Modification of Quantity and Quality of Safflower Oil Through Plant Breeding[1]

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Abstract

Less than 20 years have passed since safflower was established commercially in the southwestern area of the United States. Already hybrid varieties are available, oil and protein contents have been raised greatly, and oil quality has been modified sufficiently to constitute another oil crop for American agriculture. It is hoped that the next 20 years will be equally productive in terms of improvements and modifications of the oil and protein of this crop.

Introduction

Safflower (*Carthamus tinctorius* L.) has been grown as a commercial crop in California for 18 years. In 1950, it was grown on 23,000 acres, and now it occupies between 150,000 and 300,000 acres. Safflower is also established in Arizona and portions of the western part of the Northern Great Plains. State and USDA breeding programs of various dimensions are located in Arizona, California, Nebraska, Montana and Utah. The USDA is also developing safflower varieties at Beltsville, Maryland. Varieties are being developed by several companies located in California and Arizona.

Objectives in plant breeding programs to improve safflower have been similar to those in most other crops. Among them would be greater resistance to diseases and insects, higher yields of seed per acre, higher oil contents of the seed, higher protein contents and, more recently, modifications in oil quality. This paper will focus on progress that has been made in modifying the seed itself with a view to increasing oil contents and changing oil quality. Less attention has been given to protein.

The term "seed" is used here to include the hull (or pericarp), the seed coat which adheres to the hull, and the embryo, which contains practically all of the oil and protein. Safflower seed with 37% oil has about 50% of its total weight in the hull and seed coat, neither of which has any food or feed value. Major increases in oil and protein contents have been made by reducing hull content. Changes in oil quality have been independent of changes in hull thickness.

Changes in Hull and Seed Coat

Leadership in achieving modifications in the hull and seed coat has rested with Rubis and his associates at the University of Arizona. A major step was his discovery of the recessive *th* gene which made the hull so thin that it had a gray color because the phytomelanin layer showed through (16–18). It was soon evident that the thin-hulled plants usually had weak stems and were partially or completely male-sterile. Ebert and Knowles found that the *th* gene was responsible for weak stems and male sterility, and not other genes linked to *th* in inheritance (2). The primary effect of this gene was to reduce secondary thickening of the walls of certain cells in the hull, in the stem and in the anther. Because cells in outer layers of the hull had little or no secondary walls they collapsed on drying into a thin transparent layer. Fiber cells of the stem with reduced secondary walls failed to provide rigidity to the stems. Reduction in both secondary wall development and rib formation in endothecial cells of the anther meant that the anther did not release its pollen in a normal manner. Often no pollen was deposited on the emerging stigma, and the flower was structurally male-sterile.

Because of the effects of the *th* gene on stem strength and pollen release, it has not been incorporated into pure-line varieties. There is a possibility, however, by selecting the appropriate modifying genes, that varieties may be developed with thin hulls, adequate stem strength, and sufficient pollen release to insure a crop.

The most important use of the *th* gene is in production of hybrid varieties, as proposed by Rubis (17). Because thin-hulled plants are structurally male-sterile they can serve as a female parent in single crosses. Such a female parent should: release sufficient pollen to reproduce itself under isolation, in the presence of bees which will help to remove pollen from the anthers; produce little or no selfed seed in a crossing block in the presence of a male parent having abundant pollen; and combine well with the male parent to produce a vigorous hybrid.

Striped safflower seeds have reduced amounts of hull. Rubis has shown that the various degrees of striping are controlled by genes at one locus (18). These genes influence the secondary wall development in the outer layers of the hull and canalization of the phytomelanin layer. They are symbolized as: stp^g, giving gray stripes; stp^p, giving purple stripes; and *stp*, giving brown stripes. The gene *Stp*, dominant to all three striping genes, gives smooth hulls. Undoubtedly the striping genes, particularly stp^g and stp^p, will be used by safflower breeders. The gene *stp* has the most pronounced effect; it localizes the phytomelanin layer into definite canals, and secondary cell wall development is restricted to regions below these canals. Hull percentage is greatly reduced, and oil and protein correspondingly increased. Unfortunately, brown-striped seeds have an odor of wet straw which carries over into the oil and protein, and the oil is dark in color.

Effects of genes *th* and *stp* on seed composition are apparent from the data of Table I.

Rubis has found that a gene, symbolized *lt*, will give seed coats that are yellowish to light tan in color instead of the usual brown color (18). Oil extracted from such seeds has usually been lighter in color.

Rubis has found another gene, symbolized *p*, which

TABLE I

The Average Composition of Safflower Seed of Different Genotypes[a]

Genotype	Appearance of hull	Hull, %	Oil, %	Meal	
				Protein, %	Fiber, %
ThThStpStp	Smooth, white	40	39	20	41
ththStpStp	Very thin, gray	20	47	40	17
ThThstpstp	Brown striped	25	46	34	25

[a] From Rubis (18).

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prevents the formation of the phytomelanin layer (18). Seeds are chalky white instead of shiny white. When present in thin-hulled types produced by *th* and *stp* genes, seeds are not colored, simply because the melanin pigment is not present to show through the outer hull. The obvious use of *p* is to combine it with *stp* to eliminate the odor and dark oil color associated with the latter gene.

Changes in Fatty Acid Composition of the Oil

Safflower oil has been used as an industrial oil in surface coatings (15), and as an edible oil, mostly in soft margarines. For both purposes the high linoleic acid content has contributed to its high quality. For other food uses safflower oil has not been widely acceptable because it tends to form polymeric materials from oxidative reactions involving linoleic acid. Such polymeric materials have been particularly objectionable when safflower oil is used at high temperatures as a frying oil.

Our studies of the fatty acid composition of safflower oil have shown that there are three genes at one chromosome locus that govern the proportions of linoleic and oleic acid (8,10). The genotypes which are possible with these genes, and their effects on linoleic and oleic acid compositions are given in Table II.

The gene present in most safflower varieties, *Ol*, produces oil with high levels of linoleic acid and low levels of oleic acid. At the other extreme, the gene *ol* gives an oil low in linoleic acid and high in oleic acid. Types high in oleic acid were first found in Indian introductions (6,7,10), and subsequently have been found in materials in East Pakistan (14).

The third gene, ol^1, usually produces an oil with equal amounts of linoleic and oleic acid, but the relative amounts of each acid seem to be strongly influenced by temperature. Under low temperatures linoleic acid increases, and under high temperatures oleic acid. The gene ol^1 was found in an introduction from the Azerbaijan area of Iran. Obviously, only three genotypes, *OlOl*, ol^1ol^1 and *olol*, breed true.

The genotype of the seed determines the fatty acid composition of its oil, not the genotype of the plant producing it (8,10,12). This has been true in similar studies with other oil crops.

The gene *ol* has been substituted for the gene *Ol* in the variety US-10 using the backcrossing technique, and the new variety, UC-1, was released as genetic stock in 1965, and as a certified variety in 1966. The oil of this variety, now under extensive test in several laboratories, looks promising as a cooking oil. It has been shown to have high-temperature oxidative stability comparable to that of hydrogenated oils (3,4). It was pointed out that there are potential industrial applications for an oil with high oleic acid content, both where the oleic acid is removed from the oil and where the oil is epoxidized for use as a plasticizer and stabilizer (3). It is expected, if the new type of safflower oil is accepted commercially, that better varieties than UC-1 will be available in the near future.

TABLE II
Linoleic and Oleic Acid Composition of Oil of Safflower with Different Genotypes

Genotypes	Linoleic acid, %	Oleic acid, %
OlOl	75–80	10–15
Olol^1	70–75	15–20
Olol	60–75	18–35
ol^1ol^1	42–54	35–50
ol^1ol	30–40	55–63
olol	12–30	64–83

The value of the oil produced by the genotype ol^1ol^1, with approximately equal amounts of oleic and linoleic acids, has not been assessed. There appears to be no commercial interest in such an oil because it can be readily synthesized from the normal safflower oil and oil high in oleic acid.

At a second locus there have been identified two genes governing levels of stearic acid (12). The gene *St*, present in most safflower varieties, gives low levels of stearic acid, in terms of 1% to 2%. When the recessive gene *st* is homozygous, acid content will be about 9%. The increase in stearic acid has occurred at the expense of both linoleic and oleic acids, but not in a consistent manner. Safflower oil with higher levels of stearic acid appears to have no commercial possibilities. The gene *st* was found in two introductions, one from Israel and one from Russia.

Little attention has been given to the modifications in fatty acid composition produced by genes with small effects. A serious search has been made in the World Collection of safflower for types having higher than the usual amount of linoleic acid (7). Where the commercial varieties US-10 and Gila had oil with linoleic acid contents of 79.5% and 79.0% respectively, several introductions were above 82%, and one was as high as 84.6%. Limited studies of these types with higher levels of linoleic acid in crosses to US-10 indicate that the differences are due to several genes with small effects.

Changes in Protein

Thin-hulled types produced by genes *th* and *stp* have given undecorticated meals with protein contents in terms of 40% and 34% respectively (Table I). Such meals would be competitive with many oil seed meals for ruminants, but for poultry they will still contain too much fiber (11).

Apparently there have been no attempts to modify the relative amounts of oil and protein in the seed. Oil contents of the embryos (kernels) of Indian varieties have varied between 56.8% and 65.4% (13). Guggolz et al. have found a range of 59.0% to 64.0% in commercial varieties and 50.8% to 62.7% in experimental types (5). It would seem that there is sufficient variability here to interest the plant breeder. It is obvious, with a constant hull content, that increases in oil content will be obtained with a reduction in protein content.

The protein of safflower seed is deficient in lysine (11). This has limited the use of safflower meal as the only protein source. The Western Utilization Research and Development Division of the USDA and the University of California cooperatively are carrying forward a survey of the World Collection, hoping to find an introduction with more lysine than commercial varieties.

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