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Sequenom MassARRAY® iPLEX™ Gold SNP genotyping for high throughput variety identification

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Sequenom® MassARRAY® iPLEX™ Gold SNP genotyping for high throughput variety identification

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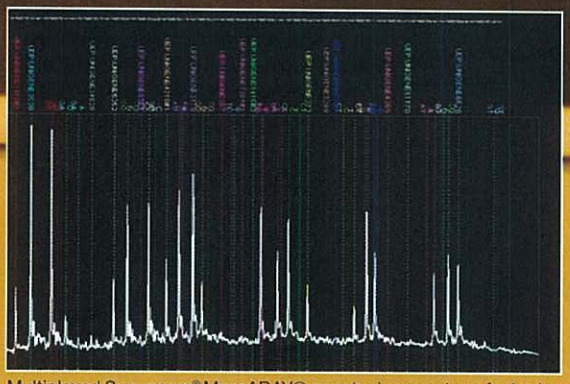


Multiplexed Sequenom® MassARRAY® genotyping spectrum for barley variety Schooner.

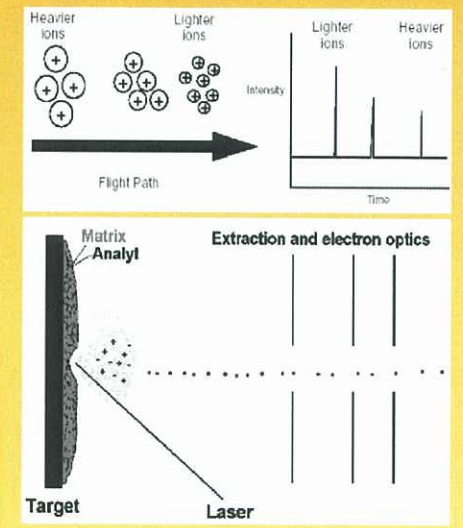
We used Sequenom® MassARRAY® iPLEX™ Gold genotyping assay to develop a multiplexed variety identification assay for the Australian barley industry.

Correct identification and traceability of barley varieties is a prominent issue for quality assurance throughout the entire barley production supply chain in Australia and worldwide.

Malting characteristics are variety dependent thus sourcing approved varieties which are uncontaminated with other malting or feed varieties is vital to product consistency. Fast, robust variety identification requires a stable marker that is not influenced by environment, and a platform which is capable of high throughput genotyping. In order to facilitate rapid, high throughput identification of barley varieties, we have developed a multiplexed SNP genotyping assay capable of determining the identity of each of 60 Australian barley varieties with precision and speed. Sequenom® MassARRAY® and iPLEX™ Gold genotyping was precise and a unique SNP barcode of up to 20 SNPs was produced for each variety. Coupled with the ability to multiplex up to 36 reactions per well on a 384-well plate in a fully automated process, this method clearly has the potential to be a high-throughput barley variety identification and purity testing method of choice.

	Assay											
Variety	1	2	3	4	5	6	7	8	9	10	11	12
Doolup	T	T	G	C	C	T	C	*	A	C	T	C
Capstan	T	T	G	C	C	T	C	G	G	C	T	C
Skiff	C	T	G	C	C	C	C	G	A	C	C	C
Unicorn	C	T	G	C	*	C	C	T	A	A	C	C
Baudin	*	T	G	C	C	T	G	T	A	C	C	C
Dash	*	T	A	G	C	T	G	*	A	C	C	G
O'Connor	T	C	G	C	C	T	G	*	A	C	T	C
Onslow	T	C	G	C	*	C	G	T	A	A	T	C
Sloop	T	C	G	C	C	C	G	*	A	A	T	C
Windich	T	C	G	C	C	T	*	*	A	C	T	C
Beecher	T	C	G	G	*	T	G	*	A	A	T	G
Bulocke	T	T	A	C	C	T	C	*	G	A	T	C
Yagan	T	T	G	G	C	T	G	T	A	A	T	G
Keel	T	T	G	G	C	C	C	*	A	A	T	G
Mundah	T	T	G	G	*	T	G	T	A	A	T	G
Hamelin	T	T	G	C	*	T	G	G	A	C	T	C
Stirling	T	T	G	C	C	C	G	T	A	C	T	C
Gairdner	T	T	G	C	C	T	*	*	A	C	T	C
Fitzgerald	T	T	G	C	*	T	G	T	A	C	T	C
Chebec	T	T	G	C	*	C	G	G	A	C	T	C
Molloy	T	T	G	C	C	T	*	*	A	A	T	C
Ketch	T	T	G	C	C	T	G	*	A	C	T	C
Harrington	T	T	G	C	C	T	G	G	A	C	T	C

SNP genotypes from a number of loci are pooled into unique "SNP barcode" for each barley variety.



Principle of MALDI-TOF mass spectrometry. The sample is embedded in a matrix then bombarded with a laser, which ionises the sample and releases the ions from the matrix into the flight tube. Here, the ions are sorted and separated according to their mass and charge in the time-of-flight analyser. The separated ions are then detected and tallied, and the results are shown as spectral peaks.

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