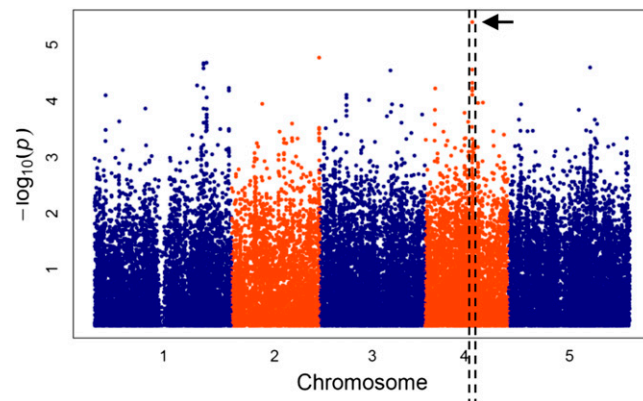


IN BRIEF

Getting There Faster: Genome-Wide Association Studies Point the Way to Increasing Nutritional Values

What if you were plunked down in front of a flying saucer and told to make it faster? Once you figured out how it moves at all, you could best choose your modifications if you knew what factors affect the saucer's speed and which of them you could readily control. Scientists aiming to understand and alter characteristics such as crop yield or nutritional value similarly need to decide where to focus their efforts. As you prepared to tinker with your saucer, you might wish you could check a slew of saucers and see what the faster (or slower) ones had in common. Plant scientists now can do just that using genome-wide association study (GWAS), wherein trait variation in diverse germplasm is associated with specific genomic differences. In contrast to traditional linkage mapping, in which relatively large quantitative trait loci are identified based on recombinant inbred populations produced from only two parental lines, GWAS takes advantage of historical recombination within populations to associate traits with individual sequence-level polymorphisms (reviewed in Zhu et al., 2008). Two new Large-Scale Biology articles underscore how GWAS can help guide research in plant biology.

Vitamin A deficiency still affects a large percentage of the global population and could be alleviated by production of seeds with higher levels of specific carotenoids, some of which (e.g., β -carotene) are dietary precursors of vitamin A (reviewed in Fitzpatrick et al., 2012). Via linkage mapping, **Gonzalez-Jorge et al. (pages 4812–4826)** first identified an *Arabidopsis thaliana* quantitative trait locus that accounts for a large portion of the variation in levels of seed carotenoids, including β -carotene, and fine-mapped it to a region containing 11 genes, one of which was *CAROTENOID CLEAVAGE DIOXYGENASE4* (*CCD4*). An independent GWAS using a diversity panel of 315 *Arabidopsis* accessions revealed that *CCD4* contained a single-nucleotide polymorphism most strongly associated with β -carotene content in seeds (see figure). Accordingly, the authors



Genome-wide association of β -carotene content in seed showing the most significant association (arrow) within *CCD4* (dashed lines). (Reprinted from Gonzalez-Jorge et al. [2013], Figure 3A.)

focused functional studies on *CCD4*, demonstrating that it is a major player in carotenoid degradation in both seeds and leaves and that differences in *CCD4* underlie natural variation in seed β -carotene content.

In the second study, **Angelovici et al. (pages 4827–4843)** examined the accumulation in *Arabidopsis* of branched-chain amino acids (Val, Leu, and Ile), which are essential amino acids that animals must obtain from their diets. The combination of GWAS with linkage and haplotype analysis directed the authors to *BRANCHED CHAIN AMINO TRANSFERASE2* (*BCAT2*), one of seven branched chain amino acid transferases in the genome. Mutant and complementation analyses showed that *BCAT2* is responsible for natural variation in seed branched-chain amino acid levels and is likely catabolic.

These two wonderfully thorough studies emphasize the value of elucidating the main determinants of a particular trait; in both cases, degradation, rather than biosynthetic, enzymes were powerful influences on the ultimate levels of the essential nutrients accumulated in seeds. Thus, given the chance to examine many other flying saucers, you might have found yourself more likely to create a faster saucer by disabling the brakes than by adding a bigger engine.

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