

Iain Wilson (Breeding & Applied Genomics)

I have worked in plant molecular biology for over 17 years, spanning basic research in the model plant *Arabidopsis*, through to more applied areas of genetics and genomics in cotton. I was involved with the development and first applications of printed cDNA microarrays for genome-wide gene expression analysis in cotton. My research has focused on plant responses to abiotic (mainly low oxygen responses during waterlogging) and biotic stresses (from fungal pathogens), and for the last 7 years has been in the identification and genetic characterisation of cotton germplasm with tolerance to fungal and viral diseases, SNP marker discovery, QTL analyses and the application of marker assisted selection into a world-renowned Australian cotton breeding program. Currently I am working on providing breeders with new genomic tools to aid in the selection of plants with superior yield and quality through genomic estimated breeding values derived from genome wide SNP genotyping.

As co-chair and future chair of the ICGI Breeding & Applied Genomics Workgroup, my interests lie in the translation of the growing wealth of cotton genomic resources into tangible knowledge and tools to help breeders improve cotton variety selection. I believe that pan-genomic DNA-level information in conjunction with low cost genotyping by sequencing provides a way forward in understanding and predicting complex heritable traits of central interest to all cotton breeders. It is clear that the next revolution in genomics will be in its direct application to commercial breeding outcomes across a multitude of crops and animals. Given the right genomic tools, cotton breeders will themselves be able to readily select cotton plants adapted to their local environment and with optimal yield and fiber quality traits that will ensure a vibrant global cotton industry into the future.