Natural trait variation for taxonomic classification and breeding
potential assessment in the genus *Camelina*

by

Jerry Wu

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Abstract

Camelina sativa (L.) Crantz or camelina has been the subject of renewed interest as a novel alternative oilseed crop suitable for uses in biofuel, food, and industrial chemical applications as well as sustainable agricultural practices. Camelina's development as an oilseed crop is currently limited by a short breeding history and a complicated allohexaploid genome structure, which hinders traditional breeding and genetic modification approaches. Therefore, our study takes an alternative approach, examining natural (phenotypic) variation in an assortment of quantitative traits of 23 accessions representing camelina and four of its crop wild relatives (CWRs) to further our understanding of the taxonomic classification and breeding potential within the *Camelina* genus.

For our first objective, to determine key traits for discriminating taxa in the genus, principal components analysis (PCA) and linear discriminants analysis (LDA) were conducted to understand the patterns of phenotypic variation observed. It was determined that C20:1 and C22:1 fatty acid traits were the most informative variables in discriminating eight group membership identifications of the *Camelina* genus in this study. Permutational MANOVAs and Welch's t-tests conducted across the eight group membership identifications as well as 23 accessions for the quantitative traits were consistent with the clustering analyses from PCA and LDA. Also, our investigations into varying morphological traits within the genus combined with patterns of variation observed for seed oil characteristics suggest that *C. hispida* Boiss. is a potential parental ancestor of camelina.

For our second objective, we established three criteria measurements to screen for candidate plant lines with desirable fatty acid profiles for further development in breeding programmes for biofuel, food, and industrial chemical applications. We identified individual

lines each of *C. sativa* (ID# S-239), *C. hispida* (ID# HG-240), and diploid *C. microcarpa* Andr. ex DC. (ID# M2-246) as well as five *C. rumelica* Velen. accessions for development in the aforementioned applications, respectively. This study provides the foundation for subsequent research on basic plant biology and directions for breeding programmes in an allopolyploid oilseed crop.

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Statement of Contribution

I, Jerry Wu, performed all the experiments and generated all the material reported in this thesis with the exception of the following:

1. Sowing and vernalization of plant accessions was done by Tracey James (Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa).
2. Flower and pod morphological measurements via microscopy was done by Sarah Endenburg (Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa).
3. Dr. Sara Martin (Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa) contributed in measuring DNA content of plant accessions via flow cytometry.
4. LDA biplot functions were written in R by Dr. Tyler Smith (Ottawa Research and Development Centre, Agriculture and Agri-Food Canada, Ottawa).

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List of Abbreviations

2C	Genome size	
2X	Diploid	
4X	Tetraploid	
6X	Hexaploid	
AvPodBeak	Average pod beak length	
AvTotalFlower	Average total flower length	
AvWidth	Average pod width	
C16:0	Palmitic acid	C _{16:0}
C18:0	Stearic acid	C _{18:0}
C18:1	Oleic acid	C _{18:1n9}
C18:2	Linoleic acid	C _{18:2n6}
C18:3	α -linolenic acid	C _{18:3n3}
C20:0	Arachidic acid	C _{20:0}
C20:1	Eicosenoic acid	C _{20:1n9}
C20:2	Eicosadienoic acid	C _{20:2n6}
C20:3	Eicosatrienoic acid	C _{20:3n3}
C22:0	Behenic acid	C _{22:0}
C22:1	Erucic acid	C _{22:1n9}
C24:0	Lignoceric acid	C _{24:0}
C24:1	Nervonic acid	C _{24:1n9}
cm	Centimetre	
CWR	Crop wild relatives	
df	Degrees of freedom	
DNA	Deoxyribonucleic acid	
FA	Fatty acid	
FAD2	Fatty acid desaturase 2	
FAD3	Fatty acid desaturase 3	
FAE1	Fatty acid elongase 1	
FAME	Fatty acid methyl ester	
FCM	Flow cytometry	
g	Gram	
GMO	Genetically modified organism	
GC-FID	Gas chromatography – flame ionization detection	
ID	Identification	
IQR	Interquartile range	
LDA	Linear discriminants analysis	
MANOVA	Multivariate analysis of variance	
m	Metre	
mm	Millimetre	
MUFA	Monounsaturated fatty acid	
PCA	Principal components analysis	
pg	Picograms	
PUFA	Polyunsaturated fatty acid	
PUFA ratio	Sum of polyunsaturated to saturated and monounsaturated fatty acids	
HH	Height at harvest	

Oil	Total oil content
Protein	Total protein content
R	Pearson's coefficient
R ²	Coefficient of determination
SFA	Saturated fatty acid
SSFA	Sum of saturated fatty acids
SVLCFA	Sum of very long chain fatty acids
TAG	Triacylglycerol
TriFD	Trichomes – forked density
TriSD	Trichomes – simple density
TriTD	Trichomes – total density
TSP	Total seed production
TSW	Thousand-seed weight
VLCFA	Very long chain fatty acid

1.0 Introduction & Literature Review

1.1 Incentives for more sustainable agricultural practices

The increased demands for food and fuel resources as a consequence of a growing world population are major challenges that the agriculture sector will face in the coming decades. This task is further complicated by the need to meet these demands without further compromising the environment. For example, predominant wheat-fallow production systems in the Great Plains of the USA have been shown to be deficient in retaining adequate soil moisture levels after crop production cycles (Obour *et al.*, 2015). Furthermore, when coupled with conventional tillage operations for weed control during the fallow period, these systems have resulted in the depletion of soil profiles which can ultimately lead to losses of arable land (DeVuyst & Halvorson, 2004).

In an effort to meet global sustainability objectives, recent strategies to mitigate this problem include intensive cropping during fallow periods combined with the adoption of reduced tillage and no-till practices as these approaches have been shown to provide long-term economic and environmental benefits (Obour *et al.*, 2015). As a result, suitable crops that combine positive agronomical properties, including growth on marginally productive agricultural lands, with diverse food and non-food applications are of interest (Gehringer *et al.*, 2006). Oilseed crops in particular have the potential to satisfy these requirements. As one of the seven bioenergy crops identified by the United States Department of Agriculture, oilseeds have been projected to represent 0.5 of 36 billion gallons of renewable transportation fuel per year by 2022 according to the U.S. Renewable Fuels Standards mandate established in 2010 (USDA Biofuels Strategic Production Report, 2010). Therefore, oilseed crops can potentially play a significant role in mitigating the effects of global warming caused by greenhouse gas emissions from fossil fuels (Obour *et al.*, 2015).

1.2 Camelina as an alternative oilseed crop

The alternative oilseed crop *Camelina sativa* (L.) Crantz has been the subject of renewed interest as a promising candidate for the aforementioned purposes. *Camelina sativa*, commonly known as camelina, “false flax”, or “gold-of-pleasure”, is a member of the mustard family (Brassicaceae) with a history of cultivation for human consumption and animal feed in Europe dating back to the Bronze Age (Iskandarov *et al.*, 2014). It is now being reconsidered as a novel alternative oilseed crop with attributes that could make it a competitor against dominant global vegetable oils such as rapeseed, sunflower, and soybean. Diversification of oil crops by adopting bioenergy crops would reduce our reliance on dominant oil crops and contribute to global sustainability goals by diversifying markets, helping to manage crop pests, and increasing overall crop productivity (Obour *et al.*, 2015).

Competitiveness in agronomic performance as compared to established oil crops is a key factor for the economically successful establishment of a new crop (Vollman & Eynck, 2015). The interest in the development of camelina is primarily based on its positive agronomic traits including its suitability for growth on temperate and marginal landscapes in North America and Europe. It is particularly competitive in semi-arid regions and in low-fertility or saline soils compared to other oilseed crops (Budin *et al.*, 1995). The ability to produce a crop with low-inputs combined with a short growth cycle (85 to 100 days), adequate resistance to pests and plant pathogens that commonly affect members of *Brassica* such as blackleg (Seguin-Swartz *et al.*, 2009), and adaptability to adverse environmental conditions such as drought- and cold-tolerance have strengthened its incentives to be implemented in sustainable agricultural practices (Gugel and Falk, 2006). Although camelina has been advocated for growth on marginal lands, a more feasible and effective strategy would be to take advantage of its short generation time and

incorporate it into multiple crop rotation systems such as a spring-sown crop for tight crop rotations (Bansal & Durrett, 2016; Gehringer *et al.*, 2006). For instance, yield returns for camelina-soybean and camelina-sunflower double cropping systems were 82% and 72% respectively of their monocropped counterparts but the net economic returns for camelina-soybean double crop were higher than soybean alone (Gesch *et al.*, 2014).

Currently, crop production for camelina continues to occur on a small scale predominantly in North America but is also grown in Slovenia, Ukraine, China, Finland, Germany, and Austria (Smith, 2015). Camelina cultivation was highest in Montana in 2007 with an acreage of 22 500 ac but has steadily declined to 1500 ac in 2013 reportedly due to the lack of perceived profitability for farmers (Smith, 2015). Interest in camelina crop development is rising slowly in Canada with approximately 5000 acres grown in Saskatchewan by 2016 mainly as a source of meal for aquaculture industries and animal feed (Arnason, 2016). Camelina's status as a novel oilseed crop will be a major challenge in marketing its appeal to farmers but we believe that the long-term implications in developing camelina will become especially relevant in meeting the global objectives pertaining to sustainable development. This can be achieved by exploring the potential uses for its oil in various industrial applications and further research in understanding basic plant biology; both of which will be discussed in subsequent sections in this chapter and throughout this thesis.

1.3 Camelina for industrial applications

Camelina possesses a unique and versatile seed oil profile that has demonstrated potential in various applications of the oil industry. The average seed oil content ranges from 30 to 49%, which is lower than that of canola (*Brassica napus* L.) (Vollman & Eynck, 2015; Francis & Warwick, 2009). The oil yield is estimated to be 106 to 907 L ha⁻¹ which is comparable to

Brassica napus and *Brassica rapa* L. and significantly higher than soybean (247 to 562 L ha⁻¹) and sunflower (500 to 750 L ha⁻¹) (Moser, 2010; Bansal & Durrett, 2016; Obour *et al.*, 2015). Although the oil yield is less than that of canola, the cost of production of seed oil from camelina can be reduced by as much as one-half due to comparatively lower input requirements (Bansal & Durrett, 2016).

The oil is characterized by high contents of oleic acid C18:1 (15-20%), linoleic acid C18:2 (15-20%), α -linolenic acid C18:3 (30-40%), and eicosenoic acid C20:1 (15-20%) and a low content of erucic acid C22:1 (~3%) (Hrastar *et al.*, 2009). The proportions of C18:2 and C18:3 in camelina oil are notably higher than soybean or canola oil (Figure 1.1). This highly polyunsaturated composition of camelina oil has been targeted in oilseed development for food and nutritive applications particularly for the high amounts of α -linolenic acid (C18:3); an essential omega 3-fatty acid known for its health benefits (Vollman & Eynck, 2015). α -linolenic acid is also abundant in flaxseed oil and has cholesterol-lowering properties in humans (Gehring *et al.*, 2006; Karvonen *et al.*, 2002). α -linolenic acid is an omega-3 fatty acid with double-bonds at carbon positions 9, 12, and 15, not to be confused with its isomer, γ -linolenic acid, which is an omega-6 fatty acid with double-bonds at carbon position 6, 9, and 12. Some studies have advocated for a reduced dietary intake of omega-6 fatty acid due to possible proinflammatory and prothrombotic effects (Harris, 2010). Although the polyunsaturated nature of the oil may contribute to oxidative instability, some studies have shown that this problem is partially offset by high amounts of phenolic and γ -tocopherols that are also present in camelina seed oil and act as antioxidants to stabilize the oil (Abramovic & Abram, 2005).

Figure 1.1. Relative proportions of fatty acid composition of seed oil from canola, soybean, and camelina (Bansal & Durrett, 2015).

The seed meal after oil extraction is very nutritive with high levels of crude protein (>45%), which is higher than that of canola (Colombini *et al.*, 2014). The meal also consists of dietary fibres, omega-3 fatty acids (>35%), and vitamin E, which have demonstrated an assortment of applicable uses in animal fodder highlighted by studies showcasing its antioxidant properties in pork meat patties and increases in unsaturated fatty acids in ewe's milk (Putnam *et al.*, 1993; Salminen *et al.*, 2006; Szumacher-Strabel *et al.*, 2011). However, the moderate proportion of anti-nutritive compounds such as erucic acid, sinapine (choline ester of sinapic acid), and glucosinolates present in camelina feed meal is currently restricting higher amounts of its incorporation into food rations for ruminants (Colombini *et al.*, 2014). For instance, higher intake of erucic acid has been associated with cardiac lipidoses based on animal experiments (Kirkhus *et al.*, 2013). Despite the promising potential for camelina in the food industry, its competitiveness is hampered by other domesticated crops that are more suitable for this purpose. Although this issue could be resolved with continued crop development, the profitability of camelina are probably best maximized if our efforts were focused on developing it for non-food applications.

Incentives to introduce novel crop plants for non-food applications are due to the recent progress in the establishment of a bio-based economy (Zhu *et al.*, 2016). The high energy density of the fatty acid components of vegetable oils have been increasingly used in recent years for the production of biofuels and various industrial materials as renewable resources (Zhu *et al.*, 2016). Oilseed crops used for these applications should be from non-human food sources so that food production will not be impacted. Camelina can fulfill this criterion given the fact that its oil has not been established as a major component of the human diet whereas domesticated oilseed crops such as soybean and rapeseed already serve this purpose. Developing food crops for industrial applications complicates matters and there are growing public and regulatory concerns associated with mixing of seeds for edible and industrial markets (Zhu *et al.*, 2016). Furthermore, studies have shown that the life cycle analysis for corn-based ethanol as a biofuel substitute for gasoline actually increases greenhouse gas emissions over time which questions the sustainability of this process (Searchinger *et al.*, 2008).

On the other hand, recent studies have provided additional incentives for camelina to be developed particularly as a renewable jet fuel as the oil has shown to be a good feedstock for biodiesel production (Frohlich & Rice, 2005; Soriano & Narani, 2012; Moser, 2010). The performance of a camelina-based jet fuel produced by Sustainable Oils in Montana was tested in various aircrafts and met all aviation fuel specifications (Sustainable Oils, 2009). In addition, a life cycle analysis of the fuel was found to reduce carbon emissions by 75% compared to petroleum products (Shonnard *et al.*, 2010). Unfortunately, the profitability of biofuel production from alternative crops is currently at a standstill due to the downward trend in oil prices.

Instead, camelina development could be geared towards niche markets involving high-value bio-based products as renewable substitutes to the variety of industrial materials currently

derived from petroleum (Bansal & Durrett, 2016; Zhu *et al.*, 2016). Development for polymers, varnishes, paints, cosmetics, and dermatological products are of particular relevance as the high levels of unsaturated fatty acids in the oil is associated with its fast-drying characteristics (Kasetaite *et al.*, 2014). Unsaturated fatty acids such as linoleic acid, α -linolenic acid, and erucic acid constitute the majority of camelina oil and have high potential to be functionalized through epoxidation for use in the biopolymer industry as pressure-sensitive adhesives, resins, and coatings (Kim *et al.*, 2015). A recent study has also demonstrated the feasibility of generating high-value wax esters from camelina seed oil via biotechnological techniques for lubricant applications (Zhu *et al.*, 2016). Camelina oil development particularly for these intended purposes is still in its infancy but the potential use, as widely demonstrated in this industry, proves to be very promising.

1.4 Camelina and genetic tools for crop development

Many studies have associated camelina oil with diverse roles in various industrial applications but the lack of a specific direction is an impediment to its development. Although the oil profile is not entirely suitable for a specific purpose, camelina is amenable to modification in its oil properties as well as other agronomic traits via breeding programs and genetic engineering. Public perception of the genetically modified organisms (GMOs), particularly for food applications, is a conscientious process whereas there may be more public acceptance for GMOs developed for non-food applications.

The camelina genome has been sequenced and shows a high degree of sequence identity with the model plant *Arabidopsis thaliana* (Kagale *et al.*, 2014). It is readily transformed by *Agrobacterium tumefaciens* using floral dip (Lu & Kang, 2008), which provides a means for highly specific genetic alterations. For instance, Horn *et al.* (2013) suppressed fatty acid

desaturase (*FAD2*) and elongase (*FAE1*) genes by RNA interference which reduced the concentrations of linoleic, linolenic, and eicosenoic acids in the oil while accumulating up to 66% of oleic acid; a fatty acid that is sought after for biofuel production. Camelina is self-compatible so any concerns of gene introgression in the field from genetically engineered camelina is very low and occurs only over short distances (Walsh *et al.*, 2012). However, it has been shown that camelina can hybridize with *Capsella bursa-pastoris* (L.) Medik or Shepherd's Purse but will not be able to establish lineages unless fertility is restored (Martin *et al.*, 2015).

1.5 Implications of natural variation in crop research

Although the genetic tools and resources from *Arabidopsis* have been successfully applied in modifying camelina for crop improvement purposes, these alterations have only been conducted on a few plant lines. In other words, current mutant or transgenic collections have been obtained using a limited number of camelina lines which represents only a small portion of its natural variation. Natural variation is defined as the phenotypic variation caused by spontaneously arising mutations that have been maintained in nature by an evolutionary processes including artificial and natural selection (Alonso-Blanco *et al.*, 2009). Natural variation has been a subject of growing interest in recent decades since it is complementary to induced mutant analysis as well as genetic engineering. In particular, documenting natural variation may uncover variants that already have desired traits that can be incorporated into crop lines while also providing a valuable resource to discover novel gene functions (Alonso-Blanco *et al.*, 2009).

Natural variation among individuals or groups of individuals or populations analyzed by a specific method or a combination of methods also allows for inference on the genetic diversity of species (Mohammadi & Prasanna, 2003). Methods to quantify measurements of such variation

remains elusive in this respect, with datasets ranging from pedigree, morphological, biochemical, and DNA-based marker data used by researchers to analyze genetic diversity in crop plants (Mohammadi & Prasanna, 2003). Therefore, a well-informed estimate of genetic diversity requires combinations of different types of approaches.

Nevertheless, genetic diversity continues to become an important component of crop improvement programs. Genetic resource management, breeding selection, and preservation of biodiversity are all topics related to studies on genetic diversity that are becoming more important particularly in the sustainable development of oilseed crop alternatives (Katepa-Mupondwa *et al.*, 2006). Estimates of genetic variation among and within populations of crop species are frequently used by breeders and population geneticists to evaluate and maintain germplasm, predict genetic gain in a breeding program, and analyze the genetic structure of crop germplasm (Katepa-Mupondwa *et al.*, 2006). Analysis of genetic diversity in germplasm collections can facilitate reliable classification of accessions, and identification of subsets of core accessions with possible utility for specific breeding purposes (Mohammadi & Prasanna, 2003).

Wild relatives of domesticated crops also possess genetic diversity useful for developing more productive, nutritious, and resilient crop varieties (Castañeda-Álvarez *et al.*, 2016). Crop wild relatives (CWR) are defined as wild plant taxa that have indirect uses derived from relatively close genetic relationships to a crop (Maxted *et al.*, 2006). The characterization of CWRs of crop species has become an increasingly important resource for improving agricultural production and maintaining sustainable agro-ecosystems due to the advent of climate change and greater ecosystem instability as a consequence of rapid human industrialization. Improving the quality and yield of crops by utilizing genetic material from CWRs via traditional breeding methods have been done by farmers for millennia with specific examples from maize, rice,

tomato, and grain legumes (Hajjar & Hodgkin, 2007). The analysis of CWRs have implications in breeding since wild populations may serve as an additional source of variation for desirable traits to enrich cultivated crops (Scossa *et al.*, 2016). Although this is not a new concept, utilization of CWRs is expected to increase due to technological advances in gathering and processing information on species and their diversity as well as improvements in breeding tools i.e. genomics (Castañeda-Álvarez *et al.*, 2016; Scossa *et al.*, 2016).

1.6 Natural variation in camelina

There have been few studies that have explored the natural variation of available camelina germplasm collections. The number of accessions maintained by several collecting institutions is relatively low due to the insignificant role of camelina as a field crop in the past (Vollman & Eynck, 2015). Despite this, phenotypic diversity has been quantified mostly on desirable agronomic characters such as disease resistance, oil quality, yield, 1000-seed weight (TSW), and plant height (Gehring *et al.*, 2006; Gugel & Falk, 2006; Manca *et al.*, 2013; Vollman *et al.*, 2005; Zubr, 2003). Seehuber (1984) described large variation and high heritability for traits such as time to flowering, plant height, and TSW with less variation for fatty acid concentrations (Vollman & Eynck, 2015). This was also confirmed by Gugel & Falk (2006) although they observed that variation in fatty acid composition was higher in camelina than other *Brassica* oilseeds.

Attempts have also been made to assess the genetic diversity and potential for directed breeding within camelina accessions using molecular marker approaches. Vollman *et al.* (2005) identified 15 random amplified polymorphic DNA (RAPD) markers for a subset of genotypes to correlate genetic and phenotypic estimates of diversity but the relationship was found to be weak. Gehring *et al.* (2006) then constructed a genetic linkage map based on amplified

fragment length polymorphism (AFLP) markers and used it to localize quantitative trait loci (QTL) related to several agronomic characteristics. A set of simple sequence repeat (SSR) primer pairs extracted by Manca *et al.* (2013) were informative for clustering 40 camelina gene bank accessions into distinct groups despite amplifying multiple fragments. Although these studies have contributed to facilitating marker-assisted breeding efforts for camelina crop development, the polyploid genome of camelina has complicated the interpretation of these results. For instance, methods for genetic mapping have been well-developed for diploid species but are lagging in more complex polyploids (Boopathi, 2013).

1.7 Current advances in camelina genome structure

Camelina is currently considered to be an allohexaploid (Hutcheon *et al.*, 2010; Kagale *et al.*, 2014) i.e. a polyploid with hybrid origin meaning that it possesses genomes of two or three parental species. The recent reference genome sequence for camelina provides additional support for this by revealing a highly undifferentiated hexaploid genome structure (Kagale *et al.*, 2014). Therefore, the current working hypothesis suggests that the camelina genome is the result of two polyploidy events involving the hybridization of parental diploids (Kagale *et al.*, 2014). A plausible explanation of the hypothesized diploid parental species giving rise to camelina's haploid genome of 20 chromosomes may consist of basal chromosome numbers of 7+7+6 (Hutcheon *et al.*, 2010; Kagale *et al.*, 2014). Kagale *et al.* (2014) also concluded that hybridization of camelina's sub-genomes was a recent event coinciding with the emergence of other polyploid crops such as canola, cotton, or wheat during the rapid expansion of agricultural practices during the past 5-10 000 years.

Polyploidy poses challenges to traditional breeding and gene manipulation approaches but knowledge of the genome organization of camelina combined with the characterization of its

germplasm diversity within and across the genus will accelerate future breeding objectives (Kagale *et al.*, 2014). In fact, Galasso *et al.* (2015) undertook a genomic fingerprinting study for *Camelina* species using introns of a family of β -tubulin genes to determine the level of genetic diversity among the genus precisely for the aforementioned purpose. Galasso *et al.* (2015) identified a high level of genetic diversity among six *Camelina* species, however, low variability was observed among and within accessions of the same species except for *Camelina hispida* Boiss.

1.8 The *Camelina* genus

The *Camelina* genus, along with seven other genera including *Arabidopsis*, currently belong to the *Camelineae* tribe in lineage I of the *Brassicaceae* family and are considered to be of Eurasian origin (Al-Shehbaz, 2012). Eight species have been updated within this genus; *Camelina alpkoyensis* Yild., *Camelina alyssum* (Mill.) Thell., *Camelina anomala* Boiss. & Hausskn., *Camelina hispida* Boiss., *Camelina laxa* C.A. Meyer, *Camelina microcarpa* Andrzej. ex DC., *Camelina rumelica* Velen., and *Camelina sativa* (L.) Crantz (Al-Shehbaz, 2012).

Chromosome counts have varied considerably between the species but $2n = 40$ has been most commonly reported among *C. alyssum*, *C. microcarpa*, and *C. sativa* (Séguin-Swartz *et al.*, 2013; Galasso *et al.*, 2015). Various chromosome counts have been documented for *C. microcarpa* ranging from $2n = 12, 16, 18-20, 26, 32, 38$, and 40 and it has recently been suggested that this species comprises three cytotypes (Warwick *et al.*, 2009; Martin *et al.*, 2016). The range of chromosome counts reported in the literature may be due in part to misidentifications that have likely been made throughout herbarium collection records for *C. microcarpa* and *Camelina* species in general. A chromosome count of $2n = 26$ has been reported for *C. rumelica* indicating a tetraploid status for this species (Galasso *et al.*, 2015; Martin *et al.*,

2016). Diploid counts of $2n = 14$ were reported for *C. hispida* which has been consistent across several studies (Al-Shehbaz, 1987; Hutcheon *et al.*, 2010; Galasso *et al.*, 2015; Martin *et al.*, 2016) whereas diploid counts of $2n = 12$ were reported for *C. laxa* (Galasso *et al.*, 2015; Martin *et al.*, 2016).

Taxonomic classification has been troublesome in the *Camelina* genus (Al-Shehbaz, 2012; Al-Shehbaz, 1987). *Camelina* species have been differentiated mainly by fruit and floral morphology as well as the type and abundance of trichomes on stems (Al-Shehbaz, 1987). However, *C. sativa* is still often confused with its close relatives *C. alyssum*, *C. microcarpa*, and *C. rumelica*. These species have naturalized populations in North America with *C. microcarpa* having the widest distribution (Francis & Warwick, 2009; Al-Shehbaz, 1987). *C. alyssum* is considered to be completely interfertile with *C. sativa* and questions whether the former should be treated as a subspecies of the latter (Al-Shehbaz, 1987). Intermediate forms between *C. rumelica* and *C. microcarpa* and between *C. microcarpa* and *C. sativa* have been found, complicating matters even further (Al-Shehbaz, 1987). Only three species, *C. anomala*, *C. laxa*, and *C. hispida*, are morphologically distinct with a range of distribution limited to Middle-Eastern countries (Al-Shehbaz, 1987).

1.9 Thesis objective statements

For the present study, we documented the natural variation for an assortment of quantitative phenotypic traits to facilitate taxonomic classification and determine the breeding potential within and among the following five species in the *Camelina* genus: *C. hispida*, *C. laxa*, *C. microcarpa*, *C. rumelica*, and *C. sativa*. Only germplasm material for these species were made accessible to us from international seed banks and seed collections at the Ottawa Research and Development Centre (ORDC), Agriculture and Agri-Food Canada (AAFC), Ottawa, Canada.

We consider the non-*C. sativa* accessions as crop wild relatives since *C. sativa* is the main species being developed as an alternative oilseed crop.

In other words, we expect the natural variation documented in our study to achieve the following two short-term objectives:

1. To identify informative traits for taxonomic classification within the genus
2. To help direct breeding efforts in improving agronomic traits for camelina

Specifically, Objective 1 focused on addressing four major taxonomic questions concerning the taxa currently available in this study:

1. Which traits are most informative for taxonomic classifications particularly among *C. microcarpa*, *C. rumelica*, and *C. sativa*?
2. Should the three identified cytotypes of *C. microcarpa* (2X, 4X, and 6X) be considered as similar or different species?
3. Should hexaploid (6X) *C. microcarpa* and *C. sativa* be considered the same species?
4. Are *C. hispida* var. *hispida* and *C. hispida* var. *grandiflora* similar enough to each other to warrant the recent demotion of *C. grandiflora* to *C. hispida* var. *grandiflora*?

Objective 2 focused mostly on improving seed oil traits via breeding for yield components and fatty acid components. Yield components were regarded as broad-level traits i.e. thousand-seed weight (TSW), oil content, and protein content. Three criteria measurements were then established for particular levels of fatty acid components to select for candidate plant lines for further development in biofuel, food, and industrial chemical applications.

Our documentation of natural trait variation in the *Camelina* genus provides support for future long-term objectives regarding relevant studies on genetic diversity to better understand the complex biology of a polyploid oilseed crop.

2.0 Methods

2.1 Plant accessions and growth conditions

Seeds from 23 *Camelina* accessions were obtained from various international seed collections (Table 2.1). The accessions comprised five different species of *Camelina*; *C. hispida* (2 accessions), *C. laxa* (1), *C. microcarpa* (6), *C. rumelica* (6), and *C. sativa* (9). The growing times were coordinated for all plants in this study so that they could all be grown in the same growth chamber (G129) at the Ottawa Research and Development Centre (ORDC) at Agriculture and Agri-Food Canada (AAFC) in Ottawa, ON, Canada (Figure 2.1). The controlled growth conditions in G129 were as follows: 16-hour light and 8-hour dark photoperiods with temperatures set at 20°C and 18°C, respectively. Seeds from *C. sativa* accessions except for S-596 were sown directly onto soil in individual 14 cm x 12 cm peat pots and placed into G129. S-596 was described as a “winter variety” of *C. sativa* and required vernalization treatment. For vernalization treatment, seeds from all other accessions including S-596 were first placed in petri dishes on filter paper moistened with 2% potassium nitrate (KNO₃) and stratified in the dark for two weeks at 4°C. The petri dishes were then placed under a growth light at room temperature to allow the seeds to germinate until the cotyledon stage. Seedlings were then sown onto soil mixture in 48-cell trays and placed in a glass house for four weeks under the same controlled conditions as described above. Once the plants grew to rosette stage, they were placed into a vernalization chamber with the following conditions: 16-hour light and 8-hour dark photoperiods with temperature set at 4°C for six weeks. The vernalized plants were then transplanted into individual pots (14 cm x 12 cm) and transferred to G129 for growth alongside the *C. sativa* accessions (Figure 2.1).

Table 2.1. Plant resource information for the complete dataset. This comprises 192 biorepetitions representing 23 *Camelina* accessions from various international seed collections used in this study.

Identifier (ID)	Species	Bioreps	Chromosome Number	Ploidy Status	Source	Accession Number	Year	Location
HG-240	<i>C. hispida</i> var. <i>grandiflora</i>	16	14	2X	NCRPIS	PI650133	2006	Turkey
HH-248	<i>C. hispida</i> var. <i>hispida</i>	16	14	2X	NCRPIS	PI650139	2006	Iran
L-612	<i>C. laxa</i>	5	12	2X	NCRPIS	PI633185	1997	Turkey
M2-246	<i>C. microcarpa</i>	8	12	2X	NCRPIS	PI650135	2005	Lozere, France
M4-168	<i>C. microcarpa</i>	6	26	4X	Martin Lab	N/A	2011	Katepwa Beach, SK, Canada
M4-718	<i>C. microcarpa</i>	8	26	4X	Martin Lab	N/A	2012	Gainsborough, SK, Canada
M4-965	<i>C. microcarpa</i>	8	26	4X	Martin Lab	N/A	2012	Cromer, MB, Canada
M6-198	<i>C. microcarpa</i>	8	40	6X	Martin Lab	N/A	2011	Bow Island, AB, Canada
M6-818	<i>C. microcarpa</i>	8	40	6X	Martin Lab	N/A	2012	Maple Creek, SK, Canada
RR-1034	<i>C. rumelica</i> subsp. <i>rumelica</i>	6	26	4X	IPK	PI650152	N/A	Germany
RR-1255	<i>C. rumelica</i> subsp. <i>rumelica</i>	7	26	4X	PGRC	No. 45-3	N/A	Crimea, Ukraine
RR-245	<i>C. rumelica</i> subsp. <i>rumelica</i>	16	26	4X	NCRPIS	PI650134	N/A	Spain
RR-247	<i>C. rumelica</i> subsp. <i>rumelica</i>	4	26	4X	NCRPIS	PI650138	N/A	Iran
RR-609	<i>C. rumelica</i> subsp. <i>rumelica</i>	8	26	4X	IPK	CAM244	N/A	Soviet Union
S-1044	<i>C. sativa</i>	8	40	6X	NCRPIS	PI650162	N/A	Poland
S-1062	<i>C. sativa</i>	8	40	6X	NCRPIS	PI650140	N/A	Germany
S-1063	<i>C. sativa</i>	8	40	6X	Rowland Lab	cv. Celine	2012	N/A
S-1662	<i>C. sativa</i>	8	40	6X	Weselake Lab	cv. Suneson	N/A	N/A

S-239	<i>C. sativa</i>	8	40	6X	NCRPIS	PI650132	2007	Germany
S-252	<i>C. sativa</i>	6	40	6X	NCRPIS	PI633194	1998	Germany
S-596	<i>C. sativa</i>	6	40	6X	IPK	CAM176	N/A	N/A
S-605	<i>C. sativa</i>	8	40	6X	IPK	CAM7	N/A	Kyrgyzstan
S-621	<i>C. sativa</i>	8	40	6X	Mercer Seeds	cv. Calena	2008	Lethbridge, AB, Canada

* *IPK Gatersleben* = Institute of Plant Genetics and Crop Plants Research IPK, Gatersleben

* *NCRPIS* = North Central Regional Plant Introduction Station

* *PGRC* = Plant Gene Resources of Canada

Figure 2.1. Growth room conditions for the biorepetitions from 23 *Camelina* accessions. Left (A) and right (B) side of plant growth chamber G129 at the ORDC.

Most accessions consisted of eight representative individual plants which we designated as biorepetitions for subsequent replicate analyses. Plants that experienced poor growth were reflected by accessions with less than eight biorepetitions but were still well-represented with at least four healthy biorepetitions in the study (Table 2.1). The pots containing each individual plant were distributed evenly to allow sufficient room for plant growth as well as using the full extent of the space available in the growth chamber. The spacing between each pot was approximately 8 cm. The positions of the plants were randomized on a biweekly basis four times throughout the growth period. The plants were watered twice daily as needed and 20-20-20 (N-P-K) fertilizer was applied every week by the greenhouse staff except for the first week where 10-52-10 fertilizer was applied to vernalized plants in order to promote root establishment after transplanting.

One of the main objectives of this study was to generate a complete seed set for all *Camelina* species and assess their seed oil characteristics for breeding purposes. Because *C. hispida* and *C. laxa* are self-incompatible, flowers within members of respective accessions of these species were randomly cross pollinated by hand on a daily basis throughout the entire growth period to induce sufficient seed production. The other species were self-compatible and were allowed to self-fertilize.

2.2 Nuclear DNA content analysis by flow cytometry (FCM)

Total nuclear DNA content was measured using flow cytometry for at least one representative biorepetition from each of the 23 accessions. This was done to validate accession identification (Martin *et al.*, 2016). Fresh young leaf tissue samples were obtained from representative biorepetitions at the rosette stage. Approximately 2 cm² area of sample leaf tissue was chopped coarsely with a sharp razor in 750 µL of Galbraith's buffer solution (Dolezel &

Bartos, 2005). Samples were co-chopped with a 1 cm² area of fresh leaf tissue from either *Raphanus sativus* L. “Saxa” (1.11 pg/2C) or *C. sativa* accession SM188 (1.59 pg ± 0.05/2C), which were grown in a separate greenhouse and used as internal standards (Martin *et al.*, 2016). The sample mixture was aspirated three times and dispensed through a 30-µm disposable filter (Partec CellTrics) into 5-mL polystyrene Falcon tubes. The sample solution was stained with 250 µL of 0.1 mg/mL propidium iodide and stored in the dark for 20 min at 4°C prior to processing on a Gallios flow cytometer (Beckman Coulter, Ontario, Canada).

Relative DNA content was determined for each sample using the fluorescence peak means for the standard and the sample via the following formula:

$$\text{Sample DNA Content} = \frac{\text{Sample Peak}}{\text{Internal Standard Peak}} \times \text{DNA Content of Internal Standard}$$

Fluorescence peak means, coefficients of variation (CVs), and nuclei numbers were determined using ModFit LT software for windows (4.0.5, 2013, Verity Software House Inc., Topsham, ME, USA) (Martin *et al.*, 2016). For each individual, three measurements with nuclei counts greater than 1000 and CVs less than 5% were taken on different days to accurately determine DNA content (Dolezel & Bartos, 2005).

2.3 Agronomic trait measurements

Data were collected on the following traits that we designated as agronomic trait measurements for each biorepetition: *days to first flower* (DFF – number of days from the date of sowing to the date at which the first flower appeared); *days to harvest* (DH – number of days from the date of sowing to the date at which the plant reached full maturity for harvesting); *height at first flower* (HFF – height from the soil interface to the appearance of the first flower

measured in cm); *height at harvest* (HH – height from the soil interface to the tip of the plant measured in cm).

2.4 Pod and flower measurements

Mature flowers and pods were obtained from each biorepetition throughout the growing period and stored in 70% ethanol for measurements made at a later date. Quantitative traits for flowers and pods of each biorepetition were each measured in triplicate using a Leica M205 C microscope with an attached Leica DFC 450 camera (Leica Microsystems Ltd., Switzerland) and associated Leica Application V 4.3.0 software program. The following nine measurements were then made for each flower and averaged in triplicate for each biorepetition; anther 1 length (AvAnther1), anther 2 length (AvAnther2), anther 3 length (AvAnther3), gynoecium length (AvGyn), petal length (AvPetalL), petal width (AvPetalW), sepal length (AvSepal), total flower length (AvTotalFlower), and style length (AvBeak) (Figure 2.2).

Figure 2.2. The nine morphological flower measurements via compound light microscopy. Example from a preserved flower of a *C. sativa* biorepetition: (A) 1 = total flower length (AvTotalFlower) and 2 = sepal length (AvSepal) and (B) 3 = petal length (AvPetalL), 4 = petal width (AvPetalW), 5 – 7 = length of three anthers (AvAnther1, AvAnther2, & AvAnther3), 8 = gynoecium length (AvGyn), and 9 = style length (AvBeak). Images taken by Sarah Endenburg.

The following seven measurements were then made for each pod and averaged for each biorepetition; pod angle 1 (AvAngle1), pod angle 2a (AvAngle2a), pod angle 2b (AvAngle2b), pod angle 3 (AvAngle3), pod length (AvLength), pod beak length (AvPodBeak), and pod width (AvWidth) (Figure 2.3).

Figure 2.3. The seven morphological pod measurements via compound light microscopy. Example from a preserved *C. microcarpa* biorepetition: 1 = pod length (AvLength), 2 = pod width (AvWidth), 3 = pod beak length (AvPodBeak), 4 = angle of the pod tip (AvAngle1), 5 – 6 = angles where the width line meets the pod edge (AvAngle2a & AvAngle2b), and 7 = angle of the pod base (AvAngle3). Image taken by Sarah Endenburg.

2.5 Trichome measurements

One side of a 10-mm lengthwise section of the stem near the base of the plant was viewed under a Leica EZ4 compound light microscope to count the number of trichomes and distinguish between forked and simple trichome types. The stem diameter was measured in the centre of the viewing area using calipers. Trichome density was then calculated by the number of trichomes divided by the total viewing area and expressed as counts/mm². The following three trichome density measurements were calculated as follows for each biorepetition:

$$\text{trichome total density (TriTD)} = \frac{(\text{forked trichome counts} + \text{simple trichome counts})}{\text{stem diameter (mm)} \times \text{stem length (10 mm)}}$$

$$\text{trichome forked density (TriFD)} = \frac{\text{forked trichome counts}}{\text{stem diameter (mm)} \times \text{stem length (10 mm)}}$$

$$\text{trichome simple density (TriSD)} = \frac{\text{simple trichome counts}}{\text{stem diameter (mm)} \times \text{stem length (10 mm)}}$$

2.6 Seed weight measurements

We waited until plants were completely brown for harvesting to ensure that seeds reached full maturity so as to achieve uniformity in seed traits across all biorepetitions. Data were collected on the following traits that we designated as seed weight measurements for each biorepetition: *average hundred-seed weight* (AvHSW – the average weight of one-hundred seeds obtained in triplicate measured in grams); *total seed production* (TSP – the total weight of seed produced measured in grams); *thousand-seed weight* (TSW – the weight of one-thousand seeds measured in grams). All seed weight measurements were performed using a Mettler AT200 analytical balance.

2.7 Protein content measurements

Approximately 10 mg of seed for each biorepetition was wrapped tightly in tin weigh boats (4 mm x 4 mm x 11 mm) with tweezers and deposited individually in an Elementar vario MICRO cube CHNS analyzer for determination of total nitrogen content via the Dumas combustion method. Total nitrogen content was converted to protein content using the standard 6.25 conversion factor (American Oil Chemist Society, 1999) and expressed on a percent dry seed weight basis. Apple leaves were used as an external standard during experimentation.

2.8 Seed oil trait measurements

The protocol used in this study to determine oil content and fatty acid composition for oilseeds was adapted from Li *et al.* (2006). Sample glass tubes (1 cm x 10 cm) and Teflon-lined

screw caps were pre-rinsed with chloroform and 1:1 methanol/distilled water, respectively, to remove any contaminating residues and were then dried. Approximately 50 mg of seed from each biorepetition was weighed on an analytical balance (Sartorius TE214S) and put into the chloroform-rinsed sample glass tubes i.e. samples. Seeds were ground manually with a glass stir rod as thoroughly as possible for each sample and were left in a desiccator filled with drierite to dry overnight. Minimizing and stabilizing any seed water content prior to following methylation reaction is important for consistency across samples as well as to remove water from impairing the transmethylation process (Li *et al.*, 2006). Samples were then weighed by difference the next day to determine the dry weight of the ground seeds.

To each sample, 1 mL of 5% (v/v) sulfuric acid in methanol (freshly prepared), 50 µg of butylated hydroxy toluene (BHT) solution, 2.5 mg of glyceryl triheptadecanoate (Sigma-Aldrich), and 100 µL of toluene co-solvent were added. Glyceryl triheptadecanoate was added as a triacylglycerol internal standard to generate methyl heptadecanoate (C17:0) for peak quantification purposes. The samples were vortexed for 30 seconds before being placed in an oven with a set temperature of 90°C for 1.5 hours. Once the samples were cooled to room temperature, 1 mL each of 0.9% (w/v) NaCl solution and hexane (Caledon Laboratories Ltd.) were added to extract the fatty acid methyl esters (FAMES). The samples were vortexed thoroughly for 30 seconds and then centrifuged (2000 rpm for 5 min. at room temperature) to facilitate phase separation. An aliquot of the hexane fraction was transferred into a 150-µL glass insert situated in a glass GC vial (Agilent Technologies).

One µL of the hexane fraction from each sample was injected and analyzed by a Varian-450 gas chromatograph (GC) equipped with an autosampler, flame ionization detector (FID), and a polar DB23 column (30 m by 0.25 mm i.d., 0.25 µm film; J & W Scientific, Folsom, CA). The

carrier gas was helium with a constant flow rate of 2.0 mL/min. The GC conditions were: split mode injection (1:40); injector and FID temperature set at 260°C and 325°C, respectively; oven temperature program 150°C for 3 min. then increasing at 10°C/min. to 240°C, and then holding this temperature for 5 min.

Raw data composed of peak areas of the resulting chromatograms were initially identified for 13 fatty acids (Table 2.2) relative to the C17:0 internal standard peak and processed using Varian Galaxie Chromatography Data System version 1.9.302.530. Other additional peaks were minor and could not be assigned to known fatty acids so they were not included. Two correction factors were then applied to the raw peak data. The first was to account for the theoretical response factor of the FID since this measurement is a function of the mass of C atoms with at least one bound H atom and thus differs for each of the FAMEs measured (Li *et al.*, 2006). These corrected areas were used to calculate the mass of each FAME in the sample by comparison to the internal standard mass. The second correction factor was to convert FAME weight to TAG weight since this is the form of lipid storage in seeds (Li *et al.*, 2006). Seed oil traits consisted of total oil content calculated as percent oil per dry seed weight as well as the accompanying 13 individual fatty acids measured in mol percent (Table 2.2).

Table 2.2. List of 13 fatty acids identified and measured in seeds of each biorepetition via GC-FID in this study.

Fatty Acid	Common name	Authentication (Hrastar <i>et al.</i>, 2009)
C16:0	Palmitic acid	C _{16:0}
C18:0	Stearic acid	C _{18:0}
C18:1	Oleic acid	C _{18:1n9}
C18:2	Linoleic acid	C _{18:2n6}
C18:3	α-linolenic acid	C _{18:3n3}
C20:0	Arachidic acid	C _{20:0}
C20:1	Eicosenoic acid	C _{20:1n9}
C20:2	Eicosadienoic acid	C _{20:2n6}
C20:3	Eicosatrienoic acid	C _{20:3n3}
C22:0	Behenic acid	C _{22:0}
C22:1	Erucic acid	C _{22:1n9}
C24:0	Lignoceric acid	C _{24:0}
C24:1	Nervonic acid	C _{24:1n9}

2.9 Fatty acid calculations

We established criteria to select accessions or biorepetitions with the best potential for future development in crop breeding programmes for applications in biofuel, food, or alternative chemical industries using combinations of fatty acid composition measurements as well as three fatty acid calculations: (1) the sum of polyunsaturated fatty acids (PUFAs) to sum of saturated fatty acids (SFAs) and monounsaturated fatty acids (MUFAs) ratio (PUFA ratio); (2) the sum of saturated fatty acids (SSFA); and (3) the sum of very long chain fatty acids (SVLCFA). The three fatty acid calculations were calculated as follows:

1. $PUFA\ ratio = \frac{C18:2+C18:3+C20:2+C20:3}{C16:0+C18:0+C18:1+C20:0+C20:1+C22:1+C24:0+C24:1}$
2. $SSFA = C16:0 + C18:0 + C20:0 + C22:0 + C24:0$
3. $SVLCFA = C20:0 + C20:1 + C20:2 + C20:3 + C22:0 + C22:1 + C24:0 + C24:1$

Biorepetitions that demonstrated highest breeding potential for biofuel applications were subjectively determined and based on the following criteria:

1. Lower degree of unsaturation (PUFA ratio).
2. Higher oleic acid (C18:1) content.

Oil crops for biofuel are desirable if the fatty acid composition is lower in the degree of polyunsaturation and higher in C18:1 content since these parameters are generally considered to be important for fuel properties such as cetane number, viscosity, cold flow, oxidative stability, and lubricity (Knothe, 2009).

Biorepetitions that demonstrated highest breeding potential for food applications were based on the following criteria from Ghamkhar *et al.* (2010):

1. More than 30% α -linolenic acid (C18:3).
2. Less than 3% erucic acid (C22:1).
3. Less than 10% saturated fatty acids i.e. lowest SSFA values.
4. Ratio of α -linolenic acid (C18:3) to linoleic acid (C18:2) greater than 1.

Biorepetitions that demonstrated highest breeding potential for industrial chemical applications were determined mainly by high SVLCFA values.

2.10 Data processing and statistical analysis

Data processing, plotting, and statistical analyses were all conducted in RStudio version 0.99.484 (RStudio Team, 2015) to assess patterns of variation in the large dataset generated in this study. The dataset was first scaled using the default “scale” function to ensure that each variable had approximately equal influence prior to conducting the following multivariate statistical techniques based on Euclidean distance measures. Principal components analysis

(PCA) and permutational MANOVAs were conducted using the “rda” and “adonis” functions in the “vegan” package, respectively (Oksanen *et al.*, 2015). Linear discriminants analysis (LDA) was conducted using the “lda” function in the “MASS” package (Venables & Ripley, 2002). The results from multivariate statistical analyses were displayed using a distance biplot in which distances between points accurately reflect the similarity among biorepetitions but the angles between arrows do not imply correlation among quantitative variables. Custom biplot functions for PCA and LDA biplots were developed by Dr. Tyler Smith, ORDC, Agriculture and Agri-Food Canada.

Boxplot figures were generated using the default “boxplot” function in RStudio where solid lines within boxes describe median values. The lower and upper hinges of the boxes represent the first and third quartile ranges to explain the interquartile range (IQR). The lower and upper extension of the box whiskers are calculated by the subtraction and addition of the formula $1.5 \times \text{IQR}$ of the first and third quartiles, respectively. Outliers are displayed as circles outside the region of the boxplot diagrams. Statistical comparisons between group ID membership and accessions were conducted using the default “t.test” function with Welch approximation applied to degrees of freedom calculations. Statistical tests of significance were all made at the $\alpha = 0.05$ level. Microsoft Excel (2013) was also used for data management and processing.

3.0 Results

3.1 Part I: Natural trait variation for taxonomic classification

3.1.1 Exploratory data analysis

Preliminary investigation on the distribution of the data points for each quantitative variable through the use of boxplots and quantile-quantile plots were indicative of a normal distribution and so data transformation was unnecessary (data not shown). Several quantitative trait variables were dropped due to incomplete measurements, high correlation with other variables, or low contribution to overall variance observed in multivariate statistical analyses. For instance, many of the morphological flower measurements were found to be highly correlated ($R > 0.80$, data not shown) and was better represented as one variable (AvTotalFlower) to avoid instances of collinearity. In total, there were 192 biorepetitions with each having a complete set of 24 quantitative trait variables measured for the 23 accessions used in this study and is hereafter referred to as the complete dataset (Table 2.1 & Table 3.1).

Table 3.1. List of 24 quantitative trait variables measured for the 192 biorepetitions in the complete dataset.

Short Form	Definition	Measurement Units
AvPodBeak	Average pod beak length	mm
AvTotalFlower	Average total flower length	mm
AvWidth	Average pod width	mm
C16:0	Palmitic acid	mol %
C18:0	Stearic acid	mol %
C18:1	Oleic acid	mol %
C18:2	Linoleic acid	mol %
C18:3	α -linolenic acid	mol %
C20:0	Arachidic acid	mol %
C20:1	Eicosenoic acid	mol %
C20:2	Eicosadienoic acid	mol %
C20:3	Eicosatrienoic acid	mol %
C22:0	Behenic acid	mol %
C22:1	Erucic acid	mol %
C24:0	Lignoceric acid	mol %
C24:1	Nervonic acid	mol %
HH	Height at harvest	cm
Oil	Total oil content	% W_{oil}/W_{dry} seed weight
Protein	Total protein content	% W_{meal}/W_{dry} seed weight
TriFD	Trichomes – forked density	counts/mm ²
TriSD	Trichomes – simple density	counts/mm ²
TriTD	Trichomes – total density	counts/mm ²
TSP	Total seed production	g
TSW	Thousand-seed weight	g

3.1.2 DNA content and validation of plant accessions via flow cytometry

DNA content measurements from at least one representative biorepetition via flow cytometry was done to confirm the ploidy status for species among the 23 accessions used in this study (Martin *et al.*, 2016). DNA content was highest among *C. sativa* (1.49 ± 0.04 pg) and M6-identified *C. microcarpa* (1.42 ± 0.05 pg) biorepetitions (hexaploids), followed by *C. rumelica* (1.16 ± 0.03 pg) and M4-identified *C. microcarpa* (0.97 ± 0.04 pg) biorepetitions (tetraploids), and HH-248 (0.73 ± 0.02 pg), HG-240 (0.65 ± 0.03 pg), L-612 (0.57 ± 0.01 pg), and M2-246 (0.53 ± 0.004 pg) biorepetitions (diploids) (Figure 3.1). The results were consistent with

previously documented DNA content measurements and accompanying chromosome counts for these *Camelina* species (Table 2.1; Martin *et al.*, 2016). Accessions were grouped by their species and ploidy status which we designate as group identification memberships (8 groups) to serve as the basis for comparative purposes and subsequent multivariate statistical analyses.

Figure 3.1. Boxplots for DNA content (pg) measured from flow cytometry. Measurements were taken from at least one representative biorepetition of the 23 accessions. Boxplots for each accession are colour-coded by their respective group identification membership.

3.1.3 Principal components analysis (PCA)

Results from the PCA showed that the first principal component (PC1) and second principal component (PC2) accounted for 29% and 22% of the total variance, respectively, together representing more than half of the total variance explained in the dataset (Figure 3.2). The top two variables with the most positive contributions were C18:1 and total seed production (TSP) on PC1 and C20:0 and C22:0 on PC2 (Figure 3.2). The top two variables with the most negative contributions were trichomes – simple density (TriSD) and total protein content (Protein) on PC1 and C18:3 and AvPodBeak on PC2 (Figure 3.2). The data points are colour coded to better visualize the biorepetitions corresponding to their previously assigned group memberships (Figure 3.2). Most of the biorepetitions formed distinct clusters according to their group memberships except for tetraploid *C. microcarpa* (M4), hexaploid *C. microcarpa* (M6), and *C. sativa* (S) biorepetitions, which clustered together on the PCA biplot (Figure 3.2).

Figure 3.2. Principle components analysis of the 24 quantitative trait variables. Group ID memberships were HG-240 (n = 16, black circles), HH-248 (n = 16, red triangles), L-612 (n = 5, green plus-signs), M2-246 (n = 8, blue crosses), M4-identified accessions (n = 22, cyan diamonds), M6-identified accessions (n = 16, magenta triangles), RR-identified accessions (n = 41, yellow boxes), and S-identified accessions (n = 68, grey asterisks). The first and second principle component axes represent 28.6% and 22.1% of the total variation in the complete dataset, respectively. The contribution of all quantitative traits are listed in Table 3.2.

Table 3.2. PCA loadings associated with the 24 quantitative trait variables. Loading scores were calculated from the first and second principal component axes from PCA of the complete dataset. The top four variables contributing to both the positive and negative directions for each axis are bolded and italicized, respectively.

Trait	PC1	PC2
AvPodBeak	1.71	<i>-1.94</i>
AvTotalFlower	2.21	-1.44
AvWidth	-1.83	1.57
C16.0	1.63	0.95
C18.0	-1.30	-0.12
C18.1	<i>-2.34</i>	<i>-1.70</i>
C18.2	-1.05	1.26
C18.3	0.22	<i>-2.67</i>
C20.0	0.37	3.05
C20.1	2.07	1.00
C20.2	1.59	2.36
C20.3	1.46	-0.75
C22.0	-0.04	3.27
C22.1	-1.46	2.52
C24.0	-0.55	2.51
C24.1	-0.27	1.56
HH	-1.80	0.63
Oil	<i>-2.01</i>	<i>-1.62</i>
Protein	2.22	0.37
TriFD	-1.19	-1.15
TriSD	2.30	0.19
TriTD	2.01	-0.21
TSP	<i>-2.69</i>	-0.11
TSW	<i>-1.95</i>	-0.37

3.1.4 *Linear discriminants analysis (LDA)*

Linear discriminants analysis (LDA) was used on the complete dataset as another ordination technique to determine variables that were most useful for discriminating members of the identified groups. TriTD, C20:0, C22:0, and C24:0 variables were dropped from the complete dataset to process the LDA due to issues with collinearity. Multivariate analysis of variance (MANOVA) was initially conducted on the dataset to test for differences among groups in selected quantitative traits and significant differences were found ($F = 32.6$, $p < 0.001$).

An LDA biplot was used to visualize group memberships and determine which variables were most important in discriminating between groups in the first two linear discriminant functions. The first linear discriminant function (LD1) explained 63.5% of the variation with C22:1 having the greatest influence in the positive direction and C20:1 having the greatest influence in the negative direction (Figure 3.3). The second linear discriminant function (LD2) explained 17.3% of the variation with AvTotalFlower having the greatest influence in the positive direction and C20:1 and thousand-seed weight (TSW) having the greatest influence in the negative direction (Figure 3.3). Cumulatively, LD1 and LD2 explained more than 80% of the between-group variance in the complete dataset (Figure 3.3).

Figure 3.3. Linear discriminants analysis biplot of 20 quantitative trait variables. Group ID memberships were HG-240 (n = 16, black circles), HH-248 (n = 16, red triangles), L-612 (n = 5, green plus-signs), M2-246 (n = 8, blue crosses), M4-identified accessions (n = 22, cyan diamonds), M6-identified accessions (n = 16, magenta triangles), RR-identified accessions (n = 41, yellow boxes), and S-identified accessions (n = 68, grey asterisks). The first and second axes account for 63.5% and 17.3% of the total between-group variance, respectively. Arrows indicate the contribution of the top variables to the formation of the discriminant axes. Contribution of all quantitative traits are listed in Table 3.3.

Table 3.3. LDA loadings associated with the 20 quantitative trait variables. Loading scores were calculated from the first and second linear discriminant functions from LDA of the complete dataset. The top four variables contributing to both the positive and negative directions for each axis are bolded and italicized, respectively.

Variable	LD1	LD2
AvPodBeak	-0.11	0.46
AvTotalFlower	<i>-0.70</i>	1.71
AvWidth	-0.03	<i>-0.98</i>
C16.0	-0.17	-0.95
C18.0	0.43	-0.36
C18.1	0.97	-0.97
C18.2	0.74	<i>-1.07</i>
C18.3	1.05	-0.29
C20.1	<i>-3.57</i>	<i>-3.40</i>
C20.2	<i>-0.86</i>	0.23
C20.3	0.87	-0.78
C22.1	4.97	-0.72
C24.1	-0.39	-0.11
HH	0.47	0.09
Oil	0.25	0.22
Protein	-0.43	-0.55
TriFD	0.29	-0.05
TriSD	0.02	-0.04
TSP	0.15	-0.66
TSW	<i>-0.65</i>	<i>-1.67</i>

3.1.5 Permutational MANOVA

To complement the findings from the above parametric-based statistical tests, a permutational MANOVA or nonparametric MANOVA was conducted using the “adonis” function from the “vegan” package in RStudio. Similar to the MANOVA test conducted earlier, significant differences in the 24 quantitative traits between all group members were observed using “adonis” with parameters set at 999 permutations (Appendix 7.1). Tests of significant differences in the quantitative traits between pairs of accessions were further investigated (Appendix 7.2). Most of the accession pairs were also significantly different from one another

when α was set at 0.05 although there were some exceptions as shown in Appendix 7.2.

Accessions that were not significantly different were M4-718 and M4-965, M6-198 and M6-818, RR-1255 and RR-247, RR-1255 and RR-609, S-1044 and S-621, S-1062 and S-252, S-1063 and S-252, S-1662 and S-252, and S-605 and S-621 (Appendix 7.2).

3.2 Part II: Natural variation for breeding potential assessment

To identify lines with breeding potential for crop development in various industrial applications, patterns of variation in common oilseed characteristics were measured. The specific quantitative variables of interest were thousand seed weight (TSW), total seed oil content (Oil), total seed protein content (Protein), C18:1, C18:2, C18:3, C20:1, and C22:1 (Table 3.1). For fatty acid composition, we chose to focus on the aforementioned five fatty acids since they comprised the vast majority of the seed oil constituents (≥ 80 mol %) for each biorepetition. Variation in saturated fatty acid compositions were measured using the sum of saturated fatty acids calculation (SSFA).

3.2.1 Patterns of variation for TSW, seed oil content, and seed protein content

TSW measurements of the *C. sativa* accessions were significantly higher than the other accessions with a maximum value of 1.45 g recorded for the S-239-1 biorepetition (Figure 3.4; Appendix 7.3 & Appendix 7.4). Oil content was also significantly higher in seeds of the *C. sativa* accessions with a maximum value of 53.9% recorded for the S-1044-2 biorepetition (Figure 3.5; Appendix 7.5 & Appendix 7.6). However, oil content was not significantly different between the seeds of *C. sativa* (S) and *C. hispida* var. *grandiflora* (HG) accessions (Figure 3.5; Appendix 7.5 & Appendix 7.6). The *C. rumelica* (RR) accessions generally had significantly higher protein contents than the other accessions except for *C. hispida* (HG and HH) accessions (Figure 3.6;

Appendix 7.7 & Appendix 7.8). A maximum value of 36.6% was obtained by the *C. rumelica* RR-1255-6 biorepetition for protein content (Figure 3.6). We further investigated the relationship between oil content and protein content and found a negative relationship across all group ID memberships (Figure 3.7; $R^2 = 0.25$, $F_{1,190} = 63.0$, $p < 0.001$).

Figure 3.4. Boxplots for the thousand-seed weight (TSW) quantitative variable. TSW was measured in grams for biorepetitions in each of the 23 accessions in this study. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.3 and Appendix 7.4 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

Figure 3.5. Boxplots for the seed oil content quantitative variable. Oil content was measured on a percent basis ($\% W_{oil}/W_{dry\ seed\ weight}$) for bioreplications in each of the 23 accessions in this study. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.5 and Appendix 7.6 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

Figure 3.6. Boxplots for the protein content quantitative variable. Protein content was measured on a percent basis ($\% W_{meal}/W_{dry\ seed\ weight}$) for bioreplications in each of the 23 accessions in this study. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.7 and Appendix 7.8 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

Figure 3.7. Correlation between oil content (% W_{oil}/W_{dry} seed weight) and protein content (% W_{meal}/W_{dry} seed weight) quantitative traits ($R^2 = 0.25$, $F_{1,190} = 63.0$, $p < 0.001$). Group ID memberships were G-240 ($n = 16$, black circles), HH-248 ($n = 16$, red triangles), L-612 ($n = 5$, green plus-signs), M2-246 ($n = 8$, blue crosses), M4-identified accessions ($n = 22$, cyan diamonds), M6-identified accessions ($n = 16$, magenta triangles), RR-identified accessions ($n = 41$, yellow boxes), and S-identified accessions ($n = 68$, grey asterisks).

3.2.2 Patterns of variation for fatty acid composition

C. sativa accessions had significantly higher C18:1 percent values than the other accessions with the widest range of values observed for the S-239 accession (Figure 3.8; Appendix 7.9 & Appendix 7.10). In particular, the S-239-1 biorepetition recorded a maximum value of 18.1 mol % (Figure 3.8). C18:2 values were highly variable although the M6-identified *C. microcarpa* accessions had significantly higher values for this fatty acid than other group ID members except for the *C. laxa* L-612 accession (Figure 3.9; Appendix 7.11 & Appendix 7.12). C18:3 was the most abundant fatty acid across all of the accessions based on mol % (Figure 3.10). *C. hispida* (HG-240, HH-248), *C. laxa* L-612, and the M6-identified *C. microcarpa*

accessions had significantly higher C18:3 values than the other group ID members but were not significantly different from each other except for HH-248 and M6-identified accessions (Figure 3.10; Appendix 7.13 & Appendix 7.14). A maximum value of 46.3 mol % for C18:3 was recorded for the HG-240-15 biorepetition (Figure 3.10). We found a negative relationship between C18:2 and C18:3 traits (Figure 3.11; $R^2 = 0.29$, $F_{1,190} = 80.0$, $p < 0.001$).

Figure 3.8. Boxplots for oleic acid (C18:1) quantitative variable. C18:1 was measured in mol % for biorepetitions in each of the 23 accessions in this study. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.9 and Appendix 7.10 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

Figure 3.9. Boxplots for linoleic acid (C18:2) quantitative variable. C18:2 was measured in mol % for biorepetitions in each of the 23 accessions in this study. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.11 and Appendix 7.12 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

Figure 3.10. Boxplots for α -linolenic acid (C18:3) quantitative variable. C18:3 was measured in mol % for biorepetitions in each of the 23 accessions in this study. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.13 and Appendix 7.14 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

Figure 3.11. Correlation between C18:2 (mol %) and C18:3 (mol %) quantitative traits ($R^2 = 0.29$, $F_{1,190} = 80.0$, $p < 0.001$). Group ID memberships were HG-240 ($n = 16$, black circles), HH-248 ($n = 16$, red triangles), L-612 ($n = 5$, green plus-signs), M2-246 ($n = 8$, blue crosses), M4-identified accessions ($n = 22$, cyan diamonds), M6-identified accessions ($n = 16$, magenta triangles), RR-identified accessions ($n = 41$, yellow boxes), and S-identified accessions ($n = 68$, grey asterisks).

C20:1 values for *C. rumelica* species were significantly higher than the other group ID members (Figure 3.12; Appendix 7.15 & Appendix 7.16). Within the *C. sativa* species, the S-239 accession had significantly lower C20:1 values than the other *C. sativa* accessions (Figure 3.12; Appendix 7.15 & Appendix 7.16). Significantly higher values for C22:1 were detected within the M2-246 *C. microcarpa* accession with a maximum value of 11.5 mol % obtained by the M2-246-2 biorepetition whereas significantly lower values were observed in the L-612 accession with a minimum value of 0.8 mol % detected for the L-612-8 biorepetition (Figure 3.13; Appendix 7.17 & Appendix 7.18). Apart from the L-612 accession, the HG-240 and HH-248 *C. hispida* accessions also had significantly lower C22:1 values but were not significantly different

from each other (Figure 3.13; Appendix 7.17 & Appendix 7.18). Within the *C. sativa* species, the S-239 accession had significantly lower C22:1 values than the other *C. sativa* accessions with the S-239-1 biorepetition recording a minimum value of 1.8 mol % (Figure 3.13; Appendix 7.17 & Appendix 7.18). It should further be noted that C20:1 and C22:1 were important classification variables from the previous LDA biplot (Figure 3.3).

Figure 3.12. Boxplots for eicosenoic acid (C20:1) quantitative variable. C20:1 was measured in mol % for biorepetitions in each of the 23 accessions in this study. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.15 and Appendix 7.16 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

Figure 3.13. Boxplots for erucic acid (C22:1) quantitative variable. C22:1 was measured in mol % for biorepetitions in each of the 23 accessions in this study. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.17 and Appendix 7.18 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

3.2.3 Criteria measurements to select lines for development in industrial applications

To assess the breeding potential for development in biofuel applications, the 192 biorepetitions were screened for lowest PUFA ratios and highest C18:1 values as these are desired components for biodiesel fuel (Knothe, 2009). *C. rumelica* accessions were observed to having lower PUFA ratios compared to the other species with RR-1034 having the lowest average value of 0.99 ± 0.013 (Figure 3.14). The lowest PUFA ratio among *C. sativa* accessions was S-1062 with an average value of 1.09 ± 0.054 (Figure 3.14). As for higher C18:1 content, the S-239 accession had the widest range of C18:1 values with a lone biorepetition (S-239-1) reaching a maximum value of 18.1 mol % as previously mentioned (Figure 3.8).

Figure 3.14. Boxplots for polyunsaturated fatty acid ratio calculation (PUFA ratio). PUFA ratio was measured for biorepetitions in each of the 23 accessions in this study to assess breeding potential for biofuel applications. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.19 and Appendix 7.20 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

To assess the breeding potential for development in food applications, the 192 biorepetitions were screened for the following four standard oil quality guidelines that have been established from canola research: (1) more than 30% C18:3; (2) less than 3% C22:1; (3) less than 10% SSFA; and (4) ratio of C18:3 to C18:2 greater than 1 (Ghamkhar *et al.*, 2010). Biorepetitions that fulfilled all four criteria belonged to the HG-240 *C. hispida* accession (Figure 3.15; Table 3.3). Biorepetitions that fulfilled criteria 1, 2, and 4 belonged to HG-240, HH-248, L-612, and S-239 (Figure 3.15; Table 3.3).

Figure 3.15. Boxplots for sum of saturated fatty acid calculation (SSFA). SSFA was measured in mol % for biorepetitions in each of the 23 accessions in this study to assess breeding potential for food applications. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.21 and Appendix 7.22 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

Table 3.4. Candidate plant lines for further development in food applications. Candidate lines were selected based on their fulfillment of four criteria established by Ghamkhar *et al.* (2010) for oilseed crop development in food applications.

Biorepetitions that fulfilled criteria 1, 2, & 4	Biorepetitions that fulfilled all criteria
HG-240 (all biorepetitions) HH-240 (all biorepetitions) L-612 (all biorepetitions) S-239 (biorepetitions 1, 3, 5, & 8)	HG-240 (biorepetitions 2, 4, 9, 11, 12, 13, 14, & 15)

To assess the breeding potential for development in industrial chemical applications, the 192 biorepetitions were screened for increased levels of very long chain fatty acids (VLCFA) as represented by the SVLCFA fatty acid calculation (see Section 2.9). The diploid *C. microcarpa* (M2-246) accession had the highest average SVLCFA value of 38.0 ± 1.4 mol % with the M2-246-8 biorepetition recording the highest individual SVLCFA value of 40.1 mol % (Figure 3.16;

Appendix 7.23 & Appendix 7.24). The *C. rumelica* RR-1034 accession also had a high SVLCFA value of 37.7 ± 0.6 mol % which was not significantly different than the M2-246 accession (Figure 3.16; Appendix 7.23 & Appendix 7.24). Apart from the M2-246 accessions, the *C. rumelica* accessions had significantly higher SVLCFA values than the other accessions (Figure 3.16; Appendix 7.23 & Appendix 7.24).

Figure 3.16. Boxplots for sum of very long chain fatty acid calculation (SVLCFA). SVLCFA was measured in mol % for biorepetitions in each of the 23 accessions in this study to assess breeding potential for industrial chemical applications. Boxplots for each accession are colour-coded by their respective group identification membership. Refer to Appendix 7.23 and Appendix 7.24 for tests of significant differences across the eight group identifications and the 23 accessions, respectively.

4.0 Discussion

4.1 *Part I: Natural trait variation for taxonomic classification*

4.1.1 *DNA content of plant accessions via flow cytometry*

Flow cytometry (FCM) was used to confirm ploidy status for the 23 *Camelina* accessions used in this study and interpreted based on previous DNA content measurements and chromosome counts completed for these *Camelina* species (Figure 3.1; Martin *et al.*, 2016). Ploidy and chromosome counts are important information for breeding purposes as they are an important factor contributing to reproductive isolation between species (Martin *et al.*, 2016). There were no deviations in DNA content and the degree of ploidy based on previous determinations (Martin *et al.*, 2016). The eight group identifications used here can be categorized further into three DNA content levels corresponding to tentative diploidy, tetraploidy, and hexaploidy classifications (Martin *et al.*, 2016). However, molecular sequencing and comparative genomics would be need to be paired with our findings to ensure accurate classification.

4.1.2 *Interpretations for PCA and LDA results*

The PCA distance biplot was initially conducted to determine general patterns of variation in the complete dataset and used as an unbiased approach to determine whether biorepetitions grouped correspondingly to their aforementioned group ID memberships. The PCA distance biplot supports the fact that the distribution of biorepetitions generally clustered closely with other biorepetitions belonging to the same group ID memberships (Table 2.1; Figure 3.2). However, there was considerable overlap between biorepetitions of the *C. sativa* accessions and tetraploid and hexaploid *C. microcarpa* accessions suggesting that their patterns of variation for the 24 quantitative traits were similar and questions whether these groups should be treated as

different species (Figure 3.2). The 24 quantitative traits all seemed to contribute to the total variance captured on PC1 (28.6%) and PC2 (22.1%) of the PCA in relatively similar amounts with C18, C20, and C22 fatty acids being among the top contributing variables on these axes (Figure 3.2; Table 3.2).

We then generated an LDA biplot for the 20 quantitative variables as another ordination method to discriminate variables based on an *a priori* grouping structure i.e. the eight group ID memberships (Figure 3.3; Table 3.3). Significant differences between groups were detected from the MANOVA ($F = 32.6$, $p < 0.001$) and served as a preliminary measure to further determine which variables were most responsible for these differences. The LDA biplot discriminated between groups most notably by C20:1 and C22:1 on LD1, which represented 63.5% of the total between-group variance (Figure 3.3). Other studies have also reported that C22:1 was an important classification variable for members of the *Brassicaceae* family, including *C. sativa* (Katepa-Mupondwa *et al.*, 2006; Enjalbert *et al.*, 2013). For instance, Katepa-Mupondwa *et al.* (2006) identified C22:1 and C18:1 as precise classification variables for accessions of *Sinapis alba* L. (yellow mustard) since they are regarded as highly heritable traits with low environmental variation. Likewise, Enjalbert *et al.* (2013) reported C22:1 to be highly correlated with PC1 for their principal components analysis for *C. sativa* accessions.

4.1.3 Interpretations for permutational MANOVA

There were significant differences in the 24 quantitative traits measured between both group ID memberships and accessions. This was expected since deviations in at least one quantitative trait compared between group ID memberships or accessions may influence tests of significant differences, which was likely the case for many of the group ID or accession-level pairings. Although significant differences were found at all levels of testing, accessions still

grouped well according to their group ID memberships as evidenced by PCA and LDA (Figure 3.2 & Figure 3.3). However, we identified the following pairs of accessions that were not significantly different across the 24 quantitative traits measured and may in fact be duplicated accessions: M4-718 and M4-965, M6-198 and M6-818, RR-1255 and RR-247, RR-1255 and RR-609, S-1044 and S-621, S-1062 and S-252, S-1063 and S-252, S-1662 and S-252, and S-605 and S-621 (Appendix 7.2).

4.1.4 Preliminary taxonomic revisions of the *Camelina* genus

As previously mentioned, we were particularly interested in answering the following four major taxonomic questions:

1. Which traits are most informative for taxonomic classifications particularly among *C. microcarpa*, *C. rumelica*, and *C. sativa*?
2. Should the three identified cytotypes of *C. microcarpa* (2X, 4X, and 6X) be considered as same or different species?
3. Should hexaploid (6X) *C. microcarpa* and *C. sativa* be considered the same species?
4. Are *C. hispida* var. *hispida* and *C. hispida* var. *grandiflora* similar enough to each other to warrant the recent demotion of *C. grandiflora* to *C. hispida* var. *grandiflora*?

In general, C22:1, C20:1, C18:1, average flower size, and thousand-seed weight were informative traits for taxonomic classification in the *Camelina* genus with or without the constraints of an *a priori* grouping structure i.e. eight group ID memberships (Figure 3.2 & Figure 3.3). However, it should be noted that *C. sativa*, *C. microcarpa* (6X), and *C. microcarpa* (4X) formed an overlapping cluster of points on the PCA indicating that the variation observed from the complete dataset for these groups were similar, suggesting that they may be closely

related (Figure 3.2). The *C. microcarpa* (2X) accession also clustered closely to these groups (Figure 3.2 & Figure 3.3). Nevertheless, results from the permutational MANOVA (Appendix 7.1 & 7.2) along with Welch's t-tests across a number of quantitative traits were in support for treating the eight group ID memberships as discrete taxonomic units in the *Camelina* genus.

As for resolving the taxonomic classifications between *C. hispida* var. *hispida* and *C. hispida* var. *grandiflora*, our results show support for the demotion of *C. grandiflora* to a variety of *C. hispida*. These two taxonomic groups clustered closely on the PCA and LDA plots (Figure 3.2 & Figure 3.3). It should also be noted that there were no statistical differences between these two groups across thousand-seed weight, protein content, and C22:1 quantitative trait variables (Appendix 7.3; Appendix 7.7; Appendix 7.17).

4.1.5 Limitations

It should be noted that the PCA displays only a proportion of the variance captured within a dataset which decreases with the addition of more variables. In other words, given that our dataset follows a 192-row (biorepetitions) by 24-column (quantitative variables) matrix, it becomes difficult for the PCA to capture all of the variation and condense this information onto a two-dimensional plot. Nevertheless, we were still able to display the majority of the variation (> 50%) onto the first (28.6%) and second (22.1%) principal components which we ascribe as a good representation of our large dataset (Figure 3.2). The representation of our dataset was further improved when incorporating an *a priori* grouping structure (i.e. group ID memberships) in our LDA which captured more than 80% of the variation observed on the first (63.5%) and second (17.3%) linear discriminant functions (Figure 3.3).

PCA requires mostly linear relationships between variables (Zuur *et al.*, 2007), which was generally observed during the exploratory data analysis stage (data not shown). However, the process of conducting the LDA is dependent on a whole series of underlying assumptions in which some were violated. For instance, the number of observations in the smallest group should typically be greater than the number of variables used (Zuur *et al.*, 2007). The LDA also functions best under the homogeneity assumption in which within-group variances should be similar between groups (Zuur *et al.*, 2007). Nevertheless, violation of these assumptions are commonly observed in the literature (Zuur *et al.*, 2007) and we believe that the LDA biplot generated is still reliable for identifying variables that discriminated between group ID memberships in our dataset.

4.2 Part II: Natural trait variation for breeding potential assessment

For our second objective, we documented the natural variation in specific oilseed characteristics commonly investigated for camelina to direct breeding efforts in oilseed crop development. The specific quantitative variables of interest were thousand seed weight (TSW), seed oil content, seed protein content, C18:1, C18:2, C18:3, C20:1, and C22:1 as well as sum of saturated fatty acid composition (SSFA) (Table 3.1). For fatty acid composition, we chose to investigate the aforementioned five fatty acids since they comprised the vast majority of the seed oil constituents (> 80 mol %) in all *Camelina* species. In general, the results from our study were in agreement with previously studies on commonly measured oilseed characteristics with respect to the *C. sativa* accessions we investigated (Budin *et al.*, 1995; Enjalbert *et al.*, 2013; Gehringer *et al.*, 2006; Gugel & Falk, 2006; Hrastar *et al.*, 2009; Vollman *et al.*, 2007; Putnam *et al.*, 1993; Zubr, 1997; Zubr, 2003). To our knowledge, this was the first study to document seed oil characteristics for other *Camelina* species or crop wild relatives of *C. sativa*.

4.2.1 Patterns of variation for TSW, seed oil content, & seed protein content

TSW and seed oil content traits were significantly higher among *C. sativa* accessions (Figure 3.4 & Figure 3.5). These differences likely reveal the extent to which *C. sativa* accessions have been subjected to selection processes during ancient times and their current breeding status. However, there is little information available on germplasm material for camelina or camelina's wild relatives (Ghamkhar *et al.*, 2010; Vollman & Eynck, 2015). Species classification then becomes speculative particularly when individuals are discriminated by traits undergoing artificial selection such as TSW which may be the case for our *C. sativa* accessions and hexaploid *C. microcarpa* accessions since this was the variable that discriminated between these group identifications the most (Figure 3.3 & Figure 3.4). In other words, it could be interpreted that these accessions may belong to the same *C. sativa* species but with differences due to wild and domesticated germplasm material. It has also been established that these accessions are classified as hexaploids with similar DNA contents (Figure 3.1). It would then be imperative to compare genome sequences of these accessions to provide further evidence for this point. Nevertheless, there still remains a considerable degree of variability in TSW and oil content traits for *C. sativa* accessions in our dataset suggesting future work in potentially enhancing these traits for further improvement (Figure 3.4; Figure 3.5).

For protein content measurements, *C. rumelica* accessions in our study were highest in protein content but had comparably lower oil contents (Figure 3.5; Figure 3.6) which suggests that these species may favour allocating carbon resources towards producing proteins rather than lipids with respect to seed development and composition for major carbon-fixating pathways in plants. Protein content is generally negatively correlated with oil content (Gehringer *et al.*, 2010; Gugel & Falk, 2006), which was also observed in our study albeit to a lesser degree (Figure 3.7;

$R^2 = 0.25$, $F_{1,190} = 63.0$, $p < 0.001$). Future work will be aimed at assessing the nutritional quality of the seed proteins (amino acid analysis).

4.2.2 *Patterns of variation in fatty acid composition*

Our study confirms that seed oil composition of camelina is mostly composed of unsaturated FAs and we further extend this fact generally to other members of the *Camelina* genus although in different relative quantities. There was significant variability across all measured traits and unique FA profiles were detected. The amount of variation observed for these traits have implications in developing varieties with altered FA profiles via breeding for use in industrial applications. Specifically, we focused on identifying suitable candidates for further enhancement in biofuel, food, and industrial chemical applications using a series of FA criteria measurements. Genetic variation in FA profiles can lead to differences in engine performance of the oil extracted from diverse cultivars (Enjalbert *et al.*, 2013). Oilseed crops also need to satisfy specific oil quality requirements to have a niche in the oil market for food industries (Ghamkhar *et al.*, 2010).

The S-239 *C. sativa* accession had the most versatile FA profile suitable for further development in both biofuel and food applications. This was demonstrated by higher C18:1 values and the fulfillment of three out of four requirements for the food criteria, respectively (Figure 3.8; Table 3.3). We did not identify any accessions with lowered PUFA content meaning that camelina will likely need to be genetically modified for further improvement of this biofuel component. Nevertheless, studies have demonstrated desirable fuel properties and life-cycle analysis of camelina oil as a blend component in renewable biofuels which serves as a suitable alternative (Moser, 2010; Moser & Vaughn, 2010).

The HG-240 *C. hispida* accession fulfilled all four requirements for the food criteria making it a suitable candidate for development for this purpose (Table 3.3). The *C. hispida* HH-248, *C. laxa* L-612, and tetraploid *C. microcarpa* accessions, along with the *C. hispida* HG-240 accession, all had significantly higher C18:3 values than the other accessions (Appendix 6.8) and may have strong implications in the food industry due to its known health benefits. We also identified accessions with very low amounts of C22:1 (less than 2 mol %) most notably in the *C. laxa* L-612 accession (Figure 3.12) which complies with established industry standards that have been set for low-erucic acid canola varieties (Ghamkhar *et al.*, 2010).

The diploid *C. microcarpa* (M2-246) and *C. rumelica* accessions were identified as having the highest proportions of VLCFAs in their FA profile (Figure 3.16), which may be useful for further development in alternative bio-industrial applications. The production of high-value industrial oils is a feasible direction for camelina since its oil is currently not being used for food applications on a large scale, which would alleviate concerns of mixing seeds for edible and industrial markets (Zhu *et al.*, 2016). The downward trend in oil prices is also an impediment for farmers in adopting camelina as a biofuel crop. Therefore, the potential for camelina can be realized with continued research to develop its oil for high-value bio-materials as a renewable and sustainable alternative to petroleum-based products.

4.2.3 Limitations

Although C20:1 and C22:1 were informative traits in discriminating taxa in the *Camelina* genus, these results could be biased since seed oil characteristics may have been subjected to processes of natural or artificial selection. Given the fact that camelina has a very short breeding history, selection for specific fatty acid characters is unlikely in its current development as an oilseed crop. Instead, broad-level quantitative traits such as oil content, protein content, and

TSW would be expected to be influenced by artificial selection. The oil content and TSW boxplots are indeed indicative of this phenomenon (Figure 3.4; Figure 3.5); however, they were not the most informative variables for taxonomic classification in our study (Figure 3.3).

Environmental effects always have the potential to obscure the results in a study which is why our experimental design consisted of growing plants in a plant chamber with biweekly randomization to control for these external influences. We previously conducted a preliminary trial in a similar manner except under greenhouse conditions for growth of *C. sativa* and *C. microcarpa* accessions, some of which were incorporated into the core set of *Camelina* accessions in the present study (Wu *et al.*, 2014). We did detect differences between some oilseed characteristics across the two environments for these particular accessions; however, a number of external factors may have contributed to this difference. First, plant growth conditions in the greenhouse trial were generally poorer than the plant chambers trial, which was likely due the close spacing of the biorepetitions in the greenhouse trial. Having the biorepetitions grow in close proximity to each other may have enhanced the effects of competition for limiting resources such as light; a parameter that strongly influences seed oil content and composition (Li *et al.*, 2006). Second, seed oil characteristics were likely affected by mildew and aphid infestations that were especially prevalent during the greenhouse trial. Despite these issues, some accessions had fairly comparable seed oil characteristics across both environments particularly for *C. sativa* accessions. In this case, it would be interesting to investigate whether the degree of polyploidy confers stability of the traits of a species across different environments (Comai, 2005). Nevertheless, the plant chambers trial addressed the limitations observed from the greenhouse trial by minimizing issues such as lighting and adequate spacing under a controlled

setting. This allowed for the majority of plants to grow to full maturity under ideal conditions with a reproducible experimental design.

Vernalisation of the non-*C. sativa* accessions and one *C. sativa* accession (S-596) in our study was required to ensure growth to full maturity of these plants (induce flowering). However, O'Neill *et al.* (2003) showed that the degree of saturation for fatty acids was influenced by vernalisation but oil content was not significantly altered, at least in *Arabidopsis thaliana*. Within the *C. sativa* accessions, only S-596 was vernalized and so we compared the seed oil characteristics from this accession against the others to evaluate this relationship. The S-596 accession generally had higher PUFA and VLCFA values, represented by the PUFA ratio and SVLCFA fatty acid calculations, than the other *C. sativa* accessions which likely accentuates this relationship although these values were still comparable to other accessions in this species (Appendix 7.20 & Appendix 7.24).

The number of biorepetitions included in our study represents only a small fraction of the genetic variation of the population of an accession and to an even smaller degree in representing species within the *Camelina* genus. Some studies recommend at least a population of 59 random diploid individuals to ensure 95% probability of detecting of all alleles of 5% or greater in frequency (Mohammadi & Prasanna, 2003). The number of samples for population genetics studies would inevitably need to increase for a polyploid species such as camelina, assuming that sample material is obtained from wild populations. However, several of the accessions in our study consist of germplasm material from various seedbanks which, again, have not been consistently maintained for *Camelina*. In other words, there may be varying levels of inbreeding among the accessions used in this study especially for plants that are self-compatible. In this respect, there are no simple recommendations for an ideal sample size, number of samples, or

number of loci and depends largely on the nature of the study (Mohammad & Prasanna, 2003). For the purposes of the present study, we were able to sufficiently document an estimate of the variation observed across many levels due primarily to our robust approach in measuring traits on an individual-by-individual basis.

5.0 Future directions and conclusion

We were able to document the natural trait variation to identify informative variables for taxonomic classification and to help direct breeding efforts in improving oilseed traits in various industrial applications within the *Camelina* genus. This was a suitable approach to develop an emerging oilseed crop with a deficient breeding history and complicated genome structure. The present study can be viewed as a step forward in addressing these two goals and opens the doors for subsequent *Camelina* research in industrial applications and fundamental plant biology.

Seed lipid characters, particularly C20:1 and C22:1, were the most informative quantitative traits for discriminating between members of the *Camelina* genus. Our study solely evaluated the phenotypic variation in an assortment of quantitative traits that can be interpreted as a morphological approach. Future work would then entail complementing our findings with molecular methods such as DNA sequencing to provide a more informed estimate of the genetic diversity in the *Camelina* genus. Sequencing regions of the genomes of the accessions used in this study would also be essential to confirm their respective species status.

Understanding genetics of natural (phenotypic) variation in crop wild relatives is important not only to infer the genetic diversity in *Camelina*, but also contributes to define heritabilities of simple and complex traits and design successful introgression strategies from diverse germplasm resources (Scossa *et al.*, 2016). In other words, crop improvement relies on the identification of natural genetic variants and on the subsequent assembly of beneficial alleles in a unique individual which may minimize the yield penalties often associated with linkage drag (Scossa *et al.*, 2016). For instance, the establishment of canola in the 1970s was the direct result of breeding oilseed rape varieties low in erucic acid content (Abbadi & Leckband, 2011) and our

detection of low erucic acid lines in crop wild relatives of *Camelina* may also provide a foundation for this purpose in camelina.

Sequencing regions of the genome with respect to the well-studied seed lipid traits we investigated would be the presumptive place to start for subsequent investigations. For example, fatty acid desaturase 3 (*FAD3*), a C18:2 desaturase enzyme, may be a good candidate for natural allelic variation contributing to quantitative variation of PUFA content (O'Neill *et al.*, 2003). Quantitative trait loci (QTL) involved in lipid biosynthesis have also been identified in camelina (Gehringer *et al.*, 2006) as well as other related species which would be an appropriate technique for this potential research direction. Jasinski *et al.* (2012) used a quantitative genetics approach to identify QTLs involved in VLCFA biosynthesis in *Arabidopsis thaliana* and subsequently found that point mutations in the β -ketoacyl-CoA synthase 18 (KCS18) enzyme was responsible for the modulation of VLCFA content. The analysis of these quantitative traits may also provide insight into the underlying structure and mechanisms of camelina's polyploid genome since genome duplication has been associated with additive effects.

Another complementary approach would be to compare the sequenced genome of camelina (Kagale *et al.*, 2014) and compare their sequences to hypothesized diploid parental ancestors; perhaps a combination of the camelina relatives we chose to investigate in our study. For instance, Hutcheon *et al.* (2010) identified a weak relationship between *C. hispida* and *C. sativa* when comparing the sequences of fatty acid desaturase 2 (*FAD2*) and fatty acid elongase 1 (*FAE1*) genes and we also documented similar quantitative levels in seed oil traits between these two species. For instance, no significant difference was observed for oil content between the HG-240 *C. hispida* accession and *C. sativa* accessions (Appendix 7.5). Galasso *et al.* (2015) also observed high genetic variability within *C. hispida* accessions relative to the other *Camelina*

species perhaps indicating that this species may be a predecessor for subsequent polyploid species within the genus. In this case, we hypothesize that the parental ancestors of *C. sativa* may be the result of a hybridization event between *C. hispida* ($n = 7$) and the diploid *C. microcarpa* ($n = 6$) or *C. laxa* ($n = 6$) due to its basal chromosome numbers of $7+7+6$ (Kagale *et al.*, 2014). The rapid onset of next-generation sequencing technologies would allow testing for this hypothesis and would be imperative in resolving camelina's complex allohexaploid genome structure. It may then be possible to resynthesize camelina from alternate parental genomes to create much greater diversity in camelina to meet specific biofuel, food, or industrial chemical applications.

6.0 References

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7.0 Appendix A – Permutational MANOVAs and Welch’s t-tests

Appendix 7.1. Results for pairwise nonparametric MANOVA between combinations of the eight group ID memberships tested across 24 quantitative traits. Tests were conducted using the “adonis” function from the “vegan” package in RStudio with parameters set at 999 permutations. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID Pairs		F-statistic	p-value
HG	HH	16.0	0.001
HG	L	7.9	0.002
HG	M2	38.5	0.001
HG	M4	89.1	0.001
HG	M6	102.1	0.001
HG	RR	62.5	0.001
HG	S	72.6	0.001
HH	L	14.1	0.001
HH	M2	41.3	0.001
HH	M4	134.7	0.001
HH	M6	142.9	0.001
HH	RR	61.5	0.001
HH	S	147.8	0.001
L	M2	11.6	0.001
L	M4	33.3	0.001
L	M6	34.6	0.001
L	RR	15.0	0.001
L	S	24.7	0.001
M2	M4	65.0	0.001
M2	M6	40.2	0.001
M2	RR	18.0	0.001
M2	S	44.8	0.001
M4	M6	42.8	0.001
M4	RR	115.0	0.001
M4	S	80.9	0.001
M6	RR	61.4	0.001
M6	S	50.2	0.001
RR	S	112.9	0.001

Appendix 7.2. Results for pairwise nonparametric MANOVA between combinations of the 23 accessions tested across 24 quantitative traits. Tests were conducted using the “adonis” function from the “vegan” package in RStudio with parameters set at 999 permutations. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values greater than this value were highlighted in bold.

Accession Pairs		F-statistic	p-value	Accession Pairs		F-statistic	p-value
HG-240	HH-248	16.0	0.001	M4-965	S-1662	74.2	0.001
HG-240	L-612	7.9	0.002	M4-965	S-239	24.3	0.001
HG-240	M2-246	38.5	0.001	M4-965	S-252	37.0	0.001
HG-240	M4-168	33.5	0.001	M4-965	S-596	26.7	0.001
HG-240	M4-718	55.6	0.001	M4-965	S-605	38.9	0.001
HG-240	M4-965	47.9	0.001	M4-965	S-621	51.3	0.001
HG-240	M6-198	54.9	0.001	M6-198	M6-818	1.2	0.304
HG-240	M6-818	69.8	0.001	M6-198	RR-1034	19.4	0.002
HG-240	RR-1034	41.5	0.001	M6-198	RR-1255	29.8	0.001
HG-240	RR-1255	32.6	0.001	M6-198	RR-245	36.0	0.001
HG-240	RR-245	61.2	0.001	M6-198	RR-247	40.4	0.001
HG-240	RR-247	20.1	0.001	M6-198	RR-609	29.0	0.001
HG-240	RR-609	47.6	0.001	M6-198	S-1044	19.8	0.001
HG-240	S-1044	38.0	0.001	M6-198	S-1062	27.2	0.001
HG-240	S-1062	31.3	0.001	M6-198	S-1063	33.1	0.001
HG-240	S-1063	24.4	0.001	M6-198	S-1662	37.4	0.001
HG-240	S-1662	31.5	0.001	M6-198	S-239	7.9	0.001
HG-240	S-239	39.5	0.001	M6-198	S-252	16.5	0.002
HG-240	S-252	18.8	0.001	M6-198	S-596	18.9	0.002
HG-240	S-596	34.0	0.001	M6-198	S-605	15.7	0.001
HG-240	S-605	36.9	0.001	M6-198	S-621	21.2	0.001
HG-240	S-621	39.0	0.001	M6-818	RR-1034	52.0	0.003
HH-248	L-612	14.1	0.001	M6-818	RR-1255	50.1	0.001
HH-248	M2-246	41.3	0.001	M6-818	RR-245	63.6	0.001
HH-248	M4-168	49.3	0.001	M6-818	RR-247	128.9	0.005
HH-248	M4-718	77.2	0.001	M6-818	RR-609	52.8	0.002
HH-248	M4-965	67.8	0.001	M6-818	S-1044	37.4	0.001
HH-248	M6-198	75.2	0.001	M6-818	S-1062	59.5	0.001
HH-248	M6-818	93.9	0.001	M6-818	S-1063	73.5	0.001
HH-248	RR-1034	41.6	0.001	M6-818	S-1662	97.8	0.002
HH-248	RR-1255	25.4	0.001	M6-818	S-239	10.3	0.001
HH-248	RR-245	60.3	0.001	M6-818	S-252	34.5	0.001
HH-248	RR-247	11.3	0.001	M6-818	S-596	39.0	0.001
HH-248	RR-609	42.6	0.001	M6-818	S-605	33.4	0.002
HH-248	S-1044	67.6	0.001	M6-818	S-621	51.3	0.001

HH-248	S-1062	52.3	0.001	RR-1034	RR-1255	13.9	0.002
HH-248	S-1063	45.0	0.001	RR-1034	RR-245	10.0	0.001
HH-248	S-1662	52.1	0.001	RR-1034	RR-247	33.9	0.010
HH-248	S-239	67.9	0.001	RR-1034	RR-609	12.5	0.001
HH-248	S-252	34.6	0.001	RR-1034	S-1044	24.3	0.001
HH-248	S-596	53.7	0.001	RR-1034	S-1062	29.1	0.001
HH-248	S-605	63.9	0.001	RR-1034	S-1063	43.4	0.001
HH-248	S-621	72.4	0.001	RR-1034	S-1662	49.7	0.002
L-612	M2-246	11.6	0.001	RR-1034	S-239	19.4	0.001
L-612	M4-168	14.7	0.005	RR-1034	S-252	21.3	0.002
L-612	M4-718	33.7	0.002	RR-1034	S-596	20.9	0.002
L-612	M4-965	28.6	0.003	RR-1034	S-605	24.6	0.001
L-612	M6-198	18.9	0.001	RR-1034	S-621	35.4	0.001
L-612	M6-818	36.4	0.001	RR-1255	RR-245	8.2	0.004
L-612	RR-1034	27.8	0.001	RR-1255	RR-247	2.1	0.126
L-612	RR-1255	11.1	0.001	RR-1255	RR-609	2.1	0.139
L-612	RR-245	21.7	0.001	RR-1255	S-1044	36.0	0.002
L-612	RR-247	12.6	0.001	RR-1255	S-1062	28.9	0.001
L-612	RR-609	18.0	0.001	RR-1255	S-1063	31.0	0.001
L-612	S-1044	24.0	0.001	RR-1255	S-1662	37.1	0.001
L-612	S-1062	23.9	0.002	RR-1255	S-239	35.7	0.001
L-612	S-1063	20.9	0.001	RR-1255	S-252	20.1	0.002
L-612	S-1662	27.8	0.001	RR-1255	S-596	33.3	0.001
L-612	S-239	16.9	0.001	RR-1255	S-605	31.5	0.001
L-612	S-252	11.8	0.002	RR-1255	S-621	39.7	0.001
L-612	S-596	26.5	0.001	RR-245	RR-247	15.6	0.001
L-612	S-605	20.6	0.001	RR-245	RR-609	7.5	0.001
L-612	S-621	26.9	0.002	RR-245	S-1044	40.6	0.001
M2-246	M4-168	22.1	0.001	RR-245	S-1062	37.0	0.001
M2-246	M4-718	42.0	0.001	RR-245	S-1063	48.5	0.001
M2-246	M4-965	36.8	0.001	RR-245	S-1662	52.3	0.001
M2-246	M6-198	20.3	0.001	RR-245	S-239	43.6	0.001
M2-246	M6-818	29.2	0.001	RR-245	S-252	25.5	0.001
M2-246	RR-1034	17.2	0.001	RR-245	S-596	39.6	0.001
M2-246	RR-1255	8.4	0.001	RR-245	S-605	35.3	0.001
M2-246	RR-245	22.7	0.001	RR-245	S-621	45.4	0.001
M2-246	RR-247	9.2	0.002	RR-247	RR-609	7.7	0.007
M2-246	RR-609	8.5	0.001	RR-247	S-1044	54.0	0.002
M2-246	S-1044	22.7	0.001	RR-247	S-1062	42.6	0.001
M2-246	S-1062	18.4	0.001	RR-247	S-1063	42.3	0.004
M2-246	S-1063	19.8	0.001	RR-247	S-1662	61.6	0.006

M2-246	S-1662	24.9	0.001	RR-247	S-239	41.7	0.001
M2-246	S-239	27.3	0.001	RR-247	S-252	27.0	0.004
M2-246	S-252	13.5	0.003	RR-247	S-596	58.7	0.002
M2-246	S-596	21.7	0.002	RR-247	S-605	52.9	0.001
M2-246	S-605	17.0	0.001	RR-247	S-621	79.0	0.001
M2-246	S-621	19.9	0.001	RR-609	S-1044	38.5	0.001
M4-168	M4-718	2.7	0.030	RR-609	S-1062	34.9	0.001
M4-168	M4-965	3.7	0.017	RR-609	S-1063	43.8	0.001
M4-168	M6-198	9.8	0.001	RR-609	S-1662	50.0	0.001
M4-168	M6-818	12.6	0.001	RR-609	S-239	35.9	0.001
M4-168	RR-1034	22.2	0.001	RR-609	S-252	24.1	0.001
M4-168	RR-1255	31.4	0.001	RR-609	S-596	37.9	0.001
M4-168	RR-245	47.9	0.001	RR-609	S-605	33.4	0.001
M4-168	RR-247	32.5	0.004	RR-609	S-621	42.8	0.001
M4-168	RR-609	38.2	0.001	S-1044	S-1062	5.1	0.003
M4-168	S-1044	17.9	0.001	S-1044	S-1063	10.5	0.002
M4-168	S-1062	24.0	0.001	S-1044	S-1662	8.1	0.001
M4-168	S-1063	27.2	0.003	S-1044	S-239	5.8	0.001
M4-168	S-1662	26.7	0.003	S-1044	S-252	3.1	0.027
M4-168	S-239	11.0	0.001	S-1044	S-596	3.8	0.010
M4-168	S-252	15.5	0.001	S-1044	S-605	2.7	0.040
M4-168	S-596	10.4	0.001	S-1044	S-621	2.2	0.064
M4-168	S-605	16.1	0.001	S-1062	S-1063	4.9	0.011
M4-168	S-621	18.7	0.001	S-1062	S-1662	5.2	0.002
M4-718	M4-965	1.8	0.166	S-1062	S-239	13.6	0.001
M4-718	M6-198	22.9	0.001	S-1062	S-252	1.2	0.327
M4-718	M6-818	44.0	0.001	S-1062	S-596	10.3	0.002
M4-718	RR-1034	58.4	0.002	S-1062	S-605	5.7	0.001
M4-718	RR-1255	64.0	0.001	S-1062	S-621	6.2	0.001
M4-718	RR-245	91.3	0.001	S-1063	S-1662	4.6	0.008
M4-718	RR-247	116.5	0.003	S-1063	S-239	19.7	0.001
M4-718	RR-609	81.4	0.001	S-1063	S-252	2.7	0.057
M4-718	S-1044	49.9	0.001	S-1063	S-596	16.9	0.001
M4-718	S-1062	72.0	0.001	S-1063	S-605	12.4	0.002
M4-718	S-1063	83.4	0.001	S-1063	S-621	13.9	0.001
M4-718	S-1662	91.4	0.001	S-1662	S-239	16.5	0.001
M4-718	S-239	25.2	0.001	S-1662	S-252	2.5	0.058
M4-718	S-252	45.8	0.001	S-1662	S-596	14.9	0.001
M4-718	S-596	31.1	0.001	S-1662	S-605	12.0	0.001
M4-718	S-605	48.7	0.001	S-1662	S-621	15.7	0.001
M4-718	S-621	64.1	0.002	S-239	S-252	7.7	0.001

M4-965	M6-198	24.9	0.001	S-239	S-596	7.9	0.001
M4-965	M6-818	54.8	0.001	S-239	S-605	6.4	0.001
M4-965	RR-1034	54.3	0.002	S-239	S-621	8.7	0.001
M4-965	RR-1255	57.9	0.001	S-252	S-596	7.5	0.001
M4-965	RR-245	77.7	0.001	S-252	S-605	3.1	0.017
M4-965	RR-247	109.4	0.005	S-252	S-621	3.6	0.003
M4-965	RR-609	73.5	0.001	S-596	S-605	7.8	0.002
M4-965	S-1044	40.6	0.001	S-596	S-621	6.0	0.007
M4-965	S-1062	58.1	0.001	S-605	S-621	1.9	0.127
M4-965	S-1063	69.4	0.001				

Appendix 7.3. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the TSW quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean (g)	ID2 mean (g)
HG	HH	-2.0	28.3	0.054	0.28	0.31
HG	L	0.8	4.7	0.474	0.28	0.25
HG	M2	5.0	16.0	0.000	0.28	0.19
HG	M4	8.7	18.7	0.000	0.28	0.18
HG	M6	4.4	20.7	0.000	0.28	0.23
HG	RR	2.4	47.4	0.021	0.28	0.24
HG	S	-25.7	81.9	0.000	0.28	0.93
HH	L	1.7	5.2	0.154	0.31	0.25
HH	M2	6.3	19.6	0.000	0.31	0.19
HH	M4	9.4	17.3	0.000	0.31	0.18
HH	M6	6.0	18.6	0.000	0.31	0.23
HH	RR	4.0	37.7	0.000	0.31	0.24
HH	S	-23.1	79.7	0.000	0.31	0.93
L	M2	1.5	5.1	0.201	0.25	0.19
L	M4	1.9	4.1	0.125	0.25	0.18
L	M6	0.6	4.1	0.563	0.25	0.23
L	RR	0.2	4.9	0.824	0.25	0.24
L	S	-16.2	8.2	0.000	0.25	0.93
M2	M4	1.0	8.2	0.361	0.19	0.18
M2	M6	-2.4	8.9	0.041	0.19	0.23
M2	RR	-2.7	20.4	0.014	0.19	0.24
M2	S	-27.8	60.3	0.000	0.19	0.93
M4	M6	-7.7	30.9	0.000	0.18	0.23
M4	RR	-4.9	47.5	0.000	0.18	0.24
M4	S	-31.9	70.2	0.000	0.18	0.93
M6	RR	-1.1	50.5	0.278	0.23	0.24
M6	S	-29.7	71.9	0.000	0.23	0.93
RR	S	-26.6	94.4	0.000	0.24	0.93

Appendix 7.4. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the TSW quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	-2.0	28.3	0.054	M4-965	S-1662	-44.0	7.6	0.000
HG-240	L-612	0.8	4.7	0.474	M4-965	S-239	-11.9	7.0	0.000
HG-240	M2-246	5.0	16.0	0.000	M4-965	S-252	-7.6	5.0	0.001
HG-240	M4-168	7.0	14.4	0.000	M4-965	S-596	-28.5	5.2	0.000
HG-240	M4-718	8.1	20.5	0.000	M4-965	S-605	-25.2	7.1	0.000
HG-240	M4-965	8.5	17.2	0.000	M4-965	S-621	-23.0	7.1	0.000
HG-240	M6-198	3.8	20.6	0.001	M6-198	M6-818	1.4	12.5	0.176
HG-240	M6-818	4.5	22.0	0.000	M6-198	RR-1034	-4.5	5.3	0.006
HG-240	RR-1034	-3.0	6.1	0.022	M6-198	RR-1255	4.1	7.6	0.004
HG-240	RR-1255	6.1	12.9	0.000	M6-198	RR-245	-0.3	20.0	0.791
HG-240	RR-245	3.6	22.8	0.002	M6-198	RR-247	2.5	4.3	0.064
HG-240	RR-247	4.9	9.2	0.001	M6-198	RR-609	0.6	9.1	0.555
HG-240	RR-609	3.1	15.6	0.006	M6-198	S-1044	-14.3	7.2	0.000
HG-240	S-1044	-13.1	7.7	0.000	M6-198	S-1062	-18.0	7.2	0.000
HG-240	S-1062	-16.6	7.8	0.000	M6-198	S-1063	-33.1	9.5	0.000
HG-240	S-1063	-24.4	17.0	0.000	M6-198	S-1662	-38.8	8.9	0.000
HG-240	S-1662	-30.4	15.1	0.000	M6-198	S-239	-11.3	7.1	0.000
HG-240	S-239	-10.6	7.3	0.000	M6-198	S-252	-7.1	5.0	0.001
HG-240	S-252	-6.6	5.1	0.001	M6-198	S-596	-25.7	5.6	0.000
HG-240	S-596	-21.7	7.8	0.000	M6-198	S-605	-23.7	7.3	0.000
HG-240	S-605	-21.7	8.2	0.000	M6-198	S-621	-21.6	7.2	0.000
HG-240	S-621	-20.0	8.0	0.000	M6-818	RR-1034	-4.8	5.5	0.004
HH-248	L-612	1.7	5.2	0.154	M6-818	RR-1255	3.1	9.2	0.013
HH-248	M2-246	6.3	19.6	0.000	M6-818	RR-245	-1.6	15.0	0.127
HH-248	M4-168	8.1	17.9	0.000	M6-818	RR-247	1.3	5.7	0.241
HH-248	M4-718	9.0	18.8	0.000	M6-818	RR-609	-0.3	10.9	0.788
HH-248	M4-965	9.2	16.4	0.000	M6-818	S-1044	-14.5	7.4	0.000
HH-248	M6-198	5.5	18.9	0.000	M6-818	S-1062	-18.2	7.4	0.000
HH-248	M6-818	6.0	21.3	0.000	M6-818	S-1063	-31.7	11.6	0.000
HH-248	RR-1034	-2.0	6.8	0.090	M6-818	S-1662	-37.4	10.7	0.000
HH-248	RR-1255	7.2	16.5	0.000	M6-818	S-239	-11.4	7.1	0.000
HH-248	RR-245	5.3	20.0	0.000	M6-818	S-252	-7.2	5.1	0.001
HH-248	RR-247	6.3	12.6	0.000	M6-818	S-596	-25.5	6.3	0.000
HH-248	RR-609	4.6	19.2	0.000	M6-818	S-605	-23.8	7.6	0.000
HH-248	S-1044	-12.2	8.2	0.000	M6-818	S-621	-21.8	7.5	0.000
HH-248	S-1062	-15.6	8.3	0.000	RR-1034	RR-1255	5.9	6.9	0.001
HH-248	S-1063	-19.7	20.4	0.000	RR-1034	RR-245	4.4	5.3	0.006

HH-248	S-1662	-25.6	18.7	0.000	RR-1034	RR-247	5.2	6.1	0.002
HH-248	S-239	-10.1	7.5	0.000	RR-1034	RR-609	4.5	6.7	0.003
HH-248	S-252	-6.3	5.2	0.001	RR-1034	S-1044	-9.2	11.6	0.000
HH-248	S-596	-19.0	9.6	0.000	RR-1034	S-1062	-11.8	11.8	0.000
HH-248	S-605	-20.3	9.0	0.000	RR-1034	S-1063	-8.3	6.4	0.000
HH-248	S-621	-18.8	8.7	0.000	RR-1034	S-1662	-12.0	6.8	0.000
L-612	M2-246	1.5	5.1	0.201	RR-1034	S-239	-8.5	9.5	0.000
L-612	M4-168	2.1	4.8	0.094	RR-1034	S-252	-5.4	6.0	0.002
L-612	M4-718	1.9	4.2	0.134	RR-1034	S-596	-10.3	8.5	0.000
L-612	M4-965	1.8	4.1	0.146	RR-1034	S-605	-14.6	11.9	0.000
L-612	M6-198	0.4	4.2	0.678	RR-1034	S-621	-13.9	12.0	0.000
L-612	M6-818	0.8	4.4	0.465	RR-1255	RR-245	-4.2	7.9	0.003
L-612	RR-1034	-2.8	8.7	0.023	RR-1255	RR-247	-1.8	8.9	0.112
L-612	RR-1255	2.1	5.3	0.092	RR-1255	RR-609	-2.8	12.8	0.017
L-612	RR-245	0.4	4.2	0.717	RR-1255	S-1044	-15.1	8.3	0.000
L-612	RR-247	1.3	4.8	0.268	RR-1255	S-1062	-18.6	8.4	0.000
L-612	RR-609	0.7	5.2	0.541	RR-1255	S-1063	-26.8	12.4	0.000
L-612	S-1044	-11.2	11.0	0.000	RR-1255	S-1662	-32.2	12.9	0.000
L-612	S-1062	-13.8	11.0	0.000	RR-1255	S-239	-11.9	7.5	0.000
L-612	S-1063	-11.2	5.0	0.000	RR-1255	S-252	-7.6	5.2	0.001
L-612	S-1662	-14.7	5.2	0.000	RR-1255	S-596	-24.4	9.1	0.000
L-612	S-239	-10.0	9.7	0.000	RR-1255	S-605	-23.9	9.1	0.000
L-612	S-252	-6.6	6.1	0.001	RR-1255	S-621	-22.0	8.7	0.000
L-612	S-596	-13.0	6.6	0.000	RR-245	RR-247	2.6	4.6	0.052
L-612	S-605	-16.7	10.2	0.000	RR-245	RR-609	0.7	9.5	0.473
L-612	S-621	-15.9	10.7	0.000	RR-245	S-1044	-14.2	7.2	0.000
M2-246	M4-168	1.3	12.0	0.219	RR-245	S-1062	-17.9	7.2	0.000
M2-246	M4-718	0.8	9.1	0.452	RR-245	S-1063	-32.6	10.1	0.000
M2-246	M4-965	0.6	7.7	0.547	RR-245	S-1662	-38.3	9.4	0.000
M2-246	M6-198	-2.8	9.2	0.020	RR-245	S-239	-11.2	7.1	0.000
M2-246	M6-818	-1.8	11.1	0.104	RR-245	S-252	-7.1	5.0	0.001
M2-246	RR-1034	-5.4	6.6	0.001	RR-245	S-596	-25.5	5.7	0.000
M2-246	RR-1255	1.2	12.7	0.255	RR-245	S-605	-23.6	7.3	0.000
M2-246	RR-245	-2.9	9.7	0.015	RR-245	S-621	-21.6	7.3	0.000
M2-246	RR-247	-0.5	9.3	0.616	RR-247	RR-609	-1.2	9.4	0.242
M2-246	RR-609	-1.6	14.0	0.122	RR-247	S-1044	-14.6	7.8	0.000
M2-246	S-1044	-14.7	8.1	0.000	RR-247	S-1062	-18.2	7.9	0.000
M2-246	S-1062	-18.2	8.2	0.000	RR-247	S-1063	-28.3	8.9	0.000
M2-246	S-1063	-26.8	13.9	0.000	RR-247	S-1662	-33.9	9.6	0.000
M2-246	S-1662	-32.3	13.9	0.000	RR-247	S-239	-11.6	7.3	0.000
M2-246	S-239	-11.7	7.4	0.000	RR-247	S-252	-7.4	5.1	0.001

M2-246	S-252	-7.4	5.2	0.001	RR-247	S-596	-24.6	7.3	0.000
M2-246	S-596	-24.1	8.8	0.000	RR-247	S-605	-23.6	8.3	0.000
M2-246	S-605	-23.5	8.8	0.000	RR-247	S-621	-21.7	8.1	0.000
M2-246	S-621	-21.7	8.5	0.000	RR-609	S-1044	-14.0	8.1	0.000
M4-168	M4-718	-0.9	7.2	0.390	RR-609	S-1062	-17.5	8.3	0.000
M4-168	M4-965	-1.2	5.7	0.276	RR-609	S-1063	-24.7	13.9	0.000
M4-168	M6-198	-5.1	7.2	0.001	RR-609	S-1662	-30.3	14.0	0.000
M4-168	M6-818	-3.7	9.2	0.005	RR-609	S-239	-11.2	7.5	0.000
M4-168	RR-1034	-6.1	6.1	0.001	RR-609	S-252	-7.1	5.2	0.001
M4-168	RR-1255	0.0	10.7	0.964	RR-609	S-596	-22.6	8.9	0.000
M4-168	RR-245	-5.2	7.8	0.001	RR-609	S-605	-22.6	8.9	0.000
M4-168	RR-247	-2.0	7.4	0.087	RR-609	S-621	-20.9	8.6	0.000
M4-168	RR-609	-3.1	12.0	0.010	S-1044	S-1062	-2.0	14.0	0.071
M4-168	S-1044	-15.3	7.8	0.000	S-1044	S-1063	4.9	7.9	0.001
M4-168	S-1062	-18.9	7.9	0.000	S-1044	S-1662	2.0	8.2	0.080
M4-168	S-1063	-30.5	11.9	0.000	S-1044	S-239	-1.9	11.8	0.083
M4-168	S-1662	-36.0	12.0	0.000	S-1044	S-252	-0.6	7.0	0.590
M4-168	S-239	-12.0	7.3	0.000	S-1044	S-596	2.4	9.5	0.037
M4-168	S-252	-7.7	5.1	0.001	S-1044	S-605	-3.2	13.1	0.007
M4-168	S-596	-26.0	7.6	0.000	S-1044	S-621	-3.1	13.6	0.008
M4-168	S-605	-24.5	8.3	0.000	S-1062	S-1063	7.9	8.1	0.000
M4-168	S-621	-22.5	8.1	0.000	S-1062	S-1662	4.8	8.4	0.001
M4-718	M4-965	-0.4	11.1	0.670	S-1062	S-239	-0.5	11.4	0.646
M4-718	M6-198	-6.9	14.0	0.000	S-1062	S-252	0.5	6.8	0.605
M4-718	M6-818	-4.2	12.5	0.001	S-1062	S-596	5.1	9.8	0.000
M4-718	RR-1034	-6.0	5.2	0.002	S-1062	S-605	-1.1	13.5	0.296
M4-718	RR-1255	0.8	7.6	0.452	S-1062	S-621	-1.1	13.8	0.287
M4-718	RR-245	-6.9	20.2	0.000	S-1063	S-1662	-7.4	13.8	0.000
M4-718	RR-247	-1.6	4.3	0.178	S-1063	S-239	-5.3	7.4	0.001
M4-718	RR-609	-2.9	9.0	0.017	S-1063	S-252	-2.9	5.1	0.034
M4-718	S-1044	-15.4	7.2	0.000	S-1063	S-596	-4.6	8.3	0.002
M4-718	S-1062	-19.1	7.2	0.000	S-1063	S-605	-11.1	8.6	0.000
M4-718	S-1063	-37.0	9.4	0.000	S-1063	S-621	-10.3	8.3	0.000
M4-718	S-1662	-42.3	8.9	0.000	S-1662	S-239	-3.5	7.5	0.009
M4-718	S-239	-12.0	7.1	0.000	S-1662	S-252	-1.5	5.2	0.181
M4-718	S-252	-7.6	5.0	0.001	S-1662	S-596	1.1	9.2	0.312
M4-718	S-596	-28.1	5.6	0.000	S-1662	S-605	-7.4	9.0	0.000
M4-718	S-605	-25.1	7.3	0.000	S-1662	S-621	-6.9	8.7	0.000
M4-718	S-621	-22.9	7.2	0.000	S-239	S-252	0.8	9.6	0.444
M4-965	M6-198	-8.0	11.0	0.000	S-239	S-596	3.8	8.1	0.005
M4-965	M6-818	-4.4	9.1	0.002	S-239	S-605	-0.3	10.1	0.802

M4-965	RR-1034	-6.0	5.1	0.002	S-239	S-621	-0.3	10.7	0.772
M4-965	RR-1255	1.0	6.5	0.351	S-252	S-596	1.8	5.4	0.131
M4-965	RR-245	-7.9	21.0	0.000	S-252	S-605	-1.1	6.2	0.304
M4-965	RR-247	-1.5	3.4	0.222	S-252	S-621	-1.1	6.5	0.294
M4-965	RR-609	-2.9	7.7	0.022	S-596	S-605	-7.5	10.8	0.000
M4-965	S-1044	-15.4	7.1	0.000	S-596	S-621	-7.1	10.3	0.000
M4-965	S-1062	-19.2	7.1	0.000	S-605	S-621	-0.1	13.9	0.945
M4-965	S-1063	-38.9	7.8	0.000					

Appendix 7.5. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the oil content quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean (% w/w)	ID2 mean (% w/w)
HG	HH	4.3	28.3	0.000	41.4	34.1
HG	L	4.1	12.1	0.001	41.4	33.3
HG	M2	4.4	12.7	0.001	41.4	30.1
HG	M4	2.8	22.0	0.010	41.4	37.2
HG	M6	3.2	23.7	0.004	41.4	36.5
HG	RR	5.8	29.6	0.000	41.4	31.9
HG	S	-1.7	18.7	0.100	41.4	43.9
HH	L	0.4	9.0	0.664	34.1	33.3
HH	M2	1.7	10.5	0.126	34.1	30.1
HH	M4	-2.5	26.0	0.020	34.1	37.2
HH	M6	-1.8	27.3	0.083	34.1	36.5
HH	RR	1.6	38.0	0.124	34.1	31.9
HH	S	-8.5	21.2	0.000	34.1	43.9
L	M2	1.2	10.8	0.241	33.3	30.1
L	M4	-2.5	5.9	0.048	33.3	37.2
L	M6	-2.0	6.6	0.094	33.3	36.5
L	RR	0.8	8.0	0.426	33.3	31.9
L	S	-7.1	4.9	0.001	33.3	43.9
M2	M4	-3.1	8.3	0.013	30.1	37.2
M2	M6	-2.8	8.8	0.022	30.1	36.5
M2	RR	-0.8	9.7	0.465	30.1	31.9
M2	S	-6.3	7.7	0.000	30.1	43.9
M4	M6	0.7	32.6	0.476	37.2	36.5
M4	RR	4.7	61.0	0.000	37.2	31.9
M4	S	-8.4	43.8	0.000	37.2	43.9
M6	RR	3.8	50.2	0.000	36.5	31.9
M6	S	-8.3	27.2	0.000	36.5	43.9
RR	S	-11.7	60.7	0.000	31.9	43.9

Appendix 7.6. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the oil content quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	4.3	28.3	0.000	M4-965	S-1662	-6.1	10.5	0.000
HG-240	L-612	4.1	12.1	0.001	M4-965	S-239	-2.7	7.8	0.026
HG-240	M2-246	4.4	12.7	0.001	M4-965	S-252	-3.1	5.7	0.022
HG-240	M4-168	1.8	9.4	0.102	M4-965	S-596	-4.6	5.5	0.005
HG-240	M4-718	2.6	22.0	0.017	M4-965	S-605	-4.2	10.4	0.002
HG-240	M4-965	2.8	17.9	0.012	M4-965	S-621	-5.7	8.9	0.000
HG-240	M6-198	2.9	20.0	0.008	M6-198	M6-818	-0.6	12.7	0.547
HG-240	M6-818	2.7	22.0	0.012	M6-198	RR-1034	-2.0	11.9	0.065
HG-240	RR-1034	1.1	16.9	0.301	M6-198	RR-1255	4.0	10.0	0.003
HG-240	RR-1255	6.1	11.3	0.000	M6-198	RR-245	1.3	13.7	0.209
HG-240	RR-245	4.7	25.5	0.000	M6-198	RR-247	5.4	9.8	0.000
HG-240	RR-247	8.7	17.7	0.000	M6-198	RR-609	3.1	12.1	0.010
HG-240	RR-609	5.3	14.1	0.000	M6-198	S-1044	-5.3	13.2	0.000
HG-240	S-1044	-2.6	16.3	0.021	M6-198	S-1062	-4.4	13.7	0.001
HG-240	S-1062	-1.1	21.4	0.284	M6-198	S-1063	-5.4	11.1	0.000
HG-240	S-1063	-1.6	21.1	0.134	M6-198	S-1662	-4.8	12.3	0.000
HG-240	S-1662	-1.2	21.9	0.239	M6-198	S-239	-3.0	12.5	0.011
HG-240	S-239	-0.5	14.7	0.611	M6-198	S-252	-3.3	9.9	0.008
HG-240	S-252	-0.7	11.7	0.496	M6-198	S-596	-4.6	9.1	0.001
HG-240	S-596	-2.2	10.3	0.056	M6-198	S-605	-3.6	12.3	0.004
HG-240	S-605	0.0	21.9	0.979	M6-198	S-621	-5.0	13.9	0.000
HG-240	S-621	-1.8	20.7	0.091	M6-818	RR-1034	-1.7	10.1	0.117
HH-248	L-612	0.4	9.0	0.664	M6-818	RR-1255	4.7	8.2	0.002
HH-248	M2-246	1.7	10.5	0.126	M6-818	RR-245	2.4	18.3	0.029
HH-248	M4-168	-1.2	7.7	0.276	M6-818	RR-247	7.7	9.8	0.000
HH-248	M4-718	-2.1	20.2	0.047	M6-818	RR-609	3.8	10.0	0.004
HH-248	M4-965	-2.9	19.4	0.009	M6-818	S-1044	-5.3	11.0	0.000
HH-248	M6-198	-1.1	16.4	0.275	M6-818	S-1062	-4.5	13.6	0.001
HH-248	M6-818	-2.0	20.8	0.056	M6-818	S-1063	-5.9	13.3	0.000
HH-248	RR-1034	-3.4	13.3	0.005	M6-818	S-1662	-5.1	13.9	0.000
HH-248	RR-1255	3.3	9.2	0.009	M6-818	S-239	-2.8	10.3	0.019
HH-248	RR-245	0.1	28.9	0.908	M6-818	S-252	-3.1	7.8	0.015
HH-248	RR-247	4.7	15.7	0.000	M6-818	S-596	-4.5	7.3	0.003
HH-248	RR-609	2.4	11.4	0.037	M6-818	S-605	-3.6	13.9	0.003
HH-248	S-1044	-6.5	13.0	0.000	M6-818	S-621	-5.1	13.2	0.000
HH-248	S-1062	-6.1	18.5	0.000	RR-1034	RR-1255	5.5	9.3	0.000
HH-248	S-1063	-7.6	22.0	0.000	RR-1034	RR-245	3.8	10.7	0.003

HH-248	S-1662	-6.8	21.4	0.000	RR-1034	RR-247	8.3	7.6	0.000
HH-248	S-239	-4.0	11.8	0.002	RR-1034	RR-609	4.7	11.1	0.001
HH-248	S-252	-4.4	9.1	0.002	RR-1034	S-1044	-3.6	11.7	0.004
HH-248	S-596	-5.6	8.2	0.000	RR-1034	S-1062	-2.4	11.3	0.036
HH-248	S-605	-5.4	21.4	0.000	RR-1034	S-1063	-3.1	8.5	0.013
HH-248	S-621	-6.6	17.4	0.000	RR-1034	S-1662	-2.6	9.7	0.026
L-612	M2-246	1.2	10.8	0.241	RR-1034	S-239	-1.4	11.3	0.181
L-612	M4-168	-1.4	8.4	0.196	RR-1034	S-252	-1.7	8.9	0.131
L-612	M4-718	-2.2	7.7	0.057	RR-1034	S-596	-3.1	8.3	0.014
L-612	M4-965	-2.8	4.8	0.040	RR-1034	S-605	-1.3	9.7	0.211
L-612	M6-198	-1.4	9.5	0.193	RR-1034	S-621	-3.0	11.7	0.010
L-612	M6-818	-2.2	7.3	0.066	RR-1255	RR-245	-3.4	8.1	0.009
L-612	RR-1034	-3.4	8.3	0.009	RR-1255	RR-247	-0.8	7.3	0.445
L-612	RR-1255	2.8	9.7	0.020	RR-1255	RR-609	-0.9	12.6	0.370
L-612	RR-245	-0.4	7.3	0.713	RR-1255	S-1044	-7.7	11.8	0.000
L-612	RR-247	3.3	5.8	0.017	RR-1255	S-1062	-7.2	9.2	0.000
L-612	RR-609	1.8	11.0	0.093	RR-1255	S-1063	-7.9	7.4	0.000
L-612	S-1044	-6.3	10.8	0.000	RR-1255	S-1662	-7.5	8.0	0.000
L-612	S-1062	-5.6	8.5	0.000	RR-1255	S-239	-5.9	12.4	0.000
L-612	S-1063	-6.6	6.1	0.001	RR-1255	S-252	-6.2	10.9	0.000
L-612	S-1662	-6.1	7.0	0.001	RR-1255	S-596	-7.1	11.0	0.000
L-612	S-239	-4.0	11.0	0.002	RR-1255	S-605	-6.7	8.0	0.000
L-612	S-252	-4.4	8.9	0.002	RR-1255	S-621	-7.6	9.6	0.000
L-612	S-596	-5.5	8.7	0.000	RR-245	RR-247	5.3	13.0	0.000
L-612	S-605	-4.9	7.0	0.002	RR-245	RR-609	2.4	10.0	0.039
L-612	S-621	-6.1	9.1	0.000	RR-245	S-1044	-7.0	11.0	0.000
M2-246	M4-168	-2.2	11.7	0.045	RR-245	S-1062	-6.7	15.6	0.000
M2-246	M4-718	-3.0	9.7	0.014	RR-245	S-1063	-8.8	21.2	0.000
M2-246	M4-965	-3.3	7.6	0.011	RR-245	S-1662	-7.7	19.2	0.000
M2-246	M6-198	-2.3	11.3	0.038	RR-245	S-239	-4.3	10.3	0.002
M2-246	M6-818	-2.9	9.4	0.016	RR-245	S-252	-4.7	7.7	0.002
M2-246	RR-1034	-3.8	10.5	0.003	RR-245	S-596	-5.9	7.1	0.001
M2-246	RR-1255	1.3	13.0	0.225	RR-245	S-605	-6.2	19.2	0.000
M2-246	RR-245	-1.6	9.3	0.133	RR-245	S-621	-7.3	14.6	0.000
M2-246	RR-247	0.9	8.4	0.392	RR-247	RR-609	-0.4	8.7	0.686
M2-246	RR-609	0.4	13.8	0.686	RR-247	S-1044	-10.5	9.1	0.000
M2-246	S-1044	-6.2	13.1	0.000	RR-247	S-1062	-11.7	10.0	0.000
M2-246	S-1062	-5.5	10.4	0.000	RR-247	S-1063	-15.6	8.5	0.000
M2-246	S-1063	-6.0	8.6	0.000	RR-247	S-1662	-13.8	9.5	0.000
M2-246	S-1662	-5.7	9.2	0.000	RR-247	S-239	-7.4	8.8	0.000
M2-246	S-239	-4.4	13.6	0.001	RR-247	S-252	-8.1	6.5	0.000

M2-246	S-252	-4.7	12.0	0.001	RR-247	S-596	-9.0	6.2	0.000
M2-246	S-596	-5.7	12.0	0.000	RR-247	S-605	-12.0	9.5	0.000
M2-246	S-605	-4.9	9.2	0.001	RR-247	S-621	-12.0	9.9	0.000
M2-246	S-621	-5.9	10.9	0.000	RR-609	S-1044	-7.1	13.7	0.000
M4-168	M4-718	-0.1	7.1	0.916	RR-609	S-1062	-6.5	11.2	0.000
M4-168	M4-965	-0.3	5.4	0.803	RR-609	S-1063	-7.3	8.9	0.000
M4-168	M6-198	0.4	8.5	0.721	RR-609	S-1662	-6.9	9.7	0.000
M4-168	M6-818	0.0	6.9	0.981	RR-609	S-239	-5.2	14.0	0.000
M4-168	RR-1034	-1.1	7.9	0.312	RR-609	S-252	-5.5	12.0	0.000
M4-168	RR-1255	3.6	10.9	0.005	RR-609	S-596	-6.5	11.7	0.000
M4-168	RR-245	1.3	6.8	0.241	RR-609	S-605	-6.0	9.7	0.000
M4-168	RR-247	3.9	6.0	0.007	RR-609	S-621	-7.0	11.7	0.000
M4-168	RR-609	2.8	11.2	0.017	S-1044	S-1062	1.8	12.2	0.099
M4-168	S-1044	-3.7	10.2	0.004	S-1044	S-1063	1.7	9.6	0.120
M4-168	S-1062	-2.7	7.7	0.028	S-1044	S-1662	1.9	10.6	0.086
M4-168	S-1063	-3.1	6.2	0.020	S-1044	S-239	1.7	13.8	0.105
M4-168	S-1662	-2.8	6.6	0.026	S-1044	S-252	1.7	11.5	0.125
M4-168	S-239	-2.0	10.9	0.065	S-1044	S-596	0.2	10.8	0.882
M4-168	S-252	-2.2	9.6	0.051	S-1044	S-605	2.9	10.6	0.015
M4-168	S-596	-3.4	9.9	0.007	S-1044	S-621	1.1	12.7	0.285
M4-168	S-605	-2.0	6.7	0.087	S-1062	S-1063	-0.4	12.1	0.724
M4-168	S-621	-3.2	8.1	0.013	S-1062	S-1662	0.0	13.2	0.988
M4-718	M4-965	-0.3	9.8	0.775	S-1062	S-239	0.3	11.5	0.738
M4-718	M6-198	0.7	13.1	0.478	S-1062	S-252	0.2	8.9	0.852
M4-718	M6-818	0.1	14.0	0.884	S-1062	S-596	-1.4	8.2	0.192
M4-718	RR-1034	-1.5	10.5	0.151	S-1062	S-605	1.3	13.2	0.202
M4-718	RR-1255	4.7	8.5	0.001	S-1062	S-621	-0.8	13.9	0.443
M4-718	RR-245	2.5	17.5	0.025	S-1063	S-1662	0.4	13.6	0.692
M4-718	RR-247	7.6	9.9	0.000	S-1063	S-239	0.6	9.1	0.554
M4-718	RR-609	3.8	10.3	0.003	S-1063	S-252	0.5	6.8	0.655
M4-718	S-1044	-5.1	11.3	0.000	S-1063	S-596	-1.3	6.4	0.238
M4-718	S-1062	-4.2	13.8	0.001	S-1063	S-605	2.1	13.6	0.056
M4-718	S-1063	-5.5	13.0	0.000	S-1063	S-621	-0.6	11.6	0.576
M4-718	S-1662	-4.8	13.8	0.000	S-1662	S-239	0.4	9.9	0.717
M4-718	S-239	-2.6	10.6	0.023	S-1662	S-252	0.2	7.5	0.835
M4-718	S-252	-3.0	8.1	0.018	S-1662	S-596	-1.5	7.0	0.181
M4-718	S-596	-4.3	7.5	0.003	S-1662	S-605	1.6	14.0	0.141
M4-718	S-605	-3.3	13.8	0.005	S-1662	S-621	-0.9	12.8	0.407
M4-718	S-621	-4.9	13.5	0.000	S-239	S-252	-0.1	11.9	0.893
M4-965	M6-198	1.1	8.7	0.301	S-239	S-596	-1.5	11.4	0.171
M4-965	M6-818	0.5	10.1	0.626	S-239	S-605	0.6	10.0	0.585

M4-965	RR-1034	-1.6	6.4	0.153	S-239	S-621	-0.9	12.0	0.375
M4-965	RR-1255	5.2	6.5	0.002	S-252	S-596	-1.4	9.9	0.199
M4-965	RR-245	3.6	20.8	0.002	S-252	S-605	0.8	7.5	0.460
M4-965	RR-247	11.3	5.4	0.000	S-252	S-621	-0.8	9.4	0.443
M4-965	RR-609	4.3	7.7	0.003	S-596	S-605	2.4	7.0	0.049
M4-965	S-1044	-5.5	8.0	0.001	S-596	S-621	0.8	8.6	0.429
M4-965	S-1062	-5.0	9.2	0.001	S-605	S-621	-2.2	12.8	0.051
M4-965	S-1063	-7.5	11.6	0.000					

Appendix 7.7. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the protein content quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean (% w/w)	ID2 mean (% w/w)
HG	HH	-0.5	27.8	0.638	29.4	29.8
HG	L	1.0	13.8	0.336	29.4	28.6
HG	M2	1.6	12.9	0.134	29.4	27.6
HG	M4	10.3	21.3	0.000	29.4	22.4
HG	M6	6.3	27.3	0.000	29.4	24.6
HG	RR	-1.1	27.4	0.268	29.4	30.3
HG	S	4.6	16.9	0.000	29.4	26.5
HH	L	1.6	9.8	0.133	29.8	28.6
HH	M2	2.1	10.3	0.066	29.8	27.6
HH	M4	13.6	25.9	0.000	29.8	22.4
HH	M6	8.0	30.0	0.000	29.8	24.6
HH	RR	-0.8	36.6	0.452	29.8	30.3
HH	S	6.8	18.5	0.000	29.8	26.5
L	M2	0.9	10.5	0.395	28.6	27.6
L	M4	9.6	6.1	0.000	28.6	22.4
L	M6	5.5	9.4	0.000	28.6	24.6
L	RR	-2.4	8.3	0.041	28.6	30.3
L	S	3.5	4.6	0.019	28.6	26.5
M2	M4	5.1	8.2	0.001	27.6	22.4
M2	M6	2.8	10.1	0.019	27.6	24.6
M2	RR	-2.6	9.4	0.030	27.6	30.3
M2	S	1.1	7.4	0.292	27.6	26.5
M4	M6	-4.1	26.5	0.000	22.4	24.6
M4	RR	-16.3	61.0	0.000	22.4	30.3
M4	S	-12.5	34.5	0.000	22.4	26.5
M6	RR	-9.5	37.8	0.000	24.6	30.3
M6	S	-3.9	18.8	0.001	24.6	26.5
RR	S	9.1	53.2	0.000	30.3	26.5

Appendix 7.8. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the protein content quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	-0.5	27.8	0.638	M4-965	S-1662	-14.7	12.2	0.000
HG-240	L-612	1.0	13.8	0.336	M4-965	S-239	-11.5	11.0	0.000
HG-240	M2-246	1.6	12.9	0.134	M4-965	S-252	-9.1	6.6	0.000
HG-240	M4-168	7.0	10.9	0.000	M4-965	S-596	-3.9	6.1	0.008
HG-240	M4-718	9.0	21.6	0.000	M4-965	S-605	-7.5	8.8	0.000
HG-240	M4-965	10.4	17.2	0.000	M4-965	S-621	-6.6	9.2	0.000
HG-240	M6-198	4.8	15.7	0.000	M6-198	M6-818	0.1	12.0	0.927
HG-240	M6-818	6.1	21.4	0.000	M6-198	RR-1034	-2.8	10.4	0.017
HG-240	RR-1034	3.0	19.6	0.007	M6-198	RR-1255	-6.4	11.9	0.000
HG-240	RR-1255	-2.8	11.1	0.017	M6-198	RR-245	-5.5	12.2	0.000
HG-240	RR-245	-0.3	27.9	0.793	M6-198	RR-247	-7.2	9.8	0.000
HG-240	RR-247	-2.6	10.8	0.024	M6-198	RR-609	-6.1	13.7	0.000
HG-240	RR-609	-1.7	17.8	0.108	M6-198	S-1044	-2.0	11.4	0.072
HG-240	S-1044	3.8	21.8	0.001	M6-198	S-1062	-1.6	10.8	0.147
HG-240	S-1062	4.5	22.0	0.000	M6-198	S-1063	-2.4	11.3	0.037
HG-240	S-1063	3.4	21.9	0.002	M6-198	S-1662	-3.3	8.5	0.010
HG-240	S-1662	3.0	19.5	0.006	M6-198	S-239	-2.7	9.2	0.026
HG-240	S-239	3.7	20.7	0.002	M6-198	S-252	-2.7	10.6	0.023
HG-240	S-252	3.1	19.3	0.005	M6-198	S-596	-0.3	11.6	0.754
HG-240	S-596	5.4	17.1	0.000	M6-198	S-605	-2.1	11.7	0.054
HG-240	S-605	3.5	21.6	0.002	M6-198	S-621	-1.4	11.1	0.203
HG-240	S-621	4.7	22.0	0.000	M6-818	RR-1034	-3.9	12.0	0.002
HH-248	L-612	1.6	9.8	0.133	M6-818	RR-1255	-7.4	9.0	0.000
HH-248	M2-246	2.1	10.3	0.066	M6-818	RR-245	-7.4	18.0	0.000
HH-248	M4-168	8.0	8.3	0.000	M6-818	RR-247	-9.2	7.4	0.000
HH-248	M4-718	11.1	18.3	0.000	M6-818	RR-609	-7.6	12.9	0.000
HH-248	M4-965	14.2	18.8	0.000	M6-818	S-1044	-2.8	13.9	0.016
HH-248	M6-198	5.7	12.1	0.000	M6-818	S-1062	-2.2	13.6	0.043
HH-248	M6-818	7.6	17.9	0.000	M6-818	S-1063	-3.3	13.9	0.006
HH-248	RR-1034	4.2	16.4	0.001	M6-818	S-1662	-4.9	10.5	0.001
HH-248	RR-1255	-2.7	8.8	0.026	M6-818	S-239	-3.9	11.7	0.002
HH-248	RR-245	0.2	30.0	0.807	M6-818	S-252	-3.7	12.0	0.003
HH-248	RR-247	-2.5	7.4	0.040	M6-818	S-596	-0.5	11.4	0.606
HH-248	RR-609	-1.4	13.7	0.171	M6-818	S-605	-2.9	14.0	0.011
HH-248	S-1044	5.1	19.1	0.000	M6-818	S-621	-1.9	13.7	0.074
HH-248	S-1062	6.0	20.2	0.000	RR-1034	RR-1255	-5.2	8.1	0.001
HH-248	S-1063	4.6	19.2	0.000	RR-1034	RR-245	-3.9	16.5	0.001

HH-248	S-1662	4.5	21.4	0.000	RR-1034	RR-247	-6.2	6.0	0.001
HH-248	S-239	5.2	22.0	0.000	RR-1034	RR-609	-4.8	11.1	0.001
HH-248	S-252	4.3	15.9	0.001	RR-1034	S-1044	1.1	11.9	0.284
HH-248	S-596	6.8	12.8	0.000	RR-1034	S-1062	1.9	11.7	0.088
HH-248	S-605	4.7	18.4	0.000	RR-1034	S-1063	0.6	11.9	0.568
HH-248	S-621	6.1	19.8	0.000	RR-1034	S-1662	-0.4	8.7	0.668
L-612	M2-246	0.9	10.5	0.395	RR-1034	S-239	0.5	9.9	0.623
L-612	M4-168	6.3	8.5	0.000	RR-1034	S-252	0.2	10.0	0.852
L-612	M4-718	8.4	9.2	0.000	RR-1034	S-596	3.2	9.5	0.010
L-612	M4-965	9.7	4.8	0.000	RR-1034	S-605	0.8	12.0	0.429
L-612	M6-198	4.1	11.0	0.002	RR-1034	S-621	2.1	11.8	0.056
L-612	M6-818	5.3	9.4	0.000	RR-1255	RR-245	2.8	8.9	0.020
L-612	RR-1034	2.0	7.7	0.081	RR-1255	RR-247	0.9	8.8	0.382
L-612	RR-1255	-3.6	9.2	0.005	RR-1255	RR-609	1.4	10.9	0.176
L-612	RR-245	-1.4	9.9	0.188	RR-1255	S-1044	5.8	8.6	0.000
L-612	RR-247	-3.7	6.8	0.008	RR-1255	S-1062	6.2	8.2	0.000
L-612	RR-609	-2.7	10.9	0.021	RR-1255	S-1063	5.5	8.6	0.000
L-612	S-1044	2.9	8.8	0.018	RR-1255	S-1662	5.2	6.8	0.001
L-612	S-1062	3.6	8.2	0.007	RR-1255	S-239	5.6	7.2	0.001
L-612	S-1063	2.4	8.7	0.038	RR-1255	S-252	5.3	8.2	0.001
L-612	S-1662	1.9	5.7	0.106	RR-1255	S-596	6.9	9.2	0.000
L-612	S-239	2.6	6.4	0.039	RR-1255	S-605	5.5	8.9	0.000
L-612	S-252	2.1	7.9	0.065	RR-1255	S-621	6.4	8.4	0.000
L-612	S-596	4.6	8.7	0.001	RR-245	RR-247	-2.7	7.5	0.029
L-612	S-605	2.6	9.1	0.028	RR-245	RR-609	-1.6	13.8	0.124
L-612	S-621	3.8	8.4	0.005	RR-245	S-1044	4.8	19.3	0.000
M2-246	M4-168	4.2	12.0	0.001	RR-245	S-1062	5.7	20.4	0.000
M2-246	M4-718	4.9	10.4	0.001	RR-245	S-1063	4.3	19.4	0.000
M2-246	M4-965	4.9	7.5	0.001	RR-245	S-1662	4.2	21.4	0.000
M2-246	M6-198	2.4	13.4	0.034	RR-245	S-239	4.9	22.0	0.000
M2-246	M6-818	2.8	10.5	0.019	RR-245	S-252	4.0	16.0	0.001
M2-246	RR-1034	0.4	9.4	0.691	RR-245	S-596	6.6	13.0	0.000
M2-246	RR-1255	-3.7	12.9	0.003	RR-245	S-605	4.4	18.5	0.000
M2-246	RR-245	-1.9	10.4	0.085	RR-245	S-621	5.9	19.9	0.000
M2-246	RR-247	-3.6	9.9	0.005	RR-247	RR-609	0.8	9.3	0.470
M2-246	RR-609	-2.9	12.5	0.013	RR-247	S-1044	7.0	6.8	0.000
M2-246	S-1044	1.1	10.0	0.315	RR-247	S-1062	7.8	6.3	0.000
M2-246	S-1062	1.5	9.6	0.175	RR-247	S-1063	6.5	6.8	0.000
M2-246	S-1063	0.7	10.0	0.473	RR-247	S-1662	6.7	4.2	0.002
M2-246	S-1662	0.2	8.0	0.838	RR-247	S-239	7.2	4.8	0.001
M2-246	S-239	0.7	8.5	0.511	RR-247	S-252	6.3	6.2	0.001

M2-246	S-252	0.5	9.6	0.617	RR-247	S-596	8.4	7.2	0.000
M2-246	S-596	2.4	10.6	0.038	RR-247	S-605	6.6	7.2	0.000
M2-246	S-605	0.9	10.3	0.395	RR-247	S-621	7.9	6.5	0.000
M2-246	S-621	1.6	9.8	0.137	RR-609	S-1044	5.5	12.4	0.000
M4-168	M4-718	-0.1	8.3	0.914	RR-609	S-1062	6.2	11.8	0.000
M4-168	M4-965	-0.7	5.4	0.523	RR-609	S-1063	5.1	12.3	0.000
M4-168	M6-198	-2.2	11.4	0.051	RR-609	S-1662	5.0	9.0	0.001
M4-168	M6-818	-2.5	8.5	0.037	RR-609	S-239	5.5	9.9	0.000
M4-168	RR-1034	-5.3	7.4	0.001	RR-609	S-252	4.9	11.3	0.000
M4-168	RR-1255	-8.2	10.9	0.000	RR-609	S-596	7.0	12.0	0.000
M4-168	RR-245	-7.8	8.4	0.000	RR-609	S-605	5.2	12.7	0.000
M4-168	RR-247	-9.3	7.9	0.000	RR-609	S-621	6.3	12.0	0.000
M4-168	RR-609	-8.2	10.5	0.000	S-1044	S-1062	0.7	13.9	0.523
M4-168	S-1044	-4.5	8.0	0.002	S-1044	S-1063	-0.5	14.0	0.613
M4-168	S-1062	-4.1	7.5	0.004	S-1044	S-1662	-1.7	11.0	0.110
M4-168	S-1063	-4.9	8.0	0.001	S-1044	S-239	-0.8	12.3	0.449
M4-168	S-1662	-6.0	6.0	0.001	S-1044	S-252	-0.9	11.8	0.376
M4-168	S-239	-5.3	6.4	0.001	S-1044	S-596	2.1	10.9	0.059
M4-168	S-252	-5.2	7.6	0.001	S-1044	S-605	-0.3	14.0	0.799
M4-168	S-596	-2.8	8.5	0.021	S-1044	S-621	0.9	14.0	0.374
M4-168	S-605	-4.6	8.3	0.002	S-1062	S-1063	-1.2	13.9	0.251
M4-168	S-621	-3.9	7.7	0.005	S-1062	S-1662	-2.7	11.6	0.020
M4-718	M4-965	-0.9	8.7	0.388	S-1062	S-239	-1.6	12.9	0.132
M4-718	M6-198	-2.6	11.8	0.024	S-1062	S-252	-1.6	11.5	0.128
M4-718	M6-818	-3.3	14.0	0.006	S-1062	S-596	1.6	10.3	0.145
M4-718	RR-1034	-7.5	12.0	0.000	S-1062	S-605	-0.9	13.7	0.380
M4-718	RR-1255	-9.5	8.9	0.000	S-1062	S-621	0.3	14.0	0.779
M4-718	RR-245	-10.8	18.4	0.000	S-1063	S-1662	-1.1	11.1	0.290
M4-718	RR-247	-12.3	7.2	0.000	S-1063	S-239	-0.2	12.4	0.860
M4-718	RR-609	-10.4	12.8	0.000	S-1063	S-252	-0.4	11.8	0.701
M4-718	S-1044	-6.2	13.9	0.000	S-1063	S-596	2.6	10.8	0.026
M4-718	S-1062	-5.8	13.7	0.000	S-1063	S-605	0.2	14.0	0.812
M4-718	S-1063	-6.7	13.9	0.000	S-1063	S-621	1.5	14.0	0.169
M4-718	S-1662	-9.2	10.7	0.000	S-1662	S-239	1.2	13.6	0.253
M4-718	S-239	-7.9	11.9	0.000	S-1662	S-252	0.7	8.4	0.526
M4-718	S-252	-7.2	12.0	0.000	S-1662	S-596	4.0	7.3	0.004
M4-718	S-596	-3.7	11.2	0.003	S-1662	S-605	1.4	10.7	0.204
M4-718	S-605	-6.3	14.0	0.000	S-1662	S-621	2.9	11.4	0.013
M4-718	S-621	-5.4	13.8	0.000	S-239	S-252	-0.3	9.6	0.787
M4-965	M6-198	-2.4	7.7	0.045	S-239	S-596	3.1	8.3	0.014
M4-965	M6-818	-3.4	8.7	0.008	S-239	S-605	0.5	11.9	0.659

M4-965	RR-1034	-9.7	6.7	0.000	S-239	S-621	1.9	12.6	0.081
M4-965	RR-1255	-10.0	6.4	0.000	S-252	S-596	3.0	9.6	0.014
M4-965	RR-245	-13.8	18.7	0.000	S-252	S-605	0.6	12.0	0.542
M4-965	RR-247	-14.6	3.6	0.000	S-252	S-621	1.9	11.7	0.084
M4-965	RR-609	-11.8	7.9	0.000	S-596	S-605	-2.3	11.2	0.042
M4-965	S-1044	-7.5	9.0	0.000	S-596	S-621	-1.3	10.6	0.220
M4-965	S-1062	-7.2	9.3	0.000	S-605	S-621	1.2	13.9	0.266
M4-965	S-1063	-8.2	9.0	0.000					

Appendix 7.9. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the C18:1 quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean (mol %)	ID2 mean (mol %)
HG	HH	3.6	29.5	0.001	10.0	8.8
HG	L	-0.6	6.8	0.568	10.0	10.3
HG	M2	11	17.8	0.000	10.0	6.5
HG	M4	2.4	33	0.024	10.0	9.3
HG	M6	-4.3	30	0.000	10.0	11.3
HG	RR	7	31.6	0.000	10.0	8.1
HG	S	-7.4	40.1	0.000	10.0	12.1
HH	L	-3.2	7.7	0.014	8.8	10.3
HH	M2	6.9	19.7	0.000	8.8	6.5
HH	M4	-1.6	30.4	0.130	8.8	9.3
HH	M6	-7.6	29.3	0.000	8.8	11.3
HH	RR	2.4	27.9	0.022	8.8	8.1
HH	S	-10.6	34.2	0.000	8.8	12.1
L	M2	8.5	7.1	0.000	10.3	6.5
L	M4	2.2	6.2	0.067	10.3	9.3
L	M6	-2.4	6.7	0.052	10.3	11.3
L	RR	5.2	5.5	0.003	10.3	8.1
L	S	-4.3	6.1	0.005	10.3	12.1
M2	M4	-9.4	16.7	0.000	6.5	9.3
M2	M6	-15.2	17.5	0.000	6.5	11.3
M2	RR	-5.8	14.1	0.000	6.5	8.1
M2	S	-18.8	17.5	0.000	6.5	12.1
M4	M6	-6.9	33.4	0.000	9.3	11.3
M4	RR	4.8	47.8	0.000	9.3	8.1
M4	S	-10.5	62.2	0.000	9.3	12.1
M6	RR	12	32.3	0.000	11.3	8.1
M6	S	-2.9	41.1	0.006	11.3	12.1
RR	S	-16.4	106.1	0.000	8.1	12.1

Appendix 7.10. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the C18:1 quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	3.6	29.5	0.001	M4-965	S-1662	-17.6	12.3	0.000
HG-240	L-612	-0.6	6.8	0.568	M4-965	S-239	-5.2	7.2	0.001
HG-240	M2-246	11.0	17.8	0.000	M4-965	S-252	-4.7	5.4	0.004
HG-240	M4-168	-0.2	6.9	0.825	M4-965	S-596	-8.5	8.7	0.000
HG-240	M4-718	3.2	18.7	0.005	M4-965	S-605	-4.4	7.9	0.002
HG-240	M4-965	3.9	21.4	0.001	M4-965	S-621	-14.8	12.1	0.000
HG-240	M6-198	-3.1	13.3	0.008	M6-198	M6-818	-0.3	13.8	0.775
HG-240	M6-818	-3.7	14.7	0.002	M6-198	RR-1034	7.1	11.6	0.000
HG-240	RR-1034	5.2	9.7	0.000	M6-198	RR-1255	7.8	12.9	0.000
HG-240	RR-1255	6.0	11.4	0.000	M6-198	RR-245	6.3	10.7	0.000
HG-240	RR-245	3.9	27.9	0.001	M6-198	RR-247	9.8	8.0	0.000
HG-240	RR-247	8.3	5.7	0.000	M6-198	RR-609	8.9	11.7	0.000
HG-240	RR-609	7.3	20.0	0.000	M6-198	S-1044	-1.4	12.7	0.197
HG-240	S-1044	-4.0	10.3	0.002	M6-198	S-1062	-2.4	13.0	0.031
HG-240	S-1062	-6.7	17.2	0.000	M6-198	S-1063	-1.8	13.1	0.098
HG-240	S-1063	-5.9	17.1	0.000	M6-198	S-1662	-4.5	11.0	0.001
HG-240	S-1662	-10.2	21.1	0.000	M6-198	S-239	-2.8	8.6	0.022
HG-240	S-239	-4.1	7.7	0.004	M6-198	S-252	-1.2	7.6	0.269
HG-240	S-252	-3.1	6.2	0.021	M6-198	S-596	0.6	11.0	0.572
HG-240	S-596	-3.4	16.4	0.003	M6-198	S-605	0.0	12.3	0.967
HG-240	S-605	-2.3	10.0	0.045	M6-198	S-621	0.1	7.9	0.953
HG-240	S-621	-5.2	18.7	0.000	M6-818	RR-1034	7.7	11.1	0.000
HH-248	L-612	-3.2	7.7	0.014	M6-818	RR-1255	8.5	12.5	0.000
HH-248	M2-246	6.9	19.7	0.000	M6-818	RR-245	7.2	11.6	0.000
HH-248	M4-168	-2.3	7.5	0.052	M6-818	RR-247	10.5	7.3	0.000
HH-248	M4-718	-0.5	20.4	0.610	M6-818	RR-609	9.9	12.4	0.000
HH-248	M4-965	-0.7	20.6	0.494	M6-818	S-1044	-1.2	12.0	0.265
HH-248	M6-198	-5.9	15.0	0.000	M6-818	S-1062	-2.2	13.6	0.042
HH-248	M6-818	-6.6	16.6	0.000	M6-818	S-1063	-1.6	13.6	0.139
HH-248	RR-1034	2.2	11.0	0.054	M6-818	S-1662	-4.5	11.7	0.001
HH-248	RR-1255	2.9	12.9	0.011	M6-818	S-239	-2.7	8.3	0.027
HH-248	RR-245	-0.4	26.1	0.721	M6-818	S-252	-1.0	7.1	0.335
HH-248	RR-247	5.3	6.6	0.001	M6-818	S-596	1.0	11.5	0.342
HH-248	RR-609	3.2	21.3	0.005	M6-818	S-605	0.3	11.6	0.791
HH-248	S-1044	-6.1	11.3	0.000	M6-818	S-621	0.5	8.1	0.638
HH-248	S-1062	-9.7	19.1	0.000	RR-1034	RR-1255	0.7	10.9	0.494
HH-248	S-1063	-8.9	19.0	0.000	RR-1034	RR-245	-2.7	7.6	0.028

HH-248	S-1662	-13.3	21.9	0.000	RR-1034	RR-247	2.8	7.3	0.025
HH-248	S-239	-5.2	7.9	0.001	RR-1034	RR-609	0.3	8.6	0.766
HH-248	S-252	-4.7	6.6	0.002	RR-1034	S-1044	-7.2	11.8	0.000
HH-248	S-596	-6.9	18.1	0.000	RR-1034	S-1062	-10.4	10.0	0.000
HH-248	S-605	-4.4	10.8	0.001	RR-1034	S-1063	-9.7	10.0	0.000
HH-248	S-621	-9.1	17.9	0.000	RR-1034	S-1662	-13.2	8.0	0.000
L-612	M2-246	8.5	7.1	0.000	RR-1034	S-239	-6.0	8.5	0.000
L-612	M4-168	0.2	8.8	0.834	RR-1034	S-252	-5.8	7.5	0.001
L-612	M4-718	2.9	6.8	0.026	RR-1034	S-596	-8.0	8.2	0.000
L-612	M4-965	3.1	4.8	0.028	RR-1034	S-605	-5.6	11.6	0.000
L-612	M6-198	-1.9	9.2	0.085	RR-1034	S-621	-9.6	5.6	0.000
L-612	M6-818	-2.3	8.4	0.051	RR-1255	RR-245	-3.6	9.1	0.006
L-612	RR-1034	4.6	8.4	0.002	RR-1255	RR-247	2.1	7.8	0.069
L-612	RR-1255	5.2	8.9	0.001	RR-1255	RR-609	-0.5	10.1	0.597
L-612	RR-245	3.2	5.6	0.021	RR-1255	S-1044	-7.8	12.4	0.000
L-612	RR-247	7.1	7.0	0.000	RR-1255	S-1062	-11.1	11.5	0.000
L-612	RR-609	5.7	6.3	0.001	RR-1255	S-1063	-10.5	11.5	0.000
L-612	S-1044	-2.9	10.9	0.014	RR-1255	S-1662	-14.0	9.4	0.000
L-612	S-1062	-4.3	7.3	0.003	RR-1255	S-239	-6.3	8.6	0.000
L-612	S-1063	-3.7	7.4	0.007	RR-1255	S-252	-6.2	7.6	0.000
L-612	S-1662	-6.3	5.9	0.001	RR-1255	S-596	-8.8	9.6	0.000
L-612	S-239	-3.7	9.0	0.005	RR-1255	S-605	-6.2	12.1	0.000
L-612	S-252	-2.4	7.9	0.040	RR-1255	S-621	-10.5	6.7	0.000
L-612	S-596	-1.7	6.1	0.133	RR-245	RR-247	6.1	4.5	0.002
L-612	S-605	-1.5	11.0	0.153	RR-245	RR-609	4.3	16.1	0.001
L-612	S-621	-2.4	4.4	0.067	RR-245	S-1044	-6.3	8.9	0.000
M2-246	M4-168	-6.6	7.2	0.000	RR-245	S-1062	-11.0	13.3	0.000
M2-246	M4-718	-7.8	14.0	0.000	RR-245	S-1063	-10.1	13.3	0.000
M2-246	M4-965	-9.6	10.5	0.000	RR-245	S-1662	-16.2	17.6	0.000
M2-246	M6-198	-11.8	12.8	0.000	RR-245	S-239	-5.2	7.4	0.001
M2-246	M6-818	-13.0	13.4	0.000	RR-245	S-252	-4.8	5.7	0.004
M2-246	RR-1034	-3.6	9.6	0.005	RR-245	S-596	-8.1	12.4	0.000
M2-246	RR-1255	-2.8	11.2	0.017	RR-245	S-605	-4.5	8.7	0.002
M2-246	RR-245	-8.6	13.9	0.000	RR-245	S-621	-12.4	20.6	0.000
M2-246	RR-247	-0.3	5.9	0.747	RR-247	RR-609	-3.1	5.2	0.027
M2-246	RR-609	-4.4	13.7	0.001	RR-247	S-1044	-9.5	9.8	0.000
M2-246	S-1044	-10.8	10.6	0.000	RR-247	S-1062	-13.3	6.2	0.000
M2-246	S-1062	-16.8	14.0	0.000	RR-247	S-1063	-12.6	6.2	0.000
M2-246	S-1063	-16.0	14.0	0.000	RR-247	S-1662	-16.2	4.8	0.000
M2-246	S-1662	-21.6	13.2	0.000	RR-247	S-239	-7.3	8.6	0.000
M2-246	S-239	-7.6	7.8	0.000	RR-247	S-252	-7.5	7.3	0.000

M2-246	S-252	-8.2	6.4	0.000	RR-247	S-596	-11.1	5.0	0.000
M2-246	S-596	-14.7	12.0	0.000	RR-247	S-605	-7.8	9.9	0.000
M2-246	S-605	-8.9	10.2	0.000	RR-247	S-621	-13.0	3.3	0.001
M2-246	S-621	-19.0	8.6	0.000	RR-609	S-1044	-8.4	9.7	0.000
M4-168	M4-718	2.0	7.0	0.082	RR-609	S-1062	-13.8	13.5	0.000
M4-168	M4-965	2.1	5.6	0.082	RR-609	S-1063	-12.9	13.4	0.000
M4-168	M6-198	-1.8	8.9	0.100	RR-609	S-1662	-18.7	13.9	0.000
M4-168	M6-818	-2.1	8.3	0.067	RR-609	S-239	-6.3	7.6	0.000
M4-168	RR-1034	3.6	8.6	0.006	RR-609	S-252	-6.4	6.0	0.001
M4-168	RR-1255	4.2	8.9	0.003	RR-609	S-596	-11.3	11.7	0.000
M4-168	RR-245	2.2	6.1	0.066	RR-609	S-605	-6.5	9.4	0.000
M4-168	RR-247	5.8	7.9	0.000	RR-609	S-621	-15.6	9.2	0.000
M4-168	RR-609	4.2	6.6	0.004	S-1044	S-1062	-0.4	10.9	0.662
M4-168	S-1044	-2.7	11.1	0.019	S-1044	S-1063	0.1	10.9	0.961
M4-168	S-1062	-3.7	7.4	0.007	S-1044	S-1662	-1.9	9.2	0.091
M4-168	S-1063	-3.3	7.4	0.013	S-1044	S-239	-2.0	9.9	0.080
M4-168	S-1662	-5.2	6.3	0.002	S-1044	S-252	-0.1	9.5	0.904
M4-168	S-239	-3.6	10.3	0.005	S-1044	S-596	2.0	9.4	0.077
M4-168	S-252	-2.4	9.5	0.038	S-1044	S-605	1.2	13.9	0.255
M4-168	S-596	-1.6	6.5	0.152	S-1044	S-621	1.7	7.4	0.131
M4-168	S-605	-1.5	11.4	0.149	S-1062	S-1063	0.7	14.0	0.476
M4-168	S-621	-2.1	5.3	0.085	S-1062	S-1662	-2.2	12.9	0.044
M4-718	M4-965	-0.1	10.9	0.941	S-1062	S-239	-1.9	7.9	0.101
M4-718	M6-198	-5.6	12.4	0.000	S-1062	S-252	0.2	6.5	0.851
M4-718	M6-818	-6.4	13.1	0.000	S-1062	S-596	3.8	12.0	0.002
M4-718	RR-1034	2.7	9.3	0.025	S-1062	S-605	1.9	10.5	0.089
M4-718	RR-1255	3.5	10.8	0.005	S-1062	S-621	3.9	8.5	0.004
M4-718	RR-245	0.2	14.6	0.816	S-1063	S-1662	-3.1	12.8	0.009
M4-718	RR-247	5.8	5.6	0.001	S-1063	S-239	-2.1	7.9	0.068
M4-718	RR-609	3.9	13.9	0.002	S-1063	S-252	-0.2	6.5	0.863
M4-718	S-1044	-5.9	10.2	0.000	S-1063	S-596	3.0	12.0	0.011
M4-718	S-1062	-9.6	13.9	0.000	S-1063	S-605	1.4	10.5	0.191
M4-718	S-1063	-8.8	13.8	0.000	S-1063	S-621	2.9	8.5	0.019
M4-718	S-1662	-13.5	13.5	0.000	S-1662	S-239	-1.2	7.5	0.273
M4-718	S-239	-5.1	7.7	0.001	S-1662	S-252	1.2	5.8	0.263
M4-718	S-252	-4.5	6.2	0.004	S-1662	S-596	7.1	11.3	0.000
M4-718	S-596	-6.7	12.0	0.000	S-1662	S-605	3.3	9.0	0.009
M4-718	S-605	-4.2	9.9	0.002	S-1662	S-621	8.5	9.7	0.000
M4-718	S-621	-9.3	8.8	0.000	S-239	S-252	1.7	11.4	0.114
M4-965	M6-198	-6.3	8.9	0.000	S-239	S-596	3.1	7.6	0.016
M4-965	M6-818	-7.3	9.4	0.000	S-239	S-605	2.7	10.2	0.024

M4-965	RR-1034	3.1	6.4	0.020	S-239	S-621	2.9	7.1	0.021
M4-965	RR-1255	4.0	7.6	0.004	S-252	S-596	1.6	5.9	0.159
M4-965	RR-245	0.4	21.8	0.683	S-252	S-605	1.1	10.0	0.297
M4-965	RR-247	6.6	3.8	0.003	S-252	S-621	1.4	5.2	0.231
M4-965	RR-609	5.1	11.6	0.000	S-596	S-605	-0.4	9.2	0.712
M4-965	S-1044	-6.3	8.0	0.000	S-596	S-621	-0.9	6.7	0.377
M4-965	S-1062	-11.6	10.3	0.000	S-605	S-621	0.0	7.4	0.994
M4-965	S-1063	-10.6	10.2	0.000					

Appendix 7.11. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the C18:2 quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean (mol %)	ID2 mean (mol %)
HG	HH	6.5	23.2	0.000	15.9	12.1
HG	L	-1.3	4.9	0.249	15.9	18.1
HG	M2	-2.8	10.6	0.018	15.9	19.2
HG	M4	2.5	17.7	0.021	15.9	14.6
HG	M6	-9.9	22.6	0.000	15.9	21.7
HG	RR	-0.6	27.1	0.577	15.9	16.3
HG	S	-1.1	19.6	0.283	15.9	16.5
HH	L	-3.8	4.3	0.018	12.1	18.1
HH	M2	-6.6	8.1	0.000	12.1	19.2
HH	M4	-7.7	23.7	0.000	12.1	14.6
HH	M6	-24.5	29.9	0.000	12.1	21.7
HH	RR	-9.8	48.3	0.000	12.1	16.3
HH	S	-12.9	31.5	0.000	12.1	16.5
L	M2	-0.6	7.4	0.587	18.1	19.2
L	M4	2.2	4.1	0.088	18.1	14.6
L	M6	-2.3	4.2	0.084	18.1	21.7
L	RR	1.1	4.3	0.315	18.1	16.3
L	S	1	4.1	0.381	18.1	16.5
M2	M4	4.4	7.3	0.003	19.2	14.6
M2	M6	-2.3	8	0.047	19.2	21.7
M2	RR	2.7	8.4	0.028	19.2	16.3
M2	S	2.5	7.5	0.040	19.2	16.5
M4	M6	-22.9	24.5	0.000	14.6	21.7
M4	RR	-4.8	55.1	0.000	14.6	16.3
M4	S	-7.9	79.5	0.000	14.6	16.5
M6	RR	12.9	49.8	0.000	21.7	16.3
M6	S	15.4	33.2	0.000	21.7	16.5
RR	S	-0.7	70.3	0.479	16.3	16.5

Appendix 7.12. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the C18:2 quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	6.5	23.2	0.000	M4-965	S-1662	-0.6	12.4	0.549
HG-240	L-612	-1.3	4.9	0.249	M4-965	S-239	-8.2	7.9	0.000
HG-240	M2-246	-2.8	10.6	0.018	M4-965	S-252	-3.5	5.5	0.014
HG-240	M4-168	0.9	20.0	0.361	M4-965	S-596	-4.0	10.0	0.003
HG-240	M4-718	3.0	17.7	0.008	M4-965	S-605	-11.9	11.1	0.000
HG-240	M4-965	3.2	17.2	0.005	M4-965	S-621	-8.3	8.9	0.000
HG-240	M6-198	-8.9	20.9	0.000	M6-198	M6-818	1.3	11.9	0.234
HG-240	M6-818	-9.2	21.3	0.000	M6-198	RR-1034	12.1	11.6	0.000
HG-240	RR-1034	2.3	17.0	0.036	M6-198	RR-1255	5.8	9.0	0.000
HG-240	RR-1255	-0.4	10.4	0.720	M6-198	RR-245	10.0	15.1	0.000
HG-240	RR-245	-0.8	26.0	0.460	M6-198	RR-247	13.3	9.4	0.000
HG-240	RR-247	2.6	14.7	0.019	M6-198	RR-609	4.6	12.6	0.001
HG-240	RR-609	-3.1	16.1	0.007	M6-198	S-1044	10.5	10.9	0.000
HG-240	S-1044	-1.3	20.3	0.213	M6-198	S-1062	10.8	13.7	0.000
HG-240	S-1062	0.4	21.9	0.706	M6-198	S-1063	12.9	7.8	0.000
HG-240	S-1063	-0.3	16.3	0.789	M6-198	S-1662	15.5	9.9	0.000
HG-240	S-1662	2.8	19.2	0.010	M6-198	S-239	4.4	13.4	0.001
HG-240	S-239	-3.9	18.2	0.001	M6-198	S-252	7.2	9.6	0.000
HG-240	S-252	-0.7	12.2	0.527	M6-198	S-596	14.2	9.3	0.000
HG-240	S-596	1.4	18.3	0.165	M6-198	S-605	8.5	11.1	0.000
HG-240	S-605	-3.0	20.5	0.007	M6-198	S-621	7.5	13.7	0.000
HG-240	S-621	-2.6	21.9	0.016	M6-818	RR-1034	13.1	8.8	0.000
HH-248	L-612	-3.8	4.3	0.018	M6-818	RR-1255	5.5	7.3	0.001
HH-248	M2-246	-6.6	8.1	0.000	M6-818	RR-245	11.1	21.2	0.000
HH-248	M4-168	-7.8	13.5	0.000	M6-818	RR-247	15.1	6.6	0.000
HH-248	M4-718	-6.9	21.4	0.000	M6-818	RR-609	4.2	9.7	0.002
HH-248	M4-965	-6.6	20.8	0.000	M6-818	S-1044	12.4	13.7	0.000
HH-248	M6-198	-18.8	12.8	0.000	M6-818	S-1062	11.9	13.0	0.000
HH-248	M6-818	-23.1	18.9	0.000	M6-818	S-1063	17.3	9.0	0.000
HH-248	RR-1034	-4.3	9.2	0.002	M6-818	S-1662	19.8	12.8	0.000
HH-248	RR-1255	-4.6	7.3	0.002	M6-818	S-239	4.0	10.5	0.002
HH-248	RR-245	-9.7	29.0	0.000	M6-818	S-252	7.1	7.1	0.000
HH-248	RR-247	-4.6	7.0	0.003	M6-818	S-596	18.1	11.4	0.000
HH-248	RR-609	-9.1	9.9	0.000	M6-818	S-605	9.7	13.8	0.000
HH-248	S-1044	-12.2	20.8	0.000	M6-818	S-621	7.8	12.9	0.000
HH-248	S-1062	-7.6	14.7	0.000	RR-1034	RR-1255	-2.0	8.8	0.082
HH-248	S-1063	-13.1	18.9	0.000	RR-1034	RR-245	-3.6	11.2	0.004

HH-248	S-1662	-6.4	21.9	0.000	RR-1034	RR-247	0.2	8.0	0.845
HH-248	S-239	-10.9	10.8	0.000	RR-1034	RR-609	-5.2	11.7	0.000
HH-248	S-252	-6.3	7.1	0.000	RR-1034	S-1044	-4.5	7.9	0.002
HH-248	S-596	-8.9	19.6	0.000	RR-1034	S-1062	-2.2	10.8	0.047
HH-248	S-605	-14.6	20.5	0.000	RR-1034	S-1063	-3.7	5.6	0.012
HH-248	S-621	-11.6	14.6	0.000	RR-1034	S-1662	0.0	7.2	0.969
L-612	M2-246	-0.6	7.4	0.587	RR-1034	S-239	-6.3	12.0	0.000
L-612	M4-168	1.7	4.3	0.158	RR-1034	S-252	-2.7	9.1	0.024
L-612	M4-718	2.4	4.1	0.074	RR-1034	S-596	-1.6	6.7	0.162
L-612	M4-965	2.5	4.1	0.068	RR-1034	S-605	-6.4	8.1	0.000
L-612	M6-198	-2.4	4.7	0.065	RR-1034	S-621	-5.5	10.8	0.000
L-612	M6-818	-2.0	4.3	0.107	RR-1255	RR-245	-0.1	7.9	0.927
L-612	RR-1034	2.3	4.7	0.075	RR-1255	RR-247	2.2	7.8	0.064
L-612	RR-1255	1.0	6.5	0.356	RR-1255	RR-609	-2.0	11.3	0.073
L-612	RR-245	1.1	4.4	0.346	RR-1255	S-1044	-0.4	6.9	0.705
L-612	RR-247	2.4	4.4	0.069	RR-1255	S-1062	0.6	8.2	0.534
L-612	RR-609	-0.2	5.3	0.843	RR-1255	S-1063	0.3	6.2	0.802
L-612	S-1044	0.9	4.2	0.418	RR-1255	S-1662	2.2	6.7	0.068
L-612	S-1062	1.5	4.5	0.203	RR-1255	S-239	-2.5	10.3	0.032
L-612	S-1063	1.3	4.0	0.268	RR-1255	S-252	-0.1	10.4	0.889
L-612	S-1662	2.4	4.1	0.075	RR-1255	S-596	1.3	6.6	0.236
L-612	S-239	-0.5	5.0	0.660	RR-1255	S-605	-1.5	7.0	0.186
L-612	S-252	1.0	5.3	0.377	RR-1255	S-621	-1.4	8.3	0.209
L-612	S-596	1.9	4.1	0.133	RR-245	RR-247	4.2	8.9	0.002
L-612	S-605	0.3	4.2	0.792	RR-245	RR-609	-2.8	11.2	0.016
L-612	S-621	0.3	4.5	0.780	RR-245	S-1044	-0.6	21.9	0.525
M2-246	M4-168	3.5	8.2	0.008	RR-245	S-1062	1.4	17.5	0.182
M2-246	M4-718	4.6	7.3	0.002	RR-245	S-1063	0.9	17.8	0.382
M2-246	M4-965	4.7	7.3	0.002	RR-245	S-1662	5.1	21.8	0.000
M2-246	M6-198	-2.5	9.5	0.031	RR-245	S-239	-3.8	12.5	0.002
M2-246	M6-818	-2.0	8.0	0.077	RR-245	S-252	-0.1	8.1	0.929
M2-246	RR-1034	4.2	9.4	0.002	RR-245	S-596	3.2	20.0	0.004
M2-246	RR-1255	2.1	12.9	0.056	RR-245	S-605	-2.9	21.9	0.007
M2-246	RR-245	2.5	8.5	0.034	RR-245	S-621	-2.4	17.4	0.030
M2-246	RR-247	4.5	8.6	0.002	RR-247	RR-609	-5.7	9.9	0.000
M2-246	RR-609	0.6	11.6	0.568	RR-247	S-1044	-5.4	5.7	0.002
M2-246	S-1044	2.3	7.8	0.049	RR-247	S-1062	-2.7	8.5	0.026
M2-246	S-1062	3.1	8.8	0.012	RR-247	S-1063	-4.7	3.5	0.013
M2-246	S-1063	3.0	7.2	0.021	RR-247	S-1662	-0.2	5.0	0.828
M2-246	S-1662	4.5	7.6	0.002	RR-247	S-239	-6.9	10.0	0.000
M2-246	S-239	0.2	10.7	0.810	RR-247	S-252	-3.0	7.6	0.018

M2-246	S-252	2.2	11.0	0.048	RR-247	S-596	-2.1	4.6	0.093
M2-246	S-596	3.8	7.5	0.006	RR-247	S-605	-7.5	5.9	0.000
M2-246	S-605	1.4	7.8	0.195	RR-247	S-621	-6.3	8.6	0.000
M2-246	S-621	1.4	8.9	0.196	RR-609	S-1044	2.6	9.1	0.028
M4-168	M4-718	3.0	7.6	0.019	RR-609	S-1062	3.7	11.5	0.003
M4-168	M4-965	3.4	7.1	0.011	RR-609	S-1063	3.7	7.4	0.007
M4-168	M6-198	-12.2	11.6	0.000	RR-609	S-1662	6.1	8.5	0.000
M4-168	M6-818	-14.1	11.2	0.000	RR-609	S-239	-0.5	13.7	0.620
M4-168	RR-1034	1.8	8.9	0.102	RR-609	S-252	2.2	11.7	0.047
M4-168	RR-1255	-1.0	7.5	0.345	RR-609	S-596	5.0	8.2	0.001
M4-168	RR-245	-2.2	16.3	0.040	RR-609	S-605	1.2	9.2	0.272
M4-168	RR-247	2.3	6.7	0.057	RR-609	S-621	1.1	11.5	0.284
M4-168	RR-609	-4.4	10.0	0.001	S-1044	S-1062	2.2	12.0	0.051
M4-168	S-1044	-3.3	10.3	0.008	S-1044	S-1063	2.2	9.7	0.053
M4-168	S-1062	-0.6	12.0	0.528	S-1044	S-1662	7.2	13.6	0.000
M4-168	S-1063	-2.1	6.2	0.074	S-1044	S-239	-3.7	9.7	0.005
M4-168	S-1662	2.7	9.2	0.024	S-1044	S-252	0.3	6.5	0.770
M4-168	S-239	-5.5	10.7	0.000	S-1044	S-596	4.9	11.9	0.000
M4-168	S-252	-1.6	7.3	0.161	S-1044	S-605	-2.8	14.0	0.015
M4-168	S-596	0.6	8.2	0.543	S-1044	S-621	-2.1	11.9	0.061
M4-168	S-605	-5.7	10.5	0.000	S-1062	S-1063	-1.0	8.2	0.354
M4-168	S-621	-4.5	12.0	0.001	S-1062	S-1662	3.1	10.9	0.011
M4-718	M4-965	0.6	13.8	0.536	S-1062	S-239	-4.8	12.4	0.000
M4-718	M6-198	-16.2	8.8	0.000	S-1062	S-252	-1.1	8.5	0.320
M4-718	M6-818	-21.5	11.0	0.000	S-1062	S-596	1.3	10.0	0.223
M4-718	RR-1034	-0.1	6.3	0.936	S-1062	S-605	-4.3	12.2	0.001
M4-718	RR-1255	-2.2	6.4	0.066	S-1062	S-621	-3.6	14.0	0.003
M4-718	RR-245	-5.5	20.2	0.000	S-1063	S-1662	7.3	10.6	0.000
M4-718	RR-247	0.2	4.1	0.857	S-1063	S-239	-5.0	7.6	0.001
M4-718	RR-609	-6.3	7.9	0.000	S-1063	S-252	-0.6	5.3	0.570
M4-718	S-1044	-8.0	12.0	0.000	S-1063	S-596	4.3	8.2	0.002
M4-718	S-1062	-3.3	9.4	0.009	S-1063	S-605	-5.7	9.5	0.000
M4-718	S-1063	-9.0	12.4	0.000	S-1063	S-621	-3.9	8.1	0.005
M4-718	S-1662	-0.1	13.1	0.940	S-1662	S-239	-7.7	9.0	0.000
M4-718	S-239	-7.9	8.2	0.000	S-1662	S-252	-3.2	6.1	0.018
M4-718	S-252	-3.3	5.6	0.018	S-1662	S-596	-2.8	11.9	0.017
M4-718	S-596	-3.3	10.7	0.008	S-1662	S-605	-10.1	13.5	0.000
M4-718	S-605	-11.1	11.8	0.000	S-1662	S-621	-7.5	10.8	0.000
M4-718	S-621	-7.9	9.3	0.000	S-239	S-252	2.9	11.0	0.015
M4-965	M6-198	-16.7	8.4	0.000	S-239	S-596	6.4	8.6	0.000
M4-965	M6-818	-22.4	10.3	0.000	S-239	S-605	2.0	9.8	0.071

M4-965	RR-1034	-0.4	6.0	0.722	S-239	S-621	1.9	12.5	0.084
M4-965	RR-1255	-2.4	6.3	0.053	S-252	S-596	2.0	5.9	0.091
M4-965	RR-245	-6.0	19.5	0.000	S-252	S-605	-1.7	6.6	0.126
M4-965	RR-247	-0.1	3.9	0.892	S-252	S-621	-1.6	8.6	0.154
M4-965	RR-609	-6.5	7.7	0.000	S-596	S-605	-7.9	11.8	0.000
M4-965	S-1044	-8.7	11.2	0.000	S-596	S-621	-5.8	10.0	0.000
M4-965	S-1062	-3.7	8.9	0.005	S-605	S-621	0.1	12.1	0.942
M4-965	S-1063	-10.4	13.1	0.000					

Appendix 7.13. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the C18:3 quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean (mol %)	ID2 mean (mol %)
HG	HH	2.8	29.4	0.009	42.0	40.0
HG	L	1.1	4.8	0.317	42.0	39.9
HG	M2	14	12.8	0.000	42.0	28.2
HG	M4	1.1	22.5	0.270	42.0	41.3
HG	M6	16.7	21.8	0.000	42.0	32.1
HG	RR	18.8	28.9	0.000	42.0	30.0
HG	S	14.4	19.4	0.000	42.0	33.8
HH	L	0	4.6	0.967	40.0	39.9
HH	M2	12.5	11.4	0.000	40.0	28.2
HH	M4	-2.4	24.8	0.023	40.0	41.3
HH	M6	15.1	23.8	0.000	40.0	32.1
HH	RR	17.4	33.3	0.000	40.0	30.0
HH	S	12.4	20.9	0.000	40.0	33.8
L	M2	6.1	5.9	0.001	39.9	28.2
L	M4	-0.8	4.2	0.480	39.9	41.3
L	M6	4.4	4.2	0.010	39.9	32.1
L	RR	5.6	4.3	0.004	39.9	30.0
L	S	3.5	4.1	0.024	39.9	33.8
M2	M4	-15	8.5	0.000	28.2	41.3
M2	M6	-4.5	8.4	0.002	28.2	32.1
M2	RR	-2.1	9.6	0.066	28.2	30.0
M2	S	-6.6	7.8	0.000	28.2	33.8
M4	M6	24.8	35.2	0.000	41.3	32.1
M4	RR	25.7	60.9	0.000	41.3	30.0
M4	S	22.6	46.3	0.000	41.3	33.8
M6	RR	4.7	53.1	0.000	32.1	30.0
M6	S	-5.3	34.7	0.000	32.1	33.8
RR	S	-9.4	65.6	0.000	30.0	33.8

Appendix 7.14. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the C18:3 quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	2.8	29.4	0.009	M4-965	S-1662	22.1	14.0	0.000
HG-240	L-612	1.1	4.8	0.317	M4-965	S-239	6.5	7.8	0.000
HG-240	M2-246	14.0	12.8	0.000	M4-965	S-252	12.6	6.7	0.000
HG-240	M4-168	4.1	18.7	0.001	M4-965	S-596	10.8	6.7	0.000
HG-240	M4-718	-0.4	21.1	0.689	M4-965	S-605	22.9	13.3	0.000
HG-240	M4-965	0.6	19.7	0.556	M4-965	S-621	16.2	10.6	0.000
HG-240	M6-198	16.4	22.0	0.000	M6-198	M6-818	-2.3	13.7	0.040
HG-240	M6-818	15.3	21.5	0.000	M6-198	RR-1034	2.5	10.4	0.029
HG-240	RR-1034	17.2	17.8	0.000	M6-198	RR-1255	2.4	11.4	0.034
HG-240	RR-1255	16.6	18.7	0.000	M6-198	RR-245	2.3	20.6	0.035
HG-240	RR-245	17.6	27.6	0.000	M6-198	RR-247	-3.4	5.1	0.020
HG-240	RR-247	10.0	8.4	0.000	M6-198	RR-609	6.9	12.0	0.000
HG-240	RR-609	19.7	19.0	0.000	M6-198	S-1044	-3.0	11.7	0.011
HG-240	S-1044	11.0	18.4	0.000	M6-198	S-1062	-1.4	14.0	0.170
HG-240	S-1062	15.2	22.0	0.000	M6-198	S-1063	-3.5	13.9	0.004
HG-240	S-1063	13.2	21.9	0.000	M6-198	S-1662	-6.8	12.2	0.000
HG-240	S-1662	13.1	19.7	0.000	M6-198	S-239	-3.7	8.9	0.005
HG-240	S-239	6.1	11.6	0.000	M6-198	S-252	-3.7	8.6	0.006
HG-240	S-252	10.3	14.1	0.000	M6-198	S-596	-5.5	8.8	0.000
HG-240	S-596	8.9	14.4	0.000	M6-198	S-605	-3.4	13.6	0.005
HG-240	S-605	14.7	21.3	0.000	M6-198	S-621	-3.5	13.3	0.004
HG-240	S-621	12.2	21.2	0.000	M6-818	RR-1034	4.6	9.4	0.001
HH-248	L-612	0.0	4.6	0.967	M6-818	RR-1255	4.4	10.4	0.001
HH-248	M2-246	12.5	11.4	0.000	M6-818	RR-245	4.5	21.7	0.000
HH-248	M4-168	0.7	19.4	0.481	M6-818	RR-247	-1.9	4.6	0.118
HH-248	M4-718	-4.1	21.8	0.000	M6-818	RR-609	8.9	11.1	0.000
HH-248	M4-965	-3.1	20.7	0.005	M6-818	S-1044	-1.5	10.8	0.169
HH-248	M6-198	14.7	21.8	0.000	M6-818	S-1062	0.7	13.7	0.493
HH-248	M6-818	13.5	22.0	0.000	M6-818	S-1063	-1.6	13.3	0.143
HH-248	RR-1034	15.6	15.7	0.000	M6-818	S-1662	-4.7	13.1	0.000
HH-248	RR-1255	15.0	16.6	0.000	M6-818	S-239	-2.7	8.4	0.024
HH-248	RR-245	16.0	29.3	0.000	M6-818	S-252	-2.2	7.8	0.064
HH-248	RR-247	8.1	7.0	0.000	M6-818	S-596	-4.1	7.9	0.004
HH-248	RR-609	18.3	16.8	0.000	M6-818	S-605	-1.2	14.0	0.258
HH-248	S-1044	9.0	16.2	0.000	M6-818	S-621	-1.7	12.4	0.106
HH-248	S-1062	13.4	21.7	0.000	RR-1034	RR-1255	0.0	11.0	0.995
HH-248	S-1063	11.2	21.2	0.000	RR-1034	RR-245	-0.4	13.5	0.700

HH-248	S-1662	11.0	20.7	0.000	RR-1034	RR-247	-5.0	6.0	0.002
HH-248	S-239	4.5	10.4	0.001	RR-1034	RR-609	4.3	12.0	0.001
HH-248	S-252	8.3	12.0	0.000	RR-1034	S-1044	-4.8	11.9	0.000
HH-248	S-596	6.8	12.3	0.000	RR-1034	S-1062	-3.8	10.5	0.003
HH-248	S-605	12.7	21.9	0.000	RR-1034	S-1063	-5.6	11.0	0.000
HH-248	S-621	10.2	19.6	0.000	RR-1034	S-1662	-8.6	7.8	0.000
L-612	M2-246	6.1	5.9	0.001	RR-1034	S-239	-5.0	9.7	0.001
L-612	M4-168	0.2	4.1	0.880	RR-1034	S-252	-5.4	9.4	0.000
L-612	M4-718	-1.3	4.2	0.264	RR-1034	S-596	-7.1	9.5	0.000
L-612	M4-965	-1.0	4.1	0.390	RR-1034	S-605	-5.6	9.2	0.000
L-612	M6-198	4.7	4.3	0.008	RR-1034	S-621	-5.5	11.7	0.000
L-612	M6-818	4.1	4.2	0.013	RR-1255	RR-245	-0.4	14.3	0.709
L-612	RR-1034	5.4	4.5	0.004	RR-1255	RR-247	-4.9	6.6	0.002
L-612	RR-1255	5.4	4.6	0.004	RR-1255	RR-609	4.2	13.0	0.001
L-612	RR-245	5.3	4.4	0.004	RR-1255	S-1044	-4.6	12.9	0.000
L-612	RR-247	3.3	4.9	0.023	RR-1255	S-1062	-3.6	11.5	0.004
L-612	RR-609	7.0	4.8	0.001	RR-1255	S-1063	-5.3	12.0	0.000
L-612	S-1044	3.5	4.8	0.019	RR-1255	S-1662	-8.0	8.8	0.000
L-612	S-1062	4.3	4.3	0.011	RR-1255	S-239	-4.9	10.2	0.001
L-612	S-1063	3.7	4.4	0.018	RR-1255	S-252	-5.2	10.3	0.000
L-612	S-1662	3.1	4.1	0.033	RR-1255	S-596	-6.9	10.4	0.000
L-612	S-239	2.3	6.4	0.057	RR-1255	S-605	-5.3	10.1	0.000
L-612	S-252	3.2	4.8	0.024	RR-1255	S-621	-5.2	12.7	0.000
L-612	S-596	2.6	4.8	0.050	RR-245	RR-247	-4.9	5.8	0.003
L-612	S-605	3.9	4.2	0.016	RR-245	RR-609	4.9	14.6	0.000
L-612	S-621	3.6	4.5	0.019	RR-245	S-1044	-4.6	14.0	0.000
M2-246	M4-168	-13.4	7.9	0.000	RR-245	S-1062	-3.6	20.4	0.002
M2-246	M4-718	-16.0	8.6	0.000	RR-245	S-1063	-5.5	19.5	0.000
M2-246	M4-965	-15.6	8.1	0.000	RR-245	S-1662	-8.8	21.6	0.000
M2-246	M6-198	-3.8	9.4	0.004	RR-245	S-239	-4.8	9.5	0.001
M2-246	M6-818	-5.0	8.8	0.001	RR-245	S-252	-5.3	10.2	0.000
M2-246	RR-1034	-2.1	10.3	0.059	RR-245	S-596	-7.1	10.4	0.000
M2-246	RR-1255	-2.1	10.9	0.062	RR-245	S-605	-5.6	21.9	0.000
M2-246	RR-245	-2.4	10.2	0.036	RR-245	S-621	-5.4	17.4	0.000
M2-246	RR-247	-5.6	9.9	0.000	RR-247	RR-609	8.4	7.5	0.000
M2-246	RR-609	1.0	11.9	0.340	RR-247	S-1044	0.4	7.8	0.670
M2-246	S-1044	-5.4	12.2	0.000	RR-247	S-1062	2.3	5.1	0.067
M2-246	S-1062	-4.6	9.4	0.001	RR-247	S-1063	0.8	5.5	0.481
M2-246	S-1063	-5.7	9.8	0.000	RR-247	S-1662	-0.7	3.9	0.498
M2-246	S-1662	-7.2	8.1	0.000	RR-247	S-239	-1.3	10.0	0.233
M2-246	S-239	-5.7	13.8	0.000	RR-247	S-252	-0.1	7.2	0.929

M2-246	S-252	-5.8	11.5	0.000	RR-247	S-596	-1.5	7.1	0.166
M2-246	S-596	-7.0	11.4	0.000	RR-247	S-605	1.2	4.5	0.291
M2-246	S-605	-5.6	8.7	0.000	RR-247	S-621	0.5	6.3	0.642
M2-246	S-621	-5.7	10.6	0.000	RR-609	S-1044	-8.3	14.0	0.000
M4-168	M4-718	-7.3	11.8	0.000	RR-609	S-1062	-8.0	12.2	0.000
M4-168	M4-965	-6.3	12.0	0.000	RR-609	S-1063	-9.5	12.7	0.000
M4-168	M6-198	20.0	10.9	0.000	RR-609	S-1662	-12.4	9.5	0.000
M4-168	M6-818	19.2	11.6	0.000	RR-609	S-239	-7.5	11.1	0.000
M4-168	RR-1034	19.7	7.2	0.000	RR-609	S-252	-8.8	11.4	0.000
M4-168	RR-1255	18.4	8.2	0.000	RR-609	S-596	-10.4	11.5	0.000
M4-168	RR-245	20.9	19.9	0.000	RR-609	S-605	-9.8	10.8	0.000
M4-168	RR-247	9.0	3.7	0.001	RR-609	S-621	-9.2	13.5	0.000
M4-168	RR-609	21.8	9.0	0.000	S-1044	S-1062	1.9	11.9	0.080
M4-168	S-1044	10.3	8.8	0.000	S-1044	S-1063	0.3	12.4	0.798
M4-168	S-1062	18.0	10.9	0.000	S-1044	S-1662	-1.4	9.3	0.193
M4-168	S-1063	14.5	10.5	0.000	S-1044	S-239	-1.6	11.4	0.130
M4-168	S-1662	16.9	12.0	0.000	S-1044	S-252	-0.6	11.6	0.589
M4-168	S-239	4.5	7.7	0.002	S-1044	S-596	-2.1	11.7	0.061
M4-168	S-252	9.5	6.3	0.000	S-1044	S-605	0.7	10.6	0.500
M4-168	S-596	7.6	6.4	0.000	S-1044	S-621	0.0	13.3	0.998
M4-168	S-605	18.3	11.7	0.000	S-1062	S-1063	-2.1	13.9	0.056
M4-168	S-621	12.5	9.8	0.000	S-1062	S-1662	-5.0	12.1	0.000
M4-718	M4-965	1.6	13.5	0.129	S-1062	S-239	-3.0	8.9	0.014
M4-718	M6-198	23.8	13.4	0.000	S-1062	S-252	-2.6	8.8	0.031
M4-718	M6-818	23.2	13.9	0.000	S-1062	S-596	-4.4	8.9	0.002
M4-718	RR-1034	23.2	9.0	0.000	S-1062	S-605	-1.8	13.5	0.095
M4-718	RR-1255	21.9	9.9	0.000	S-1062	S-621	-2.2	13.4	0.044
M4-718	RR-245	24.5	21.9	0.000	S-1063	S-1662	-2.3	11.5	0.041
M4-718	RR-247	12.4	4.4	0.000	S-1063	S-239	-1.9	9.2	0.085
M4-718	RR-609	24.9	10.6	0.000	S-1063	S-252	-0.9	9.3	0.387
M4-718	S-1044	13.9	10.4	0.000	S-1063	S-596	-2.7	9.4	0.024
M4-718	S-1062	21.9	13.3	0.000	S-1063	S-605	0.5	13.1	0.593
M4-718	S-1063	18.6	12.9	0.000	S-1063	S-621	-0.3	13.7	0.769
M4-718	S-1662	21.4	13.5	0.000	S-1662	S-239	-1.0	7.8	0.361
M4-718	S-239	7.0	8.2	0.000	S-1662	S-252	0.7	6.7	0.526
M4-718	S-252	13.1	7.5	0.000	S-1662	S-596	-1.3	6.8	0.236
M4-718	S-596	11.3	7.6	0.000	S-1662	S-605	3.5	13.3	0.004
M4-718	S-605	22.5	14.0	0.000	S-1662	S-621	1.7	10.6	0.118
M4-718	S-621	16.5	11.9	0.000	S-239	S-252	1.2	10.9	0.246
M4-965	M6-198	24.1	12.2	0.000	S-239	S-596	0.1	10.8	0.885
M4-965	M6-818	23.7	13.1	0.000	S-239	S-605	2.3	8.3	0.053

M4-965	RR-1034	23.3	7.8	0.000	S-239	S-621	1.7	9.9	0.117
M4-965	RR-1255	21.8	8.8	0.000	S-252	S-596	-1.5	10.0	0.163
M4-965	RR-245	24.7	21.6	0.000	S-252	S-605	1.4	7.6	0.204
M4-965	RR-247	11.9	3.9	0.000	S-252	S-621	0.6	10.3	0.550
M4-965	RR-609	24.9	9.5	0.000	S-596	S-605	3.3	7.7	0.011
M4-965	S-1044	13.4	9.3	0.000	S-596	S-621	2.3	10.4	0.043
M4-965	S-1062	22.1	12.0	0.000	S-605	S-621	-0.8	12.1	0.424
M4-965	S-1063	18.5	11.5	0.000					

Appendix 7.15. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the C20:1 quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean (mol %)	ID2 mean (mol %)
HG	HH	-16.9	29.5	0.000	15.3	19.5
HG	L	4.4	7	0.003	15.3	13.7
HG	M2	-1.8	8.4	0.100	15.3	16.5
HG	M4	12.4	25.9	0.000	15.3	12.7
HG	M6	6.2	25.4	0.000	15.3	14.0
HG	RR	-26.7	47.1	0.000	15.3	22.6
HG	S	-1.2	43.5	0.239	15.3	15.6
HH	L	16.3	6.3	0.000	19.5	13.7
HH	M2	4.9	8.1	0.001	19.5	16.5
HH	M4	34.5	28.5	0.000	19.5	12.7
HH	M6	27.6	27.3	0.000	19.5	14.0
HH	RR	-12.2	51.3	0.000	19.5	22.6
HH	S	16.5	51.3	0.000	19.5	15.6
L	M2	-4.1	10.1	0.002	13.7	16.5
L	M4	3.2	5.1	0.024	13.7	12.7
L	M6	-0.8	5.2	0.471	13.7	14.0
L	RR	-23.9	7.8	0.000	13.7	22.6
L	S	-5.4	6.6	0.001	13.7	15.6
M2	M4	6.4	7.5	0.000	16.5	12.7
M2	M6	4.1	7.6	0.004	16.5	14.0
M2	RR	-9.9	8.7	0.000	16.5	22.6
M2	S	1.4	8.2	0.205	16.5	15.6
M4	M6	-8.1	34.7	0.000	12.7	14.0
M4	RR	-43.1	58.3	0.000	12.7	22.6
M4	S	-14.7	85.3	0.000	12.7	15.6
M6	RR	-37.1	54.9	0.000	14.0	22.6
M6	S	-8.1	72.1	0.000	14.0	15.6
RR	S	26.7	89	0.000	22.6	15.6

Appendix 7.16. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the C20:1 quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	-16.9	29.5	0.000	M4-965	S-1662	-12.8	9.9	0.000
HG-240	L-612	4.4	7.0	0.003	M4-965	S-239	-3.1	10.0	0.010
HG-240	M2-246	-1.8	8.4	0.100	M4-965	S-252	-4.4	5.3	0.006
HG-240	M4-168	10.1	19.9	0.000	M4-965	S-596	-11.8	6.1	0.000
HG-240	M4-718	11.5	18.9	0.000	M4-965	S-605	-8.0	10.8	0.000
HG-240	M4-965	12.4	22.0	0.000	M4-965	S-621	-9.5	10.7	0.000
HG-240	M6-198	5.0	18.8	0.000	M6-198	M6-818	0.4	13.3	0.717
HG-240	M6-818	5.9	21.4	0.000	M6-198	RR-1034	-43.7	11.4	0.000
HG-240	RR-1034	-38.5	19.6	0.000	M6-198	RR-1255	-10.4	6.7	0.000
HG-240	RR-1255	-8.8	6.6	0.000	M6-198	RR-245	-32.3	18.5	0.000
HG-240	RR-245	-27.6	30.0	0.000	M6-198	RR-247	-17.6	4.4	0.000
HG-240	RR-247	-14.6	4.4	0.000	M6-198	RR-609	-15.2	8.7	0.000
HG-240	RR-609	-12.9	8.7	0.000	M6-198	S-1044	-4.0	11.1	0.002
HG-240	S-1044	-0.6	11.5	0.570	M6-198	S-1062	-7.3	10.8	0.000
HG-240	S-1062	-4.0	11.1	0.002	M6-198	S-1063	-8.6	13.6	0.000
HG-240	S-1063	-3.3	20.9	0.003	M6-198	S-1662	-7.1	12.6	0.000
HG-240	S-1662	-3.1	13.8	0.008	M6-198	S-239	1.7	12.8	0.116
HG-240	S-239	5.8	14.1	0.000	M6-198	S-252	-2.3	5.8	0.062
HG-240	S-252	-0.5	5.7	0.666	M6-198	S-596	-7.7	7.5	0.000
HG-240	S-596	-4.6	7.5	0.002	M6-198	S-605	-2.2	13.5	0.050
HG-240	S-605	2.3	16.0	0.036	M6-198	S-621	-3.5	13.4	0.004
HG-240	S-621	0.9	15.7	0.389	M6-818	RR-1034	-51.2	12.0	0.000
HH-248	L-612	16.3	6.3	0.000	M6-818	RR-1255	-10.6	6.4	0.000
HH-248	M2-246	4.9	8.1	0.001	M6-818	RR-245	-36.3	21.3	0.000
HH-248	M4-168	32.9	19.9	0.000	M6-818	RR-247	-18.4	3.9	0.000
HH-248	M4-718	29.1	17.0	0.000	M6-818	RR-609	-15.6	8.1	0.000
HH-248	M4-965	33.9	21.7	0.000	M6-818	S-1044	-4.4	9.7	0.001
HH-248	M6-198	22.0	16.9	0.000	M6-818	S-1062	-7.8	9.5	0.000
HH-248	M6-818	25.2	20.1	0.000	M6-818	S-1063	-10.1	13.9	0.000
HH-248	RR-1034	-21.6	18.5	0.000	M6-818	S-1662	-7.9	11.0	0.000
HH-248	RR-1255	-3.8	6.5	0.008	M6-818	S-239	1.5	11.2	0.159
HH-248	RR-245	-12.2	29.6	0.000	M6-818	S-252	-2.5	5.5	0.053
HH-248	RR-247	-5.2	4.1	0.006	M6-818	S-596	-8.2	6.6	0.000
HH-248	RR-609	-5.5	8.3	0.000	M6-818	S-605	-2.7	12.1	0.020
HH-248	S-1044	10.6	10.4	0.000	M6-818	S-621	-4.1	12.0	0.001
HH-248	S-1062	6.8	10.2	0.000	RR-1034	RR-1255	1.6	6.3	0.160
HH-248	S-1063	14.7	19.3	0.000	RR-1034	RR-245	6.6	19.5	0.000

HH-248	S-1662	10.1	12.3	0.000	RR-1034	RR-247	5.3	3.6	0.008
HH-248	S-239	19.6	12.6	0.000	RR-1034	RR-609	2.4	7.8	0.042
HH-248	S-252	5.5	5.6	0.002	RR-1034	S-1044	23.5	8.9	0.000
HH-248	S-596	5.4	6.9	0.001	RR-1034	S-1062	19.0	8.7	0.000
HH-248	S-605	17.3	14.2	0.000	RR-1034	S-1063	38.4	11.9	0.000
HH-248	S-621	15.6	14.0	0.000	RR-1034	S-1662	25.6	9.7	0.000
L-612	M2-246	-4.1	10.1	0.002	RR-1034	S-239	36.1	9.9	0.000
L-612	M4-168	1.5	4.8	0.190	RR-1034	S-252	11.9	5.3	0.000
L-612	M4-718	3.8	6.8	0.007	RR-1034	S-596	16.7	6.1	0.000
L-612	M4-965	3.4	5.3	0.018	RR-1034	S-605	35.6	10.5	0.000
L-612	M6-198	-0.8	6.9	0.433	RR-1034	S-621	33.6	10.4	0.000
L-612	M6-818	-0.6	5.8	0.558	RR-1255	RR-245	0.2	6.6	0.865
L-612	RR-1034	-30.1	5.3	0.000	RR-1255	RR-247	1.0	8.3	0.351
L-612	RR-1255	-10.3	7.7	0.000	RR-1255	RR-609	0.0	10.6	0.977
L-612	RR-245	-24.1	6.9	0.000	RR-1255	S-1044	8.1	8.0	0.000
L-612	RR-247	-15.8	6.1	0.000	RR-1255	S-1062	6.5	8.2	0.000
L-612	RR-609	-14.3	10.5	0.000	RR-1255	S-1063	7.9	6.5	0.000
L-612	S-1044	-4.0	10.5	0.002	RR-1255	S-1662	7.4	7.3	0.000
L-612	S-1062	-6.8	10.6	0.000	RR-1255	S-239	10.8	7.3	0.000
L-612	S-1063	-6.9	6.1	0.000	RR-1255	S-252	6.6	10.9	0.000
L-612	S-1662	-6.4	9.1	0.000	RR-1255	S-596	6.0	8.4	0.000
L-612	S-239	0.6	9.0	0.577	RR-1255	S-605	9.5	7.0	0.000
L-612	S-252	-2.6	7.0	0.037	RR-1255	S-621	9.0	7.0	0.000
L-612	S-596	-7.2	9.0	0.000	RR-245	RR-247	1.7	4.4	0.158
L-612	S-605	-2.4	8.0	0.041	RR-245	RR-609	-0.2	8.7	0.840
L-612	S-621	-3.5	8.2	0.008	RR-245	S-1044	18.2	11.3	0.000
M2-246	M4-168	5.4	7.4	0.001	RR-245	S-1062	14.2	11.0	0.000
M2-246	M4-718	6.7	8.4	0.000	RR-245	S-1063	26.2	20.7	0.000
M2-246	M4-965	6.5	7.6	0.000	RR-245	S-1662	18.9	13.6	0.000
M2-246	M6-198	4.0	8.4	0.004	RR-245	S-239	28.3	13.9	0.000
M2-246	M6-818	4.2	7.9	0.003	RR-245	S-252	9.7	5.7	0.000
M2-246	RR-1034	-12.3	7.6	0.000	RR-245	S-596	12.4	7.5	0.000
M2-246	RR-1255	-6.1	11.4	0.000	RR-245	S-605	26.8	15.7	0.000
M2-246	RR-245	-9.7	8.3	0.000	RR-245	S-621	25.1	15.5	0.000
M2-246	RR-247	-7.4	10.0	0.000	RR-247	RR-609	-1.3	9.9	0.225
M2-246	RR-609	-7.7	13.9	0.000	RR-247	S-1044	11.9	7.2	0.000
M2-246	S-1044	1.4	11.0	0.201	RR-247	S-1062	9.2	7.5	0.000
M2-246	S-1062	-0.6	11.3	0.548	RR-247	S-1063	13.1	4.0	0.000
M2-246	S-1063	0.5	8.0	0.600	RR-247	S-1662	11.3	5.8	0.000
M2-246	S-1662	0.2	9.8	0.845	RR-247	S-239	17.4	5.7	0.000
M2-246	S-239	4.6	9.6	0.001	RR-247	S-252	7.7	7.5	0.000

M2-246	S-252	0.9	10.9	0.381	RR-247	S-596	8.1	7.3	0.000
M2-246	S-596	-1.1	11.2	0.278	RR-247	S-605	15.5	5.1	0.000
M2-246	S-605	2.9	9.0	0.019	RR-247	S-621	14.5	5.2	0.000
M2-246	S-621	2.2	9.1	0.054	RR-609	S-1044	11.2	11.8	0.000
M4-168	M4-718	4.3	10.4	0.001	RR-609	S-1062	8.9	12.0	0.000
M4-168	M4-965	4.0	12.0	0.002	RR-609	S-1063	11.6	8.2	0.000
M4-168	M6-198	-3.8	10.4	0.003	RR-609	S-1662	10.5	10.3	0.000
M4-168	M6-818	-4.0	11.5	0.002	RR-609	S-239	15.4	10.2	0.000
M4-168	RR-1034	-66.8	9.6	0.000	RR-609	S-252	8.0	10.2	0.000
M4-168	RR-1255	-11.6	6.2	0.000	RR-609	S-596	8.1	11.7	0.000
M4-168	RR-245	-44.6	20.0	0.000	RR-609	S-605	13.7	9.5	0.000
M4-168	RR-247	-20.8	3.4	0.000	RR-609	S-621	12.9	9.6	0.000
M4-168	RR-609	-17.3	7.5	0.000	S-1044	S-1062	-2.8	14.0	0.014
M4-168	S-1044	-6.7	8.2	0.000	S-1044	S-1063	-1.6	10.0	0.142
M4-168	S-1062	-10.2	8.1	0.000	S-1044	S-1662	-1.9	13.4	0.086
M4-168	S-1063	-15.5	11.2	0.000	S-1044	S-239	4.9	13.2	0.000
M4-168	S-1662	-11.0	8.9	0.000	S-1044	S-252	-0.1	7.4	0.900
M4-168	S-239	-1.0	8.9	0.363	S-1044	S-596	-3.4	11.0	0.006
M4-168	S-252	-3.5	5.2	0.015	S-1044	S-605	2.2	12.4	0.046
M4-168	S-596	-10.4	5.7	0.000	S-1044	S-621	1.2	12.5	0.254
M4-168	S-605	-5.8	9.5	0.000	S-1062	S-1063	2.0	9.8	0.076
M4-168	S-621	-7.3	9.4	0.000	S-1062	S-1662	1.3	13.1	0.228
M4-718	M4-965	-1.2	12.2	0.258	S-1062	S-239	7.9	13.0	0.000
M4-718	M6-198	-6.5	14.0	0.000	S-1062	S-252	1.6	7.6	0.144
M4-718	M6-818	-6.8	13.4	0.000	S-1062	S-596	-0.7	11.3	0.481
M4-718	RR-1034	-51.7	11.5	0.000	S-1062	S-605	5.4	12.1	0.000
M4-718	RR-1255	-12.4	6.6	0.000	S-1062	S-621	4.4	12.2	0.001
M4-718	RR-245	-39.0	18.7	0.000	S-1063	S-1662	-0.7	11.4	0.525
M4-718	RR-247	-21.5	4.4	0.000	S-1063	S-239	8.7	11.6	0.000
M4-718	RR-609	-18.2	8.7	0.000	S-1063	S-252	0.7	5.6	0.513
M4-718	S-1044	-8.5	11.0	0.000	S-1063	S-596	-2.8	6.8	0.029
M4-718	S-1062	-11.6	10.7	0.000	S-1063	S-605	5.3	12.5	0.000
M4-718	S-1063	-15.6	13.7	0.000	S-1063	S-621	3.8	12.4	0.002
M4-718	S-1662	-12.4	12.5	0.000	S-1662	S-239	7.7	14.0	0.000
M4-718	S-239	-3.7	12.7	0.003	S-1662	S-252	0.9	6.5	0.378
M4-718	S-252	-4.7	5.8	0.004	S-1662	S-596	-2.0	9.6	0.074
M4-718	S-596	-11.8	7.4	0.000	S-1662	S-605	4.8	13.7	0.000
M4-718	S-605	-8.0	13.5	0.000	S-1662	S-621	3.6	13.7	0.003
M4-718	S-621	-9.3	13.4	0.000	S-239	S-252	-3.0	6.5	0.023
M4-965	M6-198	-6.4	12.1	0.000	S-239	S-596	-8.3	9.4	0.000
M4-965	M6-818	-7.0	13.5	0.000	S-239	S-605	-3.4	13.8	0.004

M4-965	RR-1034	-64.3	11.6	0.000	S-239	S-621	-4.6	13.8	0.000
M4-965	RR-1255	-12.3	6.3	0.000	S-252	S-596	-2.1	7.8	0.072
M4-965	RR-245	-45.0	22.0	0.000	S-252	S-605	1.4	6.1	0.216
M4-965	RR-247	-22.1	3.6	0.000	S-252	S-621	0.8	6.2	0.448
M4-965	RR-609	-18.3	7.8	0.000	S-596	S-605	5.9	8.5	0.000
M4-965	S-1044	-8.4	8.9	0.000	S-596	S-621	5.0	8.6	0.001
M4-965	S-1062	-11.7	8.8	0.000	S-605	S-621	-1.3	14.0	0.230
M4-965	S-1063	-17.6	13.2	0.000					

Appendix 7.17. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the C22:1 quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean (mol %)	ID2 mean (mol %)
HG	HH	-1	27.3	0.312	1.7	1.8
HG	L	9.9	16.3	0.000	1.7	0.9
HG	M2	-46.9	8.9	0.000	1.7	11.0
HG	M4	-41.5	34.2	0.000	1.7	5.6
HG	M6	-18.9	29.4	0.000	1.7	3.7
HG	RR	-19.1	44.7	0.000	1.7	3.6
HG	S	-23.1	82	0.000	1.7	5.3
HH	L	13	11.6	0.000	1.8	0.9
HH	M2	-47.9	8	0.000	1.8	11.0
HH	M4	-47	35.7	0.000	1.8	5.6
HH	M6	-20.3	25.2	0.000	1.8	3.7
HH	RR	-20.7	54	0.000	1.8	3.6
HH	S	-23.6	79.1	0.000	1.8	5.3
L	M2	-52.5	8.1	0.000	0.9	11.0
L	M4	-56.9	17.2	0.000	0.9	5.6
L	M6	-29.7	17.9	0.000	0.9	3.7
L	RR	-30.9	23	0.000	0.9	3.6
L	S	-29.7	65.4	0.000	0.9	5.3
M2	M4	27.6	8.7	0.000	11.0	5.6
M2	M6	36.3	9.6	0.000	11.0	3.7
M2	RR	37.5	9.1	0.000	11.0	3.6
M2	S	24.4	16.7	0.000	11.0	5.3
M4	M6	18.8	31.5	0.000	5.6	3.7
M4	RR	21.3	57.8	0.000	5.6	3.6
M4	S	1.7	85.8	0.097	5.6	5.3
M6	RR	1	38.9	0.304	3.7	3.6
M6	S	-10.2	80.4	0.000	3.7	5.3
RR	S	-11.2	94.4	0.000	3.6	5.3

Appendix 7.18. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the C22:1 quantitative trait. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	-1.0	27.3	0.312	M4-965	S-1662	2.1	13.9	0.053
HG-240	L-612	9.9	16.3	0.000	M4-965	S-239	7.7	7.6	0.000
HG-240	M2-246	-46.9	8.9	0.000	M4-965	S-252	0.5	5.2	0.657
HG-240	M4-168	-48.3	17.6	0.000	M4-965	S-596	-0.8	6.3	0.464
HG-240	M4-718	-40.5	20.7	0.000	M4-965	S-605	-1.2	7.5	0.259
HG-240	M4-965	-40.6	19.9	0.000	M4-965	S-621	-4.2	9.3	0.002
HG-240	M6-198	-20.1	21.8	0.000	M6-198	M6-818	-5.5	12.3	0.000
HG-240	M6-818	-21.7	17.4	0.000	M6-198	RR-1034	-3.8	8.6	0.005
HG-240	RR-1034	-19.3	12.0	0.000	M6-198	RR-1255	-0.3	7.3	0.758
HG-240	RR-1255	-10.3	8.3	0.000	M6-198	RR-245	2.8	15.4	0.013
HG-240	RR-245	-19.4	24.4	0.000	M6-198	RR-247	0.1	3.3	0.953
HG-240	RR-247	-6.6	3.5	0.004	M6-198	RR-609	-9.8	13.7	0.000
HG-240	RR-609	-27.5	20.6	0.000	M6-198	S-1044	-5.5	7.4	0.001
HG-240	S-1044	-10.8	7.7	0.000	M6-198	S-1062	-12.6	7.8	0.000
HG-240	S-1062	-19.8	8.3	0.000	M6-198	S-1063	-22.1	13.9	0.000
HG-240	S-1063	-38.6	21.3	0.000	M6-198	S-1662	-24.4	13.8	0.000
HG-240	S-1662	-40.5	21.0	0.000	M6-198	S-239	1.3	7.4	0.243
HG-240	S-239	-4.0	7.6	0.004	M6-198	S-252	-4.0	5.1	0.009
HG-240	S-252	-7.7	5.2	0.000	M6-198	S-596	-12.2	5.9	0.000
HG-240	S-596	-21.0	6.6	0.000	M6-198	S-605	-7.1	7.3	0.000
HG-240	S-605	-11.8	7.5	0.000	M6-198	S-621	-17.0	8.5	0.000
HG-240	S-621	-26.5	9.8	0.000	M6-818	RR-1034	1.2	11.2	0.267
HH-248	L-612	13.0	11.6	0.000	M6-818	RR-1255	2.6	8.7	0.031
HH-248	M2-246	-47.9	8.0	0.000	M6-818	RR-245	8.0	11.0	0.000
HH-248	M4-168	-55.8	13.0	0.000	M6-818	RR-247	2.0	3.6	0.123
HH-248	M4-718	-46.3	16.3	0.000	M6-818	RR-609	-2.8	13.3	0.014
HH-248	M4-965	-45.9	15.3	0.000	M6-818	S-1044	-3.8	7.8	0.005
HH-248	M6-198	-22.8	18.4	0.000	M6-818	S-1062	-10.1	8.6	0.000
HH-248	M6-818	-23.5	13.0	0.000	M6-818	S-1063	-12.5	12.8	0.000
HH-248	RR-1034	-20.6	8.7	0.000	M6-818	S-1662	-14.5	13.0	0.000
HH-248	RR-1255	-10.2	7.2	0.000	M6-818	S-239	2.8	7.8	0.024
HH-248	RR-245	-22.7	28.9	0.000	M6-818	S-252	-2.9	5.3	0.031
HH-248	RR-247	-6.4	3.2	0.006	M6-818	S-596	-9.0	6.9	0.000
HH-248	RR-609	-31.0	16.1	0.000	M6-818	S-605	-5.6	7.7	0.001
HH-248	S-1044	-10.6	7.3	0.000	M6-818	S-621	-13.1	10.2	0.000
HH-248	S-1062	-19.8	7.7	0.000	RR-1034	RR-1255	1.8	9.0	0.108
HH-248	S-1063	-44.5	17.2	0.000	RR-1034	RR-245	6.0	7.4	0.000

HH-248	S-1662	-46.5	16.8	0.000	RR-1034	RR-247	1.5	3.7	0.218
HH-248	S-239	-3.8	7.3	0.006	RR-1034	RR-609	-4.0	9.7	0.003
HH-248	S-252	-7.6	5.1	0.001	RR-1034	S-1044	-4.2	8.0	0.003
HH-248	S-596	-21.2	5.8	0.000	RR-1034	S-1062	-10.6	8.9	0.000
HH-248	S-605	-11.7	7.3	0.000	RR-1034	S-1063	-13.0	9.1	0.000
HH-248	S-621	-27.1	8.4	0.000	RR-1034	S-1662	-14.9	9.3	0.000
L-612	M2-246	-52.5	8.1	0.000	RR-1034	S-239	2.4	8.0	0.045
L-612	M4-168	-66.1	9.0	0.000	RR-1034	S-252	-3.2	5.3	0.022
L-612	M4-718	-56.6	10.7	0.000	RR-1034	S-596	-9.5	7.2	0.000
L-612	M4-965	-55.9	10.9	0.000	RR-1034	S-605	-5.9	7.8	0.000
L-612	M6-198	-34.7	10.0	0.000	RR-1034	S-621	-13.6	10.4	0.000
L-612	M6-818	-33.0	10.9	0.000	RR-1255	RR-245	1.5	6.8	0.189
L-612	RR-1034	-29.6	8.2	0.000	RR-1255	RR-247	0.2	5.5	0.823
L-612	RR-1255	-15.8	7.3	0.000	RR-1255	RR-609	-4.3	7.8	0.003
L-612	RR-245	-35.8	9.1	0.000	RR-1255	S-1044	-4.8	10.2	0.001
L-612	RR-247	-10.1	3.3	0.001	RR-1255	S-1062	-10.4	12.2	0.000
L-612	RR-609	-41.7	10.8	0.000	RR-1255	S-1063	-9.8	7.5	0.000
L-612	S-1044	-13.5	7.4	0.000	RR-1255	S-1662	-11.0	7.6	0.000
L-612	S-1062	-23.8	7.8	0.000	RR-1255	S-239	1.3	10.1	0.222
L-612	S-1063	-55.2	10.4	0.000	RR-1255	S-252	-3.7	6.2	0.009
L-612	S-1662	-57.0	10.6	0.000	RR-1255	S-596	-9.2	10.6	0.000
L-612	S-239	-6.7	7.4	0.000	RR-1255	S-605	-6.4	9.6	0.000
L-612	S-252	-9.6	5.1	0.000	RR-1255	S-621	-12.3	12.9	0.000
L-612	S-596	-26.2	5.9	0.000	RR-245	RR-247	-0.7	3.2	0.548
L-612	S-605	-14.3	7.3	0.000	RR-245	RR-609	-13.3	13.4	0.000
L-612	S-621	-32.6	8.5	0.000	RR-245	S-1044	-6.1	7.2	0.000
M2-246	M4-168	25.9	8.2	0.000	RR-245	S-1062	-13.6	7.5	0.000
M2-246	M4-718	28.9	8.4	0.000	RR-245	S-1063	-27.1	14.4	0.000
M2-246	M4-965	28.0	8.6	0.000	RR-245	S-1662	-29.5	14.0	0.000
M2-246	M6-198	39.3	8.1	0.000	RR-245	S-239	0.7	7.2	0.506
M2-246	M6-818	35.2	9.3	0.000	RR-245	S-252	-4.5	5.1	0.006
M2-246	RR-1034	35.4	9.6	0.000	RR-245	S-596	-13.4	5.5	0.000
M2-246	RR-1255	31.0	12.9	0.000	RR-245	S-605	-7.6	7.2	0.000
M2-246	RR-245	40.8	7.7	0.000	RR-245	S-621	-18.5	8.0	0.000
M2-246	RR-247	24.6	6.5	0.000	RR-247	RR-609	-3.1	3.4	0.045
M2-246	RR-609	34.8	8.4	0.000	RR-247	S-1044	-4.4	9.7	0.001
M2-246	S-1044	16.0	11.4	0.000	RR-247	S-1062	-8.7	7.7	0.000
M2-246	S-1062	16.3	13.6	0.000	RR-247	S-1063	-6.7	3.3	0.005
M2-246	S-1063	30.4	8.2	0.000	RR-247	S-1662	-7.5	3.3	0.003
M2-246	S-1662	29.3	8.3	0.000	RR-247	S-239	1.0	9.7	0.354
M2-246	S-239	21.7	11.3	0.000	RR-247	S-252	-3.6	7.3	0.008

M2-246	S-252	11.6	6.7	0.000	RR-247	S-596	-7.4	5.9	0.000
M2-246	S-596	21.1	11.9	0.000	RR-247	S-605	-5.9	10.0	0.000
M2-246	S-605	12.8	10.6	0.000	RR-247	S-621	-9.6	5.5	0.000
M2-246	S-621	19.9	13.5	0.000	RR-609	S-1044	-3.0	7.5	0.018
M4-168	M4-718	7.4	11.8	0.000	RR-609	S-1062	-9.1	8.0	0.000
M4-168	M4-965	5.6	12.0	0.000	RR-609	S-1063	-11.0	13.9	0.000
M4-168	M6-198	33.3	11.2	0.000	RR-609	S-1662	-13.3	14.0	0.000
M4-168	M6-818	21.6	11.8	0.000	RR-609	S-239	3.7	7.5	0.007
M4-168	RR-1034	21.6	8.8	0.000	RR-609	S-252	-2.3	5.2	0.065
M4-168	RR-1255	15.0	7.5	0.000	RR-609	S-596	-7.8	6.2	0.000
M4-168	RR-245	39.5	10.5	0.000	RR-609	S-605	-4.8	7.4	0.002
M4-168	RR-247	10.1	3.3	0.001	RR-609	S-621	-12.0	9.1	0.000
M4-168	RR-609	21.5	11.9	0.000	S-1044	S-1062	-3.0	12.6	0.012
M4-168	S-1044	2.5	7.5	0.037	S-1044	S-1063	0.2	7.4	0.847
M4-168	S-1062	-1.4	7.9	0.192	S-1044	S-1662	-0.5	7.5	0.658
M4-168	S-1063	11.0	11.6	0.000	S-1044	S-239	4.8	14.0	0.000
M4-168	S-1662	8.2	11.7	0.000	S-1044	S-252	-0.2	9.3	0.844
M4-168	S-239	9.2	7.4	0.000	S-1044	S-596	-1.3	10.6	0.215
M4-168	S-252	1.5	5.2	0.189	S-1044	S-605	-1.6	13.8	0.127
M4-168	S-596	1.8	6.0	0.117	S-1044	S-621	-2.9	10.2	0.014
M4-168	S-605	0.1	7.4	0.907	S-1062	S-1063	5.2	7.9	0.001
M4-168	S-621	-1.3	8.8	0.216	S-1062	S-1662	4.3	7.9	0.003
M4-718	M4-965	-1.5	13.9	0.157	S-1062	S-239	8.5	12.5	0.000
M4-718	M6-198	24.7	13.7	0.000	S-1062	S-252	2.0	7.4	0.082
M4-718	M6-818	14.9	13.2	0.000	S-1062	S-596	2.3	11.9	0.037
M4-718	RR-1034	15.3	9.6	0.000	S-1062	S-605	0.9	11.8	0.391
M4-718	RR-1255	11.3	7.7	0.000	S-1062	S-621	0.4	12.5	0.699
M4-718	RR-245	29.6	13.6	0.000	S-1063	S-1662	-2.6	14.0	0.020
M4-718	RR-247	7.7	3.4	0.003	S-1063	S-239	6.5	7.4	0.000
M4-718	RR-609	13.7	14.0	0.000	S-1063	S-252	-0.4	5.1	0.718
M4-718	S-1044	0.6	7.5	0.552	S-1063	S-596	-2.9	6.0	0.026
M4-718	S-1062	-4.1	8.0	0.004	S-1063	S-605	-2.3	7.4	0.051
M4-718	S-1063	3.2	13.9	0.006	S-1063	S-621	-6.6	8.8	0.000
M4-718	S-1662	0.6	14.0	0.542	S-1662	S-239	7.1	7.5	0.000
M4-718	S-239	7.3	7.5	0.000	S-1662	S-252	0.1	5.2	0.943
M4-718	S-252	0.2	5.2	0.858	S-1662	S-596	-1.8	6.1	0.125
M4-718	S-596	-1.5	6.2	0.185	S-1662	S-605	-1.7	7.4	0.124
M4-718	S-605	-1.6	7.4	0.154	S-1662	S-621	-5.3	8.9	0.000
M4-718	S-621	-5.0	9.0	0.001	S-239	S-252	-4.1	9.4	0.003
M4-965	M6-198	25.2	13.4	0.000	S-239	S-596	-7.2	10.5	0.000
M4-965	M6-818	15.8	13.6	0.000	S-239	S-605	-6.2	13.9	0.000

M4-965	RR-1034	16.1	10.1	0.000	S-239	S-621	-9.0	10.2	0.000
M4-965	RR-1255	11.9	8.0	0.000	S-252	S-596	-0.7	6.4	0.485
M4-965	RR-245	29.9	12.7	0.000	S-252	S-605	-1.1	10.1	0.283
M4-965	RR-247	8.2	3.4	0.002	S-252	S-621	-1.9	6.2	0.105
M4-965	RR-609	14.7	14.0	0.000	S-596	S-605	-0.7	10.0	0.475
M4-965	S-1044	1.0	7.6	0.336	S-596	S-621	-2.4	11.1	0.037
M4-965	S-1062	-3.5	8.1	0.008	S-605	S-621	-0.7	9.6	0.510
M4-965	S-1063	4.6	13.8	0.000					

Appendix 7.19. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the PUFA fatty acid ratio calculation. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean	ID2 mean
HG	HH	15.7	29.2	0.000	1.62	1.30
HG	L	0.3	6.0	0.757	1.62	1.61
HG	M2	26.5	20.7	0.000	1.62	1.07
HG	M4	5.6	31.1	0.000	1.62	1.51
HG	M6	17.4	22.0	0.000	1.62	1.32
HG	RR	33.1	23.6	0.000	1.62	1.04
HG	S	22.5	36.1	0.000	1.62	1.18
HH	L	-8.9	5.4	0.000	1.30	1.61
HH	M2	12.1	18.6	0.000	1.30	1.07
HH	M4	-11.6	34.2	0.000	1.30	1.51
HH	M6	-1.2	24.3	0.252	1.30	1.32
HH	RR	16.9	27.1	0.000	1.30	1.04
HH	S	6.9	44.5	0.000	1.30	1.18
L	M2	15.5	5.5	0.000	1.61	1.07
L	M4	2.9	5.3	0.032	1.61	1.51
L	M6	8.8	4.5	0.001	1.61	1.32
L	RR	17.3	4.5	0.000	1.61	1.04
L	S	12.7	5.2	0.000	1.61	1.18
M2	M4	-23.8	18.9	0.000	1.07	1.51
M2	M6	-15.7	11.6	0.000	1.07	1.32
M2	RR	2.0	12.5	0.066	1.07	1.04
M2	S	-5.7	21.2	0.000	1.07	1.18
M4	M6	13.1	33.5	0.000	1.51	1.32
M4	RR	31.8	39.1	0.000	1.51	1.04
M4	S	19.2	63.0	0.000	1.51	1.18
M6	RR	24.9	45.4	0.000	1.32	1.04
M6	S	9.9	76.5	0.000	1.32	1.18
RR	S	-9.3	104.9	0.000	1.04	1.18

Appendix 7.20. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the PUFA fatty acid ratio calculation. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	15.7	29.2	0.000	M4-965	S-1662	25.4	13.2	0.000
HG-240	L-612	0.3	6.0	0.757	M4-965	S-239	4.3	8.6	0.002
HG-240	M2-246	26.5	20.7	0.000	M4-965	S-252	9.9	6.5	0.000
HG-240	M4-168	9.5	19.9	0.000	M4-965	S-596	11.6	8.1	0.000
HG-240	M4-718	2.8	16.5	0.012	M4-965	S-605	12.7	12.3	0.000
HG-240	M4-965	5.1	21.0	0.000	M4-965	S-621	14.1	13.5	0.000
HG-240	M6-198	17.5	21.4	0.000	M6-198	M6-818	-1.4	12.7	0.178
HG-240	M6-818	14.7	21.6	0.000	M6-198	RR-1034	31.5	11.0	0.000
HG-240	RR-1034	38.6	17.9	0.000	M6-198	RR-1255	11.8	8.4	0.000
HG-240	RR-1255	22.7	13.9	0.000	M6-198	RR-245	21.9	17.9	0.000
HG-240	RR-245	32.7	22.4	0.000	M6-198	RR-247	6.7	3.7	0.003
HG-240	RR-247	16.5	5.5	0.000	M6-198	RR-609	25.6	14.0	0.000
HG-240	RR-609	35.2	21.1	0.000	M6-198	S-1044	4.6	8.5	0.002
HG-240	S-1044	14.4	12.0	0.000	M6-198	S-1062	12.2	10.0	0.000
HG-240	S-1062	23.3	16.6	0.000	M6-198	S-1063	11.8	12.0	0.000
HG-240	S-1063	24.4	20.9	0.000	M6-198	S-1662	16.2	13.6	0.000
HG-240	S-1662	28.5	22.0	0.000	M6-198	S-239	-0.7	7.7	0.513
HG-240	S-239	6.7	9.2	0.000	M6-198	S-252	4.3	5.7	0.006
HG-240	S-252	12.4	7.2	0.000	M6-198	S-596	4.2	6.4	0.005
HG-240	S-596	14.8	9.6	0.000	M6-198	S-605	4.3	9.6	0.002
HG-240	S-605	16.2	15.6	0.000	M6-198	S-621	4.7	10.8	0.001
HG-240	S-621	17.8	18.7	0.000	M6-818	RR-1034	25.7	9.4	0.000
HH-248	L-612	-8.9	5.4	0.000	M6-818	RR-1255	11.9	10.3	0.000
HH-248	M2-246	12.1	18.6	0.000	M6-818	RR-245	19.2	13.2	0.000
HH-248	M4-168	-8.9	19.0	0.000	M6-818	RR-247	7.1	4.4	0.001
HH-248	M4-718	-11.1	14.2	0.000	M6-818	RR-609	22.3	12.4	0.000
HH-248	M4-965	-11.5	19.0	0.000	M6-818	S-1044	5.1	9.8	0.000
HH-248	M6-198	-0.5	22.0	0.650	M6-818	S-1062	12.2	12.2	0.000
HH-248	M6-818	-1.6	20.1	0.126	M6-818	S-1063	11.6	13.9	0.000
HH-248	RR-1034	22.1	18.7	0.000	M6-818	S-1662	15.0	13.6	0.000
HH-248	RR-1255	10.4	11.8	0.000	M6-818	S-239	-0.2	8.3	0.882
HH-248	RR-245	16.3	24.7	0.000	M6-818	S-252	4.8	6.3	0.003
HH-248	RR-247	6.0	4.8	0.002	M6-818	S-596	4.8	7.6	0.002
HH-248	RR-609	19.3	21.9	0.000	M6-818	S-605	5.0	11.7	0.000
HH-248	S-1044	4.1	10.6	0.002	M6-818	S-621	5.3	13.1	0.000
HH-248	S-1062	10.6	14.3	0.000	RR-1034	RR-1255	-3.5	6.9	0.011
HH-248	S-1063	9.6	18.9	0.000	RR-1034	RR-245	-6.4	19.7	0.000

HH-248	S-1662	12.6	21.7	0.000	RR-1034	RR-247	-5.4	3.3	0.010
HH-248	S-239	-0.8	8.6	0.423	RR-1034	RR-609	-1.2	11.2	0.237
HH-248	S-252	3.9	6.6	0.006	RR-1034	S-1044	-7.1	7.5	0.000
HH-248	S-596	3.6	8.3	0.006	RR-1034	S-1062	-3.8	8.1	0.005
HH-248	S-605	3.6	13.4	0.003	RR-1034	S-1063	-9.2	9.0	0.000
HH-248	S-621	3.7	16.3	0.002	RR-1034	S-1662	-9.0	10.2	0.000
L-612	M2-246	15.5	5.5	0.000	RR-1034	S-239	-8.7	7.2	0.000
L-612	M4-168	4.9	4.7	0.005	RR-1034	S-252	-5.0	5.2	0.004
L-612	M4-718	1.5	6.7	0.170	RR-1034	S-596	-8.9	5.5	0.000
L-612	M4-965	2.7	5.4	0.040	RR-1034	S-605	-11.2	8.0	0.000
L-612	M6-198	9.1	4.6	0.000	RR-1034	S-621	-14.0	8.5	0.000
L-612	M6-818	8.2	5.2	0.000	RR-1255	RR-245	0.4	8.1	0.703
L-612	RR-1034	19.2	4.2	0.000	RR-1255	RR-247	-2.2	6.4	0.064
L-612	RR-1255	14.8	6.9	0.000	RR-1255	RR-609	2.7	8.2	0.026
L-612	RR-245	17.0	4.5	0.000	RR-1255	S-1044	-3.7	12.4	0.003
L-612	RR-247	11.8	7.0	0.000	RR-1255	S-1062	-0.1	12.8	0.910
L-612	RR-609	18.5	4.6	0.000	RR-1255	S-1063	-2.7	10.9	0.022
L-612	S-1044	10.4	9.0	0.000	RR-1255	S-1662	-1.5	9.2	0.160
L-612	S-1062	14.9	6.7	0.000	RR-1255	S-239	-6.3	10.1	0.000
L-612	S-1063	14.1	5.4	0.000	RR-1255	S-252	-2.6	8.1	0.031
L-612	S-1662	15.5	4.8	0.000	RR-1255	S-596	-4.7	10.2	0.001
L-612	S-239	5.4	11.0	0.000	RR-1255	S-605	-5.7	12.9	0.000
L-612	S-252	9.7	9.0	0.000	RR-1255	S-621	-6.6	12.1	0.000
L-612	S-596	10.2	7.7	0.000	RR-245	RR-247	-3.0	3.6	0.046
L-612	S-605	10.5	7.0	0.000	RR-245	RR-609	4.2	18.5	0.000
L-612	S-621	10.8	6.0	0.000	RR-245	S-1044	-4.7	8.3	0.001
M2-246	M4-168	-22.4	11.7	0.000	RR-245	S-1062	-0.6	9.7	0.584
M2-246	M4-718	-20.9	12.9	0.000	RR-245	S-1063	-4.6	12.2	0.001
M2-246	M4-965	-23.4	14.0	0.000	RR-245	S-1662	-3.2	15.4	0.006
M2-246	M6-198	-14.6	11.9	0.000	RR-245	S-239	-7.1	7.6	0.000
M2-246	M6-818	-14.1	13.8	0.000	RR-245	S-252	-3.2	5.6	0.021
M2-246	RR-1034	5.7	9.0	0.000	RR-245	S-596	-6.1	6.2	0.001
M2-246	RR-1255	0.6	11.1	0.557	RR-245	S-605	-7.8	9.4	0.000
M2-246	RR-245	1.4	11.9	0.178	RR-245	S-621	-9.8	10.6	0.000
M2-246	RR-247	-2.0	4.8	0.107	RR-247	RR-609	4.8	3.7	0.011
M2-246	RR-609	4.5	11.6	0.001	RR-247	S-1044	-1.4	8.7	0.197
M2-246	S-1044	-3.6	10.5	0.004	RR-247	S-1062	2.2	6.2	0.070
M2-246	S-1062	0.5	12.9	0.630	RR-247	S-1063	0.3	4.7	0.780
M2-246	S-1063	-2.5	14.0	0.023	RR-247	S-1662	1.4	4.0	0.238
M2-246	S-1662	-1.1	13.0	0.282	RR-247	S-239	-4.4	10.0	0.001
M2-246	S-239	-6.3	8.7	0.000	RR-247	S-252	-0.7	8.0	0.499

M2-246	S-252	-2.4	6.7	0.050	RR-247	S-596	-2.1	7.2	0.070
M2-246	S-596	-4.8	8.2	0.001	RR-247	S-605	-2.7	6.6	0.033
M2-246	S-605	-6.0	12.5	0.000	RR-247	S-621	-3.1	5.5	0.023
M2-246	S-621	-7.2	13.7	0.000	RR-609	S-1044	-6.5	8.4	0.000
M4-168	M4-718	-5.1	10.3	0.000	RR-609	S-1062	-3.0	9.8	0.014
M4-168	M4-965	-4.2	11.8	0.001	RR-609	S-1063	-7.6	11.7	0.000
M4-168	M6-198	10.6	11.1	0.000	RR-609	S-1662	-6.9	13.4	0.000
M4-168	M6-818	7.5	12.0	0.000	RR-609	S-239	-8.3	7.6	0.000
M4-168	RR-1034	41.6	7.7	0.000	RR-609	S-252	-4.6	5.6	0.004
M4-168	RR-1255	17.9	8.7	0.000	RR-609	S-596	-8.1	6.2	0.000
M4-168	RR-245	31.6	12.2	0.000	RR-609	S-605	-10.1	9.4	0.000
M4-168	RR-247	11.7	3.9	0.000	RR-609	S-621	-12.4	10.5	0.000
M4-168	RR-609	34.9	10.9	0.000	S-1044	S-1062	3.7	12.5	0.003
M4-168	S-1044	9.5	8.8	0.000	S-1044	S-1063	2.0	10.3	0.070
M4-168	S-1062	18.6	10.3	0.000	S-1044	S-1662	3.1	9.1	0.012
M4-168	S-1063	19.8	11.8	0.000	S-1044	S-239	-3.3	12.2	0.006
M4-168	S-1662	25.2	11.8	0.000	S-1044	S-252	0.5	10.3	0.628
M4-168	S-239	2.7	7.8	0.027	S-1044	S-596	-0.6	12.0	0.538
M4-168	S-252	8.2	5.8	0.000	S-1044	S-605	-1.1	12.9	0.309
M4-168	S-596	9.5	6.6	0.000	S-1044	S-621	-1.4	11.5	0.188
M4-168	S-605	10.6	10.0	0.000	S-1062	S-1063	-2.6	12.8	0.021
M4-168	S-621	11.9	11.0	0.000	S-1062	S-1662	-1.4	11.0	0.175
M4-718	M4-965	1.6	12.7	0.134	S-1062	S-239	-6.3	9.9	0.000
M4-718	M6-198	11.9	9.9	0.000	S-1062	S-252	-2.6	7.9	0.034
M4-718	M6-818	10.1	12.1	0.000	S-1062	S-596	-4.7	10.2	0.001
M4-718	RR-1034	29.3	8.1	0.000	S-1062	S-605	-5.7	13.9	0.000
M4-718	RR-1255	18.5	12.8	0.000	S-1062	S-621	-6.7	13.7	0.000
M4-718	RR-245	25.0	9.7	0.000	S-1063	S-1662	1.8	13.1	0.103
M4-718	RR-247	13.5	6.3	0.000	S-1063	S-239	-5.2	8.6	0.001
M4-718	RR-609	27.2	9.7	0.000	S-1063	S-252	-1.1	6.6	0.327
M4-718	S-1044	11.5	12.5	0.000	S-1063	S-596	-3.0	8.1	0.016
M4-718	S-1062	18.9	14.0	0.000	S-1063	S-605	-4.0	12.3	0.002
M4-718	S-1063	18.9	12.7	0.000	S-1063	S-621	-5.0	13.6	0.000
M4-718	S-1662	21.8	10.9	0.000	S-1662	S-239	-6.0	7.9	0.000
M4-718	S-239	5.0	9.9	0.001	S-1662	S-252	-1.9	5.9	0.103
M4-718	S-252	10.2	8.0	0.000	S-1662	S-596	-4.3	6.9	0.004
M4-718	S-596	11.6	10.2	0.000	S-1662	S-605	-5.6	10.5	0.000
M4-718	S-605	12.5	14.0	0.000	S-1662	S-621	-7.0	11.9	0.000
M4-718	S-621	13.5	13.7	0.000	S-239	S-252	3.4	12.0	0.005
M4-965	M6-198	13.1	12.1	0.000	S-239	S-596	2.9	11.0	0.015
M4-965	M6-818	10.4	13.9	0.000	S-239	S-605	2.7	10.3	0.020

M4-965	RR-1034	37.1	9.1	0.000	S-239	S-621	2.6	9.2	0.026
M4-965	RR-1255	19.5	10.9	0.000	S-252	S-596	-1.1	9.0	0.315
M4-965	RR-245	30.2	12.3	0.000	S-252	S-605	-1.4	8.3	0.186
M4-965	RR-247	13.5	4.7	0.000	S-252	S-621	-1.7	7.2	0.125
M4-965	RR-609	33.0	11.8	0.000	S-596	S-605	-0.4	10.7	0.695
M4-965	S-1044	11.4	10.3	0.000	S-596	S-621	-0.7	9.2	0.485
M4-965	S-1062	20.1	12.7	0.000	S-605	S-621	-0.3	13.4	0.747
M4-965	S-1063	21.1	14.0	0.000					

Appendix 7.21. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the SSFA fatty acid calculation. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean (mol %)	ID2 mean (mol %)
HG	HH	-6.9	29.6	0.000	10.0	11.9
HG	L	-5.8	5.7	0.001	10.0	12.9
HG	M2	-5.5	9.9	0.000	10.0	12.7
HG	M4	-2.6	27.0	0.014	10.0	10.6
HG	M6	-9.6	29.8	0.000	10.0	12.7
HG	RR	-12.5	40.2	0.000	10.0	13.4
HG	S	-7.4	20.6	0.000	10.0	11.6
HH	L	-2.0	5.4	0.093	11.9	12.9
HH	M2	-1.7	9.3	0.119	11.9	12.7
HH	M4	5.5	29.5	0.000	11.9	10.6
HH	M6	-3.0	29.9	0.005	11.9	12.7
HH	RR	-6.1	44.9	0.000	11.9	13.4
HH	S	1.2	22.2	0.244	11.9	11.6
L	M2	0.2	10.3	0.829	12.9	12.7
L	M4	4.8	4.7	0.006	12.9	10.6
L	M6	0.4	5.5	0.698	12.9	12.7
L	RR	-1.2	5.5	0.274	12.9	13.4
L	S	2.7	4.3	0.051	12.9	11.6
M2	M4	4.4	8.2	0.002	12.7	10.6
M2	M6	0.1	9.5	0.910	12.7	12.7
M2	RR	-1.5	9.5	0.170	12.7	13.4
M2	S	2.3	7.5	0.050	12.7	11.6
M4	M6	-8.8	28.5	0.000	10.6	12.7
M4	RR	-12.3	61.0	0.000	10.6	13.4
M4	S	-6.3	39.8	0.000	10.6	11.6
M6	RR	-3.0	43.2	0.005	12.7	13.4
M6	S	4.9	21.6	0.000	12.7	11.6
RR	S	8.8	57.0	0.000	13.4	11.6

Appendix 7.22. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the SSFA fatty acid calculation. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	-6.9	29.6	0.000	M4-965	S-1662	-5.5	8.6	0.000
HG-240	L-612	-5.8	5.7	0.001	M4-965	S-239	-2.3	7.3	0.054
HG-240	M2-246	-5.5	9.9	0.000	M4-965	S-252	-5.6	5.6	0.002
HG-240	M4-168	0.0	8.7	0.981	M4-965	S-596	6.3	8.3	0.000
HG-240	M4-718	-3.5	21.9	0.002	M4-965	S-605	-8.9	11.1	0.000
HG-240	M4-965	-4.4	16.6	0.000	M4-965	S-621	-1.6	8.2	0.152
HG-240	M6-198	-9.5	15.4	0.000	M6-198	M6-818	3.1	10.9	0.010
HG-240	M6-818	-8.8	22.0	0.000	M6-198	RR-1034	-0.8	12.0	0.429
HG-240	RR-1034	-11.1	13.2	0.000	M6-198	RR-1255	-0.8	8.9	0.437
HG-240	RR-1255	-6.4	7.8	0.000	M6-198	RR-245	0.7	17.4	0.506
HG-240	RR-245	-9.4	29.5	0.000	M6-198	RR-247	-1.5	6.0	0.195
HG-240	RR-247	-8.9	4.9	0.000	M6-198	RR-609	-1.8	9.8	0.097
HG-240	RR-609	-7.1	8.8	0.000	M6-198	S-1044	3.7	13.9	0.003
HG-240	S-1044	-5.0	14.5	0.000	M6-198	S-1062	4.9	10.6	0.000
HG-240	S-1062	-6.8	22.0	0.000	M6-198	S-1063	2.8	8.8	0.021
HG-240	S-1063	-10.5	20.3	0.000	M6-198	S-1662	4.6	10.8	0.001
HG-240	S-1662	-7.1	22.0	0.000	M6-198	S-239	3.6	13.5	0.003
HG-240	S-239	-4.4	13.0	0.001	M6-198	S-252	3.4	11.8	0.006
HG-240	S-252	-7.3	15.8	0.000	M6-198	S-596	10.2	8.3	0.000
HG-240	S-596	-1.5	18.8	0.155	M6-198	S-605	4.9	8.4	0.001
HG-240	S-605	-8.2	19.4	0.000	M6-198	S-621	6.2	11.9	0.000
HG-240	S-621	-4.6	21.3	0.000	M6-818	RR-1034	-4.5	8.8	0.002
HH-248	L-612	-2.0	5.4	0.093	M6-818	RR-1255	-2.6	6.9	0.036
HH-248	M2-246	-1.7	9.3	0.119	M6-818	RR-245	-2.6	21.9	0.018
HH-248	M4-168	4.9	7.9	0.001	M6-818	RR-247	-4.0	3.9	0.017
HH-248	M4-718	4.7	21.9	0.000	M6-818	RR-609	-3.6	7.9	0.008
HH-248	M4-965	5.1	17.0	0.000	M6-818	S-1044	1.5	10.6	0.171
HH-248	M6-198	-3.9	13.8	0.001	M6-818	S-1062	2.6	14.0	0.021
HH-248	M6-818	-1.4	21.4	0.187	M6-818	S-1063	-0.9	12.1	0.386
HH-248	RR-1034	-5.3	11.6	0.000	M6-818	S-1662	2.2	14.0	0.048
HH-248	RR-1255	-3.1	7.5	0.016	M6-818	S-239	1.6	9.8	0.153
HH-248	RR-245	-3.5	28.3	0.002	M6-818	S-252	0.6	10.0	0.536
HH-248	RR-247	-4.6	4.5	0.007	M6-818	S-596	11.2	10.7	0.000
HH-248	RR-609	-4.0	8.4	0.003	M6-818	S-605	2.4	11.3	0.037
HH-248	S-1044	0.4	13.1	0.669	M6-818	S-621	4.5	13.8	0.001
HH-248	S-1062	0.9	21.8	0.378	RR-1034	RR-1255	-0.3	8.2	0.745
HH-248	S-1063	-2.3	21.1	0.031	RR-1034	RR-245	1.6	15.1	0.131

HH-248	S-1662	0.5	21.6	0.592	RR-1034	RR-247	-0.9	5.2	0.424
HH-248	S-239	0.6	11.8	0.553	RR-1034	RR-609	-1.4	9.1	0.193
HH-248	S-252	-0.6	14.0	0.552	RR-1034	S-1044	4.7	12.0	0.001
HH-248	S-596	7.8	19.4	0.000	RR-1034	S-1062	6.5	8.4	0.000
HH-248	S-605	0.4	20.2	0.685	RR-1034	S-1063	4.3	6.7	0.004
HH-248	S-621	2.8	20.2	0.012	RR-1034	S-1662	6.1	8.7	0.000
L-612	M2-246	0.2	10.3	0.829	RR-1034	S-239	4.5	11.8	0.001
L-612	M4-168	5.1	7.9	0.001	RR-1034	S-252	4.6	9.7	0.001
L-612	M4-718	4.3	4.7	0.009	RR-1034	S-596	12.6	6.3	0.000
L-612	M4-965	4.3	4.1	0.012	RR-1034	S-605	6.6	6.4	0.000
L-612	M6-198	-0.5	6.7	0.619	RR-1034	S-621	7.8	9.7	0.000
L-612	M6-818	1.4	4.9	0.217	RR-1255	RR-245	1.2	8.4	0.247
L-612	RR-1034	-1.1	6.1	0.312	RR-1255	RR-247	-0.3	9.0	0.778
L-612	RR-1255	-1.1	10.0	0.304	RR-1255	RR-609	-0.9	13.0	0.404
L-612	RR-245	-0.1	6.3	0.951	RR-1255	S-1044	3.2	9.2	0.011
L-612	RR-247	-1.6	7.0	0.153	RR-1255	S-1062	3.6	6.8	0.010
L-612	RR-609	-2.0	11.0	0.076	RR-1255	S-1063	2.4	6.4	0.054
L-612	S-1044	2.1	7.1	0.069	RR-1255	S-1662	3.4	6.9	0.012
L-612	S-1062	2.5	4.8	0.054	RR-1255	S-239	3.2	10.0	0.010
L-612	S-1063	1.1	4.4	0.321	RR-1255	S-252	2.8	7.6	0.024
L-612	S-1662	2.4	4.8	0.067	RR-1255	S-596	6.2	6.3	0.001
L-612	S-239	2.2	7.8	0.059	RR-1255	S-605	3.4	6.3	0.013
L-612	S-252	1.7	5.5	0.147	RR-1255	S-621	4.4	7.2	0.003
L-612	S-596	5.6	4.3	0.004	RR-245	RR-247	-2.1	5.6	0.090
L-612	S-605	2.3	4.3	0.075	RR-245	RR-609	-2.3	9.4	0.049
L-612	S-621	3.5	5.1	0.017	RR-245	S-1044	3.2	16.5	0.005
M2-246	M4-168	4.8	11.9	0.000	RR-245	S-1062	4.5	21.6	0.000
M2-246	M4-718	4.0	8.1	0.004	RR-245	S-1063	2.2	19.3	0.043
M2-246	M4-965	3.9	7.2	0.006	RR-245	S-1662	4.2	21.8	0.000
M2-246	M6-198	-0.8	11.2	0.449	RR-245	S-239	3.2	14.7	0.007
M2-246	M6-818	1.1	8.4	0.302	RR-245	S-252	2.8	17.6	0.011
M2-246	RR-1034	-1.4	10.1	0.202	RR-245	S-596	10.4	18.2	0.000
M2-246	RR-1255	-1.3	12.4	0.224	RR-245	S-605	4.4	18.5	0.000
M2-246	RR-245	-0.3	10.8	0.740	RR-245	S-621	5.9	22.0	0.000
M2-246	RR-247	-1.8	9.5	0.099	RR-247	RR-609	-0.7	10.0	0.496
M2-246	RR-609	-2.1	13.4	0.051	RR-247	S-1044	4.4	6.4	0.004
M2-246	S-1044	1.8	11.6	0.090	RR-247	S-1062	5.3	3.8	0.007
M2-246	S-1062	2.2	8.3	0.058	RR-247	S-1063	3.7	3.4	0.027
M2-246	S-1063	0.8	7.6	0.451	RR-247	S-1662	5.1	3.9	0.007
M2-246	S-1662	2.0	8.4	0.076	RR-247	S-239	4.4	7.2	0.003
M2-246	S-239	1.9	12.4	0.078	RR-247	S-252	4.2	4.6	0.010

M2-246	S-252	1.4	9.3	0.201	RR-247	S-596	9.1	3.3	0.002
M2-246	S-596	5.2	7.5	0.001	RR-247	S-605	5.2	3.3	0.011
M2-246	S-605	2.0	7.5	0.084	RR-247	S-621	6.3	4.2	0.003
M2-246	S-621	3.1	8.8	0.012	RR-609	S-1044	4.0	10.2	0.002
M4-168	M4-718	-2.3	6.5	0.058	RR-609	S-1062	4.5	7.8	0.002
M4-168	M4-965	-2.7	5.2	0.041	RR-609	S-1063	3.4	7.4	0.011
M4-168	M6-198	-7.3	10.1	0.000	RR-609	S-1662	4.3	7.9	0.003
M4-168	M6-818	-5.9	6.8	0.001	RR-609	S-239	4.0	10.9	0.002
M4-168	RR-1034	-8.3	8.7	0.000	RR-609	S-252	3.7	8.6	0.005
M4-168	RR-1255	-5.8	10.0	0.000	RR-609	S-596	6.9	7.3	0.000
M4-168	RR-245	-7.0	9.9	0.000	RR-609	S-605	4.3	7.3	0.003
M4-168	RR-247	-7.5	7.1	0.000	RR-609	S-621	5.2	8.2	0.001
M4-168	RR-609	-6.5	11.0	0.000	S-1044	S-1062	0.2	10.2	0.852
M4-168	S-1044	-3.9	10.5	0.003	S-1044	S-1063	-2.1	8.6	0.066
M4-168	S-1062	-4.5	6.6	0.003	S-1044	S-1662	-0.1	10.5	0.951
M4-168	S-1063	-6.6	5.8	0.001	S-1044	S-239	0.2	13.8	0.857
M4-168	S-1662	-4.7	6.7	0.002	S-1044	S-252	-0.9	11.6	0.385
M4-168	S-239	-3.6	11.3	0.004	S-1044	S-596	4.9	8.2	0.001
M4-168	S-252	-5.2	7.9	0.001	S-1044	S-605	-0.2	8.3	0.834
M4-168	S-596	-0.9	5.6	0.384	S-1044	S-621	1.7	11.4	0.126
M4-168	S-605	-5.1	5.6	0.003	S-1062	S-1063	-4.0	12.5	0.002
M4-168	S-621	-3.2	7.3	0.015	S-1062	S-1662	-0.4	14.0	0.696
M4-718	M4-965	-0.6	8.9	0.540	S-1062	S-239	0.1	9.6	0.960
M4-718	M6-198	-7.9	10.3	0.000	S-1062	S-252	-1.5	9.6	0.156
M4-718	M6-818	-6.9	13.8	0.000	S-1062	S-596	8.4	11.0	0.000
M4-718	RR-1034	-9.7	8.1	0.000	S-1062	S-605	-0.8	11.6	0.464
M4-718	RR-1255	-5.1	6.7	0.002	S-1062	S-621	2.2	13.5	0.045
M4-718	RR-245	-7.7	21.4	0.000	S-1063	S-1662	3.5	12.2	0.004
M4-718	RR-247	-7.5	3.8	0.002	S-1063	S-239	2.1	8.3	0.067
M4-718	RR-609	-5.9	7.7	0.000	S-1063	S-252	1.4	7.4	0.189
M4-718	S-1044	-2.9	10.0	0.015	S-1063	S-596	16.0	12.0	0.000
M4-718	S-1062	-4.4	14.0	0.001	S-1063	S-605	4.3	13.8	0.001
M4-718	S-1063	-9.3	12.8	0.000	S-1063	S-621	6.0	11.2	0.000
M4-718	S-1662	-4.7	13.9	0.000	S-1662	S-239	0.3	9.8	0.786
M4-718	S-239	-2.4	9.3	0.039	S-1662	S-252	-1.2	9.9	0.261
M4-718	S-252	-5.2	9.2	0.001	S-1662	S-596	8.7	10.8	0.000
M4-718	S-596	3.3	11.2	0.007	S-1662	S-605	-0.3	11.4	0.798
M4-718	S-605	-6.2	12.0	0.000	S-1662	S-621	2.5	13.7	0.024
M4-718	S-621	-1.7	13.3	0.110	S-239	S-252	-1.0	11.1	0.322
M4-965	M6-198	-8.3	7.5	0.000	S-239	S-596	4.1	7.9	0.004
M4-965	M6-818	-8.3	8.5	0.000	S-239	S-605	-0.4	8.0	0.679

M4-965	RR-1034	-10.6	5.4	0.000	S-239	S-621	1.3	10.6	0.226
M4-965	RR-1255	-5.1	6.1	0.002	S-252	S-596	8.2	6.8	0.000
M4-965	RR-245	-8.3	16.3	0.000	S-252	S-605	1.2	6.9	0.288
M4-965	RR-247	-7.6	3.1	0.004	S-252	S-621	3.3	10.9	0.007
M4-965	RR-609	-5.9	7.1	0.001	S-596	S-605	-12.5	11.8	0.000
M4-965	S-1044	-2.9	7.4	0.023	S-596	S-621	-4.7	10.0	0.001
M4-965	S-1062	-5.1	8.7	0.001	S-605	S-621	3.2	10.4	0.009
M4-965	S-1063	-13.3	10.3	0.000					

Appendix 7.23. Results for pairwise two-tailed Welch's t-test between combinations of the eight group ID memberships tested across the SVLCFA fatty acid calculation. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

ID1	ID2	t	df	p-value	ID1 mean	ID2 mean
HG	HH	-14.4	29.5	0.000	24.20	29.42
HG	L	4.2	5.7	0.006	24.20	21.35
HG	M2	-24.2	11.3	0.000	24.20	37.95
HG	M4	-9.1	22.8	0.000	24.20	27.00
HG	M6	-2.1	22.8	0.044	24.20	24.86
HG	RR	-29.4	42.5	0.000	24.20	35.37
HG	S	-9.6	71.2	0.000	24.20	28.72
HH	L	12.2	5.3	0.000	29.42	21.35
HH	M2	-15.4	10.4	0.000	29.42	37.95
HH	M4	8.7	24.9	0.000	29.42	27.00
HH	M6	16.3	24.6	0.000	29.42	24.86
HH	RR	-16.6	47.4	0.000	29.42	35.37
HH	S	1.5	77.2	0.129	29.42	28.72
L	M2	-20.9	8.8	0.000	21.35	37.95
L	M4	-8.9	4.4	0.001	21.35	27.00
L	M6	-5.5	4.4	0.004	21.35	24.86
L	RR	-20.9	5.6	0.000	21.35	35.37
L	S	-10.1	7.7	0.000	21.35	28.72
M2	M4	21.1	8.1	0.000	37.95	27.00
M2	M6	25.2	8.2	0.000	37.95	24.86
M2	RR	4.6	11.3	0.001	37.95	35.37
M2	S	14.6	17.2	0.000	37.95	28.72
M4	M6	10.7	34.6	0.000	27.00	24.86
M4	RR	-27.9	57.0	0.000	27.00	35.37
M4	S	-4.2	81.4	0.000	27.00	28.72
M6	RR	-34.8	54.5	0.000	24.86	35.37
M6	S	-9.4	80.1	0.000	24.86	28.72
RR	S	14.2	105.7	0.000	35.37	28.72

Appendix 7.24. Results for pairwise two-tailed Welch's t-test between combinations of the 23 accessions tested across the SVLCFA fatty acid calculation. Tests of significance were evaluated at the $\alpha = 0.05$ level and p-values less than this value were highlighted in bold.

Acc. 1	Acc. 2	t	df	p-value	Acc. 1	Acc. 2	t	df	p-value
HG-240	HH-248	-14.4	29.5	0.000	M4-965	S-1662	-5.4	10.5	0.000
HG-240	L-612	4.2	5.7	0.006	M4-965	S-239	6.0	7.8	0.000
HG-240	M2-246	-24.2	11.3	0.000	M4-965	S-252	-0.7	5.3	0.532
HG-240	M4-168	-10.2	19.9	0.000	M4-965	S-596	-5.9	5.9	0.001
HG-240	M4-718	-6.4	20.7	0.000	M4-965	S-605	-2.4	7.9	0.042
HG-240	M4-965	-9.0	21.9	0.000	M4-965	S-621	-4.3	9.7	0.002
HG-240	M6-198	-2.0	21.8	0.058	M6-198	M6-818	-0.1	12.3	0.910
HG-240	M6-818	-1.8	20.4	0.081	M6-198	RR-1034	-44.3	9.6	0.000
HG-240	RR-1034	-37.3	17.1	0.000	M6-198	RR-1255	-13.1	6.5	0.000
HG-240	RR-1255	-13.5	7.4	0.000	M6-198	RR-245	-36.9	20.9	0.000
HG-240	RR-245	-30.3	27.2	0.000	M6-198	RR-247	-24.4	4.3	0.000
HG-240	RR-247	-22.9	6.9	0.000	M6-198	RR-609	-16.6	8.0	0.000
HG-240	RR-609	-16.7	9.7	0.000	M6-198	S-1044	-4.6	7.5	0.002
HG-240	S-1044	-5.1	8.4	0.001	M6-198	S-1062	-9.8	8.0	0.000
HG-240	S-1062	-10.3	9.8	0.000	M6-198	S-1063	-19.5	14.0	0.000
HG-240	S-1063	-16.4	21.7	0.000	M6-198	S-1662	-11.3	9.5	0.000
HG-240	S-1662	-11.4	14.0	0.000	M6-198	S-239	3.3	7.6	0.012
HG-240	S-239	2.4	8.5	0.039	M6-198	S-252	-2.6	5.2	0.049
HG-240	S-252	-3.0	5.5	0.026	M6-198	S-596	-9.4	5.6	0.000
HG-240	S-596	-9.9	6.7	0.000	M6-198	S-605	-5.4	7.6	0.001
HG-240	S-605	-6.0	8.8	0.000	M6-198	S-621	-9.4	8.9	0.000
HG-240	S-621	-9.8	12.3	0.000	M6-818	RR-1034	-37.5	11.8	0.000
HH-248	L-612	12.2	5.3	0.000	M6-818	RR-1255	-12.8	7.1	0.000
HH-248	M2-246	-15.4	10.4	0.000	M6-818	RR-245	-30.1	15.6	0.000
HH-248	M4-168	7.5	20.0	0.000	M6-818	RR-247	-22.2	5.9	0.000
HH-248	M4-718	8.6	19.2	0.000	M6-818	RR-609	-16.0	9.1	0.000
HH-248	M4-965	7.0	21.1	0.000	M6-818	S-1044	-4.4	8.1	0.002
HH-248	M6-198	15.6	22.0	0.000	M6-818	S-1062	-9.4	9.2	0.000
HH-248	M6-818	13.2	18.7	0.000	M6-818	S-1063	-15.3	12.1	0.000
HH-248	RR-1034	-24.5	15.3	0.000	M6-818	S-1662	-10.3	11.9	0.000
HH-248	RR-1255	-7.4	7.1	0.000	M6-818	S-239	3.2	8.2	0.012
HH-248	RR-245	-15.9	28.8	0.000	M6-818	S-252	-2.5	5.4	0.050
HH-248	RR-247	-11.9	6.0	0.000	M6-818	S-596	-9.1	6.4	0.000
HH-248	RR-609	-9.3	9.1	0.000	M6-818	S-605	-5.3	8.4	0.001
HH-248	S-1044	0.6	8.1	0.549	M6-818	S-621	-8.7	10.8	0.000
HH-248	S-1062	-2.6	9.2	0.030	RR-1034	RR-1255	2.3	7.0	0.055
HH-248	S-1063	0.1	22.0	0.945	RR-1034	RR-245	10.8	12.3	0.000

HH-248	S-1662	-0.4	12.5	0.703	RR-1034	RR-247	7.1	5.5	0.001
HH-248	S-239	8.5	8.2	0.000	RR-1034	RR-609	2.9	8.8	0.019
HH-248	S-252	1.0	5.4	0.345	RR-1034	S-1044	9.8	8.0	0.000
HH-248	S-596	-2.7	6.3	0.034	RR-1034	S-1062	9.9	8.9	0.000
HH-248	S-605	0.3	8.3	0.788	RR-1034	S-1063	28.9	9.4	0.000
HH-248	S-621	0.1	11.1	0.899	RR-1034	S-1662	17.8	11.0	0.000
L-612	M2-246	-20.9	8.8	0.000	RR-1034	S-239	17.9	8.1	0.000
L-612	M4-168	-9.5	4.4	0.000	RR-1034	S-252	7.5	5.4	0.001
L-612	M4-718	-7.8	5.2	0.000	RR-1034	S-596	8.9	6.2	0.000
L-612	M4-965	-9.1	4.9	0.000	RR-1034	S-605	10.4	8.2	0.000
L-612	M6-198	-5.5	4.6	0.004	RR-1034	S-621	16.3	10.3	0.000
L-612	M6-818	-5.3	5.3	0.003	RR-1255	RR-245	1.6	6.7	0.146
L-612	RR-1034	-24.7	5.2	0.000	RR-1255	RR-247	1.3	8.0	0.241
L-612	RR-1255	-14.1	9.9	0.000	RR-1255	RR-609	0.0	11.8	0.990
L-612	RR-245	-20.1	4.8	0.000	RR-1255	S-1044	5.8	13.0	0.000
L-612	RR-247	-18.5	6.3	0.000	RR-1255	S-1062	4.5	11.6	0.001
L-612	RR-609	-16.3	10.3	0.000	RR-1255	S-1063	7.6	6.5	0.000
L-612	S-1044	-7.1	11.0	0.000	RR-1255	S-1662	6.8	8.7	0.000
L-612	S-1062	-11.2	10.2	0.000	RR-1255	S-239	11.7	13.0	0.000
L-612	S-1063	-12.6	4.6	0.000	RR-1255	S-252	5.1	8.8	0.001
L-612	S-1662	-11.3	7.2	0.000	RR-1255	S-596	4.2	10.9	0.002
L-612	S-239	-0.7	11.0	0.514	RR-1255	S-605	5.8	12.8	0.000
L-612	S-252	-4.8	7.2	0.002	RR-1255	S-621	6.9	9.5	0.000
L-612	S-596	-11.0	9.0	0.000	RR-245	RR-247	-0.6	4.9	0.574
L-612	S-605	-7.9	11.0	0.000	RR-245	RR-609	-2.1	8.4	0.068
L-612	S-621	-10.5	8.1	0.000	RR-245	S-1044	6.2	7.7	0.000
M2-246	M4-168	20.4	8.1	0.000	RR-245	S-1062	5.0	8.4	0.001
M2-246	M4-718	20.7	10.0	0.000	RR-245	S-1063	19.5	21.2	0.000
M2-246	M4-965	19.9	9.2	0.000	RR-245	S-1662	10.9	10.7	0.000
M2-246	M6-198	24.9	8.6	0.000	RR-245	S-239	14.3	7.8	0.000
M2-246	M6-818	23.5	10.2	0.000	RR-245	S-252	4.9	5.2	0.004
M2-246	RR-1034	0.5	9.8	0.626	RR-245	S-596	4.3	5.9	0.005
M2-246	RR-1255	2.3	10.1	0.042	RR-245	S-605	6.4	7.9	0.000
M2-246	RR-245	6.7	9.2	0.000	RR-245	S-621	10.2	9.7	0.000
M2-246	RR-247	5.4	9.9	0.000	RR-247	RR-609	-1.6	9.9	0.150
M2-246	RR-609	2.7	13.3	0.017	RR-247	S-1044	6.1	9.0	0.000
M2-246	S-1044	9.1	11.2	0.000	RR-247	S-1062	4.9	9.9	0.001
M2-246	S-1062	8.6	13.4	0.000	RR-247	S-1063	13.1	4.3	0.000
M2-246	S-1063	16.3	8.5	0.000	RR-247	S-1662	9.4	8.8	0.000
M2-246	S-1662	13.2	13.2	0.000	RR-247	S-239	13.7	9.1	0.000
M2-246	S-239	16.3	11.4	0.000	RR-247	S-252	5.0	5.8	0.003

M2-246	S-252	7.3	6.6	0.000	RR-247	S-596	4.3	7.3	0.003
M2-246	S-596	7.9	9.9	0.000	RR-247	S-605	6.3	9.3	0.000
M2-246	S-605	9.4	11.9	0.000	RR-247	S-621	9.1	9.6	0.000
M2-246	S-621	12.8	13.9	0.000	RR-609	S-1044	6.4	12.8	0.000
M4-168	M4-718	3.0	10.9	0.013	RR-609	S-1062	5.2	14.0	0.000
M4-168	M4-965	0.4	11.7	0.702	RR-609	S-1063	9.7	7.9	0.000
M4-168	M6-198	11.4	12.0	0.000	RR-609	S-1662	8.3	11.6	0.000
M4-168	M6-818	8.6	10.7	0.000	RR-609	S-239	13.0	13.0	0.000
M4-168	RR-1034	-37.5	8.2	0.000	RR-609	S-252	5.4	7.5	0.001
M4-168	RR-1255	-10.2	6.4	0.000	RR-609	S-596	4.8	11.4	0.001
M4-168	RR-245	-29.1	19.1	0.000	RR-609	S-605	6.5	13.4	0.000
M4-168	RR-247	-18.7	3.9	0.000	RR-609	S-621	8.2	12.7	0.000
M4-168	RR-609	-13.0	7.7	0.000	S-1044	S-1062	-2.1	12.6	0.055
M4-168	S-1044	-1.7	7.4	0.125	S-1044	S-1063	-0.6	7.5	0.557
M4-168	S-1062	-6.0	7.7	0.000	S-1044	S-1662	-0.8	9.7	0.455
M4-168	S-1063	-9.6	12.0	0.000	S-1044	S-239	5.6	14.0	0.000
M4-168	S-1662	-5.5	8.8	0.000	S-1044	S-252	0.5	9.4	0.628
M4-168	S-239	6.2	7.4	0.000	S-1044	S-596	-2.3	11.9	0.043
M4-168	S-252	-0.6	5.1	0.576	S-1044	S-605	-0.3	13.9	0.778
M4-168	S-596	-5.9	5.5	0.002	S-1044	S-621	-0.5	10.5	0.623
M4-168	S-605	-2.3	7.5	0.050	S-1062	S-1063	2.7	8.0	0.028
M4-168	S-621	-4.3	8.3	0.003	S-1062	S-1662	2.1	11.8	0.060
M4-718	M4-965	-2.3	13.6	0.035	S-1062	S-239	8.7	12.9	0.000
M4-718	M6-198	5.7	12.6	0.000	S-1062	S-252	2.2	7.4	0.066
M4-718	M6-818	4.8	14.0	0.000	S-1062	S-596	-0.2	11.3	0.812
M4-718	RR-1034	-33.3	11.7	0.000	S-1062	S-605	1.9	13.3	0.076
M4-718	RR-1255	-10.9	7.0	0.000	S-1062	S-621	2.3	12.8	0.039
M4-718	RR-245	-25.4	16.1	0.000	S-1063	S-1662	-0.5	9.4	0.648
M4-718	RR-247	-18.6	5.7	0.000	S-1063	S-239	8.6	7.5	0.000
M4-718	RR-609	-13.6	8.9	0.000	S-1063	S-252	1.0	5.2	0.349
M4-718	S-1044	-2.6	8.1	0.031	S-1063	S-596	-2.8	5.6	0.033
M4-718	S-1062	-7.0	9.1	0.000	S-1063	S-605	0.3	7.6	0.803
M4-718	S-1063	-10.0	12.4	0.000	S-1063	S-621	0.1	8.8	0.925
M4-718	S-1662	-6.8	11.6	0.000	S-1662	S-239	8.2	9.9	0.000
M4-718	S-239	5.1	8.1	0.001	S-1662	S-252	1.1	6.0	0.297
M4-718	S-252	-1.2	5.4	0.269	S-1662	S-596	-2.2	8.3	0.054
M4-718	S-596	-6.8	6.3	0.000	S-1662	S-605	0.5	10.3	0.653
M4-718	S-605	-3.3	8.3	0.011	S-1662	S-621	0.4	13.7	0.688
M4-718	S-621	-5.6	10.6	0.000	S-239	S-252	-4.0	9.1	0.003
M4-965	M6-198	9.2	13.6	0.000	S-239	S-596	-8.7	12.0	0.000
M4-965	M6-818	7.4	13.4	0.000	S-239	S-605	-6.2	13.9	0.000

M4-965	RR-1034	-33.6	10.8	0.000	S-239	S-621	-7.7	10.8	0.000
M4-965	RR-1255	-10.1	6.7	0.000	S-252	S-596	-2.3	7.6	0.054
M4-965	RR-245	-25.4	18.7	0.000	S-252	S-605	-0.7	8.7	0.477
M4-965	RR-247	-17.8	4.9	0.000	S-252	S-621	-0.9	6.3	0.381
M4-965	RR-609	-12.8	8.4	0.000	S-596	S-605	2.1	12.0	0.060
M4-965	S-1044	-1.8	7.8	0.108	S-596	S-621	2.5	9.2	0.036
M4-965	S-1062	-6.0	8.5	0.000	S-605	S-621	-0.2	11.2	0.862
M4-965	S-1063	-8.4	13.4	0.000					

8.0 Appendix B – Extra Plant Images

Appendix 8.1. Images for *Camelina hispida*.

Appendix 8.2. Images for *Camelina laxa*.

Appendix 8.3. Images for *Camelina microcarpa*.

Appendix 8.4. Images for *Camelina rumelica*.

Appendix 8.5. Images for *Camelina sativa*.