GWAS - where are we now?

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Farlow A (2014) *EMBnet.journal* **20**(Suppl A), e782. http://dx.doi.org/10.14806/ej.20.A.782

Genome-Wide Association Studies (GWAS) are a powerful tool for establishing correlation between phenotype and genotype. For the self-fertilising plant *Arabidopsis thaliana*, more than 1000 inbred lines have been 'fully sequenced', removing the cost of genotyping for a set of lines that can be phenotyped over and over. Does having full sequence make a difference? How important is sample size and line selection? The answers from *Arabidopsis* are that it is highly dependent on trait architecture and population structure. This offers an important insight into the fundamental advantages and limitation of GWAS.

I will also discuss how Next Generation Sequencing (NGS) data allows one to explore a number of 'genomic traits' such as genome size and centromere length, and how GWAS can be used to follow the fate of new centromeric repeats in the population.