

## **New Methods in Genomic Research of Plants**

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Association mapping (as opposed to population mapping) is becoming more important in establishing associations between a phenotype and a genotype. The major advantage of association mapping, which depends on novel statistical methods, lies in the ability to use a collection of germplasm directly rather than taking the time and expense of developing a mapping population. Another advantage of association mapping is that the linkage disequilibrium values give a stronger LOD value, hence weak QTLs are more evident. SNPs are becoming more important as the molecular marker of choice because of their relative abundance within a genome and because of their adaptation to high throughput technologies. However, as with all molecular markers association must be made between the genotype and phenotype. Since genomics by definition involves gene expression, the use of microarray technology has increased in genomic work. However, because of the cost, level of skill required, and the level of error associated with microarrays, methods to verify a result is essential. To verify or extend a result obtained from an analysis by microarray, qPCR is becoming a common practice. Of course, the ability to extract good quality RNA is required by both systems.