



High Impact Paper of the Month February 2015

Quantitative Trait Loci (QTL) Mapping and Molecular Breeding for Developing Stress Resilient Maize for Sub-Saharan Africa.

Semagn, K., Beyene, Y., Babu, R., Nair, S., Gowda, M., Das, B., ... & Prasanna, B. M. (2014). *Crop Science*.





Paper commentary

This paper by The International Maize and Wheat Improvement Centre (CIMMYT) illustrates the power of SNP markers to accelerate crop improvement work and the benefits of using KASP genotyping specifically for SNP analysis at key stages throughout crop improvement programs.

Highlights of the paper

- Successful implementation of SNP marker analysis for characterisation of existing germplasm, parentage verification, QTL mapping of desirable stress resilience traits and marker-assisted recurrent selection (MARS) and Genomic Selection (GS) of these traits.
- CIMMYT has routinely used KASP, generating in excess of a million data points annually for a range of different purposes.
- Average genotyping error rate in positive control DNA samples with KASP was lower than that observed in the Illumina GoldenGate
- KASP genotyping costs for MARS were cheaper than those of the BeadXpress and GoldenGate platforms.
- The authors conclude that *'because of the continuous change in SNP genotyping technology and high upfront costs, large-scale projects could benefit from exploiting genotyping service providers and avoid significant investment in setting up in-house SNP genotyping platforms'*.

Commentary

The average maize yield in sub-Saharan Africa (SSA) is very low compared to other maize growing regions. Drought, biotic stress and poor soil are just some of the factors which contribute to low crop productivity in SSA and which drive the intense need for stress-resilient maize in this region.

CIMMYT has undertaken multiple projects to develop stress-resilient maize germplasm for SSA, and made significant progress. This review shares their main findings from each of the following research areas below:

1. Characterisation of maize germplasm using SNP markers.
2. Using SNP markers to identify QTL. Identification of QTL in germplasm with large phenotypic effects and conserved across genetic backgrounds is one of the prerequisites for crop improvement using marker-assisted breeding.
3. Fine mapping, validation and use of production markers to select major genomic regions associated with key traits.
4. MARS and GS across bi-parental populations, evaluation of new lines and demonstration of superiority over conventional pedigree selection. For example, several new drought tolerant hybrids developed by MARS and GS have been selected for national performance trials in eastern and southern Africa.

Other articles you may be interested in

Single nucleotide polymorphism genotyping using Kompetitive Allele Specific PCR (KASP): overview of the technology and its application in crop improvement.

Semagn, K., Babu, R., Hearne, S., & Olsen, M. (2014). *Molecular Breeding*, 33(1), 1-14.