

Corn oil research and improvement: A review

A. RAJENDRAN, ¹D. CHAUDHARY AND ¹V. MAHAJAN

Indian Institute of Maize Research, Pusa Campus-110012, New Delhi

¹Indian Institute of Maize Research, PAU Campus-141004, Punjab

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ABSTRACT

Corn germ oil is an industrial product characterized by high polyunsaturated fatty acids, low saturated fatty acids, essential amino acids, fatty acids, polysterols and tocopherols. Oil is a specialty trait for plant breeders in maize which is also useful and unique. Generally, in high oil genotypes the high oil in kernel is associated with low starch, reduced endosperm and kernel size. Temperate x Tropical (HO) QPM derived lines, HKI Tall and AF-04-B-5796-A-7-1-1 are inbreds registered as sources of maize oil in India. An elaborate study to decipher the genetic control and inheritance of oil and yield related traits in maize is essential for high oil corn breeding. A combination of conventional breeding methods, marker-assisted selection and transgenic approach can aid in developing high-yielding genotypes with enhanced oil content. This paper attempts to review research options to develop specialty maize with high oil and good grain yield.

Keywords: Maize, high oil corn, maize germ

Corn is successful cereal grass useful as food, feed and in industries. Corn is also source of corn oil which is tasteless odourless and pale yellow oil derived from the corn kernel. Normal corn has usually oil ranging about 3-4 per cent oil, especially in the embryo. Corn with oil content more than six per cent is called high oil corn (HOC). Germ, including embryo and scutellum makes ten per cent of corn kernel. Germ contains 80-85 per cent of total kernel oil followed by aluerone and endosperm with 12 and 5 per cent oil respectively. Corn oil is an important product that can be extracted from the embryo/germ left over after starch extraction from kernel endosperm in wet mills. The commercial and economic value of the otherwise discarded embryo is enhanced when corn oil is extracted from it. Corn oil is extensively used in baking, salad dressings, frying, margarine, biofuels and livestock feed. HOC has larger embryo with higher total protein, good stability due to low linolenic acid, higher tocopherols, phytosterol esters and phytostanol esters as well as well-balanced amino acids (Lambert *et al.*, 1998; Wassom *et al.*, 2008; Zahir *et al.*, 2014). Table- 1 depicts the nutritional excellence of HOC over primary oil sources and normal corn.

Table 1 : Fatty acid composition of primary oils and corn oil

Types of oil	Polyunsaturated fatty acid (g teaspoon ⁻¹)	Saturated fatty acid (g teaspoon ⁻¹)
Corn oil	7.436	1.761
Soybean oil	5.114	2.026
Peanut oil	4.320	2.282
Rapeseed oil	3.940	1.031

Source: USDA, National Database for Standard Reference

The expansion of area and yield of corn, availability of good cultivars, processing and comprehensive utilization can enhance the utility of HOC. This review briefs the different features of improving oil in corn.

Corn Oil Improvement - Genetics, Conventional and Modern approaches

Corn kernel oil content ranges between 1.2 and 20.0 on weight basis (Batista and Tosello, 1982; Bergquist *et al.*, 1998). Specialty corn *i.e.*, high oil corn contains 6% or more oil on dry weight basis. Corn fatty acid composition is highly variable and heritable trait. Germ and kernel weight increases linearly upto seventh week of kernel development (Leng, 1967; Curtis *et al.*, 1968). Third and fourth week of kernel development is the period of rapid metabolism in producing oil. High oil inbreds show high rate of oil accumulation 15-45 days after pollination. Once the seed is fully mature physiologically oil production is completed. Dudley *et al.* (1977) found this trait to be controlled by nearly 69 genes. Increase in kernel oil concentration has been found to be due to increased embryo:kernel ratio and increased embryo oil concentration (Dudley and Lambert, 1992; Lambert, 2001; Miller and Brimhall, 1951; Moose *et al.*, 2004; Tanaka *et al.*, 2009). Genotype influences oil content more when compared to the effects of environment and genotype x environment interaction (Berke and Rocheford, 1995; Genter *et al.*, 1956). The additive genetic variance is the main genetic component controlling this trait (Dudley and Lambert, 1992).

Hopkins (1899) first initiated long term selection experiment with Burr's White Variety to investigate selective response of protein and oil concentration in corn kernel. After several cycles of selection, the oil

Table 2: QTLs associated with kernel oil and related traits in corn

Trait	Identified QTLs gene ¹	Chromosomal position
Kernel oil	25 QTLs 4 major QTLs 9 QTLs 20 QTLs 50 QTLs 10 QTLs 6 QTLs 9 QTLs	Across 10 chromosomes (Goldman <i>et al.</i> , 1994) Chromosomes 2,5,6 and 9 (Berke and Rocheford, 1995) Chromosomes 1,5 and 6 (Mangolin <i>et al.</i> , 2004) Across 10 chromosomes (Laurie <i>et al.</i> , 2004) Across 10 chromosomes (Song <i>et al.</i> , 2004) Chromosome 2,3,6,8 (Willmot <i>et al.</i> , 2006) Chromosome 1,2,4,6,8 (Zhang <i>et al.</i> , 2010) Across 10 chromosomes (Yang <i>et al.</i> , 2010.)
Kernel oil and fatty acid composition	<i>DGATI-2</i> (Diglyceride acyltransferase) Gene (Zheng <i>et al.</i> , 2008) 74 QTLs (Li <i>et al.</i> , 2013)	Chromosome 6
Linoleic acid	Omega 6 desaturase gene (Weselake <i>et al.</i> , 2009)	
Oleic acid: linoleic acid ratio	<i>Koc6c</i> (Goldman <i>et al.</i> , 1994; Alrefai <i>et al.</i> , 1995)	
Conversion of oleic to linoleic acid	<i>fad2</i> (fatty acid desaturation) and <i>fad6</i> gene	Chromosomes 1,4,5 and 10 (Mikkilineni and Rocheford., 2003
Oleic and linoleic acid	6cM interval	Chromosome 6 (Wassom <i>et al.</i> , 2008)
Oleic acid	<i>Oilc1-1</i> 9 QTLs	Chromosome 1 (Song and Chen, 2004) Chromosome 6,7,9 (Yang <i>et al.</i> , 2010)
Linoleic acid	9 QTLs	Chromosome 6 (Yang <i>et al.</i> , 2010)
Palmitic acid	8 QTLs	Chromosome 1,2,4,6,9,10 (Yang <i>et al.</i> , 2010)
Stearic acid	7 QTLs	Chromosome 3,6 (Yang <i>et al.</i> , 2010)
Embryo Endosperm ratio		<i>ZmGe1</i>
Chromosome 7 (Cahoon <i>et al.</i> , 2006)	<i>ZmGe2</i>	Chromosome 1 (Zhang <i>et al.</i> , 2012.)
Yield and yield related traits in HOC		18 QTLs
Chromosome 1,3,4,5,6,7,8,10 (Li <i>et al.</i> , 2009.)		

Strategies and goals

concentration of the resulting high oil strain reached more than 10 per cent (Alexander, 1988; Dudley *et al.*, 1977; Lambert *et al.*, 1998; Misevic and Alexander, 1989; Ottaviano and Camussi, 1981; Song *et al.*, 1999). Negative association of oil and grain yield has limited the development of high-oil corn genotypes/hybrids. Seeds with high oil levels have often been associated with small and shrivelled size, shorter longevity and greater deterioration than seeds with high starch content (Copeland *et al.*, 2001; Rakshit *et al.*, 2003). Reason behind rapid decline of oil rich seeds is the inability of seed to imbibe moisture and hold it tightly causing the additional water taken to become excessive (Thomison *et al.*, 2002). The capacity of the plant to produce carbohydrates and synthesize oil is physiologically independent ranging from 4 to 7 per cent oil (Alexander and Lambert, 1968). With every one per cent increase in oil, kernel starch would decrease by 1.48 to 1.83 per

cent (Song and Chen, 2004). The average grain yield of the high oil hybrids is seen to decline by 5 per cent when compared to normal hybrids. Reports of Batista and Tosello (1982), Dorsey-Redding *et al.* (1991) and Sene *et al.* (2001) indicate positive correlation between oil and starch in corn. Nevertheless, in a population derived from Reid's Yellow Dent, seven cycles of recurrent selection increased kernel oil from 40 to 90 mg g⁻¹ without significant reduction in yield (Miller *et al.*, 1981). Prospecting several accessions revealed (Temperate x Tropical(HO)QPM)-B-B-B-60-B-B, (Temperate x Tropical(HO)QPM)-B-B-B-100-B-B, DMHOC4, HKI Talar, (Temperate x Tropical (HO) QPM)-B-B-B-57-B-B, HKITall-8-1-1 and AF-04-B-5796-A-7-1-1 to be best utilized for high oil corn breeding (Rajendran *et al.*, 2012). These inbreds harbour more than 5 per cent oil in the germ.

Most literature illustrates influence of the male parent through xenia effect in the determination of oil content in corn. However, reports of Miller and Brimhall (1951); Garwood *et al.* (1970) and Song *et al.* (1999) show maternal inheritance of oil content. Male gametophyte of the high oil population has additive or dominant gene action causing the germ size of the normal oil hybrid to increase slightly and increase the concentration of oil in the germ with minimum change in grain yield. Higher oil content by xenia was confirmed in modern single-cross hybrids which were male-sterile after detasseling (Letchworth and Lambert, 1998) or by using cytoplasmic male sterility (Lambert, 2001). Identification of haploid seed is possible using the xenia effect of a high oil inducer line based on oil content or embryo size (Chen and Song, 2003). Recently, top cross or top cross blend system has been developed that includes planting two types of corn for producing high-oil corn (Thomison, 2002). One type, representing 90 to 92 per cent of the seed, is a hybrid taken as the “grain parent.” Remaining is elite high oil inbred as “pollinator”. The grain/female parent used in this system is a male sterile version of an elite commercial hybrid. The pollen shed from high oil pollinator plants contain genes that lead a kernel to produce much larger than average germ or embryo thereby exploiting xenia effect (Bergquist *et al.*, 1998; Liu *et al.*, 2010). Pollinator plants influence very little on overall grain yield without compromising the oil and protein quality of the grain produced by fertilization. Oil concentration being a quantitative trait requires understanding the nature of the quantitative genetic variation for oil content in corn to develop suitable breeding programs. QTL analyses by several workers (Table 2) have identified QTLs associated with oil in corn. Most of the QTL mapping for kernel oil in corn is done in temperate corn germplasm (Alrefai *et al.*, 1995.; Goldman *et al.*, 1994). Three main QTLs (koc5b, koc6c and koc9) located in chromosomes 5, 6 and 9 are common in temperate (Berke and Rocheford, 1995) and tropical germplasm (Mangolin *et al.*, 2004). Deployment of common QTLs (oilc6 and proc6) and separate QTLs (oilc2 and oil8) that are not negatively correlated with QTL for starch concentration would minimize the loss in grain yield as there is no reduction in starch (Zhang *et al.*, 2008). Yang *et al.* (2012) identified 58 QTL for kernel oil content and associated traits in 26 genomic regions covering ten chromosomes. Proteomic analysis has revealed a total of 83 protein spots with differential expression (Liu *et al.*, 2009). Putative enoyl-ACP reductase (ENR), putative stearoyl-ACP desaturase (SAD) and putative acetyl-CoA-C-acyl-transferase (ACA) are the three proteins with abundant expression found in high oil corn lines. Transgenic approaches are being done to enhance

maize oil quantity as well as quality. Zhang *et al.* (2012) increased total oil using wheat purindoline a and b genes in transgenic lines of maize. Embryo and seed specific over expression of maize DGATs and ZmWR11 (maize wrinkled 1) transcription factors is seen to improve kernel oil and oleic acid content (Oakes *et al.*, 2011; Shen *et al.*, 2010; Zheng *et al.*, 2008). Breeding program to increase oil content in maize kernels should be considered without compromising reduction in grain yield by bringing positive alleles distributed among genotypes. Positive alleles from different genotypes can provide transgressive segregants with higher oil content (Liu *et al.*, 2009). Successful production of HOC is limited by low grain yield potential, physiological cost of oil synthesis, low seed vigour, low kernel weight, shorter seed longevity and poor germination of HOC lines. The proportion of germ and germ oil content are the prime target traits/objectives in breeding for oil in corn. Selection for germ oil is seen to influence the germ proportion and oil to a large extent. Proportion of embryo and endosperm in oily kernel greatly influences the flow of nutrients in embryo (Cahoon *et al.*, 2006; Zhang *et al.*, 2012). Seed germinability, setting, maturation, mobilisation of oleosomes and oleosins can be studied to overcome these demerits. The study of whole kernel, embryo and endosperm ratio in relation to oil contents in right germplasm could create outcomes which can be applied to elite material.

Rakshit *et al.* (2003) found grain yield of high oil hybrids to reduce as oil increases more than eight per cent. Remarkable effect of pollen is seen to increase oil as well as size of germ without affecting yield. This effect is termed as xenia and can be well exploited for breeding for high oil in corn. The pollinators or male parent should be high in oil with heavy pollen and prolonged pollen shedding. Hence, prospecting germplasm for good pollinators is can give good male parents for improvement. Elite normal corn inbred or single cross hybrids that give good seed production can be opted as female line. Detasseled single cross hybrid can be used as female. Yield levels of HOC can be increased by using single cross hybrids or female inbreds with diverse genetic background.

Several current molecular tools have improved the knowledge of genetics of oil and oil related traits in corn. QTL mapping and trait analysis has given information of several QTLs controlling quality and quantity of oil. Good quality oil has higher oleic acid and reduced saturated fatty acid like palmitic acid. Study of relation among fatty acids, carbon flow for oil, starch and protein synthesis for improving the value and amount of oil can be done using metabolism or pathways or enzymes involved in oil, starch and protein

accumulation in kernel. Synthesis of fatty acid and triglycerol and its biochemistry has been deciphered by numerous studies (Harwood, 2005; Lung and Weselake, 2006; Ohlrogge and Browse, 1995; Poneleit, 1976; Snyder *et al.*, 2009; Stymne and Stobart, 1987; Weselake *et al.*, 2009). Genetic engineering and 'omics' approaches can lead to better understanding of plant metabolism mechanism for oil production. Efficiency of marker assisted selection and breeding can be enhanced using QTLs with nil or lower pleiotropic effects on grain yield (Berke and Rocheford, 1995), favourable QTLs from elite and non-elite lines for high oil content detectable before flowering, marker-assisted backcrossing of QTLs with larger phenotypic variation (Bouchez *et al.*, 2002; Hospital *et al.*, 1997; Stuber and Sisco, 1992). Cost-effective marker-assisted selection can be successful in plant breeding programs (Mangolin *et al.*, 2004; Mihaljevic *et al.*, 2004).

The demand of quality food products, healthy food has initiated research and development activities to develop products like corn oil. Owing to health benefits a number of non-traditional oils such as rice bran oil, corn oil are entering market and is picking up. Extraction of corn oil is an upcoming area of entrepreneurship. In the coming years, research emphasis will support corn oil to catch a better position in edible oil market.

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