05	0.03	0.045	53	131	55
B	C1763		0.92	0.00	-0.01	0.76	-0.03	0.79	0.33	0.31	0.31	0.05	0.03	0.045	57	135	55
B	C2308		0.79	0.00	-0.02	0.51	0.02	0.85	0.33	0.32	0.28	0.05	0.03	0.045	53	136	54
B	C0522		0.67	0.00	-0.03	0.50	-0.05	0.58	0.35	0.30	0.30	0.05	0.03	0.05	54	133	48
B	C0036A		0.66	0.00	-0.03	0.38	-0.02	0.83	0.35	0.31	0.29	0.05	0.03	0.045	55	139	54
B	C0284		0.38	0.01	-0.05	0.17	-0.02	0.83	0.36	0.30	0.27	0.05	0.03	0.05	53	143	48
B	C0082		0.27	0.01	-0.05	0.17	-0.07	0.46	0.38	0.30	0.29	0.05	0.03	0.05	56	144	44
C	C0050	**	0.00	0.05	0.11	0.00	-0.07	0.42	0.23	0.31	0.45	0.05	0.03	0.05	57	140	50
C	C1395	**	0.00	0.05	0.12	0.00	-0.10	0.28	0.23	0.30	0.46	0.05	0.03	0.045	58	141	51
C	C0460	*	0.01	0.04	0.10	0.00	0.03	0.76	0.22	0.33	0.41	0.05	0.03	0.045	57	130	51
C	C1378	*	0.04	0.03	0.09	0.01	-0.01	0.91	0.24	0.32	0.41	0.05	0.03	0.045	60	137	52
C	C0838	*	0.03	0.03	0.08	0.01	-0.06	0.50	0.25	0.30	0.41	0.05	0.03	0.045	59	121	55

TABLE A7. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
C	C1137		0.14	0.02	0.07	0.05	0.02	0.87	0.25	0.32	0.37	0.05	0.03	0.045	57	134	58
C	C2247		0.09	0.02	0.07	0.03	0.02	0.89	0.24	0.32	0.38	0.05	0.03	0.045	59	129	57
C	C0172		0.37	0.01	0.02	0.52	-0.12	0.20	0.32	0.29	0.36	0.05	0.03	0.045	64	118	59
C	C0896		0.28	0.01	0.03	0.39	-0.13	0.17	0.32	0.29	0.38	0.05	0.03	0.045	64	117	56
C	C0607		0.91	0.00	0.02	0.68	-0.01	0.91	0.31	0.32	0.33	0.04	0.03	0.045	68	123	59
C	C1740		0.98	0.00	0.01	0.88	-0.01	0.92	0.32	0.32	0.33	0.04	0.03	0.045	67	114	62
D	C0713		0.17	0.01	-0.06	0.06	-0.01	0.90	0.38	0.31	0.26	0.05	0.03	0.045	60	131	55
D	C2255		0.66	0.00	-0.03	0.41	-0.04	0.68	0.35	0.31	0.30	0.05	0.03	0.045	57	124	62
D	C1373		0.31	0.01	0.03	0.33	0.11	0.23	0.26	0.34	0.32	0.05	0.03	0.045	55	135	59
D	C0463E		0.23	0.01	0.04	0.24	0.12	0.19	0.25	0.34	0.32	0.05	0.03	0.04	57	119	67
D	C2008		0.34	0.01	0.04	0.20	0.07	0.48	0.26	0.33	0.34	0.05	0.03	0.045	57	131	57
D	C0360		0.67	0.00	0.02	0.60	0.07	0.47	0.29	0.34	0.32	0.05	0.03	0.045	59	127	59
D	H2169		0.71	0.00	0.02	0.51	0.05	0.63	0.29	0.33	0.33	0.05	0.03	0.045	60	129	60
D	C0823		0.73	0.00	0.02	0.60	0.06	0.55	0.29	0.33	0.32	0.05	0.03	0.045	58	132	59
E	C1203		0.54	0.01	-0.04	0.27	0.02	0.84	0.35	0.32	0.27	0.05	0.03	0.05	63	137	47
E	C0810		0.30	0.01	0.01	0.85	-0.14	0.12	0.34	0.28	0.36	0.05	0.03	0.045	57	132	55
E	C0062		0.81	0.00	0.01	0.88	-0.06	0.53	0.33	0.30	0.33	0.05	0.03	0.045	62	111	64
E	C1153		0.89	0.00	0.02	0.69	0.03	0.77	0.30	0.32	0.32	0.05	0.03	0.04	58	124	66
E	C1170		0.78	0.00	0.00	0.95	-0.06	0.48	0.33	0.30	0.34	0.05	0.03	0.045	63	124	60

TABLE A7. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
E	C0431		0.77	0.00	0.01	0.89	-0.07	0.47	0.33	0.30	0.34	0.05	0.03	0.045	60	127	54
E	C1105		0.49	0.01	0.00	0.94	-0.11	0.23	0.34	0.29	0.35	0.05	0.03	0.045	63	123	60
E	C0732		0.47	0.01	-0.03	0.33	-0.07	0.44	0.36	0.30	0.30	0.04	0.03	0.04	66	117	67
E	C0566		0.23	0.01	-0.05	0.12	-0.06	0.50	0.38	0.30	0.28	0.05	0.03	0.045	64	121	61
E	C1138		0.11	0.02	-0.06	0.09	-0.12	0.17	0.41	0.29	0.30	0.05	0.03	0.04	52	121	66
E	H2038		0.14	0.02	-0.05	0.11	-0.11	0.23	0.39	0.28	0.29	0.05	0.03	0.045	62	117	62
F	C0865		0.75	0.00	-0.02	0.55	-0.04	0.66	0.35	0.31	0.31	0.05	0.03	0.045	61	130	58
F	C0496		0.98	0.00	0.00	0.97	0.02	0.86	0.31	0.32	0.32	0.05	0.03	0.045	62	126	60
F	C0681		0.96	0.00	0.01	0.81	0.02	0.87	0.31	0.32	0.32	0.05	0.03	0.045	58	120	63
F	C1437		0.94	0.00	0.01	0.79	0.02	0.81	0.31	0.33	0.32	0.05	0.03	0.045	61	124	57
F	C1696		0.09	0.02	-0.04	0.26	0.17	0.06	0.31	0.36	0.23	0.05	0.03	0.045	52	131	53
F	C1222		0.26	0.01	-0.04	0.21	0.10	0.27	0.33	0.33	0.24	0.05	0.03	0.05	57	138	48
F	C1997		0.57	0.00	-0.03	0.47	0.08	0.41	0.32	0.33	0.27	0.05	0.03	0.055	54	131	43
F	C1176		0.51	0.01	-0.02	0.68	0.10	0.28	0.31	0.34	0.28	0.05	0.03	0.05	52	144	51
F	C0169		0.57	0.00	-0.04	0.29	0.01	0.95	0.35	0.32	0.28	0.05	0.03	0.045	59	127	64
G	C0357	****	0.00	0.48	-0.33	0.00	-0.35	0.00	0.75	0.25	0.10	0.04	0.02	0.03	50	124	58
G	C0290	****	0.00	0.70	-0.42	0.00	-0.38	0.00	0.87	0.26	0.03	0.03	0.02	0.025	47	136	65
G	C0887	****	0.00	0.42	-0.32	0.00	-0.24	0.00	0.70	0.26	0.06	0.04	0.03	0.035	54	132	54
G	C1720	****	0.00	0.19	-0.21	0.00	-0.17	0.05	0.57	0.28	0.15	0.04	0.03	0.045	55	121	52

TABLE A7. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
G	C0036C	****	0.00	0.16	-0.19	0.00	-0.16	0.05	0.53	0.27	0.17	0.04	0.03	0.04	69	121	58
G	C1168	****	0.00	0.13	-0.17	0.00	-0.06	0.48	0.50	0.29	0.15	0.04	0.03	0.045	68	127	54
G	C1470	****	0.00	0.11	-0.15	0.00	-0.15	0.08	0.49	0.27	0.20	0.04	0.03	0.045	66	125	55
G	C1002	**	0.01	0.04	-0.10	0.00	-0.02	0.82	0.41	0.30	0.22	0.04	0.03	0.045	70	120	53
G	C0277B	*	0.01	0.04	-0.09	0.01	-0.07	0.46	0.42	0.30	0.24	0.04	0.03	0.05	69	127	45
G	C1410A	*	0.03	0.03	-0.09	0.01	-0.03	0.75	0.40	0.30	0.23	0.04	0.03	0.05	69	135	42
G	C2286	*	0.02	0.03	-0.09	0.01	-0.03	0.74	0.40	0.30	0.22	0.04	0.03	0.05	72	132	43
G	C0532	*	0.02	0.03	-0.09	0.01	0.00	0.99	0.39	0.31	0.22	0.04	0.03	0.05	71	133	44
G	C1242		0.09	0.02	-0.08	0.03	0.05	0.59	0.37	0.32	0.22	0.04	0.03	0.055	67	139	41
G	C1143		0.41	0.01	-0.05	0.18	0.02	0.84	0.35	0.31	0.26	0.04	0.03	0.055	73	129	41
G	C0667	**	0.01	0.04	-0.11	0.00	0.08	0.38	0.39	0.32	0.17	0.04	0.03	0.055	65	137	38
H	C0180		0.48	0.01	-0.03	0.32	-0.06	0.48	0.36	0.30	0.30	0.05	0.03	0.045	54	126	59
H	C1715		0.29	0.01	-0.05	0.12	0.00	0.99	0.36	0.31	0.26	0.05	0.03	0.045	53	134	53
H	H2030		0.19	0.01	-0.06	0.07	0.04	0.68	0.36	0.32	0.25	0.05	0.03	0.045	58	139	53
H	C1131		0.36	0.01	-0.05	0.16	0.03	0.77	0.36	0.33	0.27	0.05	0.03	0.045	59	134	54
H	C1288		0.21	0.01	-0.06	0.09	-0.04	0.69	0.38	0.31	0.27	0.05	0.03	0.045	61	120	58
H	C1360		0.51	0.01	-0.04	0.25	-0.01	0.89	0.37	0.32	0.29	0.05	0.03	0.05	62	124	48
H	C1476		0.21	0.01	-0.06	0.08	-0.02	0.83	0.38	0.31	0.27	0.05	0.03	0.045	63	127	56
H	C0523		0.50	0.01	-0.04	0.24	-0.01	0.92	0.35	0.31	0.28	0.05	0.03	0.045	61	124	54

TABLE A7. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
H	C0515		0.08	0.02	-0.04	0.18	-0.16	0.07	0.40	0.28	0.32	0.05	0.03	0.045	65	116	65
I	C1156		0.37	0.01	0.02	0.67	0.12	0.18	0.27	0.34	0.29	0.05	0.03	0.045	60	124	58
I	C1728		0.65	0.00	0.02	0.67	0.08	0.41	0.29	0.34	0.31	0.05	0.03	0.045	60	122	58
I	C1366		0.29	0.01	0.02	0.57	0.13	0.14	0.27	0.35	0.31	0.05	0.03	0.045	59	124	61
I	C1147		0.20	0.01	0.03	0.40	0.14	0.12	0.25	0.35	0.31	0.05	0.03	0.045	59	122	56
I	C0649		0.44	0.01	0.02	0.47	0.10	0.28	0.27	0.34	0.32	0.05	0.03	0.045	57	129	64
I	C1407		0.57	0.00	0.02	0.51	0.08	0.40	0.27	0.33	0.32	0.05	0.03	0.045	56	127	62
I	C0277A		0.61	0.00	0.03	0.42	0.06	0.55	0.27	0.33	0.33	0.05	0.03	0.045	56	131	61
I	C1410B		0.86	0.00	0.02	0.59	0.02	0.88	0.29	0.32	0.33	0.05	0.03	0.04	54	126	66
I	C0175		0.73	0.00	0.02	0.61	0.06	0.53	0.29	0.33	0.32	0.05	0.03	0.045	58	121	64
I	C0331		0.46	0.01	0.04	0.27	0.06	0.49	0.26	0.33	0.33	0.05	0.03	0.04	49	127	67
I	C1077		0.16	0.01	0.06	0.06	0.01	0.97	0.25	0.31	0.37	0.05	0.03	0.04	47	131	71
I	C0717		0.15	0.02	0.05	0.14	-0.10	0.28	0.29	0.29	0.39	0.05	0.03	0.045	44	130	63
I	C1461		0.06	0.02	0.07	0.04	-0.08	0.35	0.27	0.29	0.40	0.05	0.03	0.04	50	126	72
I	C1891		0.14	0.02	0.05	0.18	-0.12	0.20	0.30	0.29	0.39	0.06	0.03	0.045	42	113	61
I	C0851		0.31	0.01	0.05	0.15	-0.04	0.69	0.28	0.30	0.37	0.05	0.03	0.04	51	124	69
J	C0268		0.17	0.01	0.05	0.10	0.07	0.45	0.25	0.34	0.36	0.04	0.03	0.05	67	131	50
J	C0007	*	0.02	0.03	0.09	0.00	-0.05	0.56	0.24	0.31	0.43	0.05	0.03	0.05	62	137	50
J	C1523	*	0.05	0.03	0.07	0.04	-0.13	0.15	0.29	0.29	0.43	0.05	0.03	0.045	64	124	53

TABLE A7. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
J	C1160	*	0.01	0.04	0.09	0.01	-0.14	0.12	0.27	0.29	0.44	0.04	0.03	0.045	68	124	54
J	C1067	**	0.00	0.05	0.10	0.00	-0.17	0.05	0.27	0.28	0.46	0.04	0.03	0.045	71	122	57
J	C1453	**	0.01	0.04	0.09	0.00	-0.14	0.12	0.26	0.28	0.44	0.04	0.03	0.045	68	122	54
J	C0026	*	0.02	0.03	0.08	0.01	-0.15	0.10	0.28	0.29	0.44	0.04	0.03	0.045	69	121	54
J	C1294	*	0.03	0.03	0.08	0.03	-0.17	0.07	0.30	0.29	0.44	0.04	0.03	0.05	68	118	43
J	C1184		0.13	0.02	0.06	0.10	-0.12	0.19	0.30	0.30	0.41	0.04	0.03	0.05	68	128	50
J	C0949		0.59	0.00	0.01	0.87	-0.09	0.31	0.33	0.29	0.34	0.04	0.03	0.045	70	115	53
J	C1446		0.90	0.00	0.00	0.97	-0.05	0.64	0.33	0.31	0.33	0.05	0.03	0.05	63	123	49
J	H2074		0.69	0.00	0.03	0.43	-0.04	0.65	0.30	0.31	0.35	0.04	0.03	0.05	70	131	47
K	C1924		0.64	0.00	-0.01	0.88	-0.08	0.35	0.33	0.29	0.32	0.05	0.03	0.045	56	128	60
K	C1139		0.92	0.00	0.01	0.87	0.04	0.69	0.30	0.33	0.31	0.05	0.03	0.045	51	131	58
K	C1400		0.58	0.00	-0.01	0.73	0.09	0.33	0.30	0.34	0.28	0.05	0.03	0.04	58	126	65
K	C1010		0.71	0.00	-0.02	0.49	0.04	0.68	0.33	0.33	0.29	0.05	0.03	0.04	63	113	73
K	C1093		0.70	0.00	-0.01	0.76	0.07	0.43	0.31	0.34	0.29	0.05	0.03	0.04	64	113	68
K	C0559		0.80	0.00	-0.01	0.85	0.06	0.53	0.31	0.33	0.30	0.05	0.03	0.045	62	117	61
K	C0307		0.96	0.00	-0.01	0.79	0.01	0.89	0.33	0.32	0.31	0.05	0.03	0.05	61	127	45
K	C0806		0.82	0.00	0.01	0.89	0.06	0.54	0.30	0.33	0.31	0.05	0.03	0.045	58	127	58
K	C0947		0.90	0.00	0.00	0.98	0.04	0.65	0.31	0.33	0.31	0.05	0.04	0.04	63	107	70
K	C0698		0.73	0.00	-0.01	0.82	0.07	0.45	0.31	0.34	0.30	0.04	0.03	0.04	66	114	69

TABLE A7. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
L	C1978		0.82	0.00	0.02	0.53	-0.01	0.96	0.30	0.32	0.34	0.05	0.03	0.05	64	133	45
L	C0822		0.91	0.00	0.02	0.67	0.01	0.97	0.30	0.31	0.33	0.05	0.03	0.05	61	131	44
L	C1451		0.53	0.01	0.03	0.38	0.06	0.50	0.27	0.33	0.33	0.05	0.03	0.05	53	141	47
L	C0728		0.30	0.01	0.02	0.51	0.13	0.17	0.27	0.35	0.31	0.05	0.03	0.045	63	124	56
L	C1517		0.35	0.01	0.04	0.24	0.07	0.44	0.27	0.34	0.34	0.04	0.03	0.045	68	123	57
L	C0383		0.34	0.01	0.03	0.48	0.11	0.24	0.27	0.35	0.32	0.04	0.03	0.05	71	124	49
L	C0619		0.14	0.02	0.04	0.19	0.12	0.20	0.25	0.35	0.33	0.04	0.03	0.05	72	123	50
L	C0230		0.38	0.01	0.03	0.44	0.10	0.28	0.27	0.34	0.32	0.04	0.03	0.045	72	115	54
L	C0628		0.78	0.00	0.01	0.81	0.06	0.51	0.30	0.33	0.31	0.05	0.03	0.045	63	125	60
L	C0481		0.79	0.00	0.01	0.75	0.06	0.54	0.29	0.33	0.31	0.05	0.03	0.045	60	124	65
L	C0589		0.93	0.00	0.01	0.89	0.03	0.73	0.31	0.33	0.31	0.05	0.03	0.045	61	124	65
L	C1524		0.76	0.00	-0.01	0.76	-0.06	0.51	0.35	0.31	0.33	0.05	0.03	0.045	60	124	59
M	C1180		0.13	0.02	-0.05	0.12	-0.11	0.21	0.39	0.29	0.30	0.04	0.03	0.045	65	123	62
M	C0181		0.27	0.01	-0.06	0.10	0.00	0.99	0.37	0.32	0.27	0.05	0.03	0.045	57	134	57
M	C0903		0.19	0.01	-0.06	0.09	0.07	0.44	0.35	0.33	0.24	0.04	0.03	0.05	65	135	48
M	C1177		0.79	0.00	-0.03	0.50	0.02	0.89	0.35	0.33	0.30	0.05	0.04	0.05	50	119	48
M	C0735		0.56	0.00	-0.04	0.28	-0.01	0.94	0.35	0.31	0.28	0.05	0.03	0.05	55	135	52
M	C0252A		0.53	0.01	-0.04	0.28	0.03	0.75	0.35	0.32	0.28	0.05	0.03	0.045	53	138	55
M	C1109		0.88	0.00	-0.01	0.70	-0.03	0.75	0.34	0.31	0.31	0.05	0.03	0.045	61	130	57

TABLE A7. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
M	C1004		0.62	0.00	-0.03	0.36	0.04	0.70	0.34	0.32	0.28	0.05	0.03	0.045	57	135	53
M	C0873		0.88	0.00	-0.01	0.72	0.04	0.70	0.32	0.32	0.30	0.05	0.03	0.045	64	125	57
M	C0027		0.84	0.00	-0.02	0.69	0.04	0.65	0.32	0.32	0.29	0.05	0.03	0.045	62	129	57
M	C1440		0.71	0.00	-0.01	0.82	0.08	0.42	0.31	0.34	0.29	0.05	0.04	0.05	60	115	51
N	H2034		0.87	0.00	-0.02	0.66	0.03	0.74	0.33	0.33	0.30	0.05	0.03	0.05	58	136	51
N	C1754		0.38	0.01	-0.04	0.21	0.06	0.54	0.34	0.33	0.26	0.05	0.03	0.05	57	132	52
N	C0941		0.39	0.01	-0.04	0.23	0.07	0.47	0.34	0.33	0.26	0.05	0.03	0.045	60	136	52
N	C1145		0.54	0.01	-0.03	0.43	0.07	0.42	0.32	0.33	0.27	0.05	0.03	0.045	56	140	53
N	C0929		0.34	0.01	-0.05	0.15	0.04	0.69	0.36	0.33	0.26	0.05	0.03	0.05	54	138	51
N	C1965		0.67	0.00	-0.03	0.41	0.04	0.66	0.33	0.32	0.27	0.05	0.03	0.05	63	121	47
N	C1562		0.77	0.00	-0.02	0.66	0.06	0.54	0.32	0.33	0.29	0.05	0.03	0.05	66	133	49
N	C2303		0.82	0.00	-0.02	0.63	0.04	0.66	0.31	0.31	0.28	0.04	0.03	0.045	64	123	51
N	C0503		0.60	0.00	-0.02	0.59	0.08	0.37	0.32	0.34	0.28	0.05	0.03	0.05	65	124	50
N	C2074		0.63	0.00	-0.02	0.54	0.07	0.47	0.32	0.33	0.28	0.05	0.03	0.045	54	126	60
N	C0057		0.99	0.00	0.00	0.96	-0.01	0.89	0.32	0.31	0.32	0.05	0.03	0.045	51	131	61
O	C0736A		0.64	0.00	-0.01	0.68	0.08	0.40	0.31	0.34	0.29	0.04	0.03	0.04	68	114	66
O	C2055		0.87	0.00	0.01	0.81	0.04	0.65	0.30	0.33	0.31	0.05	0.03	0.045	65	122	57
O	C0316		0.98	0.00	-0.01	0.88	0.02	0.88	0.31	0.32	0.30	0.05	0.03	0.045	61	127	58
O	C0925		0.97	0.00	-0.01	0.81	-0.01	0.94	0.32	0.31	0.31	0.05	0.03	0.045	63	128	58

TABLE A7. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
O	C1135		0.96	0.00	-0.01	0.79	-0.01	0.96	0.32	0.31	0.31	0.05	0.03	0.045	63	127	59
O	C0043		0.91	0.00	0.00	0.98	-0.04	0.67	0.32	0.30	0.32	0.05	0.03	0.045	63	120	61
O	C1905		0.55	0.01	-0.02	0.67	-0.09	0.32	0.35	0.29	0.32	0.05	0.03	0.045	55	127	52
O	C1249		0.77	0.00	-0.02	0.64	-0.05	0.59	0.34	0.30	0.31	0.05	0.03	0.045	58	131	58
O	C1210		0.72	0.00	-0.01	0.93	-0.07	0.43	0.34	0.30	0.33	0.05	0.03	0.05	57	128	49
O	C0296		0.86	0.00	-0.02	0.59	0.01	0.92	0.33	0.32	0.30	0.05	0.03	0.04	61	118	67
O	C0238		0.72	0.00	-0.01	0.72	0.07	0.49	0.31	0.33	0.29	0.05	0.04	0.04	51	101	69
O	C1256		0.98	0.00	-0.01	0.84	-0.01	0.93	0.32	0.31	0.31	0.05	0.04	0.04	63	110	72
O	H2001		0.98	0.00	0.01	0.90	0.01	0.89	0.31	0.32	0.32	0.05	0.04	0.04	62	113	70
O	H2074		0.97	0.00	0.01	0.85	-0.02	0.89	0.31	0.31	0.32	0.05	0.03	0.04	63	115	71
P	H2013		0.13	0.02	0.05	0.12	-0.13	0.16	0.30	0.29	0.40	0.05	0.03	0.045	64	132	54
P	C0747		0.07	0.02	0.06	0.08	-0.14	0.12	0.30	0.29	0.41	0.05	0.03	0.045	62	129	56
P	C0906		0.13	0.02	0.06	0.06	-0.09	0.34	0.28	0.30	0.40	0.04	0.03	0.045	65	131	54
P	C1423		0.40	0.01	0.05	0.19	0.03	0.77	0.27	0.33	0.36	0.05	0.03	0.05	61	128	52
P	C0866		0.36	0.01	0.04	0.20	0.05	0.62	0.26	0.33	0.35	0.04	0.03	0.05	65	133	50
P	C0704		0.52	0.01	0.03	0.35	0.05	0.56	0.27	0.33	0.33	0.05	0.03	0.05	61	137	49
P	C1000		0.74	0.00	0.01	0.71	0.06	0.52	0.29	0.33	0.31	0.05	0.03	0.05	61	132	49
P	C1418		0.62	0.00	0.02	0.60	0.07	0.47	0.28	0.33	0.32	0.05	0.03	0.055	59	143	37
P	C0616		0.53	0.01	0.04	0.31	0.03	0.73	0.28	0.33	0.35	0.05	0.03	0.055	60	145	42

TABLE A7. Continued

GROUP	MARKER	SIG	PROB	RSQ	ADDIT	ADPROB	DOM	DOPROB	MTAA	MTAB	MTBB	STAA	STAB	STBB	NAA	NAB	NBB
P	H2151		0.20	0.01	0.02	0.56	0.15	0.10	0.26	0.35	0.30	0.05	0.03	0.05	57	145	45
P	C1059		0.08	0.02	0.06	0.11	0.14	0.13	0.22	0.35	0.33	0.05	0.03	0.05	53	148	46
Q	H2011		0.36	0.01	-0.03	0.38	-0.10	0.29	0.37	0.29	0.31	0.04	0.03	0.045	68	115	59
Q	C0519		0.64	0.00	-0.03	0.36	-0.01	0.90	0.35	0.32	0.29	0.04	0.03	0.045	70	116	57
Q	C2284		0.95	0.00	-0.01	0.74	0.01	0.95	0.33	0.32	0.31	0.05	0.03	0.045	66	118	55
Q	C1201		0.85	0.00	-0.02	0.57	0.01	0.97	0.34	0.32	0.30	0.04	0.04	0.045	69	113	58
Q	C1713		0.55	0.01	-0.03	0.45	0.08	0.40	0.32	0.33	0.27	0.05	0.03	0.05	62	122	50
Q	C1380		0.63	0.00	-0.03	0.43	0.05	0.56	0.33	0.33	0.28	0.05	0.03	0.045	61	128	54
Q	C1195		0.80	0.00	0.01	0.89	0.06	0.52	0.29	0.33	0.30	0.05	0.03	0.05	57	137	51
Q	C0044		0.39	0.01	0.02	0.67	0.12	0.20	0.27	0.34	0.30	0.05	0.03	0.05	53	139	52
Q	C0827		0.20	0.01	0.06	0.11	0.07	0.48	0.25	0.33	0.36	0.05	0.03	0.05	56	137	50

*, **, ***, ****: Significance level of 0.05, 0.01, 0.001, and 0.0001, respectivelly.

RSQ: Coefficient of determination (R-square)

ADDIT and DOM: Additive and dominant effects, respectivelly.

ADPROB and DOPROB: Probability of significance for additive and dominant effects, respectively

MTAA, MTAB, and MTBB: Marker classes means for the trait

STAA, STAB, and STBB: Standard error of the marker class means.

NAA, NAB and NBB: Number of plants having each marker class.

TABLE A8. F2 field data

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
10-1	1	29	71	57.0	46
10-2	0	24	76	54.4	45.2
10-3	1	26	74	59.0	46.9
10-4	1	28	72	55.2	44.5
10-5	1	40	60	60.0	50.7
10-6	1	29	71	52.4	42.6
10-7	1	33	67	58.0	45.8
10-8	1	33	67	56.6	47.6
10-9	1	31	69	62.0	45.7
10-10					
10-11					
10-12	0	26	74	58.6	46.1
10-13	1	26	74	56.8	48.2
10-14					
10-15	1	27	73	56.2	45.6
10-16	0	41	59	54.2	48.2
10-17	1	32	68	56.2	43.7
10-18	1	43	57	47.2	33
11-1					
11-2	0	35	65	51.2	37.3
11-3	0	32	68	57.0	50.3
11-4	1	30	70	55.6	44.9
11-5	0	32	68	54.0	41.3
11-6	1	24	76	56.6	47.2
11-7	1	33	67	54.6	46.8
11-8	0	29	71	57.8	46.1

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
11-9	0	25	75	49.0	41.1
11-10	1	30	70	57.4	44.9
11-11	1	26	74	60.8	51.2
11-12	0	33	67	57.2	49.6
11-13	1	28	72	61.0	46.3
11-14	1	26	74	60.8	49.7
11-15	1	33	67	55.2	44.1
11-16	1	40	60	52.6	39.6
11-17	1	28	72	59.2	49
11-18	1	33	67	50.8	38.9
12-1	1	34	66	50.0	37.8
12-2	0	24	76	52.8	45.8
12-3					
12-4	1	40	60	55.6	42.6
12-5	1	31	69	52.0	43.3
12-6	1	27	73	59.4	46.1
12-7					
12-8					
12-9	1	38	62	56.0	43.5
12-10	0	27	73	60.0	47.9
12-11	1	31	69	53.6	43.4
12-12					
12-13					
12-14	0	27	73	56.4	46.9
12-15	1	33	67	53.4	45.6
12-16	1	31	69	57.3	45.3

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
12-17	1	26	74	60.8	48.2
13-1	1	27	73	60.2	48.5
13-2	1	31	69	58.8	46.2
13-3	0	38	62	57.6	49.3
13-4	1	28	72	53.2	43.2
13-5	1	30	70	57.4	44.7
13-6	0	25	75	57.0	50.4
13-7	1	42	58	51.4	39.2
13-8	1	31	69	53.2	43.2
13-9	1				49.6
13-10	1	35	65	53.0	41.3
13-11	1	28	72	57.6	46.3
13-12	1	27	73	50.6	41.6
13-13	1	35	65	55.8	44.6
13-14	1	29	71	61.6	49.6
13-15	1	42	58	44.0	31.9
13-16					
13-17	1				
14-1	1	27	73	53.2	43.1
14-2	1	31	69	47.0	39.2
14-3	1	27	73	55.8	43.2
14-4	0	21	79	58.0	49.9
14-5					
14-6	1				43.2
14-7	1	30	70	54.8	42.6
14-8					

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
14-9	1	37	63	58.2	43.5
14-10	1	27	73	57.0	45.9
14-11	1	34	66	54.8	41.7
14-12	1	29	71	54.8	42.6
14-13	1	44	56	56.8	45
14-14	1				
14-15					
14-16	1	31	69	50.6	39.9
14-17	1	35	65	53.3	39.5
14-18					
15-1	0	31	69	46.2	37.1
15-2	1	39	61	45.0	34.3
15-3	1	28	72	59.0	48.5
15-4	1	34	66	49.4	41.3
15-5	1	30	70	55.6	43.1
15-6	1				
15-7	1	29	71	53.2	43.4
15-8	1	36	64	59.6	49
15-9	1	31	69	52.4	41.7
15-10	1				37.2
15-11	1	26	74	59.0	48
15-12	1	30	70	58.2	45.7
15-13	1	29	71	52.8	44.5
15-14	1				
15-15					
15-16	1				35.4

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
15-17	0	42	58	53.0	46.8
15-18	1	32	68	55.0	42.2
16-1	0	28	72	56.8	45.1
16-2	1	36	64	53.6	39.7
16-3	1				48
16-4	1	29	71	57.0	46.5
16-5	1	32	68	56.6	44.5
16-6	1	33	67	60.6	45.1
16-7	1	33	67	56.8	47.2
16-8	1	39	61	55.2	46.4
16-9	1	31	69	55.8	44.4
16-10					
16-11	0	25	75	54.8	48.2
16-12	1	31	69	58.2	44.9
16-13	0				
16-14	1	30	70	55.4	44.1
16-15	1	33	67	54.2	42.5
16-16	1	32	68	60.2	47
16-17	0	31	69	54.2	40.9
16-18	1	27	73	53.8	42.9
17-1	1	35	65	53.4	41.3
17-2					
17-3	0	27	73	64.2	51.9
17-4	0	32	68	54.4	43.7
17-5	1	29	71	53.6	42.7
17-6	1	35	65	50.8	37.5

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
17-7	0	37	63	58.2	50.8
17-8	1	29	71	58.2	48.1
17-9	1	30	70	61.6	47.6
17-10	0	24	76	60.4	50.1
17-11	0	40	60	61.8	52.3
17-12	1	29	71	54.0	43
17-13	1	33	67	53.6	41
17-14	0				
17-15	1	31	69	58.0	45.5
17-16					
17-17	1	29	71	53.0	42.1
18-1					
18-2	0	29	71	54.0	44
18-3					
18-4	1	29	71	57.2	42.7
18-5	1	30	70	56.4	45.4
18-6	1	28	72	60.2	49.2
18-7	1	34	66	58.6	44.1
18-8	1	28	72	59.0	47.5
18-9	1				
18-10	1	32	68	56.4	49.2
18-11	0	25	75	52.8	44.3
18-12	1	43	57	52.4	35.7
18-13	1	27	73	62.2	49.9
18-14	0	29	71	56.6	43.8
18-15	1	37	63	57.8	48.2

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
18-16	1				49.2
18-17	0	21	79	57.6	49.2
18-18	1	34	66	52.8	40.3
19-1					
19-2	1	32	68	49.6	37.6
19-3	1	28	72	51.6	42.2
19-4	1	33	67	54.6	41.6
19-5	1				38.8
19-6					
19-7					
19-8	1	28	72	54.6	44.8
19-9	1	36	64	57.2	45.5
19-10	1	38	62	53.2	38.4
19-11					
19-12	1				
19-13	1	30	70	56.6	44
19-14	1	34	66	60.8	44.1
19-15	0	31	69	56.0	51.3
19-16	1	34	66	54.4	42.3
19-17	1	32	68	52.4	41
19-18	1	30	70	47.4	39.8
20-1	1	42	58	44.8	34.5
20-2	1	37	63	44.8	34.9
20-3	1	29	71	57.2	45.5
20-4	0	27	73	53.2	33.3
20-5	0	25	75	53.6	42.9

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
20-6					
20-7	1	34	66	57.6	44.9
20-8					
20-9	1	29	71	60.4	49.2
20-10	0	25	75	60.6	51.5
20-11	1	32	68	56.8	44.7
20-12	1				29.4
20-13	1	37	63	48.8	37.8
20-14	1	36	64	62.8	53.3
20-15	0	20	80	54.0	49.1
20-16	1	33	67	50.4	39
20-17	1	28	72	54.6	45.2
21-1					
21-2	1	40	60	55.4	39.5
21-3	1	34	66	49.6	39.5
21-4	0				
21-5	1				41.4
21-6	1	39	61	56.2	41.7
21-7	0	29	71	55.0	46.4
21-8	1	28	72	58.2	45.9
21-9	1	31	69	61.0	49.5
21-10	1	33	67	55.0	40.7
21-11	1				
21-12	1	29	71	57.4	42.8
21-13	0	31	69	54.8	44.8
21-14	1	29	71	59.2	45.4

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
21-15	1	30	70	53.2	41.9
21-16					
21-17	0	25	75	62.8	50.3
21-18	1	31	69	52.6	40.2
22-1	1	32	68	51.8	43.6
22-2	1	37	63	45.2	34.4
22-3	1	32	68	53.4	41.2
22-4	0	29	71	57.6	44.9
22-5	1	28	72	58.4	44.1
22-6	1				38
22-7	1	27	73	55.4	44.6
22-8	1	28	72	61.0	47.8
22-9	1	28	72	54.4	43.6
22-10	1	31	69	56.8	43.6
22-11	1	28	72	58.0	46.7
22-12	1	29	71	56.0	45.2
22-13	1	31	69	54.4	41.1
22-14	1	28	72	54.1	46
22-15	1	28	72	60.6	45.6
22-16	0	29	71	58.8	50.1
22-17	1	35	65	53.0	40.2
22-18					
23-1	0	27	73	57.0	46.1
23-2	1	28	72	55.8	46.1
23-3					
23-4	0	29	71	54.8	46.6

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
23-5	1				
23-6	1	26	74	58.8	50.4
23-7	1	35	65	55.6	41
23-8	1	29	71	54.8	44.3
23-9	0	36	64	61.8	51.3
23-10	1	28	72	60.4	48
23-11	1	28	72	62.6	49.3
23-12	1	26	74	61.4	52.6
23-13	1				
23-14	1	34	66	53.8	41.5
23-15	1	33	67	51.4	38.4
23-16	1	24	76	53.8	44.8
23-17	0	35	65	56.0	45.9
24-1	0	26	74	55.4	48.2
24-2	1	34	66	50.8	38.8
24-3	0	31	69	53.2	45.9
24-4	1	30	70	56.4	45.7
24-5	1	40	60	51.6	37.6
24-6	1	28	72	56.6	43.2
24-7	0	25	75	54.6	46
24-8	1	38	62	53.0	40.8
24-9					
24-10	1	31	69	48.6	39.1
24-11	1	33	67	57.4	43.3
24-12	0				
24-13	1	34	66	53.0	41.5

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
24-14	1	34	66	57.0	40.9
24-15	1				
24-16	1	28	72	62.2	49
24-17	0	22	78	54.4	47.7
24-18	1				37.2
25-1	1	35	65	55.2	47.2
25-2	1	33	67	51.0	38.1
25-3	1	28	72	55.0	44
25-4	0	25	75	57.4	47.2
25-5	1	29	71	58.2	47.2
25-6	0	21	79	56.8	48.7
25-7	1	39	61	56.2	44.7
25-8	1	35	65	59.8	41.1
25-9	1	28	72	56.2	47.1
25-10	1	33	67	53.2	43.6
25-11	1	36	64	54.0	40
25-12	1	29	71	52.0	43.7
25-13	1	30	70	57.8	44
25-14	1	29	71	57.8	43.7
25-15	1	31	69	56.8	43.9
25-16	0				
25-17	1	34	66	49.4	37.1
26-1	1	40	60	51.2	36.2
26-2	1				31.4
26-3	1	38	62	58.8	47
26-4	1	36	64	54.4	39.7

TABLE A8. Continued

Plant Code	Hypod. color	Hull %	Kernel %	Kernel Oil %	Seed Oil %
26-5	1	27	73	55.8	45.6
26-6	1	31	69	59.8	46.8
26-7	0	24	76	55.2	46.1
26-8	1	29	71	55.0	43.5
26-9	1				
26-10	1	33	67	52.8	40.2
26-11	1	30	70	56.2	43.7
26-12	1	29	71	56.8	47
26-13					
26-14	1	33	67	52.0	40.4
26-15					
26-16	1	29	71	58.2	47.6
26-17	1	36	64	51.4	38.1
26-18	1	37	63	48.0	33.7