Identification of the $G_1^2 g_1^2 G_1^3 g_3^3$ Genotype in Breeding for Glandless Cottonseed

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Development of glandless-seeded genetic stocks by McMichael in the early 1950's and discovery of the inheritance of this character by McMichael (1) and Roux (4) have afforded cotton breeders an opportunity to rid cottonseed of the pigments contained in these glands. Notable among these pigments is gossypol, a phenolic compound, which produces an undesirable color in cottonseed oil and has toxic properties that limit the usefulness of cottonseed meal as an animal feed.

As soon as McMichael had selected a genetic stock with seeds free of glands, work was begun to transfer glandless seed to commercial cottons. McMichael's fundamental work and the breeding effort that quickly followed were done at the U. S. Cotton Field Station in Shafter, Calif. Cotton breeders in the U. S. Cotton Belt and in some foreign countries have subsequently engaged in similar breeding programs.

The identification of the $G_1^2 g_1^2 G_1^3 g_3^3$ genotype (double heterozygote) is important in breeding for glandless cottonseed. It has been shown (2) that plants of the doubly heterozygous genotype produce bolls with reduced gland content, so plants of this genotype could be identified by the gland content of their bolls. The glands are embedded in the surface of the carpel walls of the cotton fruit or boll. This method of identification has been further clarified by recent investigations. These investigations have led to a more accurate means of identification which will be presented here.

McMichael (1) and Roux (4), working independently, found that the glandless seed trait in cotton is primarily controlled by two independent genes which act in a complementary-type fashion. Both investigators suggested that other genes with minor effects may also be involved. McMichael reported that the 2 major alleles act as recessives, while Roux published that these alleles act as partial dominants. The senior author has reviewed the work of both Roux and McMichael and found that the data presented by each support the hypothesis of recessive gene action (3).