

Figure 1. Soybean fatty acids: stability, typical composition



Individual fatty acids and their effects on cholesterol levels

Stearic Acid (C18:0)

- Unsaturated fatty acids, such as linolenic (C18:3) and linoleic (C18:2), are oxidatively unstable, and tend to go rancid rapidly
- These fatty acids must be hydrogenated to increase stability (Figure 1)
- The hydrogenation process results in the formation of trans fatty acids, which are tightly linked with heart problems in humans and "not generally regarded as safe" by the USDA
- Stearic acid (C18:0) is a long chain fully hydrogenated fatty acid that has been shown to have no negative effect on LDL levels (unlike other saturated fatty acids)
- Soybean oil with elevated saturated fatty acid content is desirable for solid fat baking applications, and could potentially eliminate the need for expensive solid fats like cocoa butter and heart-unhealthy fats such as palm oil

	Fatty acid							
Line	Palmitic	Stearic	Oleic	Linoleic	Linolenic	Arachidic		
				- %				
A6	8.0	28.1	19.8	35.5	6.6	2.0		
FA 8077	8.4	4.4	42.8	36.7	7.6	<1.0		

Mutant lines: A6 and 194D

A6 is a mutant characterized by several large deletions, including ~1/8 chromosome deletion on Gm14 predicted to encompass 30 genes from the Glyma 1.0 high confidence gene set, including SACPD-C.

A6 exhibits poor germination and severe field defects such as reduced height and yield

194D is an EMS-induced mutant with moderate levels of stearic acid (~12%) due to a point mutation (V211E) in SACPD-C (Figure 4)

Previous work by Zhang et al (2008) and first demonstrated that the elevated stearic acid trait in soybean is due to loss of function mutations affecting a stearoyl-acyl carrier protein-desaturase gene, SACPD-C,



SACPD-C 25E06 50E05 78E06 16E06 12.5E06 15E08 17.5E08 22.5E06 21.5E06 21.5E06 27.5E06 35E06 32.5E06 37.5E06 46E06 47.5E08

Comparative Genome Hybridization of A6 and its progenitor line

Materials and Methods

(a)		Character 27000/CAC0D_C		
18:0 g kg ⁻¹ seed oil	1kbp	Glyma14g27990/SACPD-C		
37±4	[⁺		W82 Bay	← WT
27+7			FA8077	
5/1/	-	C298∆, frameshift		
129±27	-	+	KK24 (Bay)	
119±17		73704 \/0445	M25 (Bay)	
	r +	1779A,V211E		
89±11			194d (W82) 🛑 12% 🛛
110+14				
115+9	/	(Deletion of entire locus)	\square	— 13%
11510 /			/	13/0
	/	FN8 (W82)	/	
257±44 —	,	(Deletion of entire locus) + unidentified locus A6 (FA 8077?)	\vdash	—28%

Phenotypic distributions







GBS workflow. Modified from http://www.floragenex.com/rad-seq/

27,672 SNPs were identified, with an average SNP coverage of 10.98-fold. SNPs were filtered to <20% missing data, allele frequency between 0.2 and 0.8, bringing the SNP count down to 5,423. Chi-square test removed severely distorted markers (at $F_{4:5}$), resulting in a final count of 2,977















