

Maize genotyping library

A set of 1200 **KASP™** SNP markers for maize were developed for the Global Maize Programme of CIMMYT and the Generation Challenge Program. This validated set of KASP SNP markers has been applied to over 500 projects with CIMMYT globally, and is now available to the wider maize breeding community as a valuable tool for marker-assisted selection. Markers include those for drought tolerance, nitrogen use efficiency, biotic stress resistance and aluminium tolerance, amongst many others.

Maize KASP SNP markers

The KASP maize library was developed from the mapping data against the B73 reference genome (Jones et al., 2009) and a SNP mining study from EST sequences (Bately et al., 2003). The SNPs were mapped against 284 maize recombinant inbred line populations – IBM (B736Mo17) and LHRF (F26F252), 24 proprietary Pioneer varieties and 60 Elite varieties, including North American and European lines, and 3 tropical lines.

The KASP markers developed can be used for a variety of genotyping applications including confirmation of identity and purity of lines, QTL mapping, marker-assisted back crossing and marker-assisted recurrent selection.

CIMMYT has used KASP to generate in excess of one million data points annually. The work done using the KASP maize library illustrates the power of SNP markers to accelerate crop improvement and the benefits of using KASP genotyping for SNP analysis at key stages throughout crop improvement programs.

These KASP genotyping assays are easy to run, robust, accurate and highly cost-effective.

The reagents for KASP genotyping can be delivered to you so that you can run the assays in your own laboratory; KASP can be read on most qPCR instruments and FRET-capable plate readers.

Alternatively, we can run the entire project for you in our genotyping service laboratories, and can include DNA extraction steps if required.

Advantages of the maize assays:

- Panel includes 1200 functionally validated SNP assays
- Pick and choose the assays relevant to your research from our [maize assay lists](#)
- Assays can be either:
 - a) run in your own laboratory
 - b) run through our genotyping service laboratories
- Proven KASP technology delivers superior genotyping performance.

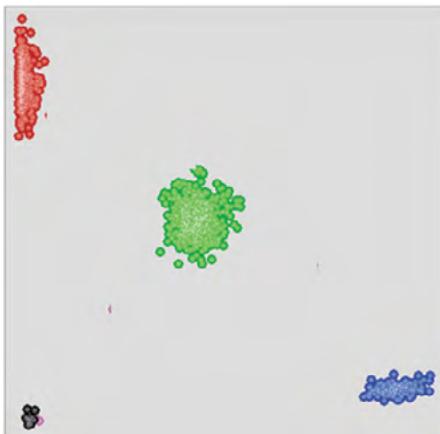


Figure 1. Typical SNP genotyping results using a pre-validated Maize KASP Assay on 1536-well plate with SNPlane instrumentation. The data was normalised with ROX and plotted using KlusterCaller™ software.

Additional genotyping panels

LGC, Biosearch Technologies™ has been providing genotyping solutions for over 15 years to a global customer base. Libraries of pre-validated KASP genotyping assays have been developed for a wide range of species, in collaboration with scientific partners who have substantial experience of working with their respective organisms.

Also available are rice, tomato, lentil and wheat [genotyping libraries](#).

Ordering information

Cat no.	Size	Description
KBS-2500-005	(2500 × 10 µL reactions)	Maize KASP Assay Mix
KBS-1050-101	500 × 10 µL reactions (2.5 mL)	KASP-TF V4.0 2X Master Mix 96/384, Standard ROX (2.5 mL)*
KBS-1050-102	5000 × 10 µL reactions (25 mL)	KASP-TF V4.0 2X Master Mix 96/384, Standard ROX (25 mL)*
KBS-1050-103	50000 × 10 µL reactions (250 mL)	KASP-TF V4.0 2X Master Mix 96/384, Standard ROX (250 mL) (10 × 25 mL)*

* Alternative master mixes with high ROX and low ROX are also available. Please ensure that you are using the optimal version of [KASP-TF Master Mix](#) for your instrument.

References

- Development of single nucleotide polymorphism (SNP) markers for use in commercial maize (*Zea mays L.*) germplasm. Jones, E., Chu, W. C., Ayele, M., Ho, J., Bruggeman, E., Yourstone, K., ... & Smith, S. (2009). Molecular Breeding, 24(2), 165-176.
- Mining for single nucleotide polymorphisms and insertions/ deletions in maize expressed sequence tag data. Batley, J., Barker, G., O'Sullivan, H., Edwards, K. J., & Edwards, D. (2003). Plant physiology, 132(1), 84-91.
- Genetic gains in grain yield through genomic selection in eight bi-parental maize populations under drought stress. Beyene, Y., Semagn, K., Mugo, S., Tarekegne, A., Babu, R., Meisel, B., ... & Crossa, J. (2015). Crop Science, 55(1), 154-163.
- 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., ... & Warburton, M. L. (2015). Crop Science, 55(1), 1-11.

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