

1739 The impact of novel sequencing technologies on molecular plant breeding

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The discovery of restriction endonucleases (1971) coupled with Southern blotting (1975) inaugurated the era of molecular plant breeding. The ability to manipulate the DNA molecule and visualize DNA sequence variation made it possible to look beyond the phenotype to the underlying DNA sequence variation and to parse plant genomes with increasing scope and resolution. Genetic linkage mapping graduated from associations of a few loci to fully resolved genome maps. Map-based cloning accelerated the pace of gene discovery, and QTL mapping was unraveling the complex genetic interactions beneath continuous phenotypes. Subsequent technical advances increased the number and types of molecular markers available and lowered the costs of implementation. But while this increased the realistic scope of application, making background selection and "breeding by design" cost-effective, molecular markers remained surrogates for DNA variation, and imperfect surrogates at that, as much of the DNA variation was either missed or was confounded. The only means of accurately sampling all the DNA variation at a locus was the relatively slow and costly method of DNA sequencing, even with the steady decline in the cost (per base) of sequencing. Plant breeders continue to focus on molecular markers, eagerly incorporating the expanding number of molecular markers emerging from genomics research. However, the new sequencing platforms, by reducing sequencing costs and time-lines by orders of magnitude, make targeted re-sequencing a viable alternative to traditional molecular markers. Consequently, it is timely to anticipate how high-throughput, low-cost genome sequencing will change how molecular markers, *i.e.*, DNA sequence variation sampling and visualization, are implemented in plant breeding.