New plant breeding strategies using an affordable and effective whole-genome profiling method.
Eric Huttner, Vanessa Caig, Jason Carling, Margaret Evers, Neil Howes, Grzegorz Uszynski, Peter Wenzl, Ling Xia, Shiying Yang, Ange-Marie Risterucci and Andrzej Kilian

Molecular technologies, both transgenesis (GM) and molecular markers, have been most successfully applied to plant breeding when dealing with a small number of genes, and with relatively simple traits. To meet the ongoing challenge of increasing food production in a more sustainable manner, we have to increase the effectiveness and speed of classical plant breeding. Many important traits are complex: they are often multigenic, involve interacting loci and genes, and may be subject to epigenetic variation. Affordable and effective molecular markers covering the whole genome will play a major role in improving crops for these complex traits.
Over the past 6 years we have developed Diversity Arrays Technology (DArT, www.DiversityArrays.com) to provide whole-genome profiles to plant breeders. The technology is now available for 18 plant species, including orphan crops for which no molecular information is available. We will present the current status of DArT and review two application case studies. For wheat, a major crop for developing and developed countries, a DArT-based whole-genome profiling service has been available for more than a year (www.Triticarte.com.au). It has served scientists in 7 different countries and has been applied to building genetic maps, identifying QTL and managing germplasm collections. In banana, an orphan crop, critical for subsistence farmers in many developing countries, DArT was established in 3 months at the end of 2005. More than 1000 polymorphic markers are now available. They will accelerate the mapping of genomic regions of agronomic importance and clarify genetic and epigenetic diversity in the plantains, a group with high phenotypic diversity but probably of oligo or monoclonal origin. For genomics studies, the markers will assist in ordering BAC libraries, anchoring genetic and physical maps and identify methylation polymorphisms.