FATTY ACID COMPOSITION IN DIVERSE OAT GERMPLASM

A Thesis
Submitted to
the College of Graduate Studies and Research
in partial fulfillment of the requirements
for the degree of
Master of Science
Department of Plant Sciences
University of Saskatchewan
Saskatoon, Saskatchewan
Canada

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ABSTRACT

Oat is an important crop for livestock feed and human food. Increased interest in the health promoting properties of oat has led to a need to explore diverse oat germplasm for improved nutritional quality. One target for improved nutritional quality could be an altered fatty acid composition. A study was conducted to explore the fatty acid profile of diverse accessions from the world oat collection preserved in the Canadian national seed genebank, Plant Gene Resources of Canada (PGRC), at the Agriculture and Agri-Food Canada (AAFC) Research Centre, Saskatoon, Saskatchewan, Canada and genotypes from the Crop Development Centre (CDC), University of Saskatchewan, Saskatoon and the Eastern Cereal and Oilseed Research Centre (ECORC), AAFC, Ottawa, Canada. Accessions included a wide range of *Avena sativa* L. and other selected species from the genus *Avena* (*A. byzantina* C. Koch, *A. sterilis* L., *A. fatua* L., *A. sativa* subsp. *nudisativa* (Husn.) Rod. et. Sold. and *A. strigosa* Schreb.). The fatty acid profiles of 917 oat accessions from these taxa were analyzed using gas chromatography, revealing significant variability for the three major fatty acids in oat oil. Oleic and linoleic acid demonstrated the greatest variation. A few *A. sativa* accessions had higher oleic and lower palmitic acid levels compared to the general average. Some hexaploid wild oat accessions (*A. sterilis*) showed relatively high oleic and below average levels of palmitic and linoleic acid compared to *A. sativa*. *A. strigosa* accessions had consistently higher levels of oleic acid than other *Avena* species. Based on initial results, 52 selected *A. sativa* accessions were grown in 2009 in replicated field trials and re-evaluated to gain insight into the influence of the growing environment on fatty acid composition. Fatty acid composition was affected by genotype, whereas location significantly affected palmitic and oleic acid content. Correlations were determined among the contents of the six fatty acids, oil content and protein content. Oleic acid content was positively correlated with oil content, which may be particularly important to plant breeders for nutritional quality improvement of future oat cultivars. The understanding gained from this research suggests the possibility of improving the fatty acid profile of future oat cultivars for food and feed.

ACKNOWLEDGMENTS

I would like to take this opportunity to acknowledge those people without whom this thesis would not have been completed. First and foremost, I would like to thank and express my deepest gratitude to my supervisors, Dr. Axel Diederichsen and Dr. Brian Rossnagel, for accepting me as their student and for offering me invaluable assistance, support and guidance throughout the course of this project. I am thankful to both of them for challenging me for constant improvement, and encouraging me throughout my degree. They have assisted me with their advice, vast experience in the field, knowledge and patience, and by offering me help every time I needed it; and have granted me the space to work in my own way. I simply could not wish for better supervisors. I am also grateful to the members of my supervisory committee for their help and support, Dr. Kirstin Bett, Dr. Bruce Coulman, and especially, Dr. Bob Tyler for offering his time and advice to help me understand the baffling world of lipids.

I am thankful to Plant Gene Resources of Canada (PGRC) staff, Dr. Ken Richards, Dallas Kessler, David Williams and Peter Kusters and to the Plant Sciences Field Lab crew for their help and support. I want to especially thank Dr. Nancy Tyler for her immense help with gas chromatography, Dan Sutherland and Dr. Wesley Taylor for their help and advice to run my laboratory experiments smoothly. It is a pleasure for me to thank Dr. Aaron Beattie for his unparalleled assistance and friendly behaviour. I also thank Dr. Nicholas Tinker from the Eastern Cereal and Oilseed Research Centre (ECORC) for his help in this work. I am grateful to Agriculture and Agri-Food, Canada (AAFC), the University of Saskatchewan (Paulden F. and Dorathea I. Knowles Postgraduate Scholarship and Rene Vandeveld Scholarship) and Dr. Rossnagel for providing me with sufficient financial support for this project.

In my daily life, I have been blessed with a friendly and cheerful group of fellow students in the department. My ex-roommates Scott and Cheryl Dakiniewich, Dr. J.P. Dahiya, Dr. Gita, Ravinder, Sangeeta, Dinesh, Pooja and Aman have helped me in adjusting to a new country and environment, both emotionally and mentally. It is hard to express my appreciation for them.

Finally, I am indebtful to my family, Anupam, Rakhee and my other friends for their love, understanding, endless encouragement and support throughout the duration of my stay in Canada.

"This thesis is dedicated to my parents, who have provided me their unconditional love and support, and have always encouraged me to follow my dreams"

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATIONS

AA	Arachidonic Acid
AAFC	Agriculture and Agri-Food Canada
CDC	Crop Development Centre
CN	Canadian National
CLA	Conjugated Linoleic Acid
DArT	Diversity Arrays Technology
DHA	Docosahexaenoic Acid
ECORC	Eastern Cereal and Oilseed Research Centre
EPA	Eicosapentaenoic Acid
FDA	Food and Drug Administration
GC	Gas Chromatography
HDL	High Density Lipoprotein
HSD	Honestly Significant Difference
IOI	Integrated Oat Improvement
LD	Linkage Disequilibrium
LDL	Low Density Lipoprotein
LSD	Least Significant Difference
PGRC	Plant Gene Resources of Canada
PUFA	Polyunsaturated Fatty Acids
RIL	Recombinant Inbred Lines
RFT	Replicated Field Trial, 2009
U of S	University of Saskatchewan

1. INTRODUCTION

Oat (*Avena sativa* L.) is a cool season, annual crop grown mainly in moist areas of temperate climatic zones. It ranks 6th among cereals in world annual production. Russia was the world production leader at 5.3 million metric tonnes in 2008-2009, followed by Canada at 4.3 million metric tonnes (Statistics Canada, 2010). Oat is a staple food in many parts of Europe, including Germany, Ireland, Scotland and the Scandinavian countries. It is well accepted as a healthy food because of its ability to lower LDL cholesterol levels and is of increasing importance for human nutrition (Prairie Oat Growers Association, 2010).

Traditionally, most oat is used as animal feed. However, its use as food or industrial raw material has increased in the last two decades. In North America, the focus on the oat crop has shifted toward food use. While most of the nutritional interest in oat is focused on dietary fibre, its oil also has nutritional potential. In general, high oil oat lines have been used for animal feed. The food industry prefers low oil lines because of the increased caloric value associated with high oil and oxidation problems associated with oils which can reduce processed product shelf-life. Oat groat oil content is low compared to commercial oilseed crops, but it is significantly higher than in most other cereal grains, with a wide range of 4 to 11% in the dehulled oat kernel (groat). Unlike other cereals, oat oil is not localized in the germ of the seed, but is also found throughout the endosperm. A number of studies indicate that oat oil content is under genetic control, thus it is possible to alter oil content via breeding (Holland et al., 2001). Oat oil is generally good for human nutrition due to a high percentage of unsaturated fatty acids such as oleic acid and linoleic acid. However, it could be improved and little information on the lipid composition of *Avena* species is available.

Based on this assessment, the present study was conducted to investigate the fatty acid composition of oat oil in germplasm from the Plant Gene Resources of Canada (PGRC) [Agriculture and Agri-Food Canada (AAFC), Saskatoon Research Centre, Saskatoon, Saskatchewan, Canada], the Crop Development Centre (CDC) [University of Saskatchewan, Saskatoon] and the Eastern Cereal and Oilseed Research Centre (ECORC) [AAFC, Ottawa, Ontario, Canada]. PGRC maintains the largest collection of genus *Avena* accessions in the world; a total of more than 27,000 accessions. Some 11,000 accessions belong to the hexaploid

cultivated oat (*A. sativa* L. s.l.), including common hulled oat (*A. sativa* L. s.str.), hulless oat (*A. sativa* subsp. *nudisativa* (Husn.) Rod et. Sold) and red oat *A. byzantina* C. Koch. Although 81% of PGRC oat germplasm is duplicated in the United States Department of Agriculture (USDA) germplasm system, Canada maintains the largest oat species collections, followed by the USA and Russia (Diederichsen et al., 2006). All genotypes from the PGRC are referred by a unique identity (CN, Canadian National) number, accessible online at the PGRC Internet accessible database GRIN-CA (http://pgrc3.agr.gc.ca/search_grinca-recherche_rirgc_e.html). The database is open to researchers and to the public and the CN numbers can be used to access passport data of any genotype. Fatty acid data generated on the PGRC oat accessions will be made available to the public through GRIN-CA.

The research project consisted of two experiments. The first experiment was an evaluation of the fatty acid profiles of selected PGRC genebank accessions, CDC breeding germplasm and a diverse set of oat accessions from ECORC. In the second experiment, selected genotypes (based on the results of the first experiment) were grown in the field to evaluate the influence of the environment on fatty acid composition.

The research project had the following objectives:

- To evaluate the fatty acid profiles of diverse oat germplasm, including current cultivars and breeding lines in the developmental pipeline of the Crop Development Centre oat breeding program; historic cultivars grown in Canada from 1886 to 2001; oat germplasm from the Nordic region; and a selection of cultivated hexaploid oat (*A. sativa* L., *A. byzantina* C. (Koch) and *A. sativa* subsp. *nudisativa* (Husn.) Rod. et. Sold) and cultivated diploid oat (*A. strigosa* Schreb.) and wild relative accessions of oat (*A. sterilis* L. and *A. fatua* L.) from the world collection available at the PGRC; and a diverse collection of hexaploid cultivated oat accessions from the International Oat Investigation project from ECORC known as 'IOI selections'.
- To evaluate the influence of the environment on oat fatty acid composition.

The focus was on cultivated and wild hexaploid *Avena* species from the PGRC collection because of cross compatibility of these species, which is an important issue in oat breeding. Important traits such as large grain size, higher protein and oil content, disease resistance and cold tolerance in *A. sativa* have been transferred from *A. sterilis* and *A. fatua* (Loskutov, 2000). The taxonomic classification of genus *Avena* is complicated and varies according to authors. Harlan and de Wet (1971) suggested a rational taxonomic classification system for crops with the idea of primary, secondary and tertiary genepools. According to their classification system, cultivated and wild hexaploid *Avena* species fall in the primary genepool category and are easy to cross with each other. The diploid species *A. strigosa*, however, is difficult to cross with the hexaploid species, but inter-ploidy crosses have recently been made to transfer crown rust resistance to *A. sativa* using special techniques such as embryo rescue (Rines and Carson, 2007).

2. LITERATURE REVIEW

2.1. Brief history of oat

Oat is a cereal grain crop belonging to family Gramineae (Poaceae) with a haploid chromosome number of seven. The genus *Avena* has three ploidy levels: diploid, tetraploid and hexaploid.

The classification of cultivated and wild species of the genus *Avena* remains somewhat confusing. Species and subspecies numbers and names vary according to author and criteria used to delineate taxa. A frequently used classification of the genus *Avena* was provided by Baum (1977). The centre of origin of oat is unknown, but it may have been domesticated in Asia Minor or the Mediterranean region. The major centre of diversity is Asia Minor where most subspecies of cultivated hexaploid oat are found (Gibson and Benson, 2002). The history of the oat crop is little known before the time of Christ. Oat was not considered an important crop to man for a long time as it was a weed in other cereals such as wheat and barley for centuries before being domesticated as a crop (Barker, 1985). Domestication most likely occurred outside the major centre of diversity. The oldest known oat grains were found in Egypt among remains of the 12th Dynasty, and are approximately 4000 years old. However, the oldest known cultivated oat were found in Western Europe from the Bronze Age (Moore-Colyer, 1995). Descriptions from the 18th century suggest oat use primarily as a horse and livestock feed in many parts of Europe (Barker, 1985; Gibson and Benson, 2002).

The evolution of oat as a cereal crop is closely related to the social and cultural development of various communities in the Western world. Oat was first brought to North America by European immigrants in 1602 to what is now the state of Massachusetts, USA. The first oat in Canada was grown during 1605 in Nova Scotia and 1617 in Quebec (McKenzie and Harder, 1995). Oat was also taken to other parts of the world such as Australia and New Zealand where it was cultivated as an important winter season crop. By the last quarter of the 19th century, oat production shifted to western North America in the middle and upper Mississippi Valley and Western Canada where it became a major spring season crop. More recently, major production is in the north central states of Iowa, Minnesota, Wisconsin, North Dakota, South Dakota, Michigan and the western Prairie region of Canada. The winter annual red oat (*A. byzantina*) was

taken to South America and southern North America by the Spanish and Portuguese, where it is primarily grown as a forage crop (Kelling and Fixen, 1992). The diploid oat (*A. strigosa*) was also taken to Latin America.

Oat is chiefly grown in Europe and North America and is 4th most important cereal in Canada after wheat, barley and maize. In the past, it has been prominently grown as feed for horses and other livestock. Russia remains a major player in world oat production followed by Canada and the United States. Since the early 1960s the Prairie Provinces have produced nearly 80% of total oat produced in Canada (Canada Grains Council, 2006). However, since oat was used primarily as a livestock feed, it was replaced by barley during late 20th century because of better nutrient composition of barley. In recent years, there has been an increase in oat production because its use has shifted from livestock feed to human food. During 2008-2009, oat was grown on 1,448,000 hectares in Canada with a total production of 4,273,000 tonnes (Statistics Canada, 2010).

2.2. Oat agronomy

Oat can be grown in climatically diverse areas but performs best under cool, moist conditions and is likely to be damaged by hot and dry weather, especially during grain fill. It can be grown on different soil types, but medium-textured soils with good water holding characteristics are most suitable. Annual precipitation in oat-growing regions ranges from 38 to 114 cm, but is often 76 cm or less (Sorrels and Simmons, 1992). Growing season precipitation is a key concern for oat production. Grain yield may be reduced greatly if there is water stress during the reproductive stages of plant growth. Oat production was limited if precipitation was less than 20 to 30 cm during the critical May to August period in Canada (Coffman and Frey, 1961). Oat can tolerate acidic soils with a pH of 4.5 but yield is lower. Highest yield is obtained over a soil pH range of 5.3 to 5.7 (Alam and Adams, 1979) while saline soils tend to reduce oat plant growth more than either wheat or barley. The major oat growing areas of North America, Europe, and Asia are found between latitudes of 40° and 60° north.

In North America, the oat-growing season is short (80-110 days) limiting grain yield. Early season seeding is possible because germination will occur at soil temperatures of 3°C to 5°C (Forsberg and Reeves, 1995), and ensures best use of available moisture, avoids mid-summer drought and heat, and circumvents damage by disease, particularly leaf (crown) and stem rust. A 34-year study in Nebraska suggested that delaying oat seeding by 10 or 20 days caused reduced yields of 10% or 26%, respectively (Forsberg and Reeves, 1995). It is also reported that later seeding dates often reduce grain test weight. May et al., (2009) reported that seeding oat during early May or early June did not affect kernel weight; however, delayed seeding to mid June caused a significant decrease in kernel weight. Early seeding (during May) resulted in significantly higher wild oat density, hence increasing crop-weed competition. Oat yield and quality were improved by early seeding and high seeding rate (May et al., 2009). In general, seeding at the earliest possible date and average daily temperatures during the growth season between 13°C to 19°C have resulted in highest grain yield (Forsberg and Reeves, 1995). Some studies have suggested that an increase in the oil content of oat can be achieved by growing oat at lower temperature, and environmental conditions might affect oat oil fatty acid composition (Welch, 1995).

2.3. Oat chemical composition

Oat grain chemical composition is variable and can be affected by genotype, growing environment and their interaction. Oat grain has a soft kernel (groat) and is considered a high-quality food and feed. The oat groat generally has the highest protein concentration of the cereals (12-20%) depending on genotype and growing environment (Peterson, 1992). Oat amino acid profile is considered nutritionally better than wheat, barley or maize, with higher levels of all essential amino acids. Oat is the only cereal which contains oil distributed throughout the seed. This quality is unique to oat but makes groat milling more difficult than for other cereals (Peterson, 1992). Oat oil percentage normally ranges between 4 and 11%, but values as high as 18% have been reported for an experimental line developed by recurrent selection (Holland et al., 2001). Higher oil oat lines are preferred as livestock feed because of the high energy density of oil versus carbohydrate. However, selection for high oil in oat groat appears to reduce potential grain yield (Holland et al., 2001). In contrast to the livestock feed industry, low oil oat

lines are often preferred for use in the food industry because of the negative high caloric value of oil.

Oat oil has a high proportion of unsaturated fatty acids, which is good for human nutrition. However, high oil content with higher levels of unsaturated fatty acids has been shown to lead to deterioration of oat product shelf life. Rancidity is a major limiting factor in processing and storage of oat. Biermann et al. (1980) reported that broken kernels during harvesting make oat more susceptible to hydrolytic and oxidative rancidity compared to wheat, and leading to development of bitter taste. Liukkonen et al. (1992) suggested that lipid hydrolysis (hydrolytic rancidity) is the major cause of deterioration of oat products, compared to lipid oxidation (oxidative rancidity). Lipase inactivation, the lipid hydrolysis initiating enzymes, is necessary to prevent lipid hydrolysis in oat, thus deterioration during processing and storage of processed oat groats and flour and for food products using those ingredients (Ekstrand et al., 1993). Thus, hydrothermic or steam treatment at 90-100°C at groat moisture levels above 12% is applied during oat groat processing to inactivate lipases (Frey and Hammond, 1975). The greater importance of hydrolytic rancidity risk suggests fatty acid composition may not be as critical for oat oil stability as is the case for many oilseed crops where oxidative rancidity is normally the greater risk.

The whole oat groat is considered nutritious because of high proportions of soluble dietary fiber, unsaturated fatty acids, high quality protein and several phytochemicals as listed in the Table 2.1 (Kirk and Sawyer, 1999).

Table 2.1. Average oat groat composition

Component	Amount
Moisture	13.3 %
Protein	13 %
Lipids	7.5 %
Fiber	10.3 %
Ash	3.1 %
Calcium	60 mg/100 g
Phosphorus	372 mg/100 g
Iodine	16 mg/100 g
Iron	3.8 mg/100 g
Zinc	3.9 mg/100 g
Thiamin	0.50 mg/100 g
Riboflavin	0.14 mg/100 g
Niacin	1.3 mg/100 g
Energy	1.61 MJ/100 g

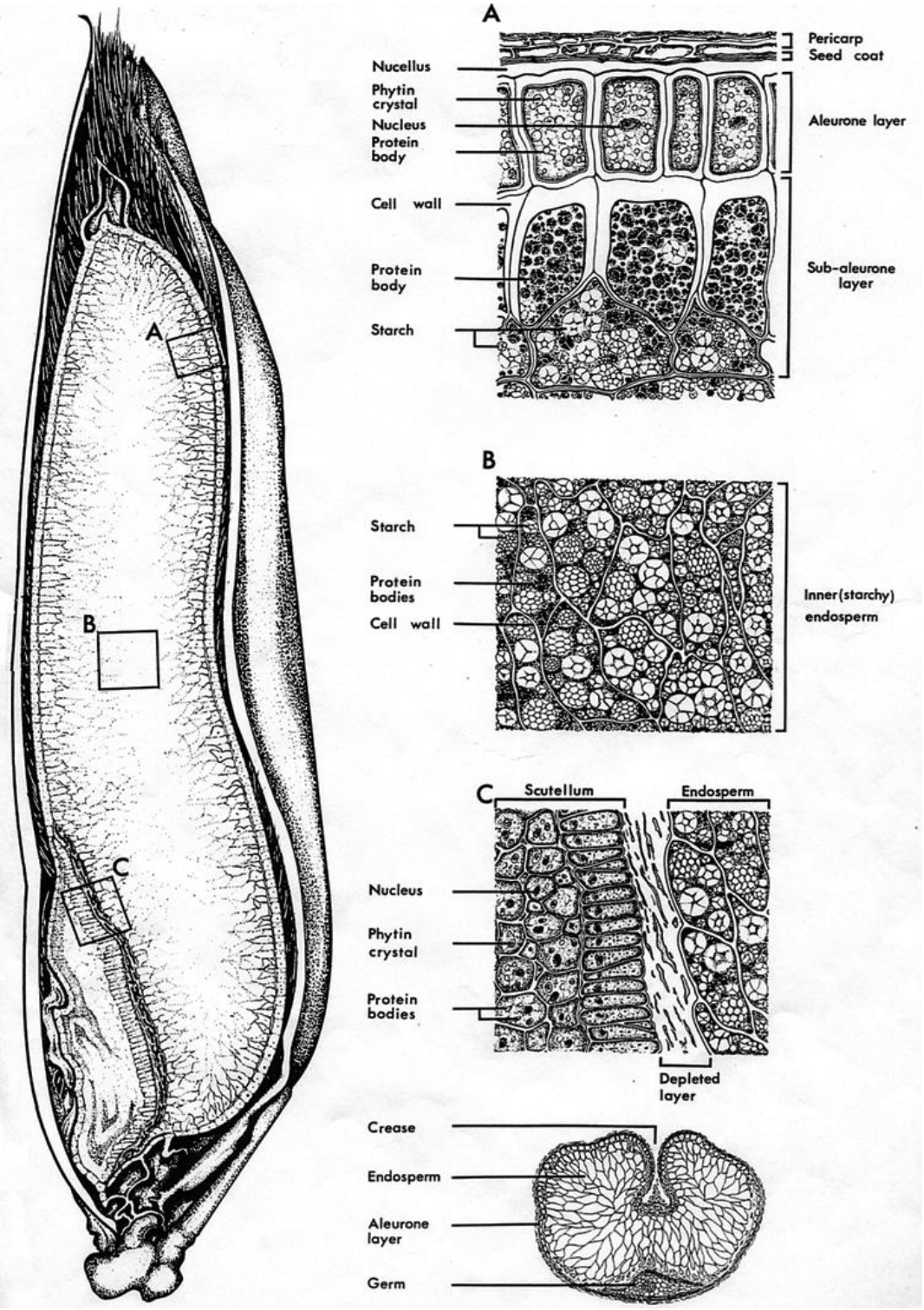
Oat bran is the outermost layer of the oat groat and generally contains a high amount of total dietary fiber and beta glucan (soluble dietary fiber). Average composition of oat bran is provided in the Table 2.2.

Table 2.2. Average oat bran composition (Marlett, 1993)

Component	Amount
Protein	12 - 26.2 %
Carbohydrates	47 - 58.5 %
Lipids	2.2 - 10.8 %
Dietary Fiber	15 - 22 %
Beta-Glucan	6.6 - 10.4 %
Potassium	441 mg/100 g
Magnesium	171 mg/100 g
Copper	0.17 mg/100 g
Iron	6.4 mg/100 g
Niacin	1.3 mg/100 g
Alpha-tocopherol	0.5 mg/100 g

The structure of the oat kernel is described in Figure 2.1. Physical grain quality is generally measured by calculating groat to hull ratio (groat weight/total grain weight). Average oat groat percentage in harvested grain is 70-75% but depending on genotype can be >80% under ideal growing conditions and is usually lower when biotic or abiotic stress negatively affect grain filling. Less hull is favorable for both food and feed cultivars. Because hull mainly contains indigestible fibre, it is considered a negative trait (Rines et al., 2006).

Figure 2.1. Structure of oat kernel (Fulcher, 1986)



The oat groat contains significant amounts of beta-glucan (2.3 to 8.5 g/ 100 g) dependent upon genotype and growing conditions (Welch et al., 2000). However, lines containing up to 14.2% beta-glucan have been reported (Cervantes-Martinez et al., 2001). Beta-glucan is distributed throughout the endosperm but is concentrated in the aleurone and sub-aleurone layers. It is found mainly in the endosperm cell walls constituting some 75% of the cell wall (Miller et al., 1995). High beta-glucan is desirable for human food and is the basis of the oat heart health claim in the United States (Peterson, 2004).

2.4. Oat oil

As stated earlier, oat has significant levels of oil in its groat. In fact, as a whole grain, oat has the highest oil concentration of all cereals. Research on increasing oil content has been conducted and oil percentage up to 18% has been achieved (Holland et al., 2001). Oil content is directly related to energy content and has a significant impact on nutritional quality. Oil also affects flavour (Heydanek et al., 1981). Oat groats collected from the field have little flavour and retain a bland and slightly bitter taste (Gansmann et al., 1995). However, they develop their characteristic flavor due to oxidation of lipids and formation of N-heterocyclic compounds due to exposure to direct heat during processing.

Conversely, lipids are also often associated with the negative trait of rancidity and off flavor development in oat products. The rate of lipid oxidation is greater in broken or damaged groats than in the undisturbed grain. Lipids of sound oat kernels are generally stable and show little change as whole grain when stored at normal storage conditions at a temperature of 20°C and 12-14% moisture. The rancid odor comes from carbonyl compounds formed during oxidation. Because oat processing usually involves grinding or flaking of groats, rancidity is a major limiting factor for the food industry (Ekstrand et al. 1993). However, there is not a single certain way for the reaction to occur and several factors play a major role in oxidation rate. Temperature, light, moisture, groat antioxidant levels and volatile compound formation may be involved (Ekstrand et al. 1993). Oat lipids are also known to have a significant effect on the oat starch pasting properties due to complexes formed between starch and lipid molecules (Tester and Karkalas, 1996).

Oat oil has been suggested as a potential edible oil source. Oat oil stability is similar to soybean oil, however, significantly higher levels of free fatty acids and lipids other than triglycerides are found in oat oil (Kalbasi-Ashtari and Hammond, 1977). Oat oil is rich in unsaturated fatty acids such as oleic (18:1) and linoleic acid (18:2). These fatty acids play a major role in the biosynthesis of long chain polyunsaturated fatty acids such as arachidonic acid (AA), eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) in the human body. Compared with other cereals, some oat species have more oleic acid and less linoleic acid. Glycolipids and antioxidants present in the oil give it excellent stability (Kalbasi-Ashtari and Hammond, 1977).

In the past, wild crop species have been used to transfer desired characters to cultivated species. Interspecific crosses between *Avena* species of different ploidy levels can be used to affect the grain quality of cultivated hexaploid oat, *A. sativa* (Loskutov, 2000). Therefore, a better understanding of the genetic variation of the oat oil composition and transferring the most desired fatty acid composition to current *A. sativa* cultivars via plant breeding may be useful for increasing the health-promoting properties of oat.

2.5. Lipid and fatty acids

The term lipid refers to a structurally diverse group of molecules generally soluble in organic solvents (e.g. chloroform) and includes a wide variety of fatty acid-derived compounds as well as certain pigments and secondary compounds not related to fatty acids. There is no single definition for lipid(s) although analysts tend to have a firm understanding of the term.

Fahy et al. (2005) developed a promising classification system for lipids. Their definition of lipid is as follows:

"Hydrophobic or amphipathic small molecules that may originate entirely or in part by carbanion-based condensations of thioesters (fatty acids, polyketides, etc.) and/or by carbocation-based condensations of isoprene units (prenols, sterols, etc.)"

The most common class of lipids in nature consists of fatty acids linked to glycerol by ester bonding. Fatty acids are considered the simplest lipids and consist of a monocarboxylic acid at

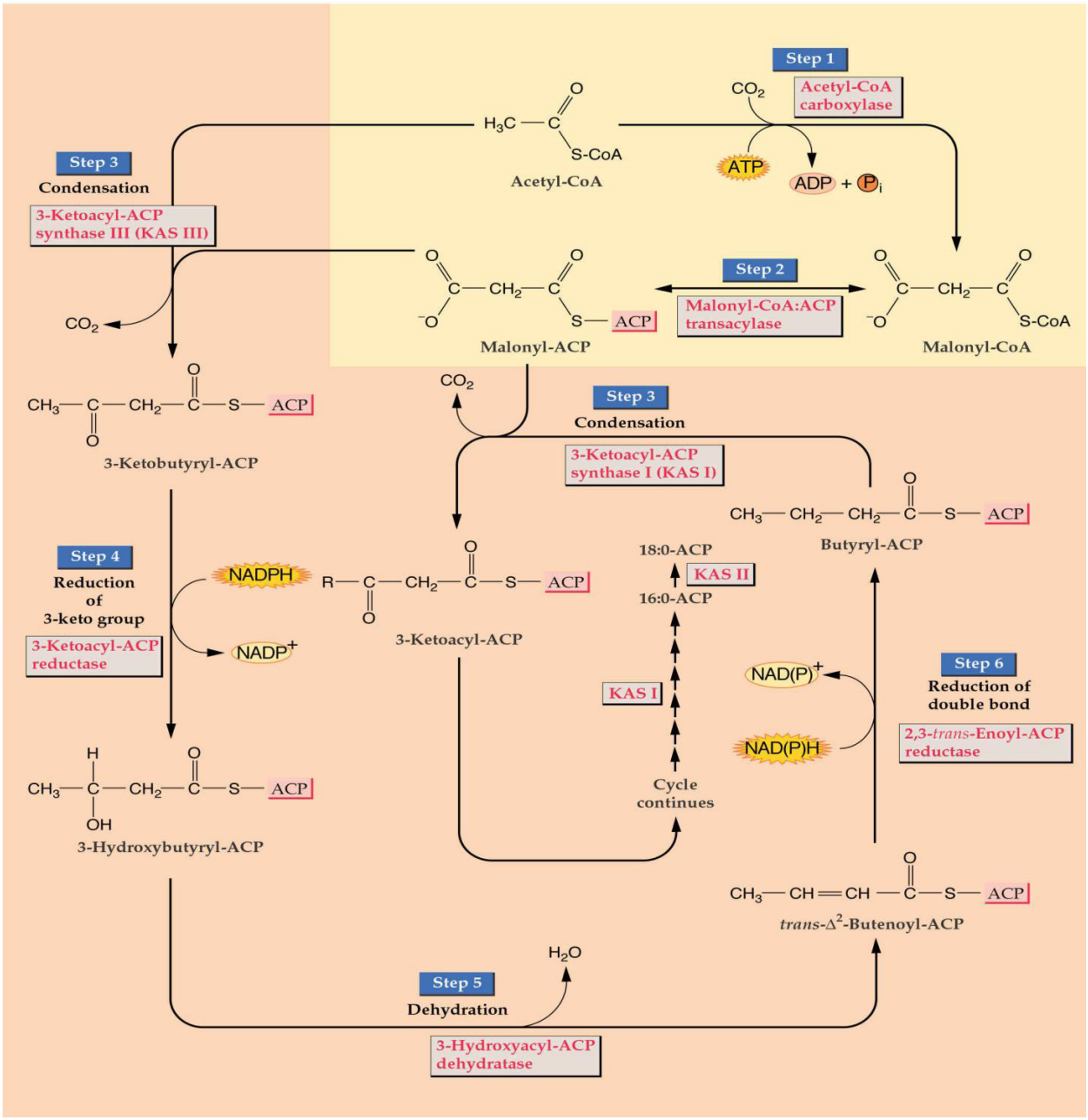
one end of a hydrocarbon chain. Other types of lipids include, but are not limited to, phospholipids, glycolipids, sphingolipids, steroids, sterols and waxes. Lipids are important for functions in living organisms including – serving as a chemical reserve of energy, building blocks of biological membranes and important biological signaling molecules (Dowhan and Bogdanov, 2002).

Glycerolipids, sphingolipids and sterols are the most notable structural components of plant membranes and act as a hydrophobic barrier to separate cells and the contents of organelles (e.g. chloroplast and mitochondria) from the cytoplasm. Triacylglycerols and waxes are storage compounds which can be an important energy source. Some examples of lipids active during signaling in biological processes include abscisic acid, gibberellins, brassinosteroids, inositol phosphates and diacylglycerols (Buchanan, 2000). Lipids are also known to have secondary function such as providing mouth feel in food (Forss, 1969).

2.6. Fatty acid biosynthesis pathway in plants

The metabolism of fatty acids and lipids is complex. The complexity is mainly because of compartmentalization of the fatty acid biosynthesis pathway in different organelles in plant cells and extensive lipid movement from one organelle to another (Buchanan, 2000). An overview of various steps in the fatty acid biosynthesis pathway in plants is illustrated in Figure 2.2.

Figure 2.2. Fatty acid biosynthesis in plants (Buchanan, 2000)



Fatty acid biosynthesis in plants is composed of the following steps:

Step 1: Fatty acid biosynthesis begins with an ATP-dependent carboxylation process in which acetyl-CoA carboxylase (also known as ACCase) catalyses the formation of malonyl-CoA (also known as activated acetyl-CoA). Biotin carboxylase activates Co_2 by attaching it to a nitrogen in the biotin ring of the biotin carboxyl carrier protein (BCCP). The flexible biotin arm of BCCP carries the activated Co_2 from the biotin carboxylase active site to the carboxyltransferase site and this enzyme transfers activated Co_2 from biotin to acetyl-CoA, producing malonyl-CoA. ACCase is highly regulated enzyme which is active in light and inhibited in dark conditions. Also, being a part of the first step of lipid synthesis, this enzyme can be inhibited by a class of herbicides called ACCase inhibitors. The herbicide compounds affect meristem of the grasses and kill them by ceasing production of cell membrane.

Step 2: Malonyl-CoA transacylase (MT) exchanges the CoA for the ACP (Acyl Carrier Protein) which is an essential protein co-factor in fatty acid biosynthesis.

Step 3: The 3-ketoacyl-ACP synthase (KAS) enzyme has three isoforms – (KAS) I, II and III.

KAS III is utilized during the first condensation reaction, which includes a carbon-carbon bond formation between C1 of an acetate primer and C2 of the malonyl-ACP. KAS I is active with C4-C14 acyl-ACPs and during production of C6:0 to C16:0. KAS II accepts only longer carbon chains and elongation of 16:0-ACP to C18:0-ACP requires KAS II.

Step 4: The 3-ketoacyl-ACP reductase (KR) enzyme reduces the keto group from 3-ketoacyl-ACP to form 3-hydroxyacyl-ACP.

Step 5: The 3-hydroxyacyl-ACP dehydratase catalyzes the removal of water from 3-hydroxyacyl-ACP to form the 2,3-*trans*-enoyl-ACP and in the next step, enoyl-ACP reductase converts 2,3-*trans*-enoyl-ACP to its corresponding saturated acyl-ACP.

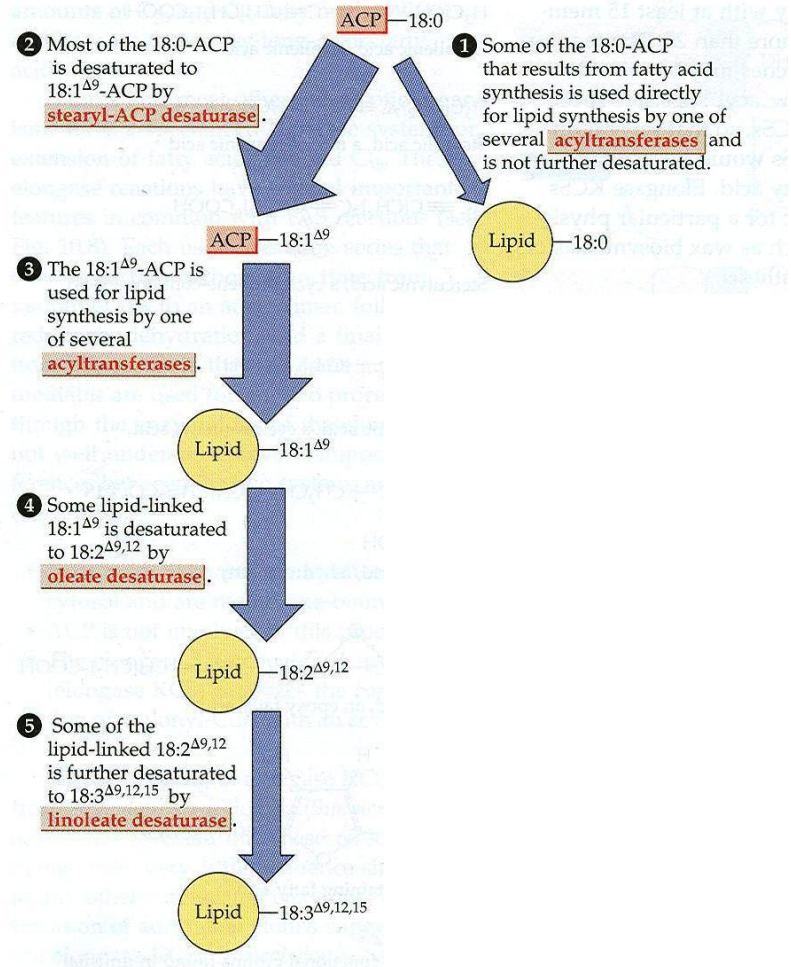
Step 6: Enoyl-ACP reductase (ER) reduces the double bond and the repetitive condensation of 2 carbon units produces 16:0=ACP and 18:0-ACP.

Each cycle of fatty acid synthesis adds two carbons to the acyl chain and the reaction stops at 16:0 or 18:0 when thioesterase terminates the biosynthesis cycle. 18:1-ACP is produced using

18:0-ACP using a stearoyl-ACP desaturase as a catalyst. 16:1-Δ9 is desaturated by using a soluble acyl-ACP Δ9 desaturase enzyme. Fatty acid elongation happens in the endoplasmic reticulum.

Several desaturase enzymes catalyze the formation of *cis*-double bonds which causes kinks in the fatty acid chain (Figure 2.3) and generate a diverse variety of unsaturated fatty acids in plant membranes and storage reserves.

Figure 2.3. Introduction of double bonds in plant lipids (Buchanan, 2000)



2.7. Modification of fatty acid composition in crops

Several examples in the literature demonstrate modification of fatty acid composition in crops using induced mutagenesis or even genetic engineering. Some examples are:

2.7.1. Canola/Rapeseed (*Brassica napus* L.)

- Canadian canola lines 45A37 and 46A40 were selected for high oleic acid and low linoleic acid compared to conventional Canadian canola varieties. These lines were developed via induced mutagenesis by exposing seeds of the canola cultivars Regent, Topas and Andor to a solution of ethylnitrosourea (8 mM) in dimethylsulfoxide. Mutation occurred within the *fad2* gene which encodes a desaturase enzyme boosting the conversion of C18:1 to C18:2 and C18:3 fatty acids in plant cells. The mutation apparently blocked the desaturase enzyme resulting in the accumulation of high levels of oleic acid (C18:1). Further, the linolenic acid level was reduced by cross-breeding the high oleic acid lines with the registered canola cultivars Stellar and Apollo which have low linolenic acid. The oleic acid content of lines 45A37 and 46A40 was 24% higher than in conventional lines, and linoleic and linolenic acid were reduced 40% and 78% respectively (Health Canada, 2009).

- High oleic acid levels have been obtained using genetic engineering in Australian *Brassica napus* and *Brassica juncea* lines. Co-suppression constructs were cloned from both species which carried the oleate desaturase gene. These constructs were then transferred to *B. napus* and *B. juncea* plants and analyzed for the presence of the selectable marker. The experiment resulted in significantly higher oleic acid levels in *B. napus* and *B. juncea*. (Stoutjesdijk et al., 2000)

2.7.2. Flax (*Linum usitatissimum* L.)

High linolenic acid content has hindered food use of flax oil due to problems related to development of off-flavors due to auto-oxidation of linolenic acid. Green(1986) described the possibility of lowering flax linolenic acid level by the development of two induced mutants ‘M1589’ and ‘M1722’. Both mutants are homozygous for a single gene mutation which results in the reduction of linolenic acid from 34% to 22% and an increase in linoleic acid from 15% to 27%. Varieties high in alpha linolenic acid, an omega-3 fatty acid, such as AC Emerson, CDC

Normandy and Linola 1084 have been developed which provide flax for the functional food market. Major objectives of the three flax breeding programs in Canada (Agriculture and Agri-Food, Canada, Morden; Crop Development Centre, University of Saskatchewan and the Viterra program at Vegreville, Alberta) include high oil content and high levels of alpha linolenic acid (Flax Council of Canada, 2010).

2.7.3. Soybean (*Glycine max* (L.) Merr.)

Kinney (1996) describes several different soybean elite lines with genetic modification of fatty acid composition. Considerably lower levels of total saturates in soybean oil were obtained by suppressing the soybean *Fat B* gene. If the soybean *Fad 2-1* gene was suppressed, oleic acid increased up to 85% with a lowered level of polyunsaturated fatty acids and saturated fatty acids. A mutation in the gene encoding delta-9 desaturase resulted in the accumulation of higher stearic acid in soy oil.

2.7.4. Sunflower (*Helianthus annuus* L.)

Soldatov (1976) described the use of chemical mutagenesis in sunflower to produce a line with significantly greater oleic acid (85%) compared to conventional lines (30%). More recently, attempts have been made to develop molecular markers for selecting high oleic acid lines in sunflower with marginal success (Dehmer and Friedt, 1998).

Modification of fatty acid composition in cereal crops is limited and few if any attempts have been made to alter specific fatty acids in cereals. Shimada et al. (2000) reported increased linolenic acid content in seeds, leaves and roots of the transgenic rice plants by introduction of a tobacco microsomal, omega-3 fatty acid desaturase gene (*NtFAD3*). Song et al. (1997) reported an increase in oil content in corn (Zea mays L.) but little to no information is available about fatty acid composition modification.

2.8. Ideal oil composition

Although oils are an important part of human and other animal diets, there is ongoing debate regarding the definition of an ideal oil profile. Generally, oil end use is the most important factor to consider when describing an ideal fatty acid composition. US health claims suggest a higher probability of coronary heart disease from diets high in saturated fats and oils (Food and Drug Administration, 1997). Saturated fats increase the level of LDL cholesterol in human blood, increasing the risk of heart attack, stroke and other problems. For selecting oil for human health, it is recommended to keep the level of saturated fatty acids (primarily palmitic and stearic acid) as low as possible. However, commercial food products such as margarine and shortenings with desired thermal stability, melting and crystallization properties may require higher levels of saturated fatty acids ranging from 15 to 25% (Wood et al. 1993, Lichtenstein et al. 1999).

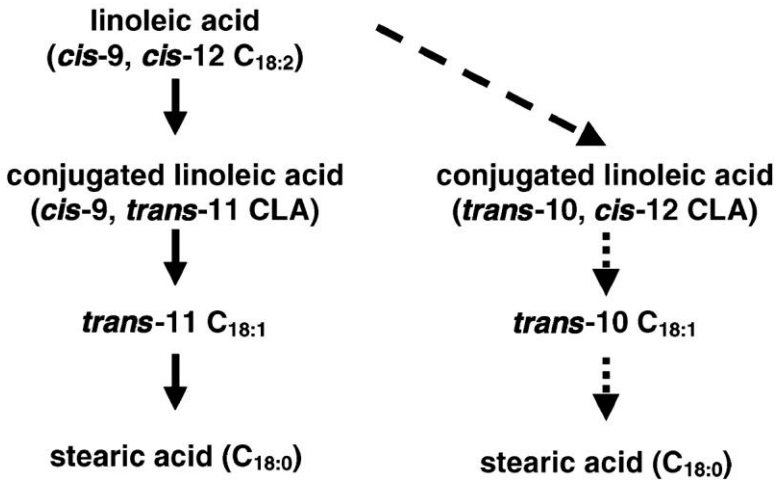
The original essential fatty acid linoleic acid (Tinaco, 1982), nutritionally is one of the two essential fatty acids, the other being linolenic acid, which the human body cannot synthesize on its own. These fatty acids act as substrates for synthesis of long chain polyunsaturated fatty acids (PUFA) and other regulatory chemicals. A daily intake of 17 grams of PUFA for adult males and 12 grams for adult females is recommended by the National Academy of Sciences, The Institute of Medicine. 1.6 grams of linolenic acid for adult males and 1.1 grams for adult females is also recommended (Food Fats and Oils, 2006). Hence, linoleic and linolenic acid are important for better oil for human diets. Linoleic and linolenic acid are poly unsaturated fatty acids and are of a concern to the food industry because of auto-oxidation and development of off-flavors. Fortunately, they are not required in high amounts in the human diet. Therefore, the food industry has adopted high oleic acid, a monosaturated fatty acid, as a desired oil profile because of better stability and improved shelf life (Fitzpatrick and Scarth, 1998; Töpfer et al., 1995). Hence, an ideal oil profile for the human diet should be low in saturated fatty acids, with sufficient amounts of essential fatty acids and high oleic acid for increased stability.

High levels of saturates are undesirable in the human diet, but preferred for ruminant diets (Moate et al., 2007). Most of the fats in a ruminant diet are digested through a process called lipolysis. Enzymes such as lipases, galactosidases and phospholipases hydrolyze the ester bonds

of triacylglycerides and other lipids, yielding glycerol and free fatty acids (Moate et al. 2008). Diglyceride and monoglyceride intermediates are metabolized rapidly, so they do not accumulate in appreciable amounts in the rumen fluid (Hawke and Silcock, 1970). Rumen microbes convert the unsaturated fatty acids into saturated fatty acids through biohydrogenation (Figure 2.4).

Feeding high levels of PUFA to lactating dairy cows can have undesirable effects, including milk fat depression. Fish oil, for example, can decrease milk fat by up to 10g/kg (Chilliard and Doreau, 1997). *Trans*-10, *cis*-12 conjugated linoleic acid (CLA) is the specific isomer responsible for milk fat depression and is produced in the rumen as an intermediate product of the biohydrogenation of linoleic acid (Bauman and Griinari, 2003). Hence, an ideal oil profile for a ruminant diet is different from the ideal oil profile for the human diet, where having high amounts of saturated fatty acids is undesirable.

Figure 2.4. Two possible pathways for biohydrogenation of linoleic acid in the rumen (Bauman and Griinari, 2003)



2.9. Gas chromatography

In analytic chemistry, gas chromatography (GC) is extensively used for detecting and identifying the components of a mixture of compounds. This technique is very similar to fractional distillation and separates the components of a mixture primarily based on boiling point differences, but at a fine micro level. GC is reliable, efficient and cost effective method of separation, requires small sample and provides fast and highly accurate quantitative analysis.

Major components of GC include:

- Gas supply – involves two types of gases, carrier gas to carry the sample through the column and a detector support gas to support the flame in the flame ionization detector.
- Introduction of sample – can be by hand or auto sampler. The most common type of sample introduction involves syringe injection of the sample into a heated injection port.
- Column – separation of components of the sample takes place in the heated column, a long tube running from the sample injector to the detector.
- Detector – detector function involves detection of sample components as they pass through the end of the column. The most common detector is a Flame Ionization Detector (FID) in which molecules of the sample are burned in the flame with produced ions detected.

A computer system is used by most GC systems to collect and analyze the data. Signals from the detector are collected and converted into user friendly information. Generally, the system generates a chromatogram which is plotted using information on the amount of the component as peak area with elution time as retention time. Contents and concentration of various components of the sample are determined by comparing various chromatograms (McNair and Miller, 2009).

To maximize GC efficiency, fatty acids in biological samples need to be split off from lipid molecules and are converted into other low boiling point derivatives such as alcoholic esters and methyl esters. In early days of GC, lipid bound fatty acids were split off by saponification using sodium hydroxide or potassium hydroxide, and then methylated with acids. Because the process was complex and time consuming, direct lipid transesterification methods were developed (Liu, 1994). A number of methods are available today for extraction and preparation of lipids for GC

analysis, including acid-catalysed transesterification, base-catalysed transesterification or specific methylation of non-esterified fatty acids (Eder, 1995). Acid-catalysed transesterification is most often used to prepare fatty acid methyl esters from seeds and other biological samples. It is simpler than other methods, but the reaction does not take place at room temperature and requires heating. Morrison and Smith (1964) reported that acid-catalysed transesterification using boron trifluoride-methanol reagent (12-14%, w/v) takes about 2 minutes to methylate free fatty acids, 10 minutes for phosphoglycerides, 30 minutes for triglycerides and 100 minutes for sphingolipids. However, methanolic acids such as sulfuric acid and hydrochloric acid with different acid concentration and different reaction times can also be used for lipid esterification. Hydrochloric acid (5%, v/v) or sulfuric acid (2%, v/v) can transesterify all the lipids available in biological samples. The fatty acid methyl esters have improved peak shape and separation in GC due to better volatility. Peaks of particular fatty acid methyl esters can be identified by comparing their retention times with those of commercially available purified samples (Liu, 1994).

3. MATERIALS AND METHODS

3.1. Sample collection

A total of 917 different oat accessions were collected and analyzed for their fatty acid profiles. Seed was provided by Plant Gene Resources of Canada (PGRC), Saskatoon Research Centre of Agriculture and Agri-Food Canada (AAFC); the Crop Development Centre (CDC), University of Saskatchewan; and the Eastern Cereal and Oilseed Research Centre (ECORC), AAFC, Ottawa (Table 3.1).

The 48 high/low oil breeding lines were a selection of genotypes from the oat breeding program at U of S. Oil content ranged from 4.5 to 12.6% (Rossnagel 2010, Unpublished data). The lines were grown in 2006 and the seed was stored at the CDC Field Laboratory.

The Historic Canadian Cultivars group consisted of 106 genotypes representing cultivars released each decade from the late 19th century to the early 21st century. The genotypes were grown at Saskatoon in 2003 and stored as a part of the seed gene bank at PGRC.

The Integrated Oat Improvement (IOI) germplasm set was received from Dr. Nicholas Tinker at the ECORC and represented a sub-set of a diverse international collection of 97 oat genotypes. The material was grown in 2008 and 2009 at the CDC in Saskatoon. However, in 2009, seed filled improperly due to severe August storm damage and, therefore, a second sample set grown in 2008 at Ottawa was sourced from the ECORC. The 'IOI selections' sub-set was included in the experiment due to its genotypic diversity.

The Nordic Oat Selection set consisted of 210 genotypes from Denmark, Finland, Norway and Sweden available from the PGRC collection.

A selection of genotypes from cultivated hexaploid *Avena* species (*A. sativa, A. byzantina* and *A. sativa* subsp. *nudisativa*), cultivated diploid *Avena* species (*A. strigosa*) and wild hexaploid *Avena* species (*A. sterilis* and *A. fatua*) from the PGRC was included.

The evaluated oat material sub-groups are listed in Table 3.1.

Table 3.1. Sub-sets of 917 oat accessions evaluated for fatty acid profile

Background/Group	Year of Production	Source and site of production	Total Number of Samples
High/low oil breeding lines	2007	U of S, Saskatoon, Canada	48
Historic Canadian Cultivars	2003	PGRC, Saskatoon, Canada	106
Integrated Oat Improvement (IOI) Germplasm set	2008	U of S, Saskatoon, and Eastern Cereal and Oilseed Research Centre, AAFC, Ottawa, Canada	97
Nordic oat selections	2007	PGRC, Saskatoon, Canada	210
A. sativa L.	From the PGRC collection	PGRC, Saskatoon, Canada	46
A. byzantina (C. Koch)	From the PGRC collection	PGRC, Saskatoon, Canada	47
A. sativa L. subsp. *nudisativa* (Husn.) Rod.Et Sold.	From the PGRC collection	PGRC, Saskatoon, Canada	17
A. strigosa Schreb	From the PGRC collection	PGRC, Saskatoon, Canada	20
A. sterilis L.	From the PGRC collection	PGRC, Saskatoon, Canada	20
A. fatua L.	From the PGRC collection	PGRC, Saskatoon, Canada	18
Selected genotypes grown at 2 locations (2 replications) in 2009		Replicated field trials at U of S & AAFC plots, Saskatoon, Canada	288
Total			917

3.2. Replicated field trial (RFT), 2009

Based on initial fatty acid profile results from samples from the first two sets analyzed, '2008 CDC high/low oil lines' and 'Historic Canadian cultivars', 34 genotypes were selected for a replicated field experiment. Eighteen cultivars and breeding lines from the U of S oat breeding program also were included. Cultivars 'CDC Sol-Fi' and 'HiFi' were included to obtain insight into their fatty acid profiles since 'CDC Sol-Fi' is a low fat genotype, 'HiFi' is a high fat genotype, and a DArT (Diversity Arrays Technology) molecular markers map for a recombinant inbred line population derived from these two parents is available. 'Aslak' and 'Matilda' are the parents of the world's only double haploid population from Finland (Tanhuanpää et al., 2008) and for which a DArT map is also available. Two recombinant inbred lines (RIL) 'OT 3033' and 'OT 3024', parents of another CDC DArT mapping population, were also included. Fatty acid profile data, along with an available DArT map for these genotypes, may be utilized in the future to identify molecular markers related to specific oat fatty acids. Breeding lines SA02984, SA071369, SA071380, SA060470, SA071192, SA071555, SA071405, SA071709, SA080473, SA080029, SA080498 and SA080511 were included in the replicated field experiment based on exceptionally high fat levels, resulting in a total of 52 genotypes for the 2009 RFT.

Genotypes were grown in a randomized complete block design field trial during the summer of 2009 with two replications, at two locations, (1) Preston plots, U of S (52° 10' N, 106° 41' W) and (2) AAFC plots, Saskatoon (52° 10' N, 106° 41' W). Five replications of four checks (CDC Dancer, CDC SO-I, SA02995 and SA96121) were included in each block, resulting in 52 samples plus 20 check samples per block. In essence, 10 replications of each check were grown at each location to measure the consistency of the field and laboratory portion of the experiment.

Three metre long single row plots were planted at the AAFC plots on May 7th, 2009, using seven grams of seed per row. Rows were separated by winter wheat rows with a row-to-row spacing of 30 cm. Micro-plots (1.2 m X 1.5 m) were planted at the U of S Preston plots on May 13th, 2009. Micro-plots were separated by 45 cm within each range and 1.8 m pathways between ranges. Twenty five grams of seed was planted per micro-plot. Single row planting was used at

AAFC because, for some lines, there was insufficient seed available for micro-plots at both locations.

The U of S micro-plots were irrigated, whereas no irrigation was provided for AAFC rows. It was discovered at flowering that the seed material for some accessions had slight admixtures. Therefore, representative plants of each genotype were identified visually and three panicles were harvested from these plants from each row at AAFC and from each plot at the U of S. Harvesting took place on September 9th, 2009, at AAFC and on September 21st, 2009, at the U of S plots. Harvested panicles were dried, threshed and whole seed was stored in PGRC seed storage system (4°C, 30% relative humidity) for fatty acid analysis.

3.3. Chemical analysis

In this experiment, transesterification was performed using methanolic sulfuric acid (2%, v/v) due to its ability to transesterify all the lipids present in oat groats except sphingolipids. The followed procedure was a modification of the procedure described by Leonova et al. (2008).

3.3.1. Sample preparation

Six seeds from each genotype were manually dehulled. The resulting groats were placed in a 5 mL plastic tube with five glass beads (5 mm). The plastic tubes were placed in a custom built shaker to crush/grind the seed into flour. The grinder was run three times for 30 min each for every group of samples to ensure uniform grinding. Groats from a few samples were very hard and were not as uniformly ground as other samples. These samples were further hand ground into fine flour using a mortar and pestle.

3.3.2. Extraction of lipids and methylation

Fine flour of each sample was transferred to a clean glass culture tube (13 mm x 100 mm) and 2.5 mL of methanolic H_2SO_4 (2 %, v/v) was added to each tube to methylate the lipids in the sample. Methanolic H_2SO_4 solution was prepared fresh by mixing 2% concentrated H_2SO_4 (Reagent A.C.S., Fisher Scientific, Nepean, Ontario, Canada) into methanol [OmniSolv Methanol for gas chromatography, EMD Chemicals Inc., (an affiliate of Merck KGaA, Darmstadt, Germany) Gibbstown, NJ, USA] volume by volume. The solution in the glass culture

tube was placed in a heated stirring module (Pierce Reacti-Therm III, Rockford, IL, USA) and heated for 80 min at 90°C. After cooling to room temperature, 1 mL of prepared solution of internal standard (0.2 mg methyl heptadecanoate per mL of hexane) and hexane (OmniSolv) was added. The glass culture tube was tilted gently twice and held overnight to allow separation of the hexane phase on top of the methanol solution. The hexane phase from the top layer of the solution was extracted and transferred to screw cap GC vials for gas chromatography (GC) analyses.

Methylated fatty acid samples were injected into a Hewlett-Packard 6890 Series GC system (Hewlett-Packard Technologies) using an Agilent 6890 Series injector (Agilent Technologies, Wilmington, DE, USA) fitted with a DB-Wax capillary column (Agilent 127-7013, 10 m x 100 µm x 0.20 µm). The injector temperature was held at 240°C. Initial column temperature was 180-220°C (held for 10 min) and increased at a rate of 4°C min^{-1} to 240°C (held for 10 min). The detector temperature was 250ºC. A standard curve based on retention times was prepared to analyze the data using Agilent GC Chemstation software, Rev. B.01.01 [164] SR1 (copyright Agilent technologies, 2001-2005). The detection limit of the GC system was set to 0.01% after calibrating the retention times for internal standard and each fatty acid.

To evaluate and maintain consistency during GC analysis of different batches of samples, two constant check samples namely 'CDC Dancer' groats and CO_2 extracted oat oil (From Nature with Love, Natural Sourcing, CT, USA) were used. 'CDC Dancer' seed was dehulled, ground and analyzed in the same way as other groat samples. For the analysis of oat oil, 10 µL of oil was added directly into methanolic H_2SO_4, followed by the procedure described above.

Fifty gram whole grain samples were analyzed for protein, hull and oil content using Near Infrared Transmittance (NIT) (Infratec 1255 Food and Feed Analyzer™, Tecator AB, Höganas). Validated calibrations for oat groat protein, hull and oil were developed at the Crop Development Centre (CDC), University of Saskatchewan and are routinely used in the CDC-Oat breeding and R&D programs.

4. RESULTS AND DISCUSSION

4.1. Initial screening

A preliminary GC analysis of the 'U of S high/low oil lines' and the 'Historic Canadian cultivars' sub-sets was conducted to identify genotypes for the subsequent replicated field trial (RFT) experiment. The 'U of S high/low oil lines' sub-set was selected to test fatty acid profile variability among genotypes with a wide range of oil contents. The 'Historic Canadian cultivars' sub-set was chosen to determine whether changes had occurred in the fatty acid profile of oat cultivars over time from the late nineteenth century to date.

Six fatty acids were detected in every oat sample: palmitic acid (16:0), stearic acid (18:0), oleic acid (18:1), linoleic acid (18:2), linolenic acid (18:3) and eicosenoic acid (20:0). Although earlier research had reported the presence of other fatty acids in oat, 14:0, 20:1 to 20:5 and 9,10-epoxy-18:0, 9,10-epoxy-18:1, 12,13-epoxy-18:1(Leonova et al. 2008) and 20:1 to 20:5, 22:0, 22:1 and 24:0 (Sahasrabudhe, 1979), none of these fatty acids was detected in this experiment. Results for the 'U of S high/low oil lines' and 'Historic Canadian cultivars' sub-sets are provided in Tables 4.1 and 4.2. Although the average fatty acid levels for the two sub-sets were very similar, palmitic acid (20.6% and 21.0%); oleic acid (36.7% and 35.8%); and linoleic acid (37.5% and 39.5%), a range was detected for each major fatty acid: palmitic acid (16.7% - 25.7%), oleic acid (24.6% - 46%) and linoleic acid (28.5% - 45.4%). There was more diversity for stearic acid (0.7% - 4.8%), linolenic acid (0.6% - 5.4%) and eicosenoic acid (0.4% - 6.3%), the small proportions of these three fatty acids would limit the scope for manipulation from an oat end-user viewpoint. Therefore, only results for the three major oat fatty acids in terms of commercial end-user products, palmitic acid, oleic acid and linoleic acid will be discussed. The sum of palmitic acid, oleic acid and linoleic acid accounted for some 95% of total fatty acid content in all genotypes except 'AC Stewart', 'Yamaska', 'OAC Woodstock', 'Larain', 'Hinoat', 'Donegal', 'Fidler', 'AC Francis', 'Cartier', 'Gemini', 'Hajira' and 'Sioux' for which the total was between 84 to 95%. Among the above listed genotypes, 'OAC Woodstock', 'AC Francis' and 'Hajira' had notably higher contents of minor fatty acids. Total detected saturated fatty acids in 'Hajira' were 31.3%. Linolenic acid content in 'Hajira' was also higher, 5.40% compared to the mean 1.39%. Results for the three minor fatty acids from a potential commercial end-user

product viewpoint, stearic, linolenic and eicosenoic acid are described in Appendix Tables 9.1 and 9.2. Higher levels of the three less abundant fatty acids were observed in the 'Historic Canadian cultivars' sub-set.

The fatty acid profiles from these sub-sets were similar to those reported by Leonova et al. (2008) except for greater mean palmitic acid content in this experiment. Leonova et al. included ten *A. sativa* accessions, and the ranges reported for palmitic acid and oleic acid content were somewhat lower and narrower(13.9 to 17.4% and 31.4 to 40.4% respectively), compared to this experiment. This difference may be the result of different genotypes evaluated or the different growing environments in the two experiments.

Table 4.1. Major fatty acid composition data of 'U of S high/low oil lines' sub-set (FA percentage based on total FA detected by GC, corresponding minor fatty acid composition in the Appendix, Table 9.1)

U of S Number	% Palmitic acid	% Oleic acid	% Linoleic acid
SA97082 §	20.1	30.6	45.4 **
SA97172	18.9	36.4	40.6
SA97178	19.8	40.9	35.0
SA97233	20.7	35.2	40.3
SA97362 §	22.3	31.7	41.9
SA97396	21.5	36.4	38.4
SA97432	18.6	35.4	42.0
SA97443	21.2	37.7	37.2
SA97116	20.7	41.8	33.7 *
SA97665 §	19.4	34.9	40.8
SA97701	20.2	35.3	39.7
SA97062	22.3	34.8	38.6
SA97250	21.2	38.1	37.1
SA97404 §	17.4	41.1	37.3
SA97407	20.8	36.6	38.7
SA97409	19.9	40.0	36.3
SA97413	19.5	36.2	40.4
SA97457	22.3	30.2	43.9 **
SA97496	19.0	38.5	38.3
SA97547 §	17.8	39.6	38.8
SA97699 §	16.7 *	37.9	39.9

SA97482 §	20.4	33.1	43.3 **
SA97668	22.7	32.2	41.2
SA97695	21.2	32.4	42.1
SA97127 §	23.6	30.3	42.6
SA97532	18.5	39.8	37.3
SA97693	19.9	40.3	35.5
Slavuj	19.6	39.4	37.4
SA96145	23.6	30.9	41.8
SA96139	21.6	33.9	41.0
SA96280	20.5	34.8	40.0
Celsia	21.0	34.2	41.1
SA98070	18.8	40.1	36.6
SA98171 §	24.0 **	29.9 *	42.3
SA98188	19.9	37.8	38.2
SA98191	21.5	34.9	40.2
SA98321 §	17.7	44.4 **	34.1 *
SA98346 §	22.8	31.7	41.2
SA98360	24.2 **	30.4	41.3
SA98379	21.4	31.7	42.2
SA98387 §	24.7 **	28.7 *	41.8
SA98416	23.3	32.3	40.4
SA98421	20.8	35.8	39.3
SA98594 §	21.7	32.3	42.4
SA98328	21.3	33.9	40.1
SA98352 §	17.1	46.0 **	33.1 *
SA98422	21.0	34.5	40.5
SA97170 §	16.8 *	42.2	36.4
Mean	20.6	35.8	39.5
Std. Deviation	2.0	4.1	2.7
Coeff. of Variation	0.10	0.11	0.07

* Lowest % of each fatty acid, ** Highest % of each fatty acid, § Genotypes selected for 2009 replicated field experiment

Table 4.2. Major fatty acid composition data of 'Historic Canadian cultivars' sub-set (FA percentage based on total FA detected by GC, corresponding minor fatty acid composition in Appendix, Table 9.2)

Cultivar	% Palmitic acid	% Oleic acid	% Linoleic acid
Mabel	21.4	38.4	36.4
CDC Dancer	21.2	36.1	38.8
Roxton	20.0	39.9	35.9
Sylva	21.6	38.9	35.6
Ultima	21.2	39.3	35.5
Kelsey [§]	19.9	38.0	37.2
CDC Pacer	22.3	35.8	37.7
Robert	21.9	40.0	33.3
Marion	20.7	40.0	35.1
Bell	20.7	42.5 **	33.2
Simcoe	17.9 *	39.2	38.4
Triple Crown	20.5	35.8	40.3
Laurel hulless	21.3	34.4	40.3
Rodney	20.0	38.3	37.2
Oxford	21.8	37.2	36.9
AC Stewart [§]	22.1	31.2	34.3
Torch hulless	19.7	41.2	35.2
Appalaches	19.7	36.9	39.9
Shaw	21.2	38.9	36.2
Yamaska [§]	19.7	36.8	33.6
Laurent	17.9 *	39.5	38.4
Fortune	18.6	36.4	41.4
OAC Woodstock [§]	23.7	35.3	28.5 *
Old Island Black	18.2	40.2	38.1
Larain	19.5	34.0	35.0
Riel	20.9	37.8	37.5
Pendek	22.1	37.9	36.5
Fundy	18.9	33.0	44.5 **
AC Juniper	19.9	39.3	36.6
Kamouraska	21.3	37.0	37.8
OAC Paisley [§]	21.5	32.5	42.0
Hinoat	21.0	35.5	34.2
Elgin	21.1	35.9	39.1
Ida	20.6	36.2	39.0
AC Pinnacle	21.5	39.2	35.4
AC Assiniboia [§]	21.7	39.8	33.7
Erban	21.5	36.3	38.3

Fraser	23.1	35.1	37.2
Dorval	19.4	37.2	39.1
Early Triumph	21.9	38.1	36.4
Beacon	21.6	38.7	36.3
Eagle	19.6	40.0	36.3
CDC Boyer	21.9	36.8	37.7
Irish	22.1	33.3	40.4
Legacy	21.0	31.3	43.4
AC Ronald §	20.8	40.6	34.0
CDC Bell	23.8	32.1	39.0
Abegweit	20.8	34.5	40.9
Gopher	22.0	29.6	43.7
Alma	17.6 *	38.8	39.2
Scotian	22.6	34.9	38.5
Terra hulless	21.3	36.9	38.0
Derby	23.1	33.2	39.7
Linwood	21.3	37.2	36.5
Alaska	19.2	36.9	39.8
Scott	21.2	36.3	38.4
Shefford	21.0	35.4	39.8
Donegal	21.2	32.2	36.4
Sentinel	22.3	34.4	39.1
Lanark	20.5	40.3	34.4
Manic	22.1	31.8	41.9
AC Marie §	19.4	43.3 **	33.0
Garry	19.5	37.0	39.0
AC Morgan	22.8	31.2	42.5
Athabasca	21.7	36.8	37.4
Dumont §	20.6	40.2	33.6
ELVY	21.4	35.2	39.6
Fidler §	20.2	37.3	33.5
Glen	17.7 *	38.4	40.1
Waldern	21.8	33.3	41.5
Ajax	18.1	37.9	40.1
Grizzly §	25.7 **	33.0	37.5
Beaver	21.2	36.3	38.6
Hudson	22.7	37.2	36.4
Valor	20.2	41.0	34.5
Lanark-RED	21.2	37.0	38.0
Random	21.4	37.1	38.2
AC Francis	21.9	29.0	35.8
Cartier	20.6	36.5	34.8

Capital	18.6	38.6	38.5
Victory	21.0	36.3	38.6
Joanette [§]	19.9	40.4	35.3
AC Rebel	20.3	40.6	34.2
AC Rigodon	20.7	41.9	33.4
Exeter [§]	25.5 **	24.6 *	45.1 **
Gemini [§]	21.0	36.3	34.4
Donald [§]	22.5	33.9	39.2
AC Mustang [§]	21.0	36.5	34.9
Russell	18.9	38.3	37.8
Quamby	23.2	37.7	35.3
Hajira [§]	21.6	24.8 *	38.6
Swedish Select	21.8	36.6	37.9
Foothill	21.5	33.5	40.8
Banner	21.2	36.7	38.3
Vanguard	19.8	39.7	36.3
Gold Rain	20.8	36.6	38.7
Sixty Day [§]	20.0	31.7	44.5 **
Cluan	22.4	35.1	38.2
Harmon	21.0	37.1	37.3
Cascade	22.7	36.3	37.7
Liberty hulless	18.1	41.8	36.2
Calibre	23.0	35.5	37.5
Sioux	19.9	37.3	35.6
AC Preakness	21.3	40.0	33.6
Hunter [§]	20.9	41.3	33.5
Jasper	21.2	37.9	36.1
Mean	21.0	36.7	37.5
Std. Deviation	1.5	3.3	2.8
Coeff. of Variation	0.07	0.09	0.08

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§] Genotypes selected for 2009 replicated field experiment

Based on this initial single sample analysis, 34 genotypes were selected for more detailed evaluation. ‘Exeter’ and ‘Hajira’ from the ‘Historic Canadian cultivars’ sub-set showed interesting variation (Table 4.2). Whereas ‘Exeter’ was low in oleic acid and high in palmitic acid and linoleic acid relative to the average, ‘Hajira’ was low in oleic acid but near average for palmitic and linoleic acid. Genotypes such as ‘Grizzly’ were selected based on comparatively high palmitic acid levels whereas ‘AC Ronald’ and ‘AC Marie’ were chosen for their high oleic acid content. ‘OAC Woodstock’ and ‘Sixty Day’ were selected based on their respective low and high linoleic acid content.

From the ‘U of S high/low oil lines’ sub-set, genotypes SA98387, SA98594, SA97127 and SA98171 (all with low fat content) were selected for their high palmitic acid and low oleic acid content whereas genotypes SA071380, SA080511 and SA080029 (all with high fat content) were selected based on their comparatively high oleic acid content. Genotypes high in oleic acid were generally lower in linoleic acid, and vice versa. Therefore genotypes high in linoleic acid, such as ‘OAC Paisley’ and SA97082 were also selected for the 2009 replicated field trial (RFT).

Data on selected genotypes with groat fat content ranging from 4.5 - 12.7%, groat protein content from 12.8 - 19.4% and repeated checks are listed in Tables 4.3 and 4.4.

Table 4.3. List of 52 genotypes selected for 2009 replicated field trial and respective groat fat content, groat protein content, palmitic, oleic and linoleic acid content mean data and standard deviation from four replications (FA percentage based on total FA detected by GC)

Cultivar	% Groat fat	% Groat protein	% Palmitic acid	% Oleic acid	% Linoleic acid
AC Assiniboia	6.9 ± 0.2	15.4 ± 1.2	20.1 ± 0.9	39.3 ± 2.1	36.6 ± 1.5
AC Marie	9.9 ± 0.3	13.3 ± 2.1	18.4 ± 1.1	42.1 ± 3.5	35.5 ± 2.1
AC Mustang	6.2 ± 0.5	13.2 ± 2.0	18.9 ± 0.3	37.2 ± 1.5	40.2 ± 1.1
AC Ronald	7.4 ± 0.7	13.5 ± 2.5	20.0 ± 0.4	38.4 ± 1.2	37.6 ± 0.8
AC Stewart	6.7 ± 0.1	16.3 ± 2.1	20.8 ± 0.6	32.4 ± 1.2	42.4 ± 1.2
Aslak	7.9 ± 0.4	17.9 ± 1.2	19.4 ± 0.4	36.7 ± 0.9	39.8 ± 0.3
CDC Sol-Fi	5.6 ± 0.3	15.5 ± 2.9	20.7 ± 0.9	32.8 ± 3.3	42.9 ± 2.6
Donald	6.8 ± 0.2	15.3 ± 1.4	19.8 ± 0.2	32.8 ± 1.6	43.4 ± 1.6
Dumont	8.1 ± 0.2	13.3 ± 2.4	19.0 ± 0.8	40.2 ± 2.3	37.0 ± 1.5
Exeter	4.5 ± 0.6	15.3 ± 3.3	22.6 ± 1.3	23.6 ± 2.4	48.5 ± 3.2
Fidler	8.6 ± 0.2	15.3 ± 1.5	19.5 ± 0.6	38.7 ± 1.3	38.5 ± 0.8
Gemini	7.6 ± 0.2	14.2 ± 1.8	20.3 ± 0.6	34.8 ± 1.5	40.9 ± 1.3
Grizzly	5.9 ± 0.2	14.6 ± 3.6	21.7 ± 0.8	31.1 ± 0.6	42.7 ± 0.9
Hajira	7.2 ± 0.4	18.1 ± 2.3	17.2 ± 2.7	34.5 ± 3.5	44.8 ± 0.9
HiFi	7.7 ± 0.2	14.9 ± 1.3	17.8 ± 1.0	37.7 ± 1.4	40.2 ± 1.0
Hunter	8.2 ± 0.3	14.0 ± 2.3	20.0 ± 0.6	39.1 ± 1.2	37.3 ± 0.8
Joanette*	-	-	17.8 ± 0.9	40.0 ± 2.4	38.0 ± 1.4
Kesley	7.8 ± 0.2	13.3 ± 1.4	18.1 ± 0.4	37.3 ± 0.6	40.6 ± 0.8
Matilda	10.3 ± 0.5	16.7 ± 1.1	18.1 ± 1.4	42.3 ± 2.7	35.1 ± 2.4
OAC Paisley	6.0 ± 0.3	15.4 ± 1.4	18.1 ± 0.7	33.0 ± 2.8	45.2 ± 2.1
OAC Woodstock	7.9 ± 0.1	15.8 ± 1.5	19.9 ± 0.3	38.0 ± 1.1	38.9 ± 0.7
OT 3024	6.3 ± 0.4	12.3 ± 2.2	19.7 ± 0.8	31.3 ± 1.8	44.6 ± 1.7
OT 3033	7.9 ± 0.5	13.1 ± 1.7	19.0 ± 0.2	38.2 ± 1.5	39.4 ± 0.8
SA02984	10.3 ± 0.6	15.5 ± 1.2	15.9 ± 0.3	43.0 ± 0.7	36.7 ± 1.3
SA060470	10.8 ± 0.5	15.7 ± 2.7	17.7 ± 0.6	43.7 ± 2.6	34.9 ± 2.3
SA071192	9.7 ± 0.4	16.1 ± 1.6	19.7 ± 0.9	41.4 ± 1.2	35.0 ± 1.0
SA071369	8.6 ± 0.6	12.8 ± 2.4	17.7 ± 0.9	41.3 ± 1.5	37.8 ± 1.1
SA071380	9.4 ± 0.5	13.3 ± 2.3	15.4 ± 0.3	44.6 ± 0.4	36.4 ± 0.7
SA071405	8.4 ± 0.2	14.8 ± 0.7	19.5 ± 1.9	37.1 ± 2.3	39.4 ± 0.9
SA071555	9.2 ± 0.6	14.0 ± 1.5	18.1 ± 0.8	41.1 ± 3.5	37.1 ± 2.8
SA071709	9.7 ± 0.3	13.9 ± 2.7	17.7 ± 0.4	41.8 ± 0.2	37.0 ± 0.3
SA080029	12.6 ± 1.0	15.1 ± 1.5	15.2 ± 0.3	45.4 ± 0.4	35.7 ± 0.7

SA080473	11.1 ± 0.2	15.1 ± 2.2	17.2 ± 1.0	45.0 ± 0.7	34.1 ± 0.8
SA080498	10.7 ± 0.4	15.5 ± 1.5	15.5 ± 0.2	43.7 ± 1.3	36.7 ± 1.4
SA080511	11.2 ± 0.5	14.8 ± 1.3	16.1 ± 0.3	44.7 ± 1.0	35.0 ± 0.8
Sixty Day	7.7 ± 0.5	19.4 ± 3.5	19.8 ± 0.7	34.3 ± 1.1	41.4 ± 0.3
SA97082	5.3 ± 0.3	14.5 ± 1.8	21.3 ± 1.6	30.6 ± 1.3	43.6 ± 2.8
SA97362	5.3 ± 0.3	14.3 ± 2.0	20.4 ± 0.9	29.9 ± 2.6	44.9 ± 1.9
SA97665	6.7 ± 0.2	14.8 ± 1.8	19.5 ± 0.5	36.1 ± 0.5	40.3 ± 0.7
SA97404	9.1 ± 0.1	16.5 ± 1.8	17.3 ± 1.5	39.6 ± 3.6	39.4 ± 2.3
SA97547	8.7 ± 0.3	14.5 ± 1.3	17.2 ± 0.3	40.6 ± 1.7	38.8 ± 1.7
SA97699	7.9 ± 0.4	16.6 ± 1.9	16.0 ± 0.7	39.9 ± 1.6	40.1 ± 2.1
SA97482	6.0 ± 0.2	15.3 ± 2.2	19.3 ± 0.4	33.6 ± 1.7	44.0 ± 1.7
SA97127	5.3 ± 0.1	14.6 ± 1.7	22.1 ± 0.3	30.3 ± 1.5	44.0 ± 0.6
SA98171	4.7 ± 0.2	14.8 ± 2.6	21.5 ± 1.0	28.8 ± 2.2	44.4 ± 2.3
SA98321	10.2 ± 0.5	14.4 ± 1.9	17.1 ± 0.4	42.5 ± 1.2	37.1 ± 0.7
SA98346	6.5 ± 0.5	17.2 ± 2.5	20.5 ± 1.1	30.9 ± 4.6	43.6 ± 4.3
SA98387	5.3 ± 0.2	16.2 ± 1.8	22.2 ± 1.3	30.2 ± 4.8	41.8 ± 4.8
SA98594	5.7 ± 0.1	14.1 ± 2.0	22.4 ± 0.9	30.8 ± 1.5	42.9 ± 0.5
SA98352	10.3 ± 0.5	14.5 ± 1.8	16.4 ± 0.7	43.5 ± 1.1	36.8 ± 0.8
SA97170	9.6 ± 0.3	14.4 ± 1.8	16.3 ± 0.4	41.2 ± 1.0	37.9 ± 1.0
Yamaska	8.5 ± 0.4	15.9 ± 2.1	19.7 ± 0.8	36.1 ± 0.8	40.5 ± 1.1

*Groat fat and protein data not available

Table 4.4. List of four repeated checks in 2009 replicated field trial and respective groat fat content, groat protein content, palmitic, oleic and linoleic acid content mean data and standard deviation from 20 replications (FA percentage based on total FA detected by GC)

Cultivar	Groat fat %	Groat protein %	% Palmitic acid	% Oleic acid	% Linoleic acid
CDC Dancer	6.1 ± 0.4	12.8 ± 1.7	19.7 ± 0.5	33.6 ± 1.5	42.0 ± 1.3
CDC SO-I	8.2 ± 0.3	15.6 ± 1.5	21.1 ± 0.6	36.9 ± 1.3	38.6 ± 1.3
SA02995	10.4 ± 0.4	15.9 ± 1.4	15.6 ± 0.4	44.4 ± 1.4	36.3 ± 1.2
SA96121	9.4 ± 0.3	16.3 ± 2.2	18.9 ± 0.6	40.2 ± 2.1	37.6 ± 1.6

4.2. Evaluation of laboratory error

During each GC run of samples, repeated checks from a single sample of each of 'CDC Dancer' groats and oat oil were analyzed to estimate laboratory error. Both samples were analyzed 14 times with results presented in Tables 4.5 and 4.6.

Table 4.5. Fatty acid composition of repeated check 'CDC Dancer' (FA percentage based on total FA detected by GC), n=14

	% Palmitic Acid	% Stearic Acid	% Oleic Acid	% Linoleic Acid	% Linolenic Acid	% Eicosenoic Acid
Maximum	22.8	2.2	37.1	39.2	1.2	0.9
Minimum	21.2	1.7	34.9	36.4	1.0	0.7
Mean	22.2	2.0	36.1	38	1.1	0.8
SD	0.52	0.24	0.81	1.04	0.12	0.10
CV	0.02	0.09	0.02	0.03	0.08	0.07

SD= Standard Deviation, CV= Coefficient of Variation

Table 4.6. Fatty acid composition of repeated check 'oat oil' (FA percentage based on total FA detected by GC), n=14

	% Palmitic Acid	% Stearic Acid	% Oleic Acid	% Linoleic Acid	% Linolenic Acid	% Eicosenoic Acid
Maximum	16.3	2.2	47.3	33.8	0.9	1
Minimum	16.0	2.1	46.1	32.7	0.8	0.6
Mean	16.2	2.1	46.6	33.3	0.9	0.9
SD	0.13	0.13	0.41	0.43	0.03	0.12
CV	0.01	0.03	0.01	0.01	0.04	0.13

SD= Standard Deviation, CV= Coefficient of Variation

Results for stearic acid, linolenic acid and eicosenoic acid showed slightly more diversity than did results for palmitic acid, oleic acid and linoleic acid for which the data was very consistent with coefficients of variation of 0.03 or less. Because their relative concentration was much lower than those of the major fatty acids, variation between maximum and minimum values for stearic acid, linolenic acid and eicosenoic acid was greater.

The consistency in repeated check fatty acid results revealed high repeatability of the laboratory measurements. A low laboratory error was an important goal in the experimental procedure because including replicates of each genotype in certain experiments was not feasible and high laboratory accuracy and repeatability provided strong confidence in the results generated during descriptive analysis of genotypes from the un-replicated experiments.

4.3. Replicated Field Trial, 2009

Summary results for genotypes in the 2009 RFT are presented in Table 4.7. The ranges for oleic acid and linoleic acid were from 23.6 - 45.4% and 34.1% - 48.5% respectively. The major saturated fatty acid, palmitic acid ranged from 15.2% - 22.6%. As stated earlier, the coefficient of variation for the minor fatty acids was greater than that for the major fatty acids. Oleic acid demonstrated greater diversity than did the other fatty acids.

Table 4.7. Fatty acid composition of 52 oat accessions in Replicated Field Trial 2009 (FA percentage based on total FA detected by GC)

	% Palmitic Acid	% Stearic Acid	% Oleic Acid	% Linoleic Acid	% Linolenic Acid	% Eicosenoic Acid
Maximum	22.6	3.1	45.4	48.5	2.2	1.7
Minimum	15.2	1.0	23.6	34.1	0.6	0.6
Mean	18.9	1.9	37.4	39.8	1.2	0.9
SD	1.92	0.51	5.14	3.42	0.42	0.34
CV	0.1	0.2	0.1	0.1	0.3	0.3
HSD ($\alpha = 0.05$)	1.8	0.89	5.0	4.4	0.67	0.82

SD= Standard Deviation, CV= Coefficient of Variation, HSD= Honestly Significant Difference

Results for Tukey's honestly significant difference (HSD) test to determine the significance of differences between genotypes for palmitic acid, oleic acid and linoleic acid content are provided in Tables 4.8 to 4.10. Genotypes followed by the same letter are not significantly different. The minimum significant difference (P=0.05) for palmitic acid was 1.8%. For example, 'Exeter' had a palmitic acid content similar to 'Grizzly' and the repeated check 'CDC SO-I', but significantly higher than that of did 'CDC Sol-Fi', 'SA97362' and 'Gemini' (Table 4.8). 'CDC Sol-Fi' contained significantly more palmitic acid than 'HiFi'. 'Aslak' and 'Matilda' had similar levels of palmitic acid. Differences between 'OT 3024' and 'OT 3033' were also non-significant. It was interesting to note that the high fat U of S breeding lines; SA080029, SA071380, SA080498, SA02984 and SA080511 had the lowest palmitic acid. Other lines with relatively high fat levels, 'SA080473' for example, also had low palmitic acid content.

Table 4.8. Tukey's HSD test for palmitic acid in Replicated Field trial 2009 (α = 0.05, minimum significant difference = 1.8 %)

Genotype	Number of replications	% Mean	Tukey grouping
Exeter	4	22.6	A
SA98594	4	22.4	A B
SA98387	4	22.2	A B C
SA97127	4	22.1	A B C D
Grizzly	4	21.7	A B C D E
SA98171	4	21.5	A B C D E F
SA97082	4	21.3	A B C D E F G
CDC SO-I	20	21.1	A B C D E F G H
AC Stewart	4	20.8	A B C D E F G H
CDC Sol-Fi	4	20.7	B C D E F G H I
SA98346	4	20.5	C D E F G H I J
SA97362	4	20.4	C D E F G H I J
Gemini	4	20.3	D E F G H I J
AC Assiniboia	4	20.1	E F G H I J K
AC Ronald	4	20.0	E F G H I J K
Hunter	4	20.0	E F G H I J K
OAC Woodstock	4	19.9	F G H I J K L
Sixty Day	4	19.8	F G H I J K L M
Donald	4	19.8	F G H I J K L M
OT 3024	4	19.7	G H I J K L M
SA071192	4	19.7	G H I J K L M
Yamaska	4	19.7	G H I J K L M
CDC Dancer	20	19.7	G H I J K L M
Fidler	4	19.5	H I J K L M N
SA071405	4	19.5	H I J K L M N
SA97665	4	19.5	H I J K L M N O

Aslak	4	19.4	H	I	J	K	L	M	N	O												
SA97482	4	19.3	H	I	J	K	L	M	N	O												
OT 3033	4	19.0		I	J	K	L	M	N	O	P											
Dumont	4	19.0		I	J	K	L	M	N	O	P											
AC Mustang	4	18.9			J	K	L	M	N	O	P	Q										
SA96121	20	18.9			J	K	L	M	N	O	P	Q										
AC Marie	4	18.4				K	L	M	N	O	P	Q										
Matilda	4	18.1					L	M	N	O	P	Q	R									
OAC Paisley	4	18.1					L	M	N	O	P	Q	R	S								
Kesley	4	18.1					L	M	N	O	P	Q	R	S								
SA071555	4	18.1						M	N	O	P	Q	R	S								
HiFi	4	17.8							N	O	P	Q	R	S	T							
Joanette	4	17.8							N	O	P	Q	R	S	T	U						
SA060470	4	17.7							N	O	P	Q	R	S	T	U						
SA071369	4	17.7							N	O	P	Q	R	S	T	U						
SA071709	4	17.7								O	P	Q	R	S	T	U						
SA97404	4	17.3									P	Q	R	S	T	U	V					
Hajira	4	17.2									P	Q	R	S	T	U	V	W				
SA97547	4	17.2									P	Q	R	S	T	U	V	W				
SA080473	4	17.2									P	Q	R	S	T	U	V	W				
SA98321	4	17.1										Q	R	S	T	U	V	W				
SA98352	4	16.4											R	S	T	U	V	W	X			
SA97170	4	16.3												S	T	U	V	W	X			
SA080511	4	16.1													T	U	V	W	X			
SA97699	4	16.0														U	V	W	X			
SA02984	4	15.9															V	W	X			
SA02995	20	15.6															V	W	X			
SA080498	4	15.5																W	X			
SA071380	4	15.4																W	X			
SA080029	4	15.2																	X			

The minimum significant difference (P=0.05) for oleic acid was 5.0%. All high fat U of S breeding lines with the exception of ‘SA071405’, contained significantly more oleic acid in the replicated field experiment, as did the repeated high fat check ‘SA02995’ and cultivars such as ‘Matilda’ (high fat) and ‘AC Marie’ (Table 4.9). ‘Matilda’ contained significantly more oleic acid than did ‘Aslak’. ‘OT 3033’ contained significantly more oleic acid than did ‘OT 3024’. However, differences between ‘CDC Sol-Fi’ and ‘HiFi’ were not significant. The repeated check ‘CDC Dancer’ had oleic acid content similar to that of ‘OT 2024’ and ‘CDC Sol-Fi’. ‘Exeter’ had the lowest oleic acid content.

Table 4.9. Tukey's HSD test for oleic acid in Replicated Field Trial 2009 (α = 0.05, minimum significant difference = 5.0 %)

Genotype	Number of replications	% Mean	Tukey grouping
SA080029	4	45.4	A
SA080473	4	45.0	A B
SA080511	4	44.7	A B C
SA071380	4	44.6	A B C D
SA02995	20	44.4	A B C D
SA060470	4	43.7	A B C D E
SA080498	4	43.7	A B C D E
SA98352	4	43.5	A B C D E
SA02984	4	43.0	A B C D E F
SA98321	4	42.5	A B C D E F G
Matilda	4	42.3	A B C D E F G H
AC Marie	4	42.1	A B C D E F G H I
SA071709	4	41.8	A B C D E F G H I J
SA071192	4	41.4	A B C D E F G H I J K
SA071369	4	41.3	A B C D E F G H I J K
SA97170	4	41.2	A B C D E F G H I J K
SA071555	4	41.1	A B C D E F G H I J K
SA97547	4	40.6	A B C D E F G H I J K L
Dumont	4	40.2	B C D E F G H I J K L
SA96121	20	40.2	B C D E F G H I J K L
Joanette	4	40.0	C D E F G H I J K L
SA97699	4	39.9	C D E F G H I J K L
SA97404	4	39.6	D E F G H I J K L M
AC Assiniboia	4	39.3	E F G H I J K L M N
Hunter	4	39.1	E F G H I J K L M N
Fidler	4	38.7	E F G H I J K L M N

AC Ronald	4	38.4		F	G	H	I	J	K	L	M	N	O									
OT 3033	4	38.2		F	G	H	I	J	K	L	M	N	O									
OAC Woodstock	4	38.0			G	H	I	J	K	L	M	N	O	P								
HiFi	4	37.7			G	H	I	J	K	L	M	N	O	P	Q							
Kesley	4	37.3				H	I	J	K	L	M	N	O	P	Q	R						
AC Mustang	4	37.2					I	J	K	L	M	N	O	P	Q	R						
SA071405	4	37.1						J	K	L	M	N	O	P	Q	R						
CDC SO-I	20	36.9						J	K	L	M	N	O	P	Q	R						
Aslak	4	36.7							K	L	M	N	O	P	Q	R						
Yamaska	4	36.1								L	M	N	O	P	Q	R	S					
SA97665	4	36.1								L	M	N	O	P	Q	R	S					
Gemini	4	34.8									M	N	O	P	Q	R	S	T				
Hajira	4	34.5										N	O	P	Q	R	S	T				
Sixty Day	4	34.3										N	O	P	Q	R	S	T				
SA97482	4	33.6											O	P	Q	R	S	T	U			
CDC Dancer	20	33.6											O	P	Q	R	S	T	U			
OAC Paisley	4	33.0												P	Q	R	S	T	U			
CDC Sol-Fi	4	32.8													Q	R	S	T	U			
Donald	4	32.8													Q	R	S	T	U			
AC Stewart	4	32.4														R	S	T	U			
OT 3024	4	31.3															S	T	U			
Grizzly	4	31.1																T	U			
SA98346	4	30.9																T	U			
SA98594	4	30.8																T	U			
SA97082	4	30.6																T	U			
SA97127	4	30.3																T	U			
SA98387	4	30.2																T	U			
SA97362	4	29.9																T	U			
SA98171	4	28.8																	U			
Exeter	4	23.6																		V		

The minimum significant difference (P=0.05) for linoleic acid was 4.4%. ‘Exeter’ along with ‘OAC Paisley’, ‘SA97362’, ‘Hazira’, ‘OT 3024’ and ‘SA98171’ contained more linoleic acid than did genotypes such as ‘CDC Sol-Fi’ and SA98594 (Table 4.10). ‘CDC Sol-Fi’ had a linoleic acid content similar to ‘HiFi’ despite the fact that ‘CDC Sol-Fi’ has low fat and ‘HiFi’ has high fat. However, ‘OT 3024’ which has relatively low fat contained significantly more linoleic acid than did ‘OT 3033’ having high percent fat. Similarly, ‘Aslak’ with its high percent fat contained significantly more linoleic acid than ‘Matilda’ which had high percent fat. Most high fat U of S breeding lines were lower in linoleic acid. ‘Aslak’ and ‘Matilda’ are the parents of the world’s only double haploid population from Finland (Tanhuanpää et al., 2008) with an available DArT map . ‘OT 3033’ and ‘OT 3024’ are two recombinant inbred lines (RIL) and are the parents of a DArT mapping population. Fatty acid profile data along with an available DArT map for these genotypes may be utilized in the future to find molecular markers related to specific fatty acid levels in oat.

Genotypes such as ‘SA98171’ and ‘SA98594’ were high in palmitic acid and linoleic acid and low in oleic acid. These genotypes were not significantly different from each other for palmitic acid and oleic acid content, but were for linoleic acid content (Tables 4.8 to 4.10).

Results for the other three minor fatty acids can be found in the Appendix, Tables 9.3 to 9.5.

Table 4.10. Tukeys HSD test for linoleic acid in Replicated Field Trial 2009 (α = 0.05, minimum significant difference = 4.4 %)

Genotype	Number of replications	% Mean	Tukey grouping
Exeter	4	48.5	A
OAC Paisley	4	45.2	A B
SA97362	4	44.9	A B C
Hajira	4	44.8	A B C
OT 3024	4	44.6	A B C D
SA98171	4	44.4	A B C D E
SA97127	4	44.0	B C D E F
SA97482	4	44.0	B C D E F
SA98346	4	43.6	B C D E F G
SA97082	4	43.6	B C D E F G
Donald	4	43.4	B C D E F G
SA98594	4	42.9	B C D E F G H
CDC Sol-Fi	4	42.9	B C D E F G H I
CDC Dancer	20	42.9	B C D E F G H I
Grizzly	4	42.7	B C D E F G H I
AC Stewart	4	42.4	B C D E F G H I J
SA98387	4	41.8	B C D E F G H I J K
Sixty Day	4	41.4	B C D E F G H I J K L
Gemini	4	40.9	B C D E F G H I J K L M
Kesley	4	40.6	C D E F G H I J K L M N
Yamaska	4	40.5	C D E F G H I J K L M N
SA97665	4	40.3	D E F G H I J K L M N
HiFi	4	40.2	D E F G H I J K L M N
AC Mustang	4	40.2	E F G H I J K L M N O
SA97699	4	40.1	E F G H I J K L M N O
Aslak	4	39.8	F G H I J K L M N O P

SA071405	4	39.4		G	H	I	J	K	L	M	N	O	P	Q							
OT 3033	4	39.4		G	H	I	J	K	L	M	N	O	P	Q							
SA97404	4	39.4		G	H	I	J	K	L	M	N	O	P	Q	R						
OAC Woodstock	4	38.9			H	I	J	K	L	M	N	O	P	Q	R	S					
SA97547	4	38.8			H	I	J	K	L	M	N	O	P	Q	R	S					
CDC SO-I	20	38.6			H	I	J	K	L	M	N	O	P	Q	R	S					
Fidler	4	38.5				I	J	K	L	M	N	O	P	Q	R	S	T				
Joanette	4	38.0					J	K	L	M	N	O	P	Q	R	S	T				
SA97170	4	37.9						K	L	M	N	O	P	Q	R	S	T				
SA071369	4	37.8						K	L	M	N	O	P	Q	R	S	T				
SA96121	20	37.6						K	L	M	N	O	P	Q	R	S	T				
AC Ronald	4	37.6						K	L	M	N	O	P	Q	R	S	T				
Hunter	4	37.3							L	M	N	O	P	Q	R	S	T				
SA071555	4	37.1							L	M	N	O	P	Q	R	S	T				
SA98321	4	37.1							L	M	N	O	P	Q	R	S	T				
Dumont	4	37.0							L	M	N	O	P	Q	R	S	T				
SA071709	4	37.0								M	N	O	P	Q	R	S	T				
SA98352	4	36.8								M	N	O	P	Q	R	S	T				
SA02984	4	36.7								M	N	O	P	Q	R	S	T				
SA080498	4	36.7								M	N	O	P	Q	R	S	T				
AC Assiniboia	4	36.6								M	N	O	P	Q	R	S	T				
SA071380	4	36.4								M	N	O	P	Q	R	S	T				
SA02995	20	36.3									N	O	P	Q	R	S	T				
SA080029	4	35.7										O	P	Q	R	S	T				
AC Marie	4	35.5											P	Q	R	S	T				
Matilda	4	35.1												Q	R	S	T				
SA080511	4	35.0												Q	R	S	T				
SA071192	4	35.0													R	S	T				
SA060470	4	34.9														S	T				
SA080473	4	34.1															T				

4.3.1. Genotype and location effects

The effects of genotype and location on fatty acid composition and interactions of genotype and location were determined using Proc Mixed model analysis in SAS version 9.1. Results are provided in Table 4.11. Genotypes were different for levels of each fatty acid, oil and protein. Location significantly affected palmitic acid, stearic acid and oleic acid content, oil and protein content. Linoleic acid, linolenic acid and eicosenoic acid content were consistent across locations. Palmitic acid content, oil content and protein content showed significant genotype x location interaction. Despite the statistically significant effect of growing location on palmitic acid, stearic acid and oleic acid content, it was observed that genotypes high or low in particular fatty acids behaved similarly at both locations.

Table 4.11. Probability for genotypes and environment effects on fatty acid composition of 52 genotypes grown in Replicated Field Trial, 2009

Effect	% Palmitic Acid	% Stearic Acid	% Oleic Acid	% Linoleic Acid	% Linolenic Acid	% Eicosenoic Acid	% Oil	% Protein
Genotype	P<.001	P<.001	P<.001	P<.001	P<.001	P<.001	P<.001	P<.001
Location	P<.001	P=.0043	P=.0003	P=0.024	P=0.60	P=0.68	P<.001	P<.001
Genotype x Location	P=0.0036	P=0.06	P=0.31	P=0.75	P=0.51	P=0.52	P<.001	P<.001
Replication	P=0.043	P<.001	P=0.56	P=0.32	P=0.0021	P<.001	P<.001	P<.001

These results showing very strong genotypic effects and only minor environmental effects indicate relatively high heritability of fatty acid composition in oat as suggested by Holland et al. (2001). Even though the absolute proportion of each fatty acid can vary due to environmental effects, relative fatty acid composition is consistent across genotypes. Lack of replication effect for palmitic, oleic and linoleic acid indicates the similar behavior of the genotypes and high stability of oat fatty acid composition. This is important for efficiency of oat breeding and germplasm evaluation at seed banks, since a high trait heritability coupled with accurate and reproducible GC results (Tables 4.5 and 4.6) means that breeders and germplasm evalutors can test large numbers of genotypes for relative fatty acid composition using small amounts of seed and with minimal replication in space or time. Similar behavior of genotypes across the locations suggests the possibility of genotype screening from a single location, therefore increasing evaluation efficiency.

4.3.2. Correlation Analysis

Pearson's correlation coefficients for each of six fatty acid levels, oil content, protein content and hull percentage were determined for the 52 genotypic means from the RFT, 2009. Results are provided in Table 4.12.

Table 4.12. Correlations among mean values of palmitic, oleic and linoleic acid content, oil content, protein content and hull percentage from Replicated Field Trial, 2009 (n=52)

	% palmitic acid	% oleic acid	% linoleic acid	% oil	% protein
% palmitic acid					
% oleic acid	-0.84**				
% linoleic acid	0.63**	-0.94**			
% oil	-0.81**	0.93**	-0.88**		
% protein	0.04	-0.13	0.14	0.005	
% hull	-0.31*	0.40**	-0.40**	0.40**	-0.12

*Significant at P=0.05, **Significant at P=0.01

In this study, palmitic acid content was negatively correlated with oleic acid content and positively correlated with linoleic acid acid. The negetive correlation between palmitic acid and oleic acid differs from the results of Zhou et al. (1998). The synthesis of linoleic acid via oleic acid desaturation explains the negative correlation between concentrations of the two fatty acids in this study.

Linoleic acid content was significantly positively correlated with linolenic acid content ($r = 0.83$, $P < 0.01$). Similar results were reported by Frey and Hammond (1976). In plants, alpha- and gamma-linolenic acid are synthesized by the desaturation of linoleic acid (Mukherjee and Kiewitt, 1987). Saastamoinen et al. (1989) suggested that a positive correlation between linoleic acid content and linolenic acid content may be the result of this biosynthetic pathway, in that synthesis of more linoleic acid results in synthesis of more linolenic acid, post desaturation.

Palmitic acid content was negatively correlated with the content of the other saturated fatty acid, stearic acid. However, there were a few genotypes such as 'SA98387' which showed high

levels of both palmitic acid (22.2%) and stearic acid (2.60%). Stearic acid content was positively correlated with oleic acid acid and oil content, and negatively correlated with linoleic acid and linolenic acid content. These results are in agreement with Saastamoinen et al. (1989) and Zhou et al. (1998). Lessire et al. (1985) demonstrated that stearoyl-CoA compared to palmitoyl-CoA, is a more effective precursor for malonyl-CoA in the biosynthesis of C_{20}-C_{26} long chain fatty acids. This can explain the positive correlation between palmitic acid and eicosenoic acid, and significant negative correlation between stearic acid and eicosenoic acid. It also has been suggested that oat synthesizes more eicosenoic acid from stearic acid, rather than palmitic acid (Saastamoinen et al., 1989).

Protein content was not correlated with the content of any fatty acid, oil content or hull percentage.

Oil content was positively correlated with oleic acid content and negatively correlated with palmitic acid and linoleic acid content. Linolenic acid and eicosenoic acid content were negatively correlated with oil content, but not significantly. Apart from Saastamoinen et al. (1989), who reported a positive correlation between the contents of all six fatty acids and oil content, results from this experiment are similar to previous studies by De La Roche et al. (1977) and Zhou et al. (1998). From a plant breeder's perspective, selection for increased oil content will likely result in increased oleic acid content meaning simultaneous improvement in oil content and quality for human food proposes is possible.

4.4. IOI selections sub-set

Fatty acid data for the 'IOI selections' sub-set is provided in Tables 4.13 and 4.14. Within the 'IOI selections' sub-set grown at Saskatoon, 'Matilda' had highest oleic acid content (47.1%) whereas 'Goslin' had highest linoleic acid content (46.3%) and 'Kolpashevskii' had the highest palmitic acid content (24.5%).

For samples of the 'IOI selections' sub-set grown at Ottawa, 'Matilda' had highest oleic acid content (47.3%), whereas 'Exeter' had the highest linoleic acid content (47.2%) and palmitic acid content (24.7%). 'Goslin' and 'Kolpashevskii' were high in linoleic acid (44.4%) and palmitic acid (21.6%), respectively. The range in the content of each fatty acid in the 'IOI selctions sub-set' was similar to that for the 2009 RFT. The mean fatty acid content was also similar, except the 'IOI selctions' sub-set demonstrated slightly higher mean palmitic acid content. Results for the other three minor fatty acids can be found in the Appendix, Table 9.6.

Table 4.13. Major fatty acid composition of oat accessions from sub-set "IOI Selections", grown at Saskatoon and Ottawa in 2008 (FA percentage based on total FA detected by GC, corresponding minor fatty acid composition in the Appendix, Table 9.6)

Cultivar	% Palmitic acid		% Oleic acid		% Linoleic acid	
	Saskatoon	Ottawa	Saskatoon	Ottawa	Saskatoon	Ottawa
06FL328	20.5	18.2	40.3	40.1	35.9	38.4
06FL930	19.1	17.8	38.1	38.2	39.2	40.8
Aarre	21	19.1	39.4	39.1	36.5	38.2
Atlas 14535	22.5	21.2	42.5	39.5	31.3 *	36.0
Auteuil	20.0	19.1	38.0	37.5	38.4	39.8
Aveny (SW 01168)	21.5	20.3	33.4	31.8	41.3	44.2
Avesta	21.6	19.5	34.6	34.6	41.1	42.5
Bage 1419/36	20.4	20.7	42.0	38.9	33.4	36.6
CDC Baler	21.0	19.9	34.2	31.6	41.4	45.3
Baragan 114	20.3	19.5	39.3	37.9	37.0	39.5
Barra	21.3	20.9	34.7	32.6	40.5	43.1
AC Baton	20.3	18.5	38.0	40.9	37.5	37.1
Belle	20.2	20.3	37.0	34.5	38.9	41.5
Borowiak	20.8	19.3	38.5	38.1	36.7	39.0

Boudrias	20.9	20.1	39.6	37.6	35.4	38.7
Boxer	22.2	20.3	33.3	34.2	40.7	42.0
CDC Boyer	21.2	20.7	38.1	36.4	37.3	39.8
Brawn	19.3	17.3	36.9	37.7	39.7	41.3
Calibre	21.4	21.3	38.0	34.5	36.7	40.8
Capital	18.7	18.7	36.5	34.2	40.5	43.2
Centennial	22.4	22.1	33.8	35.2	39.1	38.5
Chantilly	19.9	17.8	39.5	41.3	36.3	37.5
Clinton	21.4	20.6	36.5	35.2	38.1	40.2
CDC Dancer	21.0	19.8	36.3	35.5	38.8	41.2
Drummond	22.2	21.2	37.8	37.6	35.0	36.3
Evita	21.0	20.1	36.1	34.4	39.1	41.9
Exeter	24.2 **	24.7 **	25.7 *	24.7 *	46.7 **	47.2 **
Expander	21.5	20.0	35.7	36.1	39.2	40.3
Furlong	22.0	20.8	37.8	39.3	34.9	35.9
Gem	23.6	24.3 **	32.5	29.0 *	39.1	42.3
GK Pillango	21.5	20.3	35.2	33.3	39.8	43.1
Goslin	21.6	21.5	28.5 *	30.5	46.4 **	44.5
AC Gwen	21.3	20.4	40.7	41.1	33.7	34.5
Hamel	21.2	20.0	34.9	35.3	39.8	40.8
HiFi	18.5	18.2	39.1	38.8	37.6	39
IA93227-1	20.5	18.4	38.0	38.8	37.9	39.2
IAH611-447 (PI 502955)	20.3	20.5	40.6	36.2	35.4	39.8
IL2858-1	20.4	19.5	43.3	41.1	32.1	35.7
IL98-10145	18.1	16.7 *	42.9	43.0	34.3	36.4
Iltis	21.8	20.0	35.5	36.2	39.4	40.7
Irtysh 13	19.7	19.4	40.0	38.1	35.6	38.7
Ivory	21.2	19.7	33.1	34.8	42.3	42.2
Jumbo	20.4	19.0	37.5	37.4	38.4	40.2
Kangaroo	19.3	18.9	40.7	39.8	36.5	37.5
Kanota	19.5	18.8	43.9	43.0	32.7	34.6
Klein 69B	17.4	17.0	43.8	42.3	34.4	36.7
Kolpashevskii	24.5 **	21.7	34.2	34.5	37.8	40.5
Lvovskii Rannii	20.6	18.4	40.1	39.5	35.3	38.8
Maldwyn	18.2	17.3	40.3	38.4	38.0	40.3
MAM 17-5	20.8	19.6	35.2	35.0	38.6	40.4
Marathon	20.0	18.6	38.7	38.0	36.7	39.5
Marion (Canada)	19.0	18.5	35.9	33.0	41.1	44.9
Matilda	17.3 *	16.3 *	47.2 **	47.4 **	30.0 *	31.5 *

AC Medallion	20.3	19.1	40.6	41.6	34.7	35.3
Millennium	18.3	19.4	40.8	39.5	38.4	37.9
Milton	17.9	17.4	39.1	38.9	38.7	40.1
MN 811045	21.6	20.5	39.9	39.2	34.9	37.1
AC Morgan	21.9	20.7	32.6	30.7	42.1	45.3 **
Mortlock	19.5	17.8	39.3	39.0	37.5	39.5
Morton	19.0	19.5	35.2	33.6	41.8	43.1
NO58-2-75-26	17.4	16.9	42.8	42.1	35.8	37.1
Nora	18.1	17.6	41.8	40.7	36.1	37.7
Norline	19.2	19.2	45.4 **	41.4	32.0	36.0
Ogle	19.4	18.9	37.3	35.9	39.4	41.6
OMSKIJ 6922	19.8	19.1	36.0	33.4	41.2	43.9
OT2040	16.7 *	17.0	41.6	38.2	36.5	40.1
OT2045	20.7	19.8	40.7	36.1	33.9	40.2
OT2048	18.4	18.8	42.4	38.9	34.5	38.2
OT586	20.1	18.9	39.0	39.9	37.0	37.6
Powell	19.1	18.9	41.6	40.6	36.0	37.5
Proat	20.9	19.3	36.5	38.3	37.5	37.6
CDC Pro-Fi	20.7	21.4	38.5	33.8	37.0	41.3
Revisor	21.6	20.1	34.4	34.1	40.4	42.3
Richard	20.5	18.0	33.5	33.6	42.1	44.9
AC Rigodon	20.7	19.1	41.3	43.3 **	34.3	34.2 *
Rodney 0	19.9	20.7	39.0	37.4	37.2	38.2
Salomon	20.4	20.7	38.1	34.1	38.2	42.1
Silva selection	18.0	17.7	42.8	41.3	34.8	37.4
Skakun	22.5	21.3	33.0	33.7	40.6	41.3
Skrzat	20.1	19.4	41.0	39.2	35.3	38.2
CDC SO-I	21.8	21.0	38.2	39.1	36.5	36.8
CDC Sol-Fi	22.8	21.1	31.7	31.9	41.2	43.3
Spurs	19.7	18.3	36.3	34.2	40.6	44.1
SW Betania	20.1	19.8	37.1	38.8	39.5	38.4
Sylva	21.0	19.9	38.5	38.7	36.9	38.2
TAM O-301	21.6	21.4	38.8	34.4	35.7	40.9
Tartarian	20.6	19.9	37.7	35.9	38.5	40.6
Triple Crown	19.8	19.9	37.2	33.7	39.6	43.3
Trispernia	20.6	19.2	41.0	37.6	34.5	40.0
Ukraine	18.9	19.7	41.2	37.6	36.2	39.2
Ursus	21.2	20.7	39.8	36.8	35.1	39.0
Verde	19.5	18.6	37.7	38.5	39.1	39.4
Victor	19.5	19.6	40.6	39.3	36.9	38.1

Vista	19.9	17.9	39.4	39.8	36.9	39.1
WAOAT2132	20.8	20.1	40.6	38.6	34.4	36.9
WIX 7955-1	22.6	22.2	37.1	36.3	35.8	37.5
X466	21.7	20.9	38.3	35.6	34.5	38.7
Mean[§]	20.4	19.6	38.2	37.1	37.5	39.7

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

Table 4.14. Fatty acid composition of 97 oat accessions from "IOI Selections sub-set" (data based on LS means, FA percentage based on total FA detected by GC)

	% Palmitic Acid	% Stearic Acid	% Oleic Acid	% Linoleic Acid	% Linolenic Acid	% Eicosenoic Acid
Maximum	24.5	3.81	47.3	47.0	1.83	1.19
Minimum	16.8	0.95	25.2	30.8	0.62	0.41
Mean	20.0	1.88	37.6	38.6	1.12	0.81
SD	1.41	0.53	3.44	2.82	0.24	0.13
% CV	0.07	0.28	0.09	0.07	0.21	0.16
HSD($\alpha = 0.05$)	2.6	0.89	5.4	4.5	0.39	0.40

SD= Standard Deviation, CV= Coefficient of Variation

The fatty acid data from both locations was tested to determine Tukey's HSD using Proc GLM model analysis in SAS (Statistical Analysis Software) version 9.1. Corresponding data for palmitic acid, oleic acid and linoleic acid is presented in Tables 4.15 - 4.17. Data for the three minor fatty acids is in the Appendix, Tables 9.7 - 9.9. Least significant differences for palmitic acid, oleic acid and linoleic acid in the 'IOI selections' sub-set were 2.6%, 5.4% and 4.5%, compared to 2.1%, 5.6% and 5.1% in the 2009 replicated field trial (RFT). Despite having more genotypic diversity compared to the RFT, it is clear that, on average, genotypes from both experiments had similar fatty acid profiles.

'Exeter', 'CDC SO-I', 'CDC Dancer', 'HiFi' and 'Matilda' were common genotypes between the 'IOI selections' sub-set and the "RFT 2009" sub-set. Each of the common genotypes demonstrated similar fatty acid compositions in both sub-sets. As was the case for the RFT 2009 and IOI selections, 'Exeter' was high in palmitic and linoleic acid, and low in oleic acid. 'Matilda' was low in palmitic and linoleic acid and high in oleic acid. 'CDC Dancer' and 'CDC SO-I' were not significantly different from each other for the content of any fatty acid in either sub-set. It is important to note that mean fatty acid content for common genotypes were different between both sub-sets and individual genotypes demonstrated different ranges in fatty acid content; however, considering least significant differences, differences between fatty acid content means were not significant.

The similarity of results for the five common genotypes between the 'IOI selections' and the "RFT 2009" sub-set again suggest high heritability of fatty acid composition in oat, which will be beneficial for oat breeders.

Table 4.15. Tukey's HSD test for palmitic acid in 'IOI Selections' sub-set (α = 0.05, minimum significant difference = 2.6 %)

Genotype	Number of replications	% Mean	Tukey grouping
Exeter	2	24.4	A
Gem	2	24.0	A B
Kolpashevskii	2	23.1	A B C
WIX 7955-1	2	22.4	A B C D
Centennial	2	22.2	A B C D E
CDC Sol-Fi	2	21.9	A B C D E F
Skakun	2	21.9	A B C D E F G
Atlas 14535	2	21.9	B C D E F G H
Drummond	2	21.7	B C D E F G H I
Goslin	2	21.5	B C D E F G H I J
TAMO-301	2	21.5	B C D E F G H I J K
CDC SO-I	2	21.4	C D E F G H I J K L
Furlong	2	21.4	C D E F G H I J K L
Calibre	2	21.4	C D E F G H I J K L
X466	2	21.3	C D E F G H I J K L M
AC Morgan	2	21.3	C D E F G H I J K L M
Boxer	2	21.2	C D E F G H I J K L M N
Barra	2	21.1	C D E F G H I J K L M N O
MN 811045	2	21.1	C D E F G H I J K L M N O
CDC Pro-Fi	2	21.0	C D E F G H I J K L M N O
Clinton	2	21.0	C D E F G H I J K L M N O P
Ursus	2	20.9	C D E F G H I J K L M N O P
CDC Boyer	2	20.9	C D E F G H I J K L M N O P
Iltis	2	20.9	C D E F G H I J K L M N O P
Aveny (SW 01168)	2	20.9	C D E F G H I J K L M N O P

GK Pillango	2	20.9	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q					
AC Gwen	2	20.9	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
Revisor	2	20.8	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
Expander	2	20.7	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
Hamel	2	20.6	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
Avesta	2	20.6	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
Salomon	2	20.6	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
Bage 1419-36	2	20.5	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
Evita	2	20.5	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
Boudrias	2	20.5		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
WAOAT2132	2	20.5		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
CDC Baler	2	20.5		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
Sylva	2	20.5		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
Ivory	2	20.5		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R				
CDC Dancer	2	20.4		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S			
IAH611-447 (PI 502955)	2	20.4		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S			
OT2045	2	20.3		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T		
Rodney 0	2	20.3		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T		
Tartarian	2	20.3		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T		
Belle	2	20.2		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T		
MAM 17-5	2	20.2		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T		
Proat	2	20.1		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	
Borowiak	2	20.1		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	
Aarre	2	20.0		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	
IL2858-1	2	19.9		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
SW Betania	2	19.9		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
Trispernia	2	19.9		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
Baragan 114	2	19.9		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V
AC Rigodon	2	19.9		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V

Triple Crown	2	19.9	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V										
Skrzat	2	19.7		E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W									
AC Medallion	2	19.7		E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X								
Jumbo	2	19.7			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X								
Irtysh 13	2	19.5			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X								
Auteuil	2	19.5			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X								
Victor	2	19.5			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X								
OT586	2	19.5			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X								
Lvovskii Rannii	2	19.5			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X								
IA93227-1	2	19.4			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X								
OMSKIJ 6922	2	19.4			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X								
AC Baton	2	19.4			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X								
06FL328	2	19.4				G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y							
Ukraine	2	19.3					H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Marathon	2	19.3						I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Morton	2	19.2						I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Richard	2	19.2						I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Norline	2	19.2						I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Kanota	2	19.1							J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Ogle	2	19.1							J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Kangaroo	2	19.1							J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Verde	2	19.0							J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Spurs	2	19.0							J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Powell	2	19.0								K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Vista	2	18.9									L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Millennium	2	18.9									L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Chantilly	2	18.8										M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						
Marion (Canada)	2	18.8										M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z						

Capital	2	18.7														N	O	P	Q	R	S	T	U	V	W	X	Y	Z
Mortlock	2	18.6															O	P	Q	R	S	T	U	V	W	X	Y	Z
OT2048	2	18.6															O	P	Q	R	S	T	U	V	W	X	Y	Z
06FL930	2	18.4																P	Q	R	S	T	U	V	W	X	Y	Z
HiFi	2	18.3																	Q	R	S	T	U	V	W	X	Y	Z
Brawn	2	18.3																		R	S	T	U	V	W	X	Y	Z
Silva selection	2	17.9																			S	T	U	V	W	X	Y	Z
Nora	2	17.8																				T	U	V	W	X	Y	Z
Maldwyn	2	17.7																				T	U	V	W	X	Y	Z
Milton	2	17.6																					U	V	W	X	Y	Z
IL98-10145	2	17.4																						V	W	X	Y	Z
Klein 69B	2	17.2																							W	X	Y	Z
NO58-2-75-26	2	17.1																								X	Y	Z
OT2040	2	16.8																									Y	Z
Matilda	2	16.8																										Z

Table 4.16. Tukey's HSD test for oleic acid in 'IOI Selections' sub-set (α = 0.05, minimum significant difference = 5.4 %)

Genotype	Number of replications	% Mean	Tukey Grouping
Matilda	2	47.3	A
Kanota	2	43.4	A B
Norline	2	43.4	A B
Klein 69B	2	43.1	A B C
IL98-10145	2	42.9	A B C
NO58-2-75-26	2	42.5	A B C D
AC Rigodon	2	42.3	A B C D E
IL2858-1	2	42.2	A B C D E
Silva selection	2	42.0	A B C D E F
Nora	2	41.2	B C D E F G
AC Medallion	2	41.1	B C D E F G H
Powell	2	41.1	B C D E F G H
Atlas 14535	2	41.0	B C D E F G H
AC Gwen	2	40.9	B C D E F G H
OT2048	2	40.6	B C D E F G H I
Bage 1419-36	2	40.4	B C D E F G H I J
Chantilly	2	40.4	B C D E F G H I J
Kangaroo	2	40.2	B C D E F G H I J
06FL328	2	40.2	B C D E F G H I J
Millennium	2	40.2	B C D E F G H I J
Skrzat	2	40.1	B C D E F G H I J K
OT2040	2	39.9	B C D E F G H I J K L
Victor	2	39.9	B C D E F G H I J K L
Lvovskii Rannii	2	39.8	B C D E F G H I J K L M
WAOAT2132	2	39.6	B C D E F G H I J K L M N
Vista	2	39.6	B C D E F G H I J K L M N O

MN 811045	2	39.5	B	C	D	E	F	G	H	I	J	K	L	M	N	O					
AC Baton	2	39.4	B	C	D	E	F	G	H	I	J	K	L	M	N	O					
OT586	2	39.4	B	C	D	E	F	G	H	I	J	K	L	M	N	O					
Ukraine	2	39.4	B	C	D	E	F	G	H	I	J	K	L	M	N	O					
Maldwyn	2	39.4	B	C	D	E	F	G	H	I	J	K	L	M	N	O					
Trispernia	2	39.3	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P				
Aarre	2	39.2	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P				
Mortlock	2	39.2	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P				
Irtysh 13	2	39.0	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q			
Milton	2	39.0	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q			
HiFi	2	39.0	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q			
CDC SO-I	2	38.6	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
Boudrias	2	38.6	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
Sylva	2	38.6	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
Baragan 114	2	38.6	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
Furlong	2	38.5	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
IAH611-447 (PI 502955)	2	38.4	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
OT2045	2	38.4	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
IA93227-1	2	38.4	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
Marathon	2	38.4	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
Ursus	2	38.3	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
Borowiak	2	38.3	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R		
Rodney 0	2	38.2	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	
06FL930	2	38.1	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	
Verde	2	38.1	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	
SW Betania	2	37.9		C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
Auteuil	2	37.7		C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
Drummond	2	37.7		C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T
Jumbo	2	37.5			D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T

Proat	2	37.4	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T				
Brawn	2	37.3	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T				
CDC Boyer	2	37.2	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T				
X466	2	36.9		E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U			
Tartarian	2	36.8			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U			
WIX 7955-1	2	36.7			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U			
TAMO-301	2	36.6				G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U			
Ogle	2	36.6				G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U			
Calibre	2	36.2				G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U			
CDC Pro-Fi	2	36.1				G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U			
Salomon	2	36.1				G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V		
CDC Dancer	2	35.9				G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V		
Expander	2	35.9				G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V		
Iltis	2	35.8					H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V		
Clinton	2	35.8					H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V		
Belle	2	35.8					H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V		
Triple Crown	2	35.4						I	J	K	L	M	N	O	P	Q	R	S	T	U	V		
Capital	2	35.4						I	J	K	L	M	N	O	P	Q	R	S	T	U	V		
Evita	2	35.3						I	J	K	L	M	N	O	P	Q	R	S	T	U	V		
Spurs	2	35.3						I	J	K	L	M	N	O	P	Q	R	S	T	U	V		
Hamel	2	35.1							J	K	L	M	N	O	P	Q	R	S	T	U	V		
MAM 17-5	2	35.1							J	K	L	M	N	O	P	Q	R	S	T	U	V		
OMSKIJ 6922	2	34.7								K	L	M	N	O	P	Q	R	S	T	U	V	W	
Avesta	2	34.6									L	M	N	O	P	Q	R	S	T	U	V	W	
Centennial	2	34.5										M	N	O	P	Q	R	S	T	U	V	W	
Marion (Canada)	2	34.5										M	N	O	P	Q	R	S	T	U	V	W	
Morton	2	34.4											N	O	P	Q	R	S	T	U	V	W	
Kolpashevskii	2	34.4											N	O	P	Q	R	S	T	U	V	W	
Revisor	2	34.3											N	O	P	Q	R	S	T	U	V	W	
GK Pillango	2	34.2												O	P	Q	R	S	T	U	V	W	

Ivory	2	34.0	P	Q	R	S	T	U	V	W				
Boxer	2	33.7		Q	R	S	T	U	V	W				
Barra	2	33.7		Q	R	S	T	U	V	W				
Richard	2	33.5			R	S	T	U	V	W				
Skakun	2	33.3			R	S	T	U	V	W				
CDC Baler	2	32.9				S	T	U	V	W				
Aveny-SW 01168	2	32.6					T	U	V	W				
CDC Sol-Fi	2	31.8						U	V	W				
AC Morgan	2	31.6						U	V	W				
Gem	2	30.8							V	W				
Goslin	2	29.5								W	X			
Exeter	2	25.2									X			

Table 4.17. Tukey's HSD test for linoleic acid in 'IOI Selections' sub-set (α = 0.05, minimum significant difference = 4.5 %)

Genotype	Number of replications	% Mean	Tukey Grouping
Exeter	2	47.0	A
Goslin	2	45.4	A B
AC Morgan	2	43.7	A B C
Richard	2	43.5	A B C D
CDC Baler	2	43.3	A B C D
Marion (Canada)	2	43.0	A B C D E
Aveny-SW 01168	2	42.7	A B C D E F
OMSKIJ 6922	2	42.6	A B C D E F G
Morton	2	42.5	A B C D E F G H
Spurs	2	42.4	B C D E F G H I
CDC Sol-Fi	2	42.3	B C D E F G H I J
Ivory	2	42.2	B C D E F G H I J
Capital	2	41.9	B C D E F G H I J K
Avesta	2	41.8	B C D E F G H I J K L
Barra	2	41.8	B C D E F G H I J K L
Triple Crown	2	41.4	B C D E F G H I J K L M
GK Pillango	2	41.4	B C D E F G H I J K L M
Revisor	2	41.4	B C D E F G H I J K L M
Boxer	2	41.4	B C D E F G H I J K L M
Skakun	2	41.0	B C D E F G H I J K L M N
Gem	2	40.7	C D E F G H I J K L M N O
Ogle	2	40.5	C D E F G H I J K L M N O P
Evita	2	40.5	C D E F G H I J K L M N O P
Brawn	2	40.5	C D E F G H I J K L M N O P

Hamel	2	40.3	C	D	E	F	G	H	I	J	K	L	M	N	O	P											
Belle	2	40.2	C	D	E	F	G	H	I	J	K	L	M	N	O	P											
Salomon	2	40.1	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q										
Iltis	2	40.1	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R									
06FL930	2	40.0	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R									
CDC Dancer	2	40.0	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R									
Expander	2	39.7	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S								
Tartarian	2	39.6	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S								
MAM 17-5	2	39.5	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
Milton	2	39.4	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
Jumbo	2	39.3	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
Verde	2	39.2	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
Clinton	2	39.2		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
CDC Pro-Fi	2	39.2		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
Kolpashevskii	2	39.1		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
Maldwyn	2	39.1		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
Auteuil	2	39.1		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
SW Betania	2	39.0		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
Centennial	2	38.8			E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T							
Calibre	2	38.7			E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U						
IA93227-1	2	38.6			E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V					
CDC Boyer	2	38.6			E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V					
Mortlock	2	38.5			E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W				
HiFi	2	38.3				F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X			
OT2040	2	38.3				F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X			
TAMO-301	2	38.3				F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X			
Baragan 114	2	38.2				F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X			
Millennium	2	38.2					G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y		
Marathon	2	38.1					G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y		
Vista	2	38.0						H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y		

Borowiak	2	37.8	I J K L M N O P Q R S T U V W X Y
Rodney 0	2	37.7	J K L M N O P Q R S T U V W X Y
Ukraine	2	37.7	J K L M N O P Q R S T U V W X Y
IAH611-447 (PI 502955)	2	37.6	K L M N O P Q R S T U V W X Y
Sylva	2	37.6	K L M N O P Q R S T U V W X Y
Proat	2	37.6	K L M N O P Q R S T U V W X Y
Victor	2	37.5	K L M N O P Q R S T U V W X Y
AC Baton	2	37.3	K L M N O P Q R S T U V W X Y
Aarre	2	37.3	K L M N O P Q R S T U V W X Y
OT586	2	37.3	L M N O P Q R S T U V W X Y
Trispernia	2	37.2	M N O P Q R S T U V W X Y
06FL328	2	37.2	M N O P Q R S T U V W X Y
Irtysh 13	2	37.1	M N O P Q R S T U V W X Y
Ursus	2	37.1	M N O P Q R S T U V W X Y
Boudrias	2	37.0	M N O P Q R S T U V W X Y
OT2045	2	37.0	M N O P Q R S T U V W X Y
Lvovskii Rannii	2	37.0	M N O P Q R S T U V W X Y
Kangaroo	2	37.0	M N O P Q R S T U V W X Y
Chantilly	2	36.9	M N O P Q R S T U V W X Y
Nora	2	36.9	M N O P Q R S T U V W X Y
Powell	2	36.8	N O P Q R S T U V W X Y
Skrzat	2	36.8	N O P Q R S T U V W X Y
CDC SO-I	2	36.7	N O P Q R S T U V W X Y
WIX 7955-1	2	36.7	N O P Q R S T U V W X Y
X466	2	36.6	N O P Q R S T U V W X Y
NO58-2-75-26	2	36.4	N O P Q R S T U V W X Y
OT2048	2	36.3	O P Q R S T U V W X Y
Silva selection	2	36.1	P Q R S T U V W X Y

MN 811045	2	36.0											P	Q	R	S	T	U	V	W	X	Y	
Drummond	2	35.6												Q	R	S	T	U	V	W	X	Y	
WAOAT2132	2	35.6												Q	R	S	T	U	V	W	X	Y	
Klein 69B	2	35.5													R	S	T	U	V	W	X	Y	
Furlong	2	35.4														S	T	U	V	W	X	Y	
IL98-10145	2	35.3														S	T	U	V	W	X	Y	
Bage 1419-36	2	35.0															T	U	V	W	X	Y	Z
AC Medallion	2	35.0															T	U	V	W	X	Y	Z
AC Rigodon	2	34.2																U	V	W	X	Y	Z
AC Gwen	2	34.1																	V	W	X	Y	Z
Norline	2	34.0																		W	X	Y	Z
IL2858-1	2	33.9																			X	Y	Z
Kanota	2	33.7																				Y	Z
Atlas 14535	2	33.6																				Y	Z
Matilda	2	30.7																					Z

Correlation data for the 'IOI selections' sub-set is presented in Table 4.18. Correlations were similar to those from the 2009 RFT. Oleic acid content was negatively correlated with palmitic acid and linoleic acid content. Palmitic acid content was positively correlated with linoleic acid content.

Table 4.18. Fatty acid correlation Table for fatty acid means in IOI sub-group (n=97)

	% palmitic acid	% oleic acid
% palmitic acid		
% oleic acid	-0.65**	
% linoleic acid	0.29**	-0.90**

**Significant at P=0.01

5. NON-REPLICATED PGRC ACCESSIONS

The remaining material was analyzed without replication and, therefore, has been considered a descriptive analysis.

5.1. Nordic oat *A. sativa* accessions sub-set

The 'Nordic oat' sub-set consisted of 210 *A. sativa* accessions. Summarized data for palmitic acid, oleic acid and linoleic acid is provided in Tables 5.1 and 5.2. Data for the three less abundant fatty acids is in the Appendix, Tables 9.10 and 9.11. Although there was diversity present for each fatty acid within the Nordic group, the highest and lowest content of each fatty acid were not different than for genotypes from the '2009 RFT' or the 'IOI Selections' sub-set. Considering the HSD from the two relicated experiments as surrogates, these differences were not likely significant. For example, palmitic acid content in the Nordic oat sub-set ranged between 16.6% and 24.7%, whereas the range for palmitic acid in the RFT was 15.2 - 22.6%, both comparable to the Nordic accessions. The palmitic acid range for the Nordic oat sub-set (16.6 – 24.7%) was also similar to that for the IOI sub-set (16.8 - 24.5%).

To compare each sub-set in the descriptive analysis, mean contents of each fatty acid from the 2009 RFT were used to represent average oat fatty acid compositions. The 'Nordic oat selection' sub-set demonstrated a higher average plamitic acid content compared to the RFT, considering the HSD of 1.8% from the RFT as a surrogate. Oleic acid and linoleic acid content averages were not different.

Within the 'Nordic oat selection' sub-set some individual genotypes had notably divergent fatty acid levels. 'Weibulls No. 16187' had the highest (24.7%) and 'Lyngby Hede' the lowest (16.6%) palmitic acid content while 'PI 63897' had the highest oleic acid (44.3%) and low linoleic acid contents (32.5%). However, none of these genotypes was outstandingly different from similar, relatively unique lines in the RFT sub-set.

Table 5.1. Descriptive statistics for major fatty acid composition of oat accessions from 'Nordic oat selections' sub-set (FA percentage based on total FA detected by GC, corresponding data for minor fatty acid composition in the Appendix, Table 9.10) (n=210)

	% Palmitic Acid	% Oleic Acid	% Linoleic Acid
Maximum	24.7	44.3	43.6
Minimum	16.6	30.4	32.1
Mean	21.2	37.1	37.0
SD	1.24	2.61	2.03
RFT Mean	18.9	37.4	39.8
RFT HSD	1.8	5.0	4.4

SD= Standard Deviation, RFT= Replicated Field Trial

Table 5.2. Major fatty acid composition of oat accessions from 'Nordic oat selections' sub-set (FA percentage based on total FA detected by GC, corresponding minor fatty acid composition in the Appendix, Table 9.11)

Genotype	CN Number	Origin	Palmitic Acid	Oleic Acid	Linoleic Acid
Abed silver	53725	Denmark	22.7	34.2	38.9
Adelaar	90465	Sweden	20.8	35.9	35.5
Alden	82383	Sweden	22.3	34.1	39.9
Argus black	63934	Sweden	21	35.1	38.4
Awnless probsteier	53574	Sweden	20.7	40.5	33.5
Bambu	63935	Sweden	21.9	35.1	38
Bambu	88805	Sweden	21.7	37.1	37.1
Bambu i	65250	Sweden	20.3	38.2	35.6
Bambu i	67019	Sweden	21.2	36.1	38.6
Bambu ii	63936	Sweden	22.6	34.9	38.7
Bambu ii	65714	Sweden	22.6	35.7	37.6
Bambu ii	65251	Sweden	22.4	34.7	38.4
Bambu ii	64128	Sweden	21.5	37.1	35.8
Beardless probsteier	53165	Sweden	21.7	40.3	33.9
Beardless probsteier	53094	Sweden	21.2	36.6	38.3
Beiar	63966	Norway	21.5	39.7	35.1
Belgium	53429	Sweden	22.1	36.5	36.5
Belyak	90179	Sweden	21.9	38.4	35.5
Belyak	53582	Sweden	19.9	42.8	32.9
Beseler i	65150	Denmark	22	35.7	38.3
Beseler ii	88734	Denmark	21.1	36	39.1

Black bell i	53494	Sweden	22.6	37.3	36.3
Black bell ii	53229	Sweden	20.1	39	36.9
Black great mogul	53488	Sweden	20.8	40.7	34.4
Blenda	63949	Sweden	21.9	36.6	37.1
Blenda	64466	Sweden	21.8	35	38.8
Blenda	64491	Sweden	21.6	36.6	37.2
Blixt	64553	Sweden	23.2	36.5	35.9
Borris opus	55158	Denmark	19.8	38.9	36.9
C.d. 3843	55143	Sweden	21.3	36.5	37.9
C.d. 3866	55147	Sweden	20.9	35.2	39
C.d. 3899	55156	Sweden	18.6	41.1	36.4
Crown	53711	Sweden	21.8	36.5	37.5
Crown	53543	Sweden	22.7	34	39.3
Dan	80793	Sweden	21.6	37.7	35.6
Danish island yellow	53541	Denmark	24	32.3	40
Diamant	65715	Sweden	22.8	37.3	36.3
Eagle	88772	Sweden	21.1	38.4	36.2
Echo	88545	Sweden	20.9	37.2	34.7
Echo	90218	Sweden	20.9	39.2	35.9
Eho	64544	Finland	19.9	36.6	38.4
Eho	64095	Finland	19.7	41.8	34.8
Eho	64009	Finland	21.2	36.6	37.9
Eho tammisto	55102	Finland	21.4	35.7	36.2
Engelbrekt ii	63868	Sweden	21.2	41.5	33.2
Esa	64096	Finland	20.2	41.4	33.5
Esa	65902	Finland	20.5	37.9	37.9
Esakaura	88674	Finland	19.6	39.3	37.1
Extra klock ii	64499	Sweden	22.7	36.5	36.1
Extra klockhavre	63950	Sweden	21.2	38.7	36.3
Fortuna	88385	Sweden	21.4	36.2	36.7
French black	90470	Denmark	20.6	38.2	36.7
Golden	88773	Sweden	21.2	37.6	36.9
Golden rain	90396	Sweden	22.7	33.9	39.6
Golden rain	53576	Sweden	22.6	35.3	37.9
Golden rain ii	88547	Sweden	22.8	34.3	39
Gouldregen	88739	Sweden	21.6	35.9	38.7
Gray moor	53540	Denmark	24.3	34.7	36.7
Great mogul	53099	Sweden	19.8	40.9	35.5
Great mogul ii	64501	Sweden	19.5	42.4	34.4
Grossmogul	65212	Sweden	20.2	40.4	35.5

Gul naesgaard	65092	Denmark	22.5	34.3	39.2
Guldregn	65254	Sweden	22.3	33.9	38.9
Guldregn iii	65264	Sweden	22	36.6	37.4
Ha 70-81-1	73355	Finland	20.2	39.6	34.9
Ha 70-81-3	73356	Finland	18.9	42.8	32.9
Ha 70-81-3c	73357	Finland	19.9	36.8	37.1
Ha70-81-3	29842	Finland	18.8	39.1	33.8
Ha70-81-3c	29844	Finland	18.6	36.1	38
Ha70-81-4	29843	Finland	18.2	43.9**	33.7
Hankkija 773	79298	Finland	20.9	38.6	36.2
Hannes	66468	Finland	20.3	40.1	35.1
Havre stam 54	55107	Sweden	20.2	36.6	37.1
Havre stam 58	55108	Sweden	21.6	32.8	41.3
Hedvig	82382	Sweden	20.3	38.5	36.4
Hein ii	55124	Norway	21.9	31.9	35
Hja 75430	45986	Finland	21.6	37	35.8
Hja 76037n	45987	Finland	19.3	38.6	37.4
Hja 78033	45988	Finland	19.9	38.3	35.3
Hja 78156	45989	Finland	20.9	37.5	36.7
Hja 80278	45990	Finland	21.5	33.8	38.7
Holmberg 54	55106	Sweden	20.7	38.1	37.1
Hvitling	53088	Sweden	22.2	35.7	38
Jalostettu maatiais	90219	Finland	18.6	40.9	36.6
Jo 1043	35914	Finland	21.1	37.3	38
Jo0770	1772	Finland	21.7	35.6	38
Jo0794	1773	Finland	21.5	36.1	37.8
Juha	65411	Finland	20.7	41.1	33.7
Juha	64546	Finland	20.9	36.7	36.7
Kalott	77953	Sweden	20.4	39.7	36.5
Korgen	63967	Norway	21.1	41.3	32.1*
Kyro	64547	Finland	23.7	33.3	39.1
Kyto	88759	Finland	22	36.1	38
Kyto	64102	Finland	20.5	39.7	33.2
Kytokaura	90369	Finland	22.6	35.1	38.4
Lightning	64493	Sweden	21.6	38.8	35.6
Ligowo svalof	53220	Sweden	22	36.5	37.5
Linda	66608	Sweden	21	37.2	37.1
Lyngby hede	65117	Sweden	16.6*	40.1	36.7
Max	64678	Denmark	20.5	36.4	38.1
Merkur	28751	Norway	21	39.2	36.3

Minor	55160	Denmark	20.8	34	37.9
Nasta	44287	Finland	21.7	35.6	36.6
Nidar	54143	Norway	21.3	35.7	39
Nina	30886	Sweden	19.7	35.6	38.3
Nip	64492	Sweden	21	38.9	36.3
Nopsa	88387	Finland	22.4	36.2	37.4
Nova	53779	Denmark	20.4	38.7	35.8
Opus	88916	Denmark	20.2	39.7	35.8
Opus ii	64468	Denmark	20.7	36.5	38.3
Opus iii	66477	Denmark	20.5	38.2	37.2
Orion	63911	Sweden	20.9	38.3	37
Orion iii	55123	Sweden	21.6	36.7	37.6
Orion iii	63970	Sweden	22.3	36.9	36.8
Orn	63872	Sweden	20.7	39.2	35.5
Osmo	64108	Finland	19.6	41	33.8
Osmo i	90220	Finland	22.2	36.5	36.8
Osmo ii	88388	Finland	21.7	37.9	36.4
Pellervo	88760	Finland	21.8	36.4	36.6
Pelso	88477	Finland	24.4**	33.4	37.6
Penderhavre	65717	Sweden	22.7	39.7	33.7
Pi 055378	88389	Denmark	21.2	36.8	37.4
Pi 197843	63974	Sweden	23.5	33.9	38.7
Pi 224301	64131	Sweden	22.9	33.4	39.6
Pi 264267	64500	Sweden	19.4	40.6	36.7
Pi 361866	73483	Denmark	20.3	41.8	33.3
Pi 63897	99000	Finland	17.2*	44.3**	32.5*
Ponta	30887	Sweden	21.8	32.6	41.3**
Primus	88808	Sweden	20	34.6	41.3
Primus ii	55121	Sweden	18.3	36.6	39.8
Primus ii	63873	Sweden	19.4	38.5	37.3
Primus ii	55034	Sweden	18.3	36.7	38.6
Probsteier	53421	Sweden	22.7	35.5	38
Probsteier	53424	Sweden	21.7	36.3	38.5
Probsteier	53634	Sweden	19.4	41.2	34.2
Probsteier	65312	Sweden	21.8	37.7	36.4
Probsteier (cultivar)	53420	Sweden	22.9	36.9	36.5
Puhti	35909	Finland	21.4	34.8	38.7
Puhti	44288	Finland	21.3	35	36.4
Reima	35910	Finland	21.1	39.9	34.7
Rex	64025	Denmark	20.4	38.1	36.1

Risto	30885	Sweden	21.6	36.5	35.9
Risto	77954	Sweden	24.2	36.5	36
Risto	80794	Sweden	23.2	37.7	35.4
Ryhti	35911	Finland	19	41.4	35.3
Ryhti	44286	Finland	20.9	38.4	35.9
Same	63955	Sweden	19.5	39.7	35.1
Sang	1775	Sweden	21	34.7	39.9
Sang	77955	Sweden	21.7	35.7	38.5
Sang	80795	Sweden	22.3	34.6	38.9
Saxo	65885	Sweden	21.4	33.6	40.7
Seger	65909	Sweden	20.3	42.2	33.8
Selma	72374	Sweden	22	36	38.4
Simo takioincer	55103	Finland	21.3	40.4	34.2
Sirius	88672	Sweden	20.4	40.3	35.3
Sirius	63912	Sweden	21	39	35.7
Sirius ii	55122	Sweden	20.1	39.1	36.9
Sisu	64548	Finland	21.5	35.7	37
Sofi	82381	Sweden	20.6	41.5	33.7
Sol	55109	Sweden	20.7	36.1	38.3
Soleil ii	65420	Sweden	19.7	36.6	38.8
Sorbo	57866	Sweden	21.7	38.1	36.2
Star	88774	Sweden	22.2	33.8	40.2
Star	54144	Sweden	22.4	33	40.1
Sternhafer	88750	Sweden	21.5	35.6	39.1
Stormogul ii	63957	Sweden	19.7	41	33.1
Sun ii	55105	Sweden	20.9	37.2	37.6
Sv. 25/357	63973	Sweden	22.5	37.4	36
Svalof 8	54977	Sweden	20.6	37.1	38
Svea	80796	Sweden	20.5	38.6	36.8
Swedish select	88333	Sweden	20.9	31.9*	43.6**
Tammi	88761	Finland	21	34.7	40.2
Tammie tammisto	55099	Finland	20.9	36.3	37.8
Trio	54784	Sweden	20.5	39	35.3
Trio	63937	Sweden	22.6	36.5	36.8
Triumphal	88381	Sweden	21.5	35.9	37.5
Tuha	64011	Finland	21.3	38.1	35.5
Tuotto	90221	Finland	22.2	38.4	35.2
Valko	80779	Finland	23.5	35	37.8
Veli	44289	Finland	20.9	39.5	36
Victoria	52998	Denmark	21.4	35.7	39

Victory	53726	Sweden	21.7	36.2	36.8
Victory	53326	Sweden	21.6	34.5	38.9
Victory	53340	Sweden	21.6	34.6	38.3
Victory	53648	Sweden	21.8	32.4	41.3
Victory	53911	Sweden	19.7	38.4	34.2
Victory	55031	Sweden	20.9	35.4	37.2
Wasa	53778	Sweden	20.6	37.2	37.6
Wasa	53647	Sweden	22.3	35.8	37.5
Wasta	35913	Finland	21.9	36.3	36.6
Weibull 16385	65350	Sweden	21.6	38.5	34.8
Weibull 16428	65352	Sweden	20.5	39.9	35.3
Weibull 16509	66470	Sweden	22.5	34.4	39.6
Weibull 16511	66471	Sweden	22.4	35.3	38.7
Weibulls 16004	57107	Sweden	21.2	32.3	40
Weibull's 16004	64672	Sweden	22.2	34.2	39.3
Weibull's 16195	64673	Sweden	22.3	32.6	39.4
Weibull's 16229	64674	Sweden	20.7	36.6	37.2
Weibull's 16385	64675	Sweden	20.9	38	36.4
Weibulls no. 16187	64484	Sweden	24.7**	31.6*	39.7
Weibulls no. 16228	64485	Sweden	21.5	36.7	36.8
Weikus	30888	Sweden	19.6	30.4*	33.3
White probsteier	88338	Sweden	22.8	32.9	40.9
Yellow	52999	Denmark	22.4	37.6	35.9
Yellow naesgaard	53776	Denmark	21.7	36.2	36.7
Ylitornio	63971	Sweden	21.6	40.8	33.8
Zloty deszcz	90176	Sweden	21	38.9	36.4
Zonne ii	65269	Sweden	20.6	38	37.1
Weibull 16384	65349	Sweden	22	36.9	35.6
Weibull 16414	65883	Sweden	20.3	38.5	36
Mean[§]			21.2	37.1	37

* Lowest % of each fatty acid, **Highest% of each fatty acid, [§]Mean % of each fatty acid

5.2. PGRC accessions sub-set

The PGRC accessions sub-set was comprised of accessions from different species sourced from Plant Gene Resources of Canada. Genotypes included representatives from the hexaploid species *A. sativa*, *A. byzantina*, *A. sativa* subsp. *nudisativa*, *A. sterilis*, *A. fatua* and the diploid oat species *A. strigosa.*

5.2.1. *A. sativa* accessions

Forty six *A. sativa* accessions were selected to represent different geographic regions across the range of distribution of the species and analyzed. Summarized fatty acid data is provided in Tables 5.3 and 5.4. Mean palmitic acid, oleic acid and linoleic acid contents were not apparently different between the PGRC *A. sativa* accessions and the RFT, considering HSD for each fatty acid from the RFT as surrogates (Table 5.3). Respective data for the three minor fatty acids is in the Appendix, Tables 9.12 and 9.13.

'CN 3120' had the highest oleic acid content (46.1%) whereas 'CN 3109' had highest linoleic acid content (44.5%), and 'CN 55149' and 'CN 3186' had the highest palmitic acid content (22.8%). Respective mean content from the RFT were 18.2%, 37.4% and 39.8% palmitic acid, oleic acid and linoleic acid, respectively. Considering the RFT HSD as surrogates, the above listed genotypes were different. 'CN 4840' had a lower palmitic acid content (14.6%) than the RFT mean. Minimum values for palmitic acid (14.6%) and linoleic acid (29%) were lower compared to the 2009 RFT (15.2% and 34.1% for palmitic acid and linoleic acid respectively).

The lower values for the two fatty acids may show increased range of diversity in the investigated oat material, although considering the HSD for each fatty acid from the 2009 RFT, these low palmitic acid accessions were likely not significantly different from the lowest palmitic genotypes in the 2009 RFT.

Table 5.3. Descriptive statistics for major fatty acid composition of *A. sativa* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding data for minor fatty acid composition in the Appendix, Table 9.12) (n= 46)

	% Palmitic Acid	% Oleic Acid	% Linoleic Acid
Maximum	22.8	46.2	44.6
Minimum	14.6	29.6	29.0
Mean	19.6	36.4	38.7
SD	1.93	3.91	3.64
RFT Mean	18.9	37.4	39.8
RFT HSD	1.8	5.0	4.4

SD= Standard Deviation, RFT= Replicated Field Trial

Table 5.4. Major fatty acid composition of *A. sativa* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding minor fatty acid composition in the Appendix, Table 9.13)

CN Number	% Palmitic acid	% Oleic acid	% Linoleic acid
3109	19.7	32.6	44.6 **
63900	21.9	30.7 *	41.6
4367	19.4	35.6	38.5
53993	16.4	30.8	44.5 **
65156	19.9	34.6	41.7
88697	16.7	38.7	36.7
4394	19.0	36.6	39.5
2898	22.6	32.4	40.2
4271	19.0	40.4	37.4
4401	22.3	31.2	43.3
3133	20.9	38.4	32.0
90458	18.5	30.1	43.4
3180	19.1	40.2	37.0
4387	19.9	34.9	40.9
55149	22.8 **	29.6 *	42.2
2933	18.8	39.2	37.6
4907	17.8	39.5	38.2
3175	18.6	39.2	36.3
2906	22.2	38.0	35.5
88777	17.7	40.5	35.7
64015	19.7	35.7	40.7
88754	17.9	39.2	36.1

63736	20.1	41.4	34.8
82123	18.7	35.9	42.0
64061	21.0	35.7	37.7
4828	18.1	38.4	38.2
3160	19.5	34.7	41.5
2937	20.7	32.7	41.4
2841	17.0	43.8 **	32.5
1771	18.3	36.3	39.7
4840	14.6 *	34.0	42.7
4380	19.9	37.1	37.2
3189	19.3	35.2	40.9
4388	21.7	31.9	42.0
88791	22.3	31.0	43.2
4865	19.2	36.9	39.9
2822	16.6 *	38.0	39.5
3110	19.4	38.8	38.4
56233	21.4	33.7	37.7
4691	21.2	30.8	42.2
30749	19.0	36.7	37.1
2928	18.5	39.4	35.8
4360	21.3	35.4	39.3
3120	19.7	46.2 **	29.0 *
3186	22.8 **	40.6	32.1 *
2821	19.4	41.8	32.8
Mean[§]	19.6	36.4	38.7

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

5.2.2. *A. byzantina* accessions

Forty-seven *A. byzantina* accessions were analyzed. Summarized fatty acid data is provided in Tables 5.5 and 5.6. The minor fatty acids data is in the Appendix, Tables 9.14 and 9.15.

A. byzantina accessions were not apparently different from the RFT with respect to their mean palmitic acid, oleic acid and linoleic acid contents. 'CN 53687' was highest in oleic acid (45.2%), 'CN 64301' and 'CN 2807' were highest in linoleic acid (41.9%) and 'CN 21948' had the highest palmitic acid content (22.9%) within the sub-set. 'CN 64654' had the lowest palmitic acid content (16.3%) within the sub-set.

This sub-set had a narrower range for the contents of each fatty acid compared to the 2009 RFT, e.g. oleic acid content in *A. byzantina* sub-set ranged from 32.4 - 45.2% compared to the RFT range of 23.6 - 45.4%.

Table 5.5. Descriptive statistics for major fatty acid composition of *A. byzantina* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding data for minor fatty acid composition in the Appendix, Table 9.14) (n=47)

	% Palmitic Acid	% Oleic Acid	% Linoleic Acid
Maximum	22.9	45.2	41.9
Minimum	16.3	32.4	33.6
Mean	19.2	38.7	37.9
SD	1.42	2.54	2.11
RFT Mean	18.9	37.4	39.8
RFT HSD	1.8	5.0	4.4

SD= Standard Deviation, RFT= Replicated Field Trial

Table 5.6. Major fatty acid composition of *A. byzantina* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding minor fatty acid composition in the Appendix, Table 9.15)

CN Number	% Palmitic acid	% Oleic acid	% Linoleic acid
88917	18.3	39.1	38.4
88833	20.8	35.8	40.1
5212	20.8	36.6	38.5
4218	19.8	40.4	34.8
3159	17.4	39.2	35.3
54018	18.6	39.5	38.4
88594	17.7	41.6	37.5
55297	19.9	38.0	37.9
63819	19.4	37.3	39.6
64595	18.6	37.5	40.4
3171	17.5	39.5	38.6
64947	19.5	39.0	34.3
88755	17.6	39.4	37.9
3150	18.2	39.6	39.4
21948	22.9 **	35.2	36.6
64654	16.3 *	40.0	37.6
2843	21.2	35.0	40.1
64225	20.2	39.5	37.5
53687	17.6	45.2 **	33.6 *
57207	20.2	34.3	41.7
63815	19.2	42.4	34.4
64296	20.7	40.9	35.3
64188	21.3	37.4	37.8
2832	19.2	38.7	39.0
3194	17.8	39.6	37.1
55125	19.8	36.7	39.3
88783	17.2 *	39.8	38.9
65029	21.6 **	39.8	34.1 *
90489	17.4 *	39.5	39.9
88938	19.4	39.0	38.7
25055	20.6	38.6	37.8
57004	19.1	39.5	37.3
3162	20.2	39.7	36.3
57142	18.6	38.7	40.0
5197	19.6	35.5	41.0
88722	18.3	42.1	36.3
65482	18.2	43.8 **	34.2

53597	19.8	40.9	35.7
3194	18.6	39.9	38.0
57909	18.6	40.1	37.7
64293	20.0	37.5	38.3
56892	17.8	39.0	37.2
53869	19.4	33.5 *	40.0
65325	20.1	37.5	38.1
64523	19.6	40.7	36.8
2807	20.6	32.4 *	41.9 **
64301	18.9	36.1	41.9 **
Mean[§]	19.2	38.7	37.9

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

5.2.3. *A. sativa* subsp. *nudisativa* accessions

Seventeen *A. sativa* subsp. *nudisativa* accessions were evaluated. Summarized fatty acid data is provided in Tables 5.7 and 5.8. Corresponding minor fatty acids data is in the Appendix, Tables 9.18 and 9.17.

This sub-set had a lower mean linoleic acid content (34.3%), compared to the RFT (38.4%), whereas palmitic acid (19.4%) and oleic acid (41.7%) means were not different from the RFT means (20% and 37.6%, respectively), considering the RFT HSD as surrogates.

Genotype 'CN 34095' was highest in palmitic acid (23.7%), whereas 'CN 53677' had lowest in palmitic acid (16.9%). 'CN 52029' was highest in oleic acid (47.5%) and 'CN 66492' was highest in linoleic acid (38.9%) within the sub-set. Ranges for oleic acid and linoleic acid content were lower than for the 2009 RFT sub-set. However, the range for palmitic acid content range was similar.

Table 5.7. Descriptive statistics for major fatty acid composition of *A. sativa* subsp. *nudisativa* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding data for minor fatty acid composition in the Appendix, Table 9.16) (n=17)

	% Palmitic Acid	% Oleic Acid	% Linoleic Acid
Maximum	23.7	47.5	38.9
Minimum	16.9	38.0	26.1
Mean	19.4	41.7	34.3
SD	1.91	2.73	3.31
RFT Mean	18.9	37.4	39.8
RFT HSD	1.8	5.0	4.4

SD= Standard Deviation, RFT= Replicated Field Trial

Table 5.8. Major fatty acid composition of *A. sativa* subsp. *nudisativa* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding minor fatty acid composition in the Appendix, Table 9.17)

CN Number	% Palmitic acid	% Oleic acid	% Linoleic acid
63829	20.7	43.9	31.3
17824	18.9	40.1	32.5
52029	18.0	47.5 **	30.5 *
46228	19.8	42.1	33.5
46819	19.3	43.5	33.1
53677	16.9 *	40.9	37.6
29662	20.0	38.0 *	37.8
66492	19.3	38.1 *	38.9 **
42930	18.5	45.3 **	32.4
79437	19.2	39.8	36.9
79365	23.6 **	42.6	26.1 *
30730	19.5	38.4	38.3 **
4930	18.1	43.1	34.8
63700	17.5	41.7	36.9
64584	17.4 *	44.1	34.7
55263	19.7	40.4	35.4
34095	23.7 **	39.6	33.1
Mean[§]	19.4	41.7	34.3

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

5.2.4. *A. strigosa* accessions

Twenty diploid *A. strigosa* oat accessions were evaluated and corresponding summary data is provided in Tables 5.9 and 5.10. Summary data for the minor fatty acids is in the Appendix, Tables 9.18 and 9.19.

'CN 81779' had highest oleic acid content (47.7%), whereas 'CN 22000' and 'CN 25767' were highest in linoleic acid (36.3%) and palmitic acid (21.0%) respectively. This diploid oat sub-set showed lower diversity for palmitic acid and linoleic acid content, compared to the hexaploid oat species evaluated in the 2009 RFT. 'CN 81779' and 'CN 81784' had the lowest palmitic acid content (17.5% and 17.6%, respectively) within sub-set. The lower diversity of fatty acid may be due to restricted allele interaction in diploid *A. strigosa*, compared to *A. sativa*

and other hexaploid *Avena* species. *A. strigosa* genotypes may be a good starting point for more detailed fatty acid composition research such as identifying molecular markers linked to specific fatty acid composition due to the simplified nature of the *A. strigosa* genome.

This sub-set demonstrated a similar mean palmitic acid content, but a greater mean oleic acid content and a lower mean linoleic acid content compared to the RFT sub-set (Table 5.13). Oleic acid content was consistently higher in this sub-set, compared to the RFT mean oleic acid content (Table 5.14). The mean oleic acid content was highest (44.1%) in *A. strigosa* among investigated oat material whereas the linoleic acid level was lower (33.0%) compared to the 2009 replicated field trial (39.8%).

On the basis of the strong positive correlation between oleic acid content and oil content from the RFT and the IOI selections, it can be predicted that *A. strigosa* accessions will have higher oil content compared to *A. sativa* accessions. If this is the case, *A. strigosa* may be a potential germplasm resource to improve the quality and quantity of oil in future oat cultivars, although interspecifc crosses may be hard to make because of compatibility barriers between *A. sativa* and *A. strigosa*. There are a few reports of using *A. strigosa* as a germplasm source to transfer disease resistance to *A. sativa* (Rines et al. 2007), so use of this diploid oat species to transfer desired traits to *A. sativa* is possible.

Table 5.9. Descriptive statistics for major fatty acid composition of *A. strigosa* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding data for minor fatty acid composition in the Appendix, Table 9.18) (n=20)

	% Palmitic Acid	% Oleic Acid	% Linoleic Acid
Maximum	21	47.8	36.3
Minimum	17.5	39.7	30.7
Mean	19.2	44.1	33.0
SD	1.13	2.11	1.53
RFT Mean	18.9	37.4	39.8
RFT HSD	1.8	5.0	4.4

SD= Standard Deviation, RFT= Replicated Field Trial

Table 5.10. Major fatty acid composition of *A. strigosa* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding minor fatty acid composition in the Appendix, Table 9.19)

CN Number	% Palmitic acid	% Oleic acid	% Linoleic acid
54037	18.7	46.8	30.7 *
88826	19.3	44.2	33.2
88867	19.0	44.9	32.7
52909	18.3	45.2	32.5
58076	18.5	43.6	34.0
88866	19.1	42.3	34.9
25730	20.8	42.5	32.8
88330	20.3	42.7	33.4
3067	18.1	42.7	35.5 **
81779	17.5 *	47.8 **	30.9 *
3075	20.5	41.4	34.1
3068	20.6	42.7	33.0
81768	18.6	47.0 **	30.8
22002	19.6	44.2	32.8
81784	17.6*	44.8	34.3
25767	21.0 **	42.6	32.5
81762	19.0	45.8	31.8
79350	17.7	47.0 **	31.7
58062	19.4	44.0	32.7
22000	20.3	39.7 *	36.3 **
Mean[§]	19.2	44.1	33.0

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

5.2.5. *A. sterilis* accessions

Twenty *A. sterilis* samples were included in the study and summarized fatty acid data is provided in Tables 5.11 and 5.12. The minor fatty acids data can be found in the Appendix, Tables 9.20 and 9.21.

The *A. sterilis* accessions had a higher mean palmitic acid content (24.3%) and lower mean linoleic acid content (28.8%) compared to the RFT mean (18.9% and 39.8% respectively).

Mean oleic acid levels were not different. 'CN 25658' had an oleic acid content of 56.6%, the highest level among all accessions analyzed, but with much lower linoleic acid at 18.2%.

'CN 24018' had a palmitic acid content of 27.2% and a stearic acid and eicosenoic acid content of 4.6% and 2.6% respectively, the highest level of total saturated fatty acids among all the genotypes analyzed. 'CN 64586' was highest in linoleic acid (38.8%) within the sub-set whereas accession 'CN 25658' was highest in oleic acid (56.6%) among all genotypes in this project. Most *A. sterilis* accessions had higher palmitic acid levels and lower linoleic acid levels compared to *A. sativa* lines. 'CN 24248' demonstrated the lowest palmitic acid content (18.2%) within the sub-set. However, there are many genotypes in *A. sativa* accessions that had lower palmitic acid content than 'CN 24248'.

Earlier reports suggested the ability of *A. sterilis* to store more oil compared to *A. sativa* (Leonova et al., 2008), but *A. sterilis* fatty acids profiles reported from that research did not show higher levels of palmitic acid or oleic acid and were comparable to those of a normal *A. sativa* fatty acid profile.

Table 5.11. Descriptive statistics for major fatty acid composition of *A. sterilis* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding data for minor fatty acid composition in the Appendix, Table 9.20) (n=20)

	% Palmitic Acid	% Oleic Acid	% Linoleic Acid
Maximum	27.2	56.6	38.8
Minimum	18.2	34.5	18.2
Mean	24.3	41.1	28.8
SD	2.64	4.61	5.13
RFT Mean	18.9	37.4	39.8
RFT HSD	1.8	5.0	4.4

SD= Standard Deviation, RFT= Replicated Field Trial

Table 5.12. Major fatty acid composition of *A. sterilis* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding minor fatty acid composition in the Appendix, Table 9.21)

CN Number	% Palmitic acid	% Oleic acid	% Linoleic acid
20202	25.0	42.0	23.6
21749	24.3	43.7	27.7
21794	26.5	39.5	24.1
21870	23.5	37.2	32.2
22466	24.4	38.3	32.5
23016	26.2	39.5	30.0
23226	25.8	44.0	25.2
23553	25.6	38.8	31.5
23570	25.3	42.7	27.4
24018	27.2 **	39.2	22.9 *
24092	25.7	39.7	29.9
24248	18.2 *	43.6	34.0
24434	27.2 **	43.9	23.0
25658	19.5 *	56.6 **	18.2 *
64586	21.5	34.5 *	38.8 **
64610	22.8	44.6 **	26.5
64616	26.7	35.8 *	33.7
67342	26.7	41.8	26.6
67357	21.3	38.6	33.6
67381	23.1	38.2	34.3 **
Mean[§]	24.3	41.1	28.8

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

5.2.6. *A. fatua* accessions

Eighteen *A. fatua* accessions were analyzed for their fatty acid composition. Summary data is provided in Tables 5.13 and 5.14. Corresponding data for minor fatty acids is in the Appendix, Tables 9.22 and 9.23.

A. fatua accessions had apparently different mean levels for all of the three major fatty acids compared to RFT means. Mean palmitic acid (22.2%) and oleic acid content (42.8%) were higher, whereas linoleic acid content (29.2%) was lower in *A. fatua*, when compared to the RFT means (20.0%, 37.6% and 38.6% for palmitic acid, oleic acid and linoleic acid respectively).

'CN 23035' showed the highest palmitic acid content (29.5%) among all analyzed accessions and may contribute to an increase in diversity for palmitic acid in oat. 'CN 22559' and 'CN 22557' had the lowest palmitic acid levels (15.4% and 16.7% respectively) within the sub-set. 'CN 23710' and 'CN 22561' had the highest oleic acid (46.5%) and linoleic acid content (36.6%) respectively. This *A. fatua* sub-set had a lower range for oleic acid content compared to the 2009 RFT sub-set, but there were individual accessions with lower linoleic acid and higher palmitic acid content, 'CN 21985' was much lower in linoleic acid (20.2%) and higher palmitic acid content (28.9%) compared to *A. sativa* genotypes from the 2009 RFT.

Table 5.13. Descriptive statistics for major fatty acid composition of *A. fatua* accessions from 'PGRC accessions' sub-set (FA percentage based on total FA detected by GC, corresponding data for minor fatty acid composition in the Appendix, Table 9.22) (n=18)

	% Palmitic Acid	% Oleic Acid	% Linoleic Acid
Maximum	29.6	46.6	36.6
Minimum	15.4	31.2	20.2
Mean	22.2	42.8	29.2
SD	4.31	3.63	4.74
RFT Mean	18.9	37.4	39.8
RFT HSD	1.8	5.0	4.4

SD= Standard Deviation, RFT= Replicated Field Trial

Table 5.14. Major fatty acid composition of *A. fatua* accessions from 'PGRC accessions' (FA percentage based on total FA detected by GC, corresponding minor fatty acid composition in the Appendix, Table 9.23)

CN Number	% Palmitic acid	% Oleic acid	% Linoleic acid
19396	21.5	45.6	28.1
21197	28.5	40.2	25.0
21213	22.0	44.0	28.0
21229	20.1	41.5	33.5
21242	20.8	41.3	32.5
21302	24.1	42.9	28.4

22557	16.7 *	45.6	31.5
22559	15.4 *	44.3	36.2 **
22561	16.8	41.7	36.6 **
22564	20.5	40.2	34.0
22600	26.6	38.8	25.3
22613	20.6	44.0	30.8
22614	24.0	43.7	26.8
23035	29.6 **	31.2 *	30.5
23710	20.9	46.6 **	23.0
24141	18.6	45.1	31.4
21985	28.9 **	45.9 **	20.2 *
25522	26.8	45.7	21.7 *
23110	18.4	45.2	30.4
Mean[§]	22.1	42.8	29.2

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

6. GENERAL DISCUSSION AND SUMMARY

Oleic acid and linoleic acid showed the most variation among the 917 oat accessions investigated. Oleic acid content ranged from 23.5% to 56.5%, and linoleic acid content from 18.2% to 48.5%. Although both oleic acid and linoleic acid are unsaturated fatty acids, oleic acid has received more attention from the food industry due to greater stability and longer shelf life compared to linoleic acid.

Fatty acid profiles of representative (two cultivars per decade of release) accessions from the 'Historic Canadian cultivars' sub-set were plotted over time to evaluate possible fatty acid profile variation during the last century. No noticeable pattern of change in palmitic acid, oleic acid or linoleic acid composition was detected (Figure 6.1). Trendlines based on linear regression suggest no change in oleic acid, increase in palmitic acid and decrease in linoleic acid levels. The randomness of the fatty acid profiles of oat genotypes over the years probably relates to the fact that the fatty acid profile has never been a criterion for selecting oat cultivars. There may be an opportunity for plant breeders to select oat cultivars with improved fatty acid composition for human nutrition or livestock feed. Results from these experiments revealing diversity in fatty acid composition are encouraging. Oleic acid and linoleic acid contents of *Avena sativa* accessions with average oil content such as 'CDC Dancer' are comparable with available commercial oils, e.g. peanut oil (figure 6.2). This study indicates that fatty acid profiles similar to normal corn and soybean oil may be achieved in oat oil fatty acid profile by slight modification. Further, modification of the fatty acid profile of future oat cultivars may enhance the pre-acclaimed health promoting properties of oat.

Figure 6.1. Change in fatty acid proportions in the 'Historic Canadian cultivars' sub-set over years of release 1886-2001.

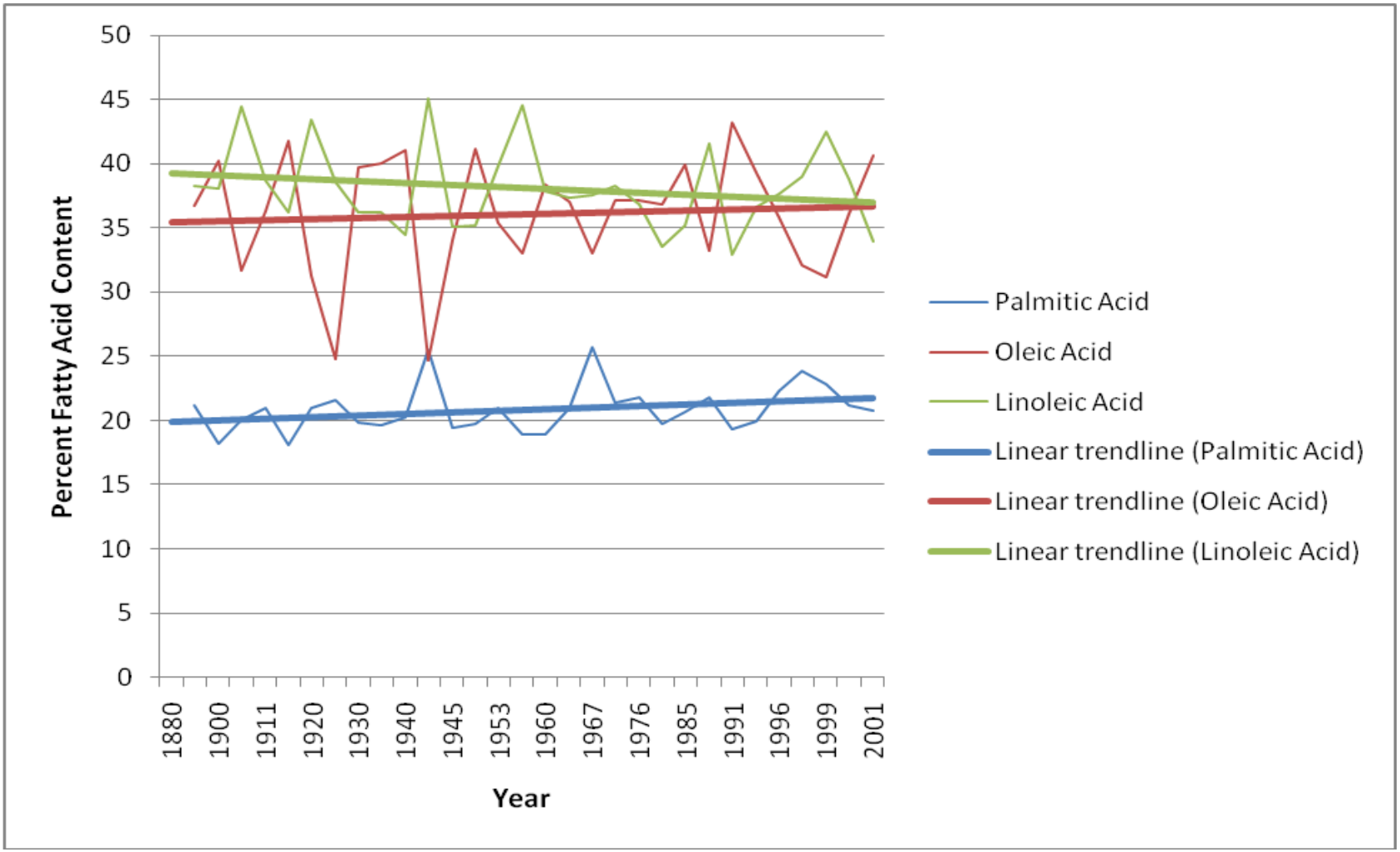
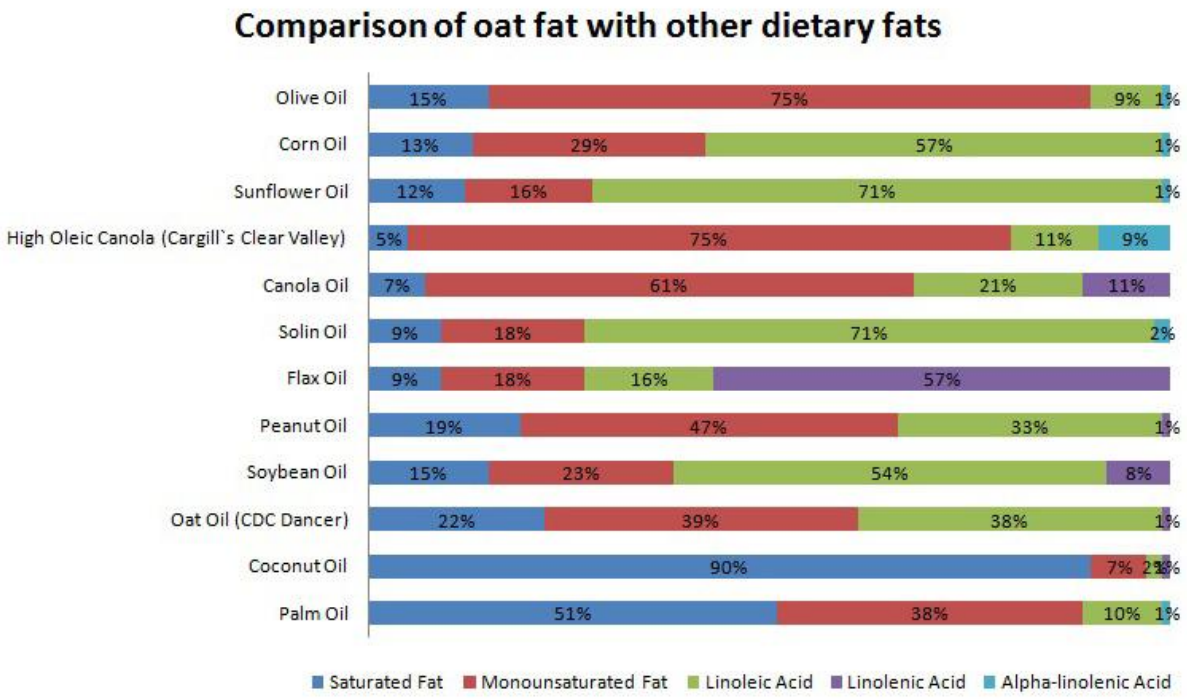


Figure 6.2. Comparison of oat fat with other dietary fats



Data sources: Mcdonald (1994) and Flax Council of Canada (2010); Solin Oil values are for Linola™; Oat oil (CDC Dancer) data from the current study

A few previous reports suggested an effect of growing conditions (especially temperature) on oat fatty acid composition. Welch (1975) and Saastamoinen et al. (1989) reported that lower growing temperature caused higher oil accumulation in oat, increasing the proportions of oleic acid and linoleic acid while palmitic acid and stearic acid contents decreased. While variable growing season temperature was not a variable in the current study the tendency for increased oil content to result in increased oleic and linoleic acid levels concommittant with reduded palmitc and and stearic acid porportions was consistent.

Rezai and Frey (1988) reported that *A. sterilis* genotypes from various geographical regions of Europe and the Mediterranean region demonstrated significantly different oil contents. Based on information from earlier studies, it was hypothesized that the fatty acid profile of *A. byzantina* accessions originating from a warmer Mediterranean climate could differ from that for *A. sativa* accessions originating from a cooler Scandinavian climate, with Nordic *A. sativa* material predicted to have more unsaturated fatty acid(s) than *A. byzantina*. All samples of *Avena sp. genotypes* included in this study, except those from 'IOI selections' sub-set grown at Ottawa, were produced at a single geographical site, Saskatoon, SK, Canada, while genotypes included in previously reported experiments were grown at different geographical sites. This may be the reason for differences in fatty acid profiles. In the current study, growing location was found to have a significant effect on absolute percentage of some fatty acids, but individual genotypic relative fatty acid porportions were consistent across locations. Therefore the hypothesis is not supported by the current study.

It is evident from the experimental results reported here that the species of genus *Avena* included in this experiment comprise a diverse range for key fatty acid composition. By using the fatty acid HSD from the 2009 RFT and 'IOI selections' sub-sets as surrogates, an orientation for comparing the non-replicated results from the PGRC accessions sub-set, genotypes with higher palmitic acid, oleic acid and linoleic acid contents were identified. These diverse lines could be used as base breeding material to alter the fatty acid composition of future oat cultivars. *Avena* species of various ploidy levels have been used to transfer desirable characters, such as large grain, higher protein, disease resistance and oil content, to cultivated oat. *A. sterilis* is considered as an important source of commercially important traits and is widely used in oat breeding

(Loskutov, 2000). Results of this experiment provide an excellent opportunity for oat breeders to use *A. strigosa, A. sterilis* and *A. fatua* to breed oat cultivars with altered fatty acid composition. In general, *A. stigosa, A. sterilis* and *A. fatua* selections had relatively more genotypes with interesting fatty acid profiles compared to *A. sativa* accessions, even though these sub-sets were of limited scope with 20 or fewer genotypes. This suggests the possibility of finding more genotypes with relatively unique fatty acid profiles if more genotypes from these *Avena* species were to be investigated.

Frey (1994) describes the importance of *A. sterilis* in the oat gene pool to improve disease resistance and increased groat protein and oil content in *A. sativa* genotypes. *A. sterilis* was demonstrated to carry diverse and complementary genes to *A. sativa*. Schipper et al. (1991) and Holland and Frey (1999) reported increased oat groat oil content with recurrent selection in *A. sativa* and *A. sterilis*. Over the various cycles of recurrent selection, the ratio of unsaturated to saturated fatty acids, oil content and oleic acid content increased, whereas palmitic acid and linoleic acid content decreased. These results support the possibility of breeding oat with the objectives of higher oil and oleic acid content.

As suggested in many reports, modern biotechnological tools such as molecular (e.g. DArT) mapping can be useful for breeders (Kilian et al., 2005, Oraguzie et al., 2007, Wenzl el al., 2007). Finding molecular markers linked to major fatty acids can make genotype selection more efficient and provide opportunities for more consistent and effective selection. DArT populations for which the parents were included in the current study along with their corresponding fatty acid data could be further used to identify molecular markers. The cultivars ‘Sol-Fi’ and ‘HiFi’ had notable differences in fat content and fatty acid composition. Whereas ‘Sol-Fi’ had below average fat content and higher palmitic acid and linoleic acid content, ‘Hifi’ demonstrated above average fat content and higher oleic acid content. Similar differences were observed in genotypes ‘OT 3033’ and ‘OT 3024’. Parents of the world’s only haploid population, ‘Aslak’ and ‘Matilda’, also showed variations in fatty acid profile. These DArT populations could be a starting point for further molecular marker investigations. Also, developing more DArT populations using parents with unique fatty acid profiles could be helpful for molecular marker assisted selection and finding interesting genotypes.

Genotypes with higher unsaturated fatty acid content and lower saturated fatty acid content such as 'SA98352' (U of S high/low oil lines sub-set), 'Millennium' and 'OT 2040' (IOI Selections sub-set, genotypes from AAFC, Winnipeg), 'IL98-10145' (IOI Selections sub-set, a breeding line from the University of Illinois), 'Matilda' (IOI Selections sub-set), 'CN 53677' (PGRC Selections, *A. sativa* subsp. *nudisativa* sub-set) or diploid oat lines such as 'CN 81784' (PGRC Selections, A. strigosa sub-set) can be crossed with genotypes with comparatively lower unsaturated fatty acid contents and higher saturated fatty acid contents (e.g. 'SA98387' from U of S high/low oil lines sub-set; 'OAC Woodstock' from Historic Canadian Cultivars sub-set and a cultivar from the University of Guelph; 'Grizzly' from Historic Canadian Cultivars sub-set and a cultivar from the University of Alberta; 'Pelso' from the Nordic Oat Selections sub-set or *A. sterilis* accessions such as 'CN 24018' and 'CN 24434', and *A. fatua* accessions such as 'CN 23035' and 'CN 21985', from PGRC Selections sub-set) to develop more DArT populations to identify more molecular markers associated with fatty acids. 'Millennium', 'OT 2040' and 'Grizzly' are noteworthy since these genotypes are already well adapted to Western Canada. Breeding *A. sativa* genotypes with diploid *A. strigosa* genotypes can be a challenge and special techniques are required for a successful crossing (Rines and Carson, 2007).

The cultivar 'Exeter' also presents an opportunity because it has been identified in this experiment as a genotype with a relatively unique fatty acid profile. A population derived using 'Exeter' and other genotypes with a normal or unique fatty acid profile could be used to develop a DArT or SNP map to identify molecular markers related to important fatty acids. One such population with 'Exeter' and 'Dal' as parents exists at the ECORC, Ottawa (Personal communication with Dr. Nicholas Tinker).

In general, the two major unsaturated fatty acids (oleic acid and linoleic acid) in oat comprised some 75% of the total fatty acid composition in *A. sativa* selections. *A. sterilis* and *A. fatua* selections demonstrated slightly lower levels of total unsaturated fatty acids (69.9% and 72%, respectively). However, certain genotypes, for example 'SA97170' and 'SA98352' from the 'U of S high/low oil lines' sub-set, had a higher proportion of unsaturated fatty acids (78.6% and 79.1%, respectively versus 16.8% and 17.1% of palmitic acid respectively). This difference in unsaturated versus saturated fatty acids is evident in *A. fatua* genotypes with an average of

72% unsaturated fatty acids. For example, a total oleic acid and linoleic acid contents of 80.5% were detected in 'CN 22559' versus a palmitic acid content of 15.4%. Matilda from the 'IOI Selections' sub-set contained a total of 77.1% unsaturated fatty acids and 17.3% of palmitic acid. Such genotypes, with higher levels of unsaturated fatty acids, were identified among all sub-sets evaluated and could be used in breeding programs to develop oat cultivars with higher unsaturated fatty acid levels for human food. Whereas oleic acid tends to increase HDL (good) cholesterol in human blood stream, linoleic acid is known to have no effect on it. Both oleic and linoleic acid are known to lower LDL (bad) cholesterol (Erickson et al. 1964), hence decreasing the risks of heart stroke and coronary heart disease. *A. stigosa* selections had generally higher mean oleic acid and lower linoleic acid contents compared to the 2009 RFT average, but demonstrated higher total unsaturated fatty acid levels compared to that for the PGRC *A. sativa* selections.

Genotypes such as SA98352 and Matilda had higher oleic acid content (46.0% and 47.2%, respectively) even though their fat content were relatively lower (10.3%) compared to genotypes with very high fat content such as SA080029 (12.6%). Such genotypes might specifically interest the oat food industry where manufacturers aim to increase the proportions of healthy fat in oat products.

On the other hand, genotypes low in unsaturated fatty acids generally demonstrated higher levels of palmitic acid. For example, 'SA98387' from the U of S high/low oil lines sub-set contained 24.7% of palmitic acid and 70.5 % of total unsaturated fatty acids. Similar differences were evident in certain *A. sterilis* and *A. fatua* genotypes. For example, *A. sterilis* lines 'CN 24018' and 'CN 24434' had a palmitic acid content of 27.2%, but total unsaturated fatty acid contents of only 62.0% and 66.9% respectively. Similarly, *A. fatua* lines 'CN 23035' and 'CN 21985' contained 29.6% and 28.9% of palmitic acid combined with 61.7% and 66.2% of unsaturated fatty acids respectively. The *A. sativa* cultivar 'Exeter' from the 'Historic Canadian Cultivars' sub-set contained 25.5% of palmitic acid and only 69.8% of unsaturated fatty acids. Such genotypes could be an important germplasm source for breeders interested in increasing saturated fat levels in feed oat cultivars. These genotypes could also be used for food products such as margarines and shortenings. Canola and soybean oil that are high in unsaturated fatty

acids need to be modified to attain desirable stability and crystallization properties by processes such as blending and hydrogenation (Rousseau, 2004). Hydrogenation introduces variable amount of *trans* fatty acids along with saturation in the oil. *Trans* fatty acids have adverse effects on human health and are better avoided (Ascherio and Willett, 1997). Blending various oils is an alternative to hydrogenation and canola oil has been blended with soybean oil or palm oil to produce margarines (Eskin and McDonald. 2007). Oat oil could be an alternative to soybean oil as a blending option with canola oil. Cargill's Clear Valley high oleic/low linoleic acid canola oil is an example of blending canola and flaxseed oil to improve fatty acid composition (Cargill, 2010). Similar blends to attain desirable stability, melting and crystallization can be made to alter the oat oil fatty acid composition for food markets.

It could be an interesting challenge for plant breeders to shift oat fatty acid composition towards a more desirable fatty acid profile. A few hypothetical examples of crosses that could be made to produce desired results for the food industry are:

<u>*A. sativa* accessions</u>

SA97170 (16/42/36 POL*) X SA97482 (20/33/43 POL*)

??? (16/42/37 POL*)

*POL: palmitic/oleic/linoleic acid

<u>*A. sterilis* and *A. fatua* accessions</u>

CN 22559 (15/44/36 POL*) X CN 25658 (19/56/18 POL*)

??? (15/56/28 POL*)

*POL: palmitic/oleic/linoleic acid

Similar types of crosses for the feed oat industry could focus on increasing saturated fatty acids and decreasing unsaturated fatty acids. Some hypothetical examples are:

<u>*A. sativa* accessions</u>

Grizzly (25/33/37 POL*) X Hajira (21/24/38 POL*)

??? (25/24/37 POL*)

*POL: palmitic/oleic/linoleic acid

<u>*A. sterilis* and *A. fatua* accessions</u>

CN 24018 (27/39/22 POL*) X CN 23035 (29/31/30 POL*)

??? (29/31/22 POL*)

*POL: palmitic/oleic/linoleic acid

In the above examples, selections can be made to select for higher stearic acid and eicosenoic acid content such as those of 'Hajira', to increase the saturated fatty acid content in the new lines.

7. MAJOR FINDINGS AND CONCLUSIONS

- Investigation of oat fatty acid composition in this experiment revealed significant fatty acid diversity among various *Avena* species.

- Oleic acid and linoleic acid generally make up some 75% of the total fatty acids in *A. sativa* and demonstrated most variation. Some genotypes from other *Avena* species in the study demonstrated higher levels of other fatty acids compared to *A. sativa*.

- Oleic acid content was positively correlated with oil content. This may be important for plant breeders trying to improve the oat oil content as well as the oil quality for human food.

- Mean oleic acid content of *A. strigosa* lines was higher than that of *A. sativa*. However, there were some interesting *A. sativa*, *A. sterilis* and *A. fatua* genotypes with higher oleic acid or higher palmitic acid content. *A. sterilis* had a higher mean palmitic acid content.

- Growing environment affected palmitic acid, stearic acid and oleic acid content in the oat fatty acid profile, but not linoleic acid, linolenic acid and eicosenoic acid content. However, despite the effect of growing environment, genotypes high or low in particular fatty acids behaved similarly at both locations, suggesting high heritability of the fatty acid composition traits which may be useful for oat breeders in effective selection and accurate evaluation of future oat genotypes and existing oat germplasm.

- There is a possibility of finding more genotypes with interesting fatty acid profiles in *A. strigosa*, *A. sterilis* and *A. fatua* species.

- Presence of parents of DArT mapping populations included in this experiment indicate a starting point for potential identification of molecular markers linked to specific fatty acid levels for more effective selection in breeding programs. Also, new DArT populations c*an be develo*p*ed using ge*notyp*es with* interesting fatty acid profiles as parents to gain more insight into fatty acid content-molecular marker association.

A recent goal for most oilseed crop improvement programs has been to alter fatty acid profiles for human food by decreasing saturated fatty acid content and increasing unsaturated fatty acids levels. While average oat oil is already relatively 'healthy', with unsaturated fatty acid levels of > 85% and saturated fatty acid levels as low as 15%, certain oat genotypes show potential as a source of even healthier oil. Oat oil content is a food industry concern because of restricted allowance of total fat level in food products on a per serving basis. However, if oil quality in oat products could be improved, it could be possible that whole grain oat products specifically could be allowed greater total fat per serving. This would benefit consumers because of healthier fat for their diet; but also aid food processors and oat product manufacturers by modifying the complexity involved in processing low fat oat varieties due to excessive groat breakage of low fat oat during dehulling and issues of bland taste of final oat products developed from low fat oat. Such a change would also be beneficial to oat breeding by allowing greater flexibility in breeding germplasm choice and reducing the emphasis on selection for low groat fat levels.

Altering oat fatty acid composition for specific needs may improve its nutritional quality in human and ruminant diets. Results of this study provide a detailed insight of oat fatty acid composition. The oat oil fatty acid diversity revealed in this study could be an important initial step to breed future oat cultivars with modified fatty acid composition to suit various markets.

8. LIST OF REFERENCES

Alam, S. M., and Adams, W. A., 1979. Effect of soil pH on the growth and mineral content of oats. Pakistan Journal of Scientific and Industrial Research. 22: 147-151.

Ascherio A., Willett W.C., 1997. Health effects of trans fatty acids. American J Clinical Nutr Oct. 1997 vol. 66 no. 4 1006S-1010S.

Barker, G. 1985. Prehistoric Farming in Europe. Cambridge University Press, Cambridge.

Baum, B.R. 1977. Oats: wild and cultivated. A monograph of the genus *Avena* L. (Poaceae). Printing and Publishing, Agriculture Canada.

Bauman, D. E. and Griinari, J. M. 2003. Nutritional regulation of milk fat synthesis. Annu. Rev. Nutr. 23: 203-227.

Biermann, U.; Wittmann, A.; and Grosch. W. (1980) Occurrence of bitter tasting hydroxy fatty acids in oats and wheat, Fette Seifen Anstrichm. 82:236–240

Buchanan B.B. 2000. Biochemistry and Molecular Biology of Plants. American Society of Plant Physiologists Rockville, Maryland.

Canada Grains Council. 2006. Handbook.
Published online: http://www.canadagrainscouncil.ca/

Cervantes-Martinez et al. 2001. Selection for greater beta glucan content in oat grain. Crop Sci. 41:1085–1091

Chilliard, Y. and Doreau, M. 1997. Influence of supplemental fish oil and rumen-protected methionine on milk yield and composition in dairy cows. J. Dairy Res. 64: 173-179.

Cargill. 2010. Clear Valley® Omega-3 oil. www.cargill.com. 2010.

http://www.cargill.com/food/na/en/products/oils-shortenings/clear-valley/oils/clear-valley-omega-3-oil/index.jsp

Coffman, F. A. 1961. Origin and history. Pages 15-40 *in* F.A. Coffman, ed. Oats and oat improvement. American Society of Agronomy, Madison, WI, USA.

Coffman, F.A. and Frey, K. J. 1961. Influence of climate and physiological factors on growth in oat. Pages 420-464 *in* F.A. Coffman, ed. Oats and oat improvement. American Society of Agronomy, Madison, WI, USA.

Dehmer K.J. and Friedt, W. 1998. Development of molecular markers for high oleic acid content in sunflower (*Helianthus annuus* L.). Industrial Crops and Products 7,(2-3), :311-315

De La Roche, I. A., Burrows, V. D., and Mckenzie, R. I. H. 1977. Variation in lipid composition among strains of oats. Crop Sci. 17:145-148.

Diederichsen, A. 2006. Assessments of genetic diversity within a world collection of cultivated hexaploid oat (*Avena sativa* L.) based on qualitative morphological characters, Genetic Resources and Crop Evolution.55,(3):419-440

Dowhan, W. and Bogdanov, M. 2002 Functional roles of lipids in membranes. New Comprehensive Biochemistry Volume 36, 2002, Pages 1-35 Biochemistry of Lipids, Lipoproteins and Membranes, 4th edition

Eder, K. 1995. Gas chromatographic analysis of fatty acid methyl esters. J Chromatography B. 617: 113-131

Ekstrand, B., Gangby, I.; Åkesson, G., Stöllman, U.; Lingnert, H. and Dahl. S. (1993) Lipase activity and development of rancidity in oats and oat products related to heat treatment during processing, J. Cereal Sci. 17:247–254

Erickson B.A., Coots R.C., Mattson F.H., Kligman A.M. 1964. The Effect of Partial Hydrogenation of Dietary Fats, of the Ratio of Polyunsaturated to Saturated Fatty Acids, and of Dietary Cholesterol upon Plasma Lipids in Man. J Clinical Invest.43(11): 2017–2025.
Eskin N.E.M., Mcdonald B.E. 2007. Canola oil. Nutrition bulletin. Vol. 16, issue 3. 2007.

Fahy et al. 2005. A comprehensive classification system for lipids, Journal of Lipid Research, Vol. 46, 839-862

Fernández-Martínez et al. 1997. Sunflower mutant containing high levels of palmitic acid in high oleic background Euphytica Volume 97, Number 1, 113-11

Fitzpatrick, K., and R. Scarth. Improving the health and nutritional value of seed oils. PBI Bulletin. (January 1998):15–19

Flax Council of Canada 2010, Growing flax. (accessed: August 2010)http://www.flaxcouncil.ca/english/index.jsp?p=growing11&mp=growing

Food and Drug Administration, Food Labeling: Health Claims; Oats and Coronary Heart Disease; Final Rule (1997) (accessed: September 2010)
Published online:
http://www.fda.gov/Food/LabelingNutrition/LabelClaims/HealthClaimsMeetingSignificantScientificAgreementSSA/ucm074719.htm

Food, Fats and Oil (2006) The Institute of Shortening and Edible Oils. (accessed: March 2009)
http://www.iseo.org/foodfats.htm

Forsberg, R. A. and Reeves, D. L. 1995. Agronomy of oats. Pages 223-251 *in* R. W. Welch, ed. The oat crop: Production and utilization. Chapman & Hall, New York, NY, USA.

Forss, D. A. 1969. Role of lipids in flavors. J. Agric. Food Chem.,17 (4): 681–685

Frey, K.J. 1994. Remaking a crop gene pool: The case history of Avena. Proc. Of the Nat. Sci. Counc, ROC, Part B: Life Sci., Vol. 18, No2, pp. 85-93

Frey, K. J. and Hammond, E. G. 1976. Genetics, characteristics, and utilization of oil in caryopses of oat species. Journal of the American Oil Chemists Society 52 (9) 358-362.

Fulcher, R.G. 1986. Morphological and chemical organization of the oat kernel. Pages 47-94 in: Oats: Chemistry and Technology. F.H. Webster, Ed. American Association of Cereal Chemists, St. Paul, MN.

Gansmann, W. and Vorwerck, K. 1995. Oat Milling, Processing and Storage, in The Oat Crop, edited by R.W. Welch, Chapman and Hall, London, pp. 369–408.

Gibson, L. and Benson G. 2002. Origin, History, and Uses of Oat (*Avena sativa*) and Wheat (*Triticum aestivum*) (accessed: May 2010)
http://www.agron.iastate.edu/courses/agron212/readings/oat_wheat_history.htm

Green, A.G. 1986. Genetic control of polyunsaturated fatty acid biosynthesis in flax (Linum usitatissimum) seed oil TAG Theoretical and Applied Genetics Volume 72, Number 5, 654-661.

Harlan, J. and J. de Wet (1971). Towards a rational classification of cultivated plants. *Taxon* **20**: 509-517.

Health Canada 2009 High Oleic Acid / Low Linolenic Acid Canola Lines 45A37, 46A40 (accessed: July 2010)

http://www.hc-sc.gc.ca/fn-an/gmf-agm/appro/ofb-096-228-a-eng.php

Hawke, J. C. and Silcock, R. W. 1970. The *in vitro* rates of lipolysis and biohydrogenation in rumen contents. Biochim. Biophys. Acta 218: 201-212.

Heydanek, M.G. and McGorrin, R.J. 1981. Gas Chromatography–Mass Spectroscopy Identification of Volatiles from Rancid Oat groats. J. Agric. Food Chem. 29:1093–1095.

Holland et al. 2001. Correlated responses of fatty acid composition, grain quality, and agronomic traits to nine cycles of recurrent selection for increased oil content in oat. Euphytica 122 (1): 69-79

Jolliffe I. 2005. Principal component analysis. Encyclopedia of Statistics in Behavioral Science. (accessed: July 2010)
Published online: http://onlinelibrary.wiley.com/doi/10.1002/0470013192.bsa501/full

Kalbasi-Ashtari A. and Hammond E. G. 1977. Oat Oil: Refining and stability. Journal of the American Oil Chemists' Society Volume 54, Number 8, 305-307

Kelling, K. A. and Fixen, P. E.. 1992. Soil and nutrient requirements for oat production. Pages 165-190 *in* Oat science and technology. American Society of Agronomy and Crop Science Society of America, Madison, WI, USA.

Kinney, A.J. 1996. Development of genetically engineered soybean oils for food applications. Journal of Food Lipids 3: 213-292

Kirk, R.S. and Sawyer, R. 1999. Pearson's compostion and analysis of foods. 9th ed. Addison-Wesley Longmam Inc., Harlow, England, p 285

Leonova et al. 2008. Analysis of Oil Composition in Cultivars and Wild Species of Oat (*Avena* sp.) J. Agric. Food Chem., 56 (17), pp 7983–7991

Lessire R., Juguelin H., Moreau P., and Cassagne C. 1985. Elongation of acyl-CoAs by microsomes from etiolated leek seedlings. Phytochemistry 24:1187

Lichtenstein A.H., Lynne M.A, Susan M.J., Ernst J.S. 1999. Effects of Different Forms of Dietary Hydrogenated Fats on Serum Lipoprotein Cholesterol Levels. N Engl J Med 1999; 341:856.

Liu, K.S. 1994. Preparation of fatty acid methyl esters for gas-chromatographic analysis of lipids in biological materials. J Am Oil Chem Soc. 71: 1179-1187

Loskutov, I.G. 2000. Interspecific Crosses in the Genus *Avena* L. Russian Journal of Genetics, 37(5): 467-475

Marlett, J.A. 1993. Comparisons of dietary fiber and selected nutrient compositions of oat and other grain fractions. In: Wood PJ (ed) Oat bran. American Association of Cereal Chemists, St. Paul, MN: 49–82

May, E. W., Shirtliffe S.J., McAndrew, D.W., Hopzapfel, C.B., Lafond, G.P. 2009. Management of wild oat (*Avena fatua* L.) in tame oat (*Avena sativa* L.) with early seeding dates and high seeding rates. Can. J. Plant Sci. 89: 763-773

Mcdonald B.E. 1994. Canola oil nutritional properties. Canola Council of Canada, Winnipeg, MB.

McKenzie, R.I.H. and D.E. Harder. 1995. "Oat." pp. 98–112 in A.E. Slinkard and D.R. Knott (eds.), Harvest of Gold. Saskatoon: University of Saskatchewan Extension Press.

McNair, H.M. and Miller, J.M. (2009). Basic Gas Chromatography, Second Edition. A Wiley-Interscience Publication. New York. Miller, S.S., Fulcher, R.G., Sen, A., and Arnason, J.T. 1995. Oat endosperm cell walls: I. Isolation, composition, and comparison with other tissues. Cereal Chem 72:421–427

Moate, P. J., Boston, R. C., Jenkins, T. C., and Lean, I. J. 2007. Kinetics of ruminal lipolysis of triacylglycerol and biohydrogenation of long-chain fatty acids: new insights from old data. J. Dairy Sci. 91: 731-742.

Moore-Colyer, R. J. 1995. Oats and oat production in history and pre-history. Pages 1-33 *in* R.W. Welch ed. The oat crop: Production and utilization. Chapman & Hall, New York, NY, USA.

Morrison, W.R. and Smith, L.M. 1964. Preparation of fatty acid methyl esters and dimethylacetals from lipids with boron fluride-methanol. J. lipid Res. 5: 600-608.

Mukherjee K.D. and Keiwitt I. 1987. Formation of gamma-linolenic acid in higher plant evening primrose (*Oenothera beinnis* L.). J. Agric. Food Chem. 35:1009

Peterson , D. M. 1992. Composition and nutritional characteristics of oat grain and products. Pages 265-292 *in* H.G. Marshall and M.E. Sorells eds. Oat science and technology. American Society of Agronomy and Crop Science Society of America, Madison, WI, USA.

Peterson, D.M. 2004. Oat – a multifunctional grain. In: Peltonen-Saino P, Topi-Hulmi M (eds) Proc 7th Intl Oat Conf, Helsinki, Finland, pp 21–26. (accessed: May 2010) www.mtt.fi/met/pdf/met51.pdf

Rines, H.W., Carson, M.L. 2007. Transfer of crown rust resistance from diploid oat Avena strigosa into hexaploid cultivated oat A. sativa [abstract]. North American Cereal Rust Workshop, April 2-4, 2007, St. Paul, MN. p. 50.

Rines, H.W., Molnar, S.J., Tinker, N.A. and Phillips, R.L. 2006. Oat Genome Mapping and Molecular Breeding in Plants. Cereals and Millets. (Vol 1) C. Kole (Ed.) Springer-Verlag Berlin Heidelberg 2006.

Rousseau D. 2004. Chemical and physical properties of canola and rapeseed oil. Rapeseed and Canola Oil: Production, Processing, Properties, and Uses – F.D. Gunstone. CRC Press. 2004

Saastamoinen M., Kumpulainen J. and Nummela S. 1989. Genetic and environmental variation in oil content and fatty acid composition of oats. Cereal Chem. 66(4):296-300

Schipper, H.; Hammond, E.G.; and Frey, K.J. (1991). Changes in fatty acid composition associated with recurrent selection for groat-oil content in oat. *Euphytica* 56: 81--88, 1991.

Soldatov, K.I. 1976. Chemical mutagenesis in sunflower breeding. In: 7th Int. Sunflower Conf., Krasnodar, pp. 352—357

Shimada, T.; Wakita, Y.; Otani, M.; Iba, K. (2000). Modification of Fatty Acid Composition in Rice Plants by Transformation with a Tobacco Microsomal .OMEGA.-3 Fatty Acid Desaturase Gene (NtFAD3). Plant Biotechnology. 17(1): 43-48

Song, T.; Su, S.; Chen, S.; Zhao, Y. (1997). Bright future of high oil corn. J maize sciences. 1997 (3). 83-88

Sorrells, M. E. and Simmons, S. R. 1992. Influence of environment on the development and adaptation of oat. Pages 115-164 *in* H.G. Marshall and M.E. Sorells eds. Oat science and technology. American Society of Agronomy and Crop Science Society of America, Madison, WI, USA.

Statistics Canada, 2010. Production of field and speciality crops; Stocks of Principal Field Crops at December 31, 2009 (accessed: June 2010)
http://www40.statcan.gc.ca/l01/cst01/Prim11b-eng.htm

http://www.statcan.gc.ca/bsolc/olc-cel/olc-cel?catno=22-002-X&lang=eng

Stoutjesdijk et al. 2000. High-oleic acid Australian *Brassica napus* and *B. juncea* varieties produced by co-suppression of endogenous *D*12-desaturases Biochemical Society Transactions (2000), Volume 28, part 6. Pages 938-940.

Tanhuanpää P.; Kalendar R.; Schulman A.H. and Kiviharju E. 2008. The first doubled haploid linkage map for cultivated oat The Genome 51: 560-569

Tester, R.F. and Karkalas J. 1996. Swelling and Gelatinization of Oat Starches, Cereal chem... 73(2):271–277.

Tinaco, J. 1982. Dietary requirements and functions of alpha linolenic acid in animals. Prog. Lipid Res. 21:1-45

Töpfer, R., N. Martini and J. Schell. 1995. Modification of plant lipid synthesis. Science 268:681–686

Welch, R. W. 1995. The chemical composition of oats. pp. 279-320 *in* R. W. Welch (ed.) The oat crop: Production and utilization. Chapman & Hall, New York, NY, USA.

Welch, R., Brown, J., Leggett, J., 2000. Interspecific and intraspecific variation in grain and groat characteristics of wild oat (*Avena*) species: Very high groat (1–3), (1–4)-b-D-glucan in an *Avena atlantica* genotype. J Cereal Sci 31:273–279

Wenzl P., Huttner E., Caig V., Heller-Uszynska K., Carling J., Jaccoud D., Evers M., Xia L., Hok P., Risterucci A.M., Uszynski G., Kilian A. 2007. Diversity Arrays Technology (DArT): a rapid and cost-effective method for generating high-density genome fingerprints. Poster presented at the REDBIO 2007 meeting, Vina del Mar, Chile, 22-26 Oct.

Whole Grains Nutrition. Prairies Oat Growers Association. (accessed: September 2010) http://www.poga.ca/default.aspx?page=13

Wood R., Kubena K., O'Brian B., Tseng S., Martin G. 1993. Effect of butter, mono- and polyunsaturated fatty acid-enriched butter, trans fatty acid margarine, and zero trans fatty acid margarine on serum lipids and lipoproteins in healthy men. J Lipid Research, 34, 1-11.

Zhou M.X., Robards, K., Glennie-Holmes, M., and Helliwell, S. 1998. Fatty Acid Composition of Lipids of Australian Oats, J. Cereal Sci. 28:311–319

Zhu S., Rossnagel B.G. and Kaeppler H.F. 2004. Genetic analysis of quantitative trait loci for groat protein and oil content in oat. Crop Sci 44:254–260

9. APPENDIX

Table 9.1. Minor fatty acid composition of 'U of S high/low oil lines' sub-set (FA percentage based on total FA detected by GC)

U of S Number	% Stearic acid	% Linolenic acid	% Eicosenoic acid
SA97082	1.18	1.95**	0.73
SA97172	2.53	1.00	0.65
SA97178	1.89	1.36	1.02
SA97233	1.90	1.16	0.80
SA97362	1.58	1.46	1.01
SA97396	1.72	1.03	0.94
SA97432	1.85	1.48	0.79
SA97443	1.96	1.04	0.94
SA97116	1.87	0.93	0.99
SA97665	2.68	1.66	0.60*
SA97701	3.11	1.09	0.64*
SA97062	1.94	1.45	0.91
SA97250	1.92	0.95	0.80
SA97404	2.55	0.82	0.76
SA97407	1.95	1.11	0.86
SA97409	2.13	0.84	0.77
SA97413	1.92	1.20	0.83
SA97457	1.07	1.62	0.94
SA97496	2.65	0.79	0.74
SA97547	2.29	0.68*	0.78
SA97699	3.90**	0.90	0.69
SA97482	0.97*	1.44	0.89
SA97668	1.60	1.48	0.91
SA97695	1.88	1.72	0.74
SA97127	0.99*	1.52	0.97
SA97532	2.63	0.98	0.73
SA97693	2.46	1.14	0.84
Slavuj	1.66	1.03	0.81
SA96145	1.23	1.63	0.84
SA96139	1.16	1.39	0.94
SA96280	2.34	1.56	0.87
Celsia	1.37	1.34	0.97
SA98070	2.93	0.84	0.67
SA98171	1.10	1.79	0.97
SA98188	1.96	1.25	0.89
SA98191	1.15	1.26	0.99

SA98321	1.91	0.73	1.12**
SA98346	1.79	1.58	0.92
SA98360	1.52	1.66	0.92
SA98379	2.03	1.78	0.91
SA98387	1.87	2.03**	0.92
SA98416	1.79	1.37	0.91
SA98421	1.98	1.20	0.90
SA98594	1.35	1.36	0.90
SA98328	2.43	1.45	0.77
SA98352	2.03	0.70*	1.07**
SA98422	1.77	1.35	0.88
SA97170	3.27**	0.73	0.64*
Mean [§]	1.95	1.27	0.86

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean% of each fatty acid

Table 9.2. Minor fatty acid composition of 'Historic Canadian Cultivars' sub-set (FA percentage based on total FA detected by GC)

Cultivar	% Stearic acid	% Linolenic acid	% Eicosenoic acid
Mabel	1.72	1.03	0.99
CDC Dancer	1.90	1.20	0.90
Roxton	2.66	0.73	0.81
Sylva	2.33	0.78	0.73
Ultima	2.20	0.89	0.97
Kelsey	3.32	0.89	0.74
CDC Pacer	2.31	1.09	0.76
Robert	3.04	0.85	0.89
Marion	2.44	0.89	0.87
Bell	2.06	0.78	0.90
Simcoe	2.67	1.05	0.78
Triple Crown	1.37*	1.02	0.91
Laurel hulless	1.86	1.00	1.07
Rodney	2.68	1.05	0.84
Oxford	2.27	0.99	0.88
AC Stewart	4.23**	5.08	3.04
Torch hulless	2.12	0.79	0.96
Appalaches	1.84	1.06	0.60
Shaw	1.95	0.94	0.82
Yamaska	2.20	4.55	3.18

Laurent	2.51	0.89	0.84
Fortune	2.11	0.95	0.62
OAC Woodstock	4.87**	4.36	3.17
Old Island Black	1.66	0.89	0.97
Larain	2.00	5.16**	4.33
Riel	2.11	0.90	0.88
Pendek	1.55	1.08	0.98
Fundy	1.98	1.13	0.48*
AC Juniper	2.48	0.93	0.84
Kamouraska	2.17	0.97	0.82
OAC Paisley	1.46	1.51	1.05
Hinoat	2.16	3.80	3.36
Elgin	2.10	0.87	0.83
Ida	2.15	1.05	1.07
AC Pinnacle	2.39	0.74	0.87
AC Assiniboia	3.15	0.86	0.84
Erban	1.98	1.01	0.86
Fraser	2.34	1.34	0.86
Dorval	2.60	0.93	0.85
Early Triumph	1.84	0.90	0.81
Beacon	1.77	0.88	0.85
Eagle	2.28	1.07	0.77
CDC Boyer	1.98	0.86	0.85
Irish	1.76	1.05	1.45
Legacy	1.97	1.42	0.94
AC Ronald	2.96	0.84	0.80
CDC Bell	1.51	1.31	2.29
Abegweit	2.23	1.12	0.55*
Gopher	1.46	1.27	2.05
Alma	2.53	1.06	0.86
Scotian	2.07	1.06	0.89
Terra hulless	1.98	0.97	0.80
Derby	1.77	1.37	0.84
Linwood	3.16	1.08	0.69
Alaska	2.17	1.13	0.84
Scott	2.34	1.00	0.81
Shefford	1.44	1.11	1.28
Donegal	3.12	3.84	3.23
Sentinel	2.34	1.05	0.83
Lanark	3.06	0.94	0.79

Manic	1.78	1.41	1.04
AC Marie	3.04	0.63*	0.78
Garry	2.93	0.94	0.74
AC Morgan	1.53	1.13	0.83
Athabasca	2.30	1.02	0.81
Dumont	3.92	0.91	0.80
ELVY	1.81	1.14	0.89
Fidler	2.82	3.40	2.82
Glen	2.10	0.92	0.80
Waldern	1.51	1.12	0.83
Ajax	1.96	0.94	0.95
Grizzly	1.68	1.08	0.99
Beaver	2.02	0.95	0.90
Hudson	1.68	1.10	0.93
Valor	2.17	1.14	0.95
Lanark-RED	1.80	1.04	0.94
Random	1.49	1.09	0.70
AC Francis	3.76	4.74	4.76**
Cartier	2.11	2.93	3.07
Capital	2.44	1.06	0.88
Victory	2.20	1.01	0.80
Joanette	2.51	1.05	0.91
AC Rebel	3.29	0.86	0.79
AC Rigodon	2.24	0.78	0.94
Exeter	1.79	1.71	1.25
Gemini	2.66	2.75	2.94
Donald	2.15	1.40	0.93
AC Mustang	1.44	3.42	2.76
Russell	3.22	0.92	0.81
Quamby	1.51	1.12	1.15
Hajira	3.33	5.40**	6.31**
Swedish Select	1.93	0.98	0.85
Foothill	2.01	1.09	1.18
Banner	1.89	1.00	0.88
Vanguard	2.36	0.86	0.96
Gold Rain	2.04	1.03	0.84
Sixty Day	1.49	1.46	0.87
Cluan	2.53	1.09	0.79
Harmon	2.79	1.05	0.78
Cascade	1.17*	1.08	1.05

Liberty hulless	2.19	0.83	0.98
Calibre	2.07	1.11	0.77
Sioux	2.50	2.57	2.22
AC Preakness	3.38	0.90	0.82
AC Hunter	2.73	0.72*	0.82
Jasper	2.99	0.96	0.87
Mean[§]	2.28	1.39	1.22

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

Table 9.3. Tukey's HSD test for stearic acid in Replicated Field Trial 2009 (α = 0.05, minimum significant difference = 0.89 %)

Genotype	Number of replications	% Mean	Tukey Grouping									
SA02984	4	3.09	A									
SA080511	4	3.00	A	B								
SA97170	4	2.84	A	B	C							
Matilda	4	2.69	A	B	C	D						
SA98387	4	2.62	A	B	C	D	E					
SA080498	4	2.57	A	B	C	D	E	F				
SA071405	4	2.51	A	B	C	D	E	F	G			
SA97699	4	2.51	A	B	C	D	E	F	G	H		
AC Ronald	4	2.34	A	B	C	D	E	F	G	H	I	
SA071192	4	2.30	A	B	C	D	E	F	G	H	I	J
Kesley	4	2.28	A	B	C	D	E	F	G	H	I	J
SA060470	4	2.25	A	B	C	D	E	F	G	H	I	J
Gemini	4	2.22	A	B	C	D	E	F	G	H	I	J
SA02995	20	2.22	A	B	C	D	E	F	G	H	I	J
SA97665	4	2.22	A	B	C	D	E	F	G	H	I	J
AC Assiniboia	4	2.21	A	B	C	D	E	F	G	H	I	J
SA071709	4	2.12	A	B	C	D	E	F	G	H	I	J
AC Marie	4	2.08	A	B	C	D	E	F	G	H	I	J K
HiFi	4	2.08	A	B	C	D	E	F	G	H	I	J K
SA071380	4	2.06	A	B	C	D	E	F	G	H	I	J K
Hunter	4	2.04	A	B	C	D	E	F	G	H	I	J K
SA080029	4	2.04	A	B	C	D	E	F	G	H	I	J K
Aslak	4	2.03	A	B	C	D	E	F	G	H	I	J K
SA97547	4	2.02	A	B	C	D	E	F	G	H	I	J K
SA071555	4	2.01	A	B	C	D	E	F	G	H	I	J K
Dumont	4	1.94		B	C	D	E	F	G	H	I	J K
SA98346	4	1.89			C	D	E	F	G	H	I	J K

SA97404	4	1.88	C	D	E	F	G	H	I	J	K
Yamaska	4	1.87	C	D	E	F	G	H	I	J	K
SA071369	4	1.84	C	D	E	F	G	H	I	J	K
CDC SO-I	20	1.80	C	D	E	F	G	H	I	J	K
OT 3033	4	1.79	C	D	E	F	G	H	I	J	K
Joanette	4	1.78	C	D	E	F	G	H	I	J	K
SA97362	4	1.73		D	E	F	G	H	I	J	K
Donald	4	1.71		D	E	F	G	H	I	J	K
SA98352	4	1.69		D	E	F	G	H	I	J	K
Sixty Day	4	1.69		D	E	F	G	H	I	J	K
OT 3024	4	1.69		D	E	F	G	H	I	J	K
SA98171	4	1.66		D	E	F	G	H	I	J	K
SA080473	4	1.65		D	E	F	G	H	I	J	K
SA96121	20	1.59			E	F	G	H	I	J	K
Grizzly	4	1.57			E	F	G	H	I	J	K
AC Mustang	4	1.55			E	F	G	H	I	J	K
SA97082	4	1.55			E	F	G	H	I	J	K
CDC Sol-Fi	4	1.54			E	F	G	H	I	J	K
SA98321	4	1.52			E	F	G	H	I	J	K
Exeter	4	1.51				F	G	H	I	J	K
CDC Dancer	20	1.43					G	H	I	J	K
Hajira	4	1.41					G	H	I	J	K
SA98594	4	1.41						H	I	J	K
AC Stewart	4	1.38							I	J	K
Fidler	4	1.36							I	J	K
OAC Paisley	4	1.26							I	J	K
OAC Woodstock	4	1.24								J	K
SA97127	4	1.22								J	K
SA97482	4	1.00									K

Table 9.4. Tukey's HSD test for linolenic acid in Replicated Field Trial 2009 (α = 0.05, minimum significant difference = 0.67 %)

Genotype	Number of replications	% Mean	Tukey Grouping											
Exeter	4	2.20	A											
SA98171	4	1.99	A	B										
AC Stewart	4	1.92	A	B	C									
SA98387	4	1.79	A	B	C	D								
SA97362	4	1.74	A	B	C	D	E							
SA97082	4	1.71	A	B	C	D	E	F						
SA98346	4	1.62	A	B	C	D	E	F	G					
OT 3024	4	1.61	A	B	C	D	E	F	G	H				
Grizzly	4	1.52		B	C	D	E	F	G	H	I			
OAC Paisley	4	1.50		B	C	D	E	F	G	H	I			
Sixty Day	4	1.50		B	C	D	E	F	G	H	I			
Donald	4	1.49		B	C	D	E	F	G	H	I			
SA98594	4	1.44		B	C	D	E	F	G	H	I	J		
CDC Dancer	20	1.44		B	C	D	E	F	G	H	I	J		
SA97127	4	1.43		B	C	D	E	F	G	H	I	J		
SA97665	4	1.33		B	C	D	E	F	G	H	I	J	K	
Joanette	4	1.27			C	D	E	F	G	H	I	J	K	L
SA97482	4	1.27			C	D	E	F	G	H	I	J	K	L
Hajira	4	1.23				D	E	F	G	H	I	J	K	L
AC Mustang	4	1.21				D	E	F	G	H	I	J	K	L
Aslak	4	1.20				D	E	F	G	H	I	J	K	L
Gemini	4	1.17				D	E	F	G	H	I	J	K	L
CDC Sol-Fi	4	1.17				D	E	F	G	H	I	J	K	L
OAC Woodstock	4	1.16				D	E	F	G	H	I	J	K	L
Yamaska	4	1.16				D	E	F	G	H	I	J	K	L
HiFi	4	1.08					E	F	G	H	I	J	K	L
Dumont	4	1.07					E	F	G	H	I	J	K	L
Kesley	4	1.06						F	G	H	I	J	K	L
AC Marie	4	1.05						F	G	H	I	J	K	L
Fidler	4	1.03							G	H	I	J	K	L
AC Assiniboia	4	1.03							G	H	I	J	K	L
Matilda	4	1.00							G	H	I	J	K	L
SA97404	4	1.00							G	H	I	J	K	L
SA071555	4	0.98							G	H	I	J	K	L
AC Ronald	4	0.94								H	I	J	K	L
OT 3033	4	0.94									I	J	K	L

CDC SO-I	20	0.93	I	J	K	L
SA080473	4	0.92	I	J	K	L
SA97699	4	0.92	I	J	K	L
SA96121	20	0.91	I	J	K	L
Hunter	4	0.89	I	J	K	L
SA071192	4	0.89	I	J	K	L
SA98321	4	0.81		J	K	L
SA97170	4	0.80		J	K	L
SA071380	4	0.80		J	K	L
SA071405	4	0.80		J	K	L
SA080498	4	0.80		J	K	L
SA02995	20	0.75			K	L
SA080029	4	0.72			K	L
SA071709	4	0.71			K	L
SA98352	4	0.71			K	L
SA02984	4	0.70			K	L
SA060470	4	0.69			K	L
SA97547	4	0.66				L
SA071369	4	0.63				L
SA080511	4	0.61				L

Table 9.5. Tukey's HSD test for eicosenoic acid in Replicated Field Trial 2009 (α = 0.05, minimum significant difference = 0.82 %)

Genotype	Number of replications	% Mean	Tukey Grouping			
Exeter	4	1.68	A			
SA98171	4	1.61	A	B		
SA98346	4	1.45	A	B	C	
Grizzly	4	1.42	A	B	C	D
SA98387	4	1.40	A	B	C	D
SA97362	4	1.37	A	B	C	D
Sixty Day	4	1.30	A	B	C	D
SA97082	4	1.24	A	B	C	D
Joanette	4	1.22	A	B	C	D
SA080473	4	1.15	A	B	C	D
AC Stewart	4	1.09	A	B	C	D
HiFi	4	1.08	A	B	C	D
OT 3024	4	1.07	A	B	C	D
SA98594	4	1.02	A	B	C	D

SA97127	4	0.98	A	B	C	D
SA98321	4	0.97	A	B	C	D
AC Mustang	4	0.97	A	B	C	D
OAC Paisley	4	0.96	A	B	C	D
SA080029	4	0.94	A	B	C	D
CDC Dancer	20	0.94	A	B	C	D
Fidler	4	0.93	A	B	C	D
SA98352	4	0.88	A	B	C	D
OAC Woodstock	4	0.87	A	B	C	D
SA97482	4	0.86	A	B	C	D
AC Assiniboia	4	0.86	A	B	C	D
Hajira	4	0.86	A	B	C	D
AC Marie	4	0.84		B	C	D
SA97170	4	0.84		B	C	D
CDC Sol-Fi	4	0.84		B	C	D
Aslak	4	0.83		B	C	D
Donald	4	0.82		B	C	D
CDC SO-I	20	0.82		B	C	D
SA96121	20	0.80		B	C	D
SA080498	4	0.80		B	C	D
Matilda	4	0.80		B	C	D
Dumont	4	0.77			C	D
SA97404	4	0.77			C	D
SA060470	4	0.75			C	D
SA071192	4	0.75			C	D
SA071709	4	0.72			C	D
SA97547	4	0.71			C	D
SA071380	4	0.70			C	D
Yamaska	4	0.69			C	D
AC Ronald	4	0.69			C	D
SA071369	4	0.69			C	D
Hunter	4	0.68			C	D
SA071555	4	0.68			C	D
SA02995	20	0.68			C	D
OT 3033	4	0.68			C	D
Kesley	4	0.67			C	D
Gemini	4	0.67			C	D
SA02984	4	0.65			C	D
SA071405	4	0.65			C	D
SA97665	4	0.64			C	D
SA97699	4	0.63			C	D
SA080511	4	0.61				D

Table 9.6. Minor fatty acid composition of oat accessions from sub-set 'IOI Selections', grown at Saskatoon and Ottawa in 2008 (FA percentage based on total FA detected by GC)

Cultivar	% Stearic acid		% Linolenic acid		% Eicosenoic acid	
	Saskatoon	Ottawa	Saskatoon	Ottawa	Saskatoon	Ottawa
06FL328	1.92	1.48	0.67	0.82	0.66	0.88
06FL930	2.15	1.73	0.77	0.80	0.67	0.75
Aarre	1.98	1.53	1.13	1.31	0.43	0.88
Atlas 14535	1.83	1.16	0.81	1.07	0.96	1.05
Auteuil	2.04	1.68	1.06	1.14	0.63	0.73
Aveny (SW 01168)	1.73	1.26	1.40	1.55	0.72	0.89
Avesta	1.28	1.07	1.44	1.43	0.15*	0.90
Bage 1419/36	2.88	2.14	0.78	1.01	0.59	0.65
CDC Baler	1.48	1.06	1.13	1.35	0.76	0.77
Baragan 114	1.78	1.37	0.85	0.85	0.83	0.87
Barra	1.41	1.02	1.29	1.53	0.81	0.88
AC Baton	2.18	1.57	1.22	1.06	0.78	0.86
Belle	2.10	1.64	0.97	1.01	0.87	1.03
Borowiak	2.04	1.61	1.20	1.14	0.75	0.81
Boudrias	2.44	1.77	0.95	1.05	0.75	0.75
Boxer	1.87	1.56	1.27	1.23	0.71	0.80
CDC Boyer	1.81	1.45	0.95	0.86	0.73	0.79
Brawn	1.84	1.42	1.35	1.43	0.94	0.90
Calibre	2.17	1.46	1.01	1.20	0.74	0.75
Capital	2.26	1.75	1.18	1.42	0.76	0.75
Centennial	2.72	2.14	1.21	1.10	0.77	0.98
Chantilly	2.50	1.67	1.21	1.06	0.66	0.73
Clinton	1.56	1.23	1.37	1.59	1.14**	1.23**
CDC Dancer	1.78	1.38	1.31	1.21	0.88	0.86
Drummond	3.43	2.95	1.03	1.20	0.62	0.71
Evita	1.70	1.37	1.34	1.38	0.74	0.85
Exeter	1.61	1.59	1.79	1.75**	0.44	0.38*
Expander	1.49	1.26	1.26	1.40	0.89	1.01
Furlong	3.36	2.20	0.96	1.03	0.72	0.81
Gem	1.93	1.73	1.95**	1.71**	0.95	0.90
GK Pillango	1.52	1.08	1.22	1.49	0.83	0.82
Goslin	0.96*	0.93*	1.86**	1.49	0.77	1.07
AC Gwen	2.60	2.21	0.94	0.89	0.80	0.86
Hamel	1.88	1.56	1.42	1.43	0.79	0.92

HiFi	3.22	2.34	0.82	0.98	0.73	0.78
IA93227-1	1.34	1.05	1.16	1.29	1.19**	1.19**
IAH611-447 (PI 502955)	1.97	1.47	0.89	1.20	0.84	0.83
IL2858-1	2.23	1.61	1.12	1.17	0.89	0.92
IL98-10145	2.98	1.97	1.06	1.05	0.77	0.93
Iltis	1.20	0.95*	1.24	1.20	0.91	0.92
Irtysh 13	2.93	1.89	1.13	1.19	0.72	0.76
Ivory	1.50	1.33	1.17	1.08	0.79	0.78
Jumbo	1.97	1.47	0.98	1.08	0.79	0.85
Kangaroo	1.92	2.11	0.91	0.97	0.69	0.76
Kanota	2.24	1.76	0.82	0.93	0.89	0.95
Klein 69B	3.03	2.49	0.74	0.86	0.65	0.69
Kolpashevskii	1.18*	1.02	1.31	1.28	1.01	1.04
Lvovskii Rannii	2.35	1.50	1.09	1.16	0.57	0.75
Maldwyn	1.42	1.59	1.21	1.37	0.9	1.02
MAM 17-5	3.09	2.64	1.45	1.54	0.87	0.86
Marathon	2.67	1.77	1.17	1.27	0.79	0.88
Marion (Canada)	1.81	1.23	1.36	1.51	0.82	0.84
Matilda	4.25**	3.37**	0.66*	0.70*	0.66	0.76
AC Medallion	2.67	2.00	0.97	1.11	0.77	0.91
Millennium	1.57	1.35	0.88	0.89	0.59	0.97
Milton	2.35	1.73	1.13	1.11	0.85	0.87
MN 811045	1.68	1.27	0.84	0.95	0.97	1.03
AC Morgan	1.56	1.28	1.09	1.27	0.69	0.80
Mortlock	1.85	1.74	1.17	1.09	0.64	0.94
Morton	1.77	1.44	1.41	1.41	0.87	0.91
NO58-2-75-26	2.39	2.10	0.90	0.99	0.71	0.85
Nora	2.51	2.38	0.77	0.88	0.81	0.79
Norline	1.92	1.55	0.78	0.89	0.74	0.98
Ogle	1.50	1.16	1.38	1.40	1.08	1.09
OMSKIJ 6922	1.80	1.26	1.22	1.41	0.45	0.92
OT2040	3.69**	2.93	0.89	1.09	0.66	0.68
OT2045	2.71	1.61	1.14	1.30	0.87	0.95
OT2048	3.32	2.21	0.80	1.05	0.69	0.89
OT586	2.18	1.80	0.88	0.91	0.81	0.92
Powell	1.72	1.26	0.71	0.78	0.84	0.90
Proat	3.28	3.13**	1.15	1.04	0.61	0.71
CDC Pro-Fi	1.92	1.42	1.01	1.16	0.88	0.95
Revisor	1.45	1.00	1.33	1.56	0.85	0.91

Richard	2.13	1.62	1.29	1.45	0.51	0.53*
AC Rigodon	2.02	1.74	0.85	0.85	0.86	0.85
Rodney 0	2.16	1.53	0.94	1.16	0.83	0.99
Salomon	1.59	1.31	0.90	1.11	0.83	0.75
Silva selection	3.04	2.00	0.80	0.95	0.59	0.61
Skakun	1.57	1.36	1.44	1.46	0.89	0.84
Skrzat	1.93	1.35	0.94	1.03	0.81	0.83
CDC SO-I	2.03	1.45	0.80	0.85	0.62	0.83
CDC Sol-Fi	2.39	1.85	1.28	1.17	0.68	0.65
Spurs	1.40	1.21	1.24	1.34	0.76	0.82
SW Betania	1.49	1.32	1.11	0.87	0.63	0.91
Sylva	1.98	1.58	0.97	0.93	0.60	0.73
TAM O-301	2.23	1.37	1.02	1.23	0.73	0.73
Tartarian	2.29	1.69	0.93	1.03	0.34*	0.83
Triple Crown	1.61	1.17	0.99	1.21	0.82	0.78
Trispernia	2.15	1.37	0.78	0.97	0.97	0.94
Ukraine	1.81	1.53	0.89	0.99	0.94	0.92
Ursus	2.18	1.54	0.89	1.10	0.77	0.82
Verde	1.43	1.26	1.32	1.18	0.99	1.13
Victor	1.80	1.57	0.54*	0.69*	0.78	0.80
Vista	2.24	1.41	0.80	0.87	0.78	0.89
WAOAT2132	2.52	2.41	0.86	1.08	0.79	0.84
WIX 7955-1	2.43	1.78	1.26	1.31	0.76	0.97
X466	3.16	2.27	1.36	1.56	1.00	1.00
Mean[§]	2.10	1.60	1.10	1.20	0.80	0.90

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

Table 9.7. Tukey's HSD test for stearic acid in 'IOI Selections' sub-set (α = 0.05, minimum significant difference = 0.86 %)

Genotype	Number of replications	% Mean	Tukey Grouping
Matilda	2	3.81	A
OT2040	2	3.31	A B
Proat	2	3.21	A B C
Drummond	2	3.19	A B C D
MAM 17-5	2	2.87	B C D E
HiFi	2	2.78	B C D E F
Furlong	2	2.78	B C D E F
OT2048	2	2.77	B C D E F
Klein 69B	2	2.76	B C D E F
X466	2	2.72	B C D E F G
Silva selection	2	2.52	B C D E F G H
Bage 1419-36	2	2.51	B C D E F G H
IL98-10145	2	2.48	B C D E F G H I
WAOAT2132	2	2.47	B C D E F G H I J
Nora	2	2.45	C D E F G H I J K
Centennial	2	2.43	C D E F G H I J K L
Irtysh 13	2	2.41	C D E F G H I J K L
AC Gwen	2	2.41	C D E F G H I J K L
AC Medallion	2	2.34	D E F G H I J K L M
NO58-2-75-26	2	2.25	E F G H I J K L M N
Marathon	2	2.22	E F G H I J K L M N O

Rodney 0	2	2.16	E F G H I J K L M N O P
CDC Sol-Fi	2	2.12	E F G H I J K L M N O P Q
WIX 7955-1	2	2.11	E F G H I J K L M N O P Q
Boudrias	2	2.11	E F G H I J K L M N O P Q
Chantilly	2	2.09	E F G H I J K L M N O P Q R
Milton	2	2.04	E F G H I J K L M N O P Q R S
Kangaroo	2	2.02	E F G H I J K L M N O P Q R S T
Capital	2	2.01	E F G H I J K L M N O P Q R S T
Kanota	2	2.00	F G H I J K L M N O P Q R S T
OT586	2	1.99	F G H I J K L M N O P Q R S T
Tartarian	2	1.99	F G H I J K L M N O P Q R S T
06FL930	2	1.94	F G H I J K L M N O P Q R S T U
Lvovskii Rannii	2	1.93	F G H I J K L M N O P Q R S T U V
IL2858-1	2	1.92	F G H I J K L M N O P Q R S T U V
AC Rigodon	2	1.88	G H I J K L M N O P Q R S T U V
Richard	2	1.88	G H I J K L M N O P Q R S T U V
AC Baton	2	1.88	G H I J K L M N O P Q R S T U V
Belle	2	1.87	G H I J K L M N O P Q R S T U V
Auteuil	2	1.86	G H I J K L M N O P Q R S T U V
Ursus	2	1.86	G H I J K L M N O P Q R S T U V
OT2045	2	1.85	H I J K L M N O P Q R S T U V
Gem	2	1.83	H I J K L M N O P Q R S T U V
Vista	2	1.83	H I J K L M N O P Q R S T U V
Borowiak	2	1.83	H I J K L M N O P Q R S T U V
Calibre	2	1.82	H I J K L M N O P Q R S T U V
TAMO-301	2	1.80	H I J K L M N O P Q R S T U V W

Mortlock	2	1.80	H I J K L M N O P Q R S T U V W
Sylva	2	1.78	H I J K L M N O P Q R S T U V W
Trispernia	2	1.76	H I J K L M N O P Q R S T U V W
Aarre	2	1.76	H I J K L M N O P Q R S T U V W
CDC SO-I	2	1.74	H I J K L M N O P Q R S T U V W
Norline	2	1.74	H I J K L M N O P Q R S T U V W
Hamel	2	1.72	H I J K L M N O P Q R S T U V W
IAH611-447 (PI 502955)	2	1.72	H I J K L M N O P Q R S T U V W
Jumbo	2	1.72	H I J K L M N O P Q R S T U V W
Boxer	2	1.72	H I J K L M N O P Q R S T U V W
06FL328	2	1.70	H I J K L M N O P Q R S T U V W
Victor	2	1.69	H I J K L M N O P Q R S T U V W
CDC Pro-Fi	2	1.67	H I J K L M N O P Q R S T U V W
Ukraine	2	1.67	H I J K L M N O P Q R S T U V W
Skrzat	2	1.64	I J K L M N O P Q R S T U V W
Iltis	2	1.63	I J K L M N O P Q R S T U V W
Brawn	2	1.63	I J K L M N O P Q R S T U V W
Morton	2	1.61	J K L M N O P Q R S T U V W
Exeter	2	1.60	K L M N O P Q R S T U V W
CDC Dancer	2	1.58	L M N O P Q R S T U V W
Baragan 114	2	1.58	L M N O P Q R S T U V W
Evita	2	1.54	M N O P Q R S T U V W
OMSKIJ 6922	2	1.53	M N O P Q R S T U V W
Marion (Canada)	2	1.52	M N O P Q R S T U V W
Maldwyn	2	1.51	M N O P Q R S T U V W
Aveny (SW 01168)	2	1.50	M N O P Q R S T U V W

Atlas 14535	2	1.50	M N O P Q R S T U V W
Powell	2	1.49	M N O P Q R S T U V W
Barra	2	1.48	M N O P Q R S T U V W
Skakun	2	1.47	N O P Q R S T U V W
Millennium	2	1.46	N O P Q R S T U V W
Salomon	2	1.45	N O P Q R S T U V W
AC Morgan	2	1.42	N O P Q R S T U V W
Ivory	2	1.42	N O P Q R S T U V W
SW Betania	2	1.41	N O P Q R S T U V W
Clinton	2	1.40	N O P Q R S T U V W
Triple Crown	2	1.39	N O P Q R S T U V W
Expander	2	1.38	O P Q R S T U V W
Verde	2	1.35	P Q R S T U V W
Ogle	2	1.33	P Q R S T U V W
Spurs	2	1.31	P Q R S T U V W
GK Pillango	2	1.30	P Q R S T U V W
CDC Baler	2	1.27	Q R S T U V W
Revisor	2	1.23	R S T U V W
MN 811045	2	1.22	S T U V W
IA93227-1	2	1.20	S T U V W
Avesta	2	1.18	T U V W
Kolpashevskii	2	1.10	U V W
CDC Boyer	2	1.08	V W
Goslin	2	0.95	W

Table 9.8. Tukey's HSD test for linolenic acid in 'IOI Selections' sub-set (α = 0.05, minimum significant difference = 0.39 %)

Genotype	Number of replications	% Mean	Tukey Grouping
Gem	2	1.83	A
Exeter	2	1.77	A B
Goslin	2	1.68	A B C
MAM 17-5	2	1.50	A B C D
Clinton	2	1.48	A B C D E
Aveny (SW 01168)	2	1.48	A B C D E
X466	2	1.46	A B C D E
Skakun	2	1.45	A B C D E F
Revisor	2	1.45	A B C D E F G
Marion (Canada)	2	1.44	A B C D E F G H
Avesta	2	1.44	A B C D E F G H
Hamel	2	1.43	B C D E F G H I
Morton	2	1.41	B C D E F G H I
MN 811045	2	1.41	B C D E F G H I
Ogle	2	1.39	B C D E F G H I J
Brawn	2	1.39	B C D E F G H I J
Richard	2	1.37	C D E F G H I J K
Evita	2	1.36	C D E F G H I J K L
GK Pillango	2	1.36	C D E F G H I J K L
Expander	2	1.33	C D E F G H I J K L M
OMSKIJ 6922	2	1.32	C D E F G H I J K L M N
Capital	2	1.30	C D E F G H I J K L M N O
Kolpashevskii	2	1.30	C D E F G H I J K L M N O P
Spurs	2	1.29	C D E F G H I J K L M N O P Q

Maldwyn	2	1.29	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q						
WIX 7955-1	2	1.29	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q						
CDC Dancer	2	1.26		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R					
Boxer	2	1.25		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R					
Verde	2	1.25		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R					
CDC Baler	2	1.24		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S				
CDC Sol-Fi	2	1.23		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T			
IA93227-1	2	1.23		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T			
Aarre	2	1.22		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U		
Rodney 0	2	1.22		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U		
CDC Boyer	2	1.22		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U		
Marathon	2	1.22		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U		
AC Morgan	2	1.18		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	
Borowiak	2	1.17		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	
Irtysh 13	2	1.16		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	
Centennial	2	1.16		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	
IL2858-1	2	1.15		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	
AC Baton	2	1.14		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
Chantilly	2	1.14		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
Mortlock	2	1.13		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
TAMO-301	2	1.13		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
Ivory	2	1.13		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
Lvovskii Rannii	2	1.13		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
Milton	2	1.12		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
Drummond	2	1.12		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
Calibre	2	1.11		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
Triple Crown	2	1.10		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
Auteuil	2	1.10		D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W
Proat	2	1.10			E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W

CDC Pro-Fi	2	1.09		E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W		
IL98-10145	2	1.06			F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	
OT2045	2	1.05				G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	
IAH611-447 (PI 502955)	2	1.05					H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	
AC Medallion	2	1.04					H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	
Jumbo	2	1.03						I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	
Salomon	2	1.01							J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
Boudrias	2	1.00							J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
Furlong	2	1.00							J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
Ursus	2	1.00							J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
SW Betania	2	0.99								K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
OT2040	2	0.99								K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
Belle	2	0.99								K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
Skrzat	2	0.99								K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
Tartarian	2	0.98								K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
WAOAT2132	2	0.97									L	M	N	O	P	Q	R	S	T	U	V	W	X	Y
Sylva	2	0.95										M	N	O	P	Q	R	S	T	U	V	W	X	Y
NO58-2-75-26	2	0.95										M	N	O	P	Q	R	S	T	U	V	W	X	Y
Kangaroo	2	0.94										M	N	O	P	Q	R	S	T	U	V	W	X	Y
Atlas 14535	2	0.94										M	N	O	P	Q	R	S	T	U	V	W	X	Y
Ukraine	2	0.94										M	N	O	P	Q	R	S	T	U	V	W	X	Y
OT2048	2	0.93											N	O	P	Q	R	S	T	U	V	W	X	Y
AC Gwen	2	0.92												O	P	Q	R	S	T	U	V	W	X	Y
Iltis	2	0.91												O	P	Q	R	S	T	U	V	W	X	Y
HiFi	2	0.90													P	Q	R	S	T	U	V	W	X	Y
OT586	2	0.90														Q	R	S	T	U	V	W	X	Y
Bage 1419-36	2	0.90														Q	R	S	T	U	V	W	X	Y
Barra	2	0.90														Q	R	S	T	U	V	W	X	Y
Millennium	2	0.89															R	S	T	U	V	W	X	Y

Kanota	2	0.88	R	S	T	U	V	W	X	Y		
Silva selection	2	0.88	R	S	T	U	V	W	X	Y		
Trispernia	2	0.88	R	S	T	U	V	W	X	Y		
AC Rigodon	2	0.85		S	T	U	V	W	X	Y		
Baragan 114	2	0.85		S	T	U	V	W	X	Y		
Vista	2	0.84			T	U	V	W	X	Y		
Norline	2	0.84			T	U	V	W	X	Y		
Nora	2	0.83				U	V	W	X	Y		
CDC SO-I	2	0.83				U	V	W	X	Y		
Klein 69B	2	0.80					V	W	X	Y		
06FL930	2	0.79					V	W	X	Y		
Powell	2	0.75						W	X	Y		
06FL328	2	0.75						W	X	Y		
Matilda	2	0.68							X	Y		
Victor	2	0.62								Y		

Table 9.9. Tukey's HSD test for eicosenoic acid in 'IOI Selections' sub-set (α = 0.05, minimum significant difference = 0.40 %)

Genotype	Number of replications	% Mean	Tukey Grouping
IA93227-1	2	1.19	A
Clinton	2	1.19	A B
Ogle	2	1.09	A B C
Verde	2	1.06	A B C D
Kolpashevskii	2	1.03	A B C D E
Atlas 14535	2	1.01	A B C D E F
X466	2	1.00	A B C D E F
Barra	2	1.00	A B C D E F
Maldwyn	2	0.96	A B C D E F G
Trispernia	2	0.96	A B C D E F G
Belle	2	0.95	A B C D E F G
Expander	2	0.95	A B C D E F G
Ukraine	2	0.93	A B C D E F G H
Gem	2	0.93	A B C D E F G H I
Goslin	2	0.92	A B C D E F G H I
Kanota	2	0.92	A B C D E F G H I
Brawn	2	0.92	A B C D E F G H I
CDC Pro-Fi	2	0.92	A B C D E F G H I
CDC Boyer	2	0.92	A B C D E F G H I
Rodney 0	2	0.91	A B C D E F G H I
OT2045	2	0.91	A B C D E F G H I
IL2858-1	2	0.91	A B C D E F G H I
Morton	2	0.89	A B C D E F G H I
Revisor	2	0.88	A B C D E F G H I
Centennial	2	0.88	A B C D E F G H I
CDC Dancer	2	0.87	A B C D E F G H I
Powell	2	0.87	A B C D E F G H I

MAM 17-5	2	0.87	A	B	C	D	E	F	G	H	I	
WIX 7955-1	2	0.87	A	B	C	D	E	F	G	H	I	
OT586	2	0.87	A	B	C	D	E	F	G	H	I	
Skakun	2	0.87	A	B	C	D	E	F	G	H	I	
Norline	2	0.86	A	B	C	D	E	F	G	H	I	
Milton	2	0.86	A	B	C	D	E	F	G	H	I	
AC Rigodon	2	0.86	A	B	C	D	E	F	G	H	I	
Hamel	2	0.86	A	B	C	D	E	F	G	H	I	
IL98-10145	2	0.85	A	B	C	D	E	F	G	H	I	
Baragan 114	2	0.85	A	B	C	D	E	F	G	H	I	
MN 811045	2	0.85	A	B	C	D	E	F	G	H	I	
AC Medallion	2	0.84	A	B	C	D	E	F	G	H	I	
Vista	2	0.84	A	B	C	D	E	F	G	H	I	
IAH611-447 (PI 502955)	2	0.84	A	B	C	D	E	F	G	H	I	
Marathon	2	0.84	A	B	C	D	E	F	G	H	I	
Marion (Canada)	2	0.83	A	B	C	D	E	F	G	H	I	
AC Gwen	2	0.83	A	B	C	D	E	F	G	H	I	
GK Pillango	2	0.83	A	B	C	D	E	F	G	H	I	
AC Baton	2	0.82	A	B	C	D	E	F	G	H	I	
Skrzat	2	0.82	A	B	C	D	E	F	G	H	I	
Jumbo	2	0.82	A	B	C	D	E	F	G	H	I	
WAOAT2132	2	0.82	A	B	C	D	E	F	G	H	I	J
Aveny (SW 01168)	2	0.81	A	B	C	D	E	F	G	H	I	J
Nora	2	0.80	A	B	C	D	E	F	G	H	I	J
Triple Crown	2	0.80	A	B	C	D	E	F	G	H	I	J
Evita	2	0.80	A	B	C	D	E	F	G	H	I	J
Ursus	2	0.80	A	B	C	D	E	F	G	H	I	J
Spurs	2	0.79	A	B	C	D	E	F	G	H	I	J
Mortlock	2	0.79	A	B	C	D	E	F	G	H	I	J

OT2048	2	0.79	A	B	C	D	E	F	G	H	I	J
Victor	2	0.79	A	B	C	D	E	F	G	H	I	J
Salomon	2	0.79	A	B	C	D	E	F	G	H	I	J
Ivory	2	0.79	A	B	C	D	E	F	G	H	I	J
Millennium	2	0.78		B	C	D	E	F	G	H	I	J
NO58-2-75-26	2	0.78		B	C	D	E	F	G	H	I	J
Borowiak	2	0.78		B	C	D	E	F	G	H	I	J
06FL328	2	0.77			C	D	E	F	G	H	I	J
SW Betania	2	0.77			C	D	E	F	G	H	I	J
CDC Baler	2	0.77			C	D	E	F	G	H	I	J
Furlong	2	0.77			C	D	E	F	G	H	I	J
Iltis	2	0.76			C	D	E	F	G	H	I	J
Capital	2	0.76			C	D	E	F	G	H	I	J
HiFi	2	0.76			C	D	E	F	G	H	I	J
Boxer	2	0.76			C	D	E	F	G	H	I	J
Boudrias	2	0.75			C	D	E	F	G	H	I	J
Calibre	2	0.75			C	D	E	F	G	H	I	J
AC Morgan	2	0.75			C	D	E	F	G	H	I	J
Irtysh 13	2	0.74			C	D	E	F	G	H	I	J
TAMO-301	2	0.73			C	D	E	F	G	H	I	J
CDC SO-I	2	0.73			C	D	E	F	G	H	I	J
Kangaroo	2	0.73			C	D	E	F	G	H	I	J
06FL930	2	0.71			C	D	E	F	G	H	I	J
Matilda	2	0.71			C	D	E	F	G	H	I	J
Chantilly	2	0.70			C	D	E	F	G	H	I	J
OMSKIJ 6922	2	0.69			C	D	E	F	G	H	I	J
Auteuil	2	0.68			C	D	E	F	G	H	I	J
OT2040	2	0.67				D	E	F	G	H	I	J
Klein 69B	2	0.67				D	E	F	G	H	I	J
CDC Sol-Fi	2	0.67				D	E	F	G	H	I	J

Drummond	2	0.67	D	E	F	G	H	I	J
Sylva	2	0.67	D	E	F	G	H	I	J
Proat	2	0.66	D	E	F	G	H	I	J
Lvovskii Rannii	2	0.66	D	E	F	G	H	I	J
Aarre	2	0.66	D	E	F	G	H	I	J
Bage 1419-36	2	0.62		E	F	G	H	I	J
Silva selection	2	0.60			F	G	H	I	J
Tartarian	2	0.59				G	H	I	J
Avesta	2	0.53					H	I	J
Richard	2	0.52						I	J
Exeter	2	0.41							J

Table 9.10. Descriptive statistics for minor fatty acid composition of oat accessions from 'Nordic oat selections' sub-set (FA percentage based on total FA detected by GC)

	% Stearic Acid	% Linolenic Acid	% Eicosenoic Acid
Maximum	7.57	3.87	5.26
Minimum	1.23	0.67	0.55
Mean	2.24	1.23	1.26
SD	0.58	0.55	0.61
RFT Mean %	1.89	1.23	0.91
RFT HSD	0.89	0.67	0.82

SD= Standard Deviation, RFT= Replicated Field Trial

Table 9.11. Minor fatty acid composition of oat accessions from 'Nordic oat selections' sub-set (FA percentage based on total FA detected by GC)

Genotype	CN Number	Origin	% Stearic acid	% Linolenic acid	% Eicosenoic acid
Abed silver	53725	Denmark	2.31	1.18	0.78
Adelaar	90465	Sweden	2.62	2.32	2.83
Alden	82383	Sweden	1.72	1.05	0.93
Argus black	63934	Sweden	2.05	1.52	1.99
Awnless probsteier	53574	Sweden	2.07	1.58	1.68
Bambu	63935	Sweden	1.85	1.8	1.38
Bambu	88805	Sweden	2.29	0.89	0.9
Bambu i	65250	Sweden	2.45	1.74	1.66
Bambu i	67019	Sweden	2.25	0.92	0.83
Bambu ii	63936	Sweden	2	0.88	0.87
Bambu ii	65714	Sweden	1.91	1.83	1.87
Bambu ii	65251	Sweden	2.09	1.01	1.46
Bambu ii	64128	Sweden	2.34	0.81	0.89
Beardless probsteier	53165	Sweden	1.97	1.11	0.83
Beardless probsteier	53094	Sweden	2.4	0.84	0.83
Beiar	63966	Norway	1.71	0.97	1.06
Belgium	53429	Sweden	2.3	0.99	1.68
Belyak	90179	Sweden	2.48	0.86	1.13
Belyak	53582	Sweden	2.63	0.83	0.78
Beseler i	65150	Denmark	2.14	1.05	0.87

Beseler ii	88734	Denmark	2.03	0.94	0.9
Black bell i	53494	Sweden	1.92	0.95	0.92
Black bell ii	53229	Sweden	2.32	1	0.69
Black great mogul	53488	Sweden	2.82	0.72	0.66
Blenda	63949	Sweden	2.58	1	0.77
Blenda	64466	Sweden	2.54	1.15	0.7
Blenda	64491	Sweden	2.41	0.99	1.25
Blixt	64553	Sweden	2.61	0.99	0.73
Borris opus	55158	Denmark	2.16	0.98	1.18
C.d. 3843	55143	Sweden	1.83	0.92	1.51
C.d. 3866	55147	Sweden	2.23	1.18	1.53
C.d. 3899	55156	Sweden	1.69	0.9	1.33
Crown	53711	Sweden	2.04	1.24	0.71
Crown	53543	Sweden	2.48	0.86	0.85
Dan	80793	Sweden	3.23	1.01	0.87
Danish island yellow	53541	Denmark	1.83	1.15	0.79
Diamant	65715	Sweden	1.85	0.88	0.96
Eagle	88772	Sweden	2.39	1.02	0.84
Echo	88545	Sweden	2.13	3.02	2.05
Echo	90218	Sweden	2.22	0.85	0.92
Eho	64544	Finland	2.28	1.08	0.95
Eho	64095	Finland	1.85	0.7	1.11
Eho	64009	Finland	2.21	1.44	1.44
Eho tammisto	55102	Finland	2.06	2.54	2.09
Engelbrekt ii	63868	Sweden	2.5	0.67*	0.95
Esa	64096	Finland	2.82	1.02	1.08
Esa	65902	Finland	1.73	1	0.96
Esakaura	88674	Finland	2.05	0.91	1.04
Extra klock ii	64499	Sweden	3.18	0.95	0.65*
Extra klockhavre	63950	Sweden	2.04	0.92	0.82
Fortuna	88385	Sweden	2.04	1.9	1.81
French black	90470	Denmark	2.3	1.33	0.86
Golden	88773	Sweden	2.48	0.9	0.89
Golden rain	90396	Sweden	2.28	1	0.97
Golden rain	53576	Sweden	2.11	0.92	0.74
Golden rain ii	88547	Sweden	2.05	1.03	0.84
Gouldregen	88739	Sweden	1.97	1.02	0.86
Gray moor	53540	Denmark	2.03	1.01	1.25
Great mogul	53099	Sweden	2.38	0.76	0.69

Great mogul ii	64501	Sweden	2.19	0.7	0.78
Grossmogul	65212	Sweden	2.48	0.72	0.67
Gul naesgaard	65092	Denmark	2.27	1.05	0.72
Guldregn	65254	Sweden	2.57	1.02	1.31
Guldregn iii	65264	Sweden	2.34	0.88	0.79
Ha 70-81-1	73355	Finland	2.92	0.89	1.45
Ha 70-81-3	73356	Finland	3.84	0.84	0.67
Ha 70-81-3c	73357	Finland	2.75	1.98	1.5
Ha70-81-3	29842	Finland	3.72	2.93	1.6
Ha70-81-3c	29844	Finland	1.99	2.38	2.96
Ha70-81-4	29843	Finland	2.4	0.88	0.93
Hankkija 773	79298	Finland	2.33	1	0.9
Hannes	66468	Finland	2.61	0.95	0.93
Havre stam 54	55107	Sweden	2.09	2.38	1.57
Havre stam 58	55108	Sweden	1.66	1.25	1.3
Hedvig	82382	Sweden	1.48	1.4	1.84
Hein ii	55124	Norway	4.61**	3.68**	2.94
Hja 75430	45986	Finland	2.32	1.8	1.5
Hja 76037n	45987	Finland	1.95	1.05	1.73
Hja 78033	45988	Finland	2.33	2.63	1.58
Hja 78156	45989	Finland	2.17	1.12	1.63
Hja 80278	45990	Finland	2.17	0.97	2.88
Holmberg 54	55106	Sweden	2.27	0.94	0.94
Hvitling	53088	Sweden	2.26	0.99	0.76
Jalostettu maatiais	90219	Finland	2	0.94	0.99
Jo 1043	35914	Finland	1.7	1.1	0.84
Jo0770	1772	Finland	2.15	1.15	1.38
Jo0794	1773	Finland	2.01	1.1	1.47
Juha	65411	Finland	1.81	1.99	1.89
Juha	64546	Finland	2.38	1	1.1
Kalott	77953	Sweden	1.5	0.83	1.07
Korgen	63967	Norway	1.43	1.85	2.22
Kyro	64547	Finland	1.91	1.26	0.79
Kyto	88759	Finland	2.26	2.13	2.25
Kyto	64102	Finland	1.95	1	1
Kytokaura	90369	Finland	1.84	1.09	0.99
Lightning	64493	Sweden	2.31	0.93	0.72
Ligowo svalof	53220	Sweden	2.15	1.04	0.8
Linda	66608	Sweden	2.47	1.17	1.01
Lyngby hede	65117	Sweden	1.44	2.9	2.24

Max	64678	Denmark	2.27	1.01	1.69
Merkur	28751	Norway	1.68	0.95	0.95
Minor	55160	Denmark	1.87	2.71	2.76
Nasta	44287	Finland	2.54	1.83	1.72
Nidar	54143	Norway	2.16	0.97	0.82
Nina	30886	Sweden	1.58	1.58	3.26**
Nip	64492	Sweden	1.99	0.95	0.82
Nopsa	88387	Finland	2.06	1.04	0.96
Nova	53779	Denmark	2.39	1.62	1.19
Opus	88916	Denmark	2.56	0.93	0.79
Opus ii	64468	Denmark	2.01	1.13	1.34
Opus iii	66477	Denmark	2.4	0.99	0.81
Orion	63911	Sweden	1.96	0.9	0.95
Orion iii	55123	Sweden	1.96	1.06	1.11
Orion iii	63970	Sweden	2.17	0.92	0.86
Orn	63872	Sweden	2.74	0.93	0.97
Osmo	64108	Finland	2.41	1.33	1.84
Osmo i	90220	Finland	2.09	1.02	1.38
Osmo ii	88388	Finland	2.01	0.98	1.01
Pellervo	88760	Finland	2.04	1.47	1.7
Pelso	88477	Finland	1.23*	1.45	1.87
Penderhavre	65717	Sweden	1.98	0.93	1
Pi 055378	88389	Denmark	2.21	0.91	1.59
Pi 197843	63974	Sweden	1.79	1.07	1.03
Pi 224301	64131	Sweden	2.11	1.26	0.76
Pi 264267	64500	Sweden	1.39	0.91	1.08
Pi 361866	73483	Denmark	2.75	0.85	0.98
Pi 63897	99000	Finland	2.66	2.4	1
Ponta	30887	Sweden	1.39	1.26	1.68
Primus	88808	Sweden	2.59	1.04	0.55*
Primus ii	55121	Sweden	2.41	1.72	2.3
Primus ii	63873	Sweden	2.8	1.03	1.45
Primus ii	55034	Sweden	2.34	0.94	1.55
Probsteier	53421	Sweden	1.94	1.04	0.84
Probsteier	53424	Sweden	1.81	0.99	0.76
Probsteier	53634	Sweden	2.02	1.35	1.78
Probsteier	65312	Sweden	2.12	1.03	0.99
Probsteier (cultivar)	53420	Sweden	2.01	0.83	0.88
Puhti	35909	Finland	2.11	1.16	1.91

Puhti	44288	Finland	2.23	1.96	3.12
Reima	35910	Finland	2.09	1.07	1.09
Rex	64025	Denmark	2.66	1.3	1.35
Risto	30885	Sweden	1.49	2.25	2.25
Risto	77954	Sweden	1.72	0.9	0.79
Risto	80794	Sweden	2.01	0.93	0.82
Ryhti	35911	Finland	2.55	0.85	0.87
Ryhti	44286	Finland	2.78	1.01	0.95
Same	63955	Sweden	1.67	2.42	1.56
Sang	1775	Sweden	2.13	1.04	1.21
Sang	77955	Sweden	2.55	0.88	0.72
Sang	80795	Sweden	2.45	0.98	0.78
Saxo	65885	Sweden	1.87	1.36	1.09
Seger	65909	Sweden	2.11	0.71	0.87
Selma	72374	Sweden	1.6	1.07	0.96
Simo takioincer	55103	Finland	2.21	0.86	0.93
Sirius	88672	Sweden	2.52	0.85	0.95
Sirius	63912	Sweden	2.18	0.79	1.01
Sirius ii	55122	Sweden	2.12	0.91	0.86
Sisu	64548	Finland	2.65	1.68	1.6
Sofi	82381	Sweden	2.79	0.68*	0.68
Sol	55109	Sweden	2.85	1.17	0.9
Soleil ii	65420	Sweden	3.16	0.95	0.75
Sorbo	57866	Sweden	2.03	0.9	1.01
Star	88774	Sweden	2.08	1.1	1.4
Star	54144	Sweden	1.96	1.05	0.77
Sternhafer	88750	Sweden	1.98	0.96	0.84
Stormogul ii	63957	Sweden	2.42	1.77	2.09
Sun ii	55105	Sweden	2.31	1.07	0.88
Sv. 25/357	63973	Sweden	2.35	0.93	0.78
Svalof 8	54977	Sweden	1.78	1.02	1.51
Svea	80796	Sweden	1.98	1.14	1.02
Swedish select	88333	Sweden	1.29*	1.45	0.91
Tammi	88761	Finland	2.11	1.17	0.89
Tammie tammisto	55099	Finland	2.49	1.03	1.49
Trio	54784	Sweden	2.9	1.02	1.23
Trio	63937	Sweden	2.23	0.99	0.8
Triumphal	88381	Sweden	2.23	0.93	1.99
Tuha	64011	Finland	1.95	1.87	1.36
Tuotto	90221	Finland	2.58	0.83	0.86

Valko	80779	Finland	1.78	1.17	0.82
Veli	44289	Finland	1.69	1.05	0.92
Victoria	52998	Denmark	2.23	0.98	0.74
Victory	53726	Sweden	2.01	1.02	2.04
Victory	53326	Sweden	2.35	1	2.22
Victory	53340	Sweden	1.89	1.17	1.51
Victory	53648	Sweden	1.99	1.91	1.37
Victory	53911	Sweden	2.36	3.11	2.24
Victory	55031	Sweden	2.42	1.79	2.17
Wasa	53778	Sweden	2.69	0.93	0.81
Wasa	53647	Sweden	1.94	0.95	1.71
Wasta	35913	Finland	2.7	0.97	1.55
Weibull 16385	65350	Sweden	2.77	1.01	1.7
Weibull 16428	65352	Sweden	3.49	0.98	0.71
Weibull 16509	66470	Sweden	2.37	0.78	2.06
Weibull 16511	66471	Sweden	2.48	0.89	0.88
Weibulls 16004	57107	Sweden	1.57	1.16	0.88
Weibull's 16004	64672	Sweden	1.5	1.15	0.96
Weibull's 16195	64673	Sweden	1.71	3.13	1.73
Weibull's 16229	64674	Sweden	2.24	1.17	0.93
Weibull's 16385	64675	Sweden	1.73	1.23	2.75
Weibulls no. 16187	64484	Sweden	2.23	1.73	1.59
Weibulls no. 16228	64485	Sweden	2.92	1	0.72
Weikus	30888	Sweden	1.67	1.19	1.18
White probsteier	88338	Sweden	2.87	0.98	1.06
Yellow	52999	Denmark	7.57**	3.87**	5.26**
Yellow naesgaard	53776	Denmark	1.63	1.03	0.78
Ylitornio	63971	Sweden	2.26	0.91	0.99
Zloty deszcz	90176	Sweden	1.97	1.85	1.63
Zonne ii	65269	Sweden	2.06	0.78	1.01
Weibull 16384	65349	Sweden	1.93	0.81	1.02
Weibull 16414	65883	Sweden	2.67	0.97	0.77
Mean[§]			2.24	1.23	1.26

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

Table 9.12. Descriptive statistics for minor fatty acid composition of *A. sativa* accessions from 'PGRC selections' sub-set (FA percentage based on total FA detected by GC)

	% Stearic Acid	% Linolenic Acid	% Eicosenoic Acid
Maximum	2.76	3.82	2.78
Minimum	1.08	0.86	0.79
Mean	1.81	2.02	1.49
SD	0.42	0.78	0.52
RFT Mean	1.89	1.23	0.91
RFT HSD	0.89	0.67	0.82

SD= Standard Deviation, RFT= Replicated Field Trial

Table 9.13. Minor fatty acid composition of *A. sativa* accessions from 'PGRC selections ' sub-set (FA percentage based on total FA detected by GC)

Genotype	% Stearic acid	% Linolenic acid	% Eicosenoic acid
3109	1.24	1.08	0.81*
63900	1.67	2.50	1.68
4367	2.48	2.31	1.66
53993	2.66**	3.82**	1.89
65156	1.64	1.13	1.02
88697	2.19	3.25	2.48
4394	1.62	1.97	1.35
2898	1.68	1.87	1.32
4271	1.15*	1.06	1.05
4401	1.08*	1.11	1.09
3133	2.76**	3.43	2.53**
90458	2.32	3.50**	2.22
3180	1.92	1.03*	0.79*
4387	1.31	1.48	1.54
55149	1.65	2.62	1.14
2933	1.41	1.91	1.07
4907	1.57	1.44	1.44
3175	1.78	2.60	1.43
2906	1.93	1.58	0.87
88777	2.34	2.31	1.40
64015	1.69	1.24	0.89

88754	1.78	2.83	2.19
63736	1.96	0.86*	0.92
82123	1.36	1.23	0.84
64061	2.02	1.49	2.04
4828	1.39	2.41	1.52
3160	1.72	1.36	1.21
2937	1.89	2.04	1.27
2841	2.08	2.70	1.90
1771	1.89	2.27	1.52
4840	2.59	3.29	2.78**
4380	1.65	2.39	1.70
3189	2.25	1.18	1.17
4388	1.40	1.73	1.38
88791	1.31	1.06	1.20
4865	1.36	1.63	1.01
2822	1.50	2.55	1.87
3110	1.36	1.11	0.96
56233	2.21	2.78	2.27
4691	1.90	2.33	1.63
30749	2.18	2.69	2.35
2928	1.79	2.60	1.93
4360	1.82	1.03	1.06
3120	2.45	1.64	1.09
3186	1.53	1.94	1.03
2821	1.81	2.33	1.87
Mean[§]	1.81	2.02	1.49

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

Table 9.14. Descriptive statistics for minor fatty acid composition of *A. byzantina* accessions from 'PGRC selections' sub-set (FA percentage based on total FA detected by GC)

	% Stearic Acid	% Linolenic Acid	% Eicosenoic Acid
Maximum	2.80	3.40	2.32
Minimum	1.32	0.69	0.06
Mean	2.03	1.33	0.79
SD	0.39	0.72	0.59
RFT Mean	1.89	1.23	0.91
RFT HSD	0.89	0.67	0.82

SD= Standard Deviation, RFT= Replicated Field Trial

Table 9.15. Minor fatty acid composition of *A. byzantina* accessions from 'PGRC selections' sub-set (FA percentage based on total FA detected by GC)

CN Number	% Stearic acid	% Linolenic acid	% Eicosenoic acid
88917	2.70	0.97	0.58
88833	1.66	0.85	0.83
5212	1.83	1.10	1.20
4218	1.86	1.93	1.21
3159	2.35	3.40**	2.32**
54018	2.24	0.92	0.42
88594	1.68	1.02	0.57
55297	2.00	1.07	1.06
63819	1.64	1.04	1.04
64595	1.88	0.82	0.75
3171	1.57	0.91	1.97
64947	2.70**	2.50	1.92
88755	1.81	1.92	1.39
3150	1.86	0.91	0.06*
21948	2.21	2.89	0.15
64654	2.27	2.64	1.26
2843	1.78	0.98	0.99
64225	1.95	0.75*	0.14
53687	2.07	0.80	0.79
57207	2.42	1.12	0.32
63815	2.30	0.87	0.82
64296	2.15	0.69*	0.24
64188	2.34	0.96	0.23
2832	1.61	1.22	0.28
3194	1.57	2.18	1.83
55125	2.65	0.97	0.62
88783	2.31	0.95	0.91
65029	2.16	1.94	0.41
90489	2.01	0.91	0.25
88938	1.67	1.00	0.20
25055	1.59	1.00	0.41
57004	1.37	1.11	1.62
3162	2.80**	0.81	0.23
57142	1.61	1.03	0.12
5197	2.30	1.26	0.32
88722	2.04	0.83	0.39
65482	2.33	0.86	0.62
53597	1.52	1.09	1.02

3194	2.06	0.90	0.59
57909	2.24	0.77	0.67
64293	2.41	1.04	0.75
56892	2.48	3.03	0.53
53869	1.91	3.10**	2.19**
65325	2.70	1.00	0.60
64523	2.05	0.84	0.09*
2807	1.36*	2.16	1.62
64301	1.32*	1.21	0.66
Mean[§]	2.03	1.33	0.79

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

Table 9.16. Descriptive statistics for minor fatty acid composition of *A. sativa* subsp. *nudisativa* accessions from 'PGRC selections' sub-set (FA percentage based on total FA detected by GC)

	% Stearic Acid	% Linolenic Acid	% Eicosenoic Acid
Maximum	2.93	2.96	2.78
Minimum	1.61	0.63	0.80
Mean	2.14	1.06	1.35
SD	0.42	0.60	0.56
RFT Mean	1.89	1.23	0.91
RFT HSD	0.89	0.67	0.82

SD= Standard Deviation, RFT= Replicated Field Trial

Table 9.17. Minor fatty acid composition of *A. sativa* subsp. *nudisativa* accessions from 'PGRC selections' (FA percentage based on total FA detected by GC)

CN Number	% Stearic acid	% Linolenic acid	% Eicosenoic acid
63829	2.18	0.69*	1.20
17824	2.85**	2.96**	2.73**
52029	2.30	0.63*	1.11
46228	2.93**	0.86	0.80*
46819	2.26	0.91	0.95*
53677	1.68	1.43	1.53
29662	1.84	0.90	1.52
66492	1.61*	0.89	1.27
42930	1.86	0.82	1.13
79437	2.26	0.84	0.96
79365	2.75	2.16**	2.78**
30730	1.64*	0.90	1.23
4930	2.27	0.77	0.99
63700	1.86	0.87	1.23
64584	1.91	0.77	1.16
55263	2.37	0.77	1.35
34095	1.73	0.83	1.06
Mean[§]	2.14	1.06	1.35

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

Table 9.18. Descriptive statistics for minor fatty acid composition of *A. strigosa* accessions from 'PGRC selections' sub-set (FA percentage based on total FA detected by GC)

	% Stearic Acid	% Linolenic Acid	% Eicosenoic Acid
Maximum	1.96	1.13	1.33
Minimum	1.30	0.79	1.06
Mean	1.59	0.92	1.18
SD	0.18	0.10	0.06
RFT Mean	1.89	1.23	0.91
RFT HSD	0.89	0.67	0.82

SD= Standard Deviation, RFT= Replicated Field Trial

Table 9.19. Minor fatty acid composition of *A. strigosa* accessions from 'PGRC selections' sub-set (FA percentage based on total FA detected by GC)

CN Number	% Stearic acid	% Linolenic acid	% Eicosenoic acid
54037	1.56	0.95	1.25**
88826	1.31	0.85	1.19
88867	1.30*	0.84	1.18
52909	1.75	1.03	1.33**
58076	1.82**	0.94	1.11
88866	1.68	0.99	1.06*
25730	1.79	0.90	1.20
88330	1.45	0.96	1.18
3067	1.70	0.83	1.16
81779	1.79	0.80	1.19
3075	1.66	1.13**	1.23
3068	1.52	1.03	1.14
81768	1.60	0.85	1.25
22002	1.31*	0.79*	1.19
81784	1.40	0.88	1.08*
25767	1.96**	0.80	1.22
81762	1.49	0.79*	1.16
79350	1.54	0.96	1.21
58062	1.64	1.04**	1.22
22000	1.60	0.96	1.10
Mean[§]	1.59	0.92	1.18

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

Table 9.20. Descriptive statistics for minor fatty acid composition of *A. sterilis* accessions from "PGRC selections" (FA percentage based on total FA detected by GC)

	% Stearic Acid	% Linolenic Acid	% Eicosenoic Acid
Maximum	4.60	3.69	3.01
Minimum	1.76	0.50	0.57
Mean	2.78	1.45	1.55
SD	0.85	0.92	0.64
RFT Mean	1.89	1.23	0.91
RFT HSD	0.89	0.67	0.82

SD= Standard Deviation, RFT= Replicated Field Trial

Table 9.21. Minor fatty acid composition of *A. sterilis* accessions from 'PGRC selections' sub-set (FA percentage based on total FA detected by GC)

CN Number	% Stearic acid	% Linolenic acid	% Eicosenoic acid
20202	3.51	2.98	2.91**
21749	2.60	0.55*	1.21
21794	3.77	3.07**	3.01**
21870	4.15	1.09	1.81
22466	2.11	0.92	1.77
23016	2.69	0.50*	1.09
23226	1.89	1.89	1.25
23553	1.76*	1.15	1.18
23570	2.11	1.36	1.12
24018	4.60**	3.69**	2.49
24092	2.68	0.69	1.37
24248	1.83*	1.05	1.33
24434	2.09	1.94	1.82
25658	2.27	1.78	1.70
64586	3.21	1.03	0.97*
64610	4.22**	0.75	1.03
64616	2.52	0.67	0.57*
67342	2.66	1.04	1.25
67357	2.54	2.22	1.81
67381	2.46	0.70	1.28
Mean[§]	2.78	1.45	1.55

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid

Table 9.22. Descriptive statistics for minor fatty acid composition of *A. fatua* accessions from 'PGRC selections' sub-set (FA percentage based on total FA detected by GC)

	Stearic Acid	Linolenic Acid	Eicosenoic Acid
Maximum	4.78	3.16	3.30
Minimum	1.96	0.57	0.64
Mean	3.03	1.46	1.40
SD	0.69	0.87	0.64
RFT Mean	1.89	1.23	0.91
RFT HSD	0.89	0.67	0.82

SD= Standard Deviation, RFT= Replicated Field Trial

Table 9.23. Fatty acid composition of *A. fatua* accessions from 'PGRC selections' sub-set (FA percentage based on total FA detected by GC)

CN Number	% Stearic acid	% Linolenic acid	% Eicosenoic acid
19396	3.12	0.58*	1.12
21197	3.75**	1.57	1.03
21213	4.78**	0.61	0.64*
21229	3.00	0.76	1.11
21242	3.56	0.76	1.09
21302	2.89	0.57*	1.24
22557	2.55	2.21	1.54
22559	2.14	0.65	1.29
22561	2.94	0.76	1.20
22564	3.17	0.87	1.19
22600	3.64	3.16**	2.48**
22613	2.66	0.74	1.17
22614	2.87	1.61	0.97
23035	3.39	2.91**	2.41
23110	3.59	2.61	3.30**
24141	2.05*	1.90	0.92*
21985	2.35	1.38	1.21
25522	3.15	1.52	1.12
23110	1.96*	2.59	1.48
Mean[§]	3.03	1.46	1.40

* Lowest % of each fatty acid, ** Highest % of each fatty acid, [§]Mean % of each fatty acid