

High-throughput genotyping of barley for variety identification

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Barley is a genotypically variable species and correct identification of barley varieties is vital for quality assurance of goods requiring different grain attributes. For example, the malting and brewing performance of barley is variety dependent, thus sourcing the correct variety is critical to product consistency. In order to facilitate rapid, high throughput identification of barley varieties, we have developed an assay capable of determining variety identity and purity with precision and speed. A comprehensive collection of Australian barley germplasm was established and molecular markers (SNPs) specific to each variety were identified. We used MALDI-TOF mass spectrometry to identify the variety-specific SNP by determining the mass of the polymorphic nucleotide itself. Genotype calling was precise and coupled with the ability to multiplex up to 25 reactions per well on a 384-well plate in a fully automated process, MALDI-TOF mass spectrometry clearly has the potential to be a high-throughput genotyping method of choice.

Theme: High throughput genotyping

Oral paper

Presenter Profile:

Julie Pattemore is a PhD Candidate supported by GRDC and the Grain Foods CRC at the Centre for Plant Conservation Genetics, Southern Cross University. Julie is developing nanotechnology-based high throughput genotyping platforms for variety identification.

