***Travel Fund Report***

***Glasshouse Crop Research Institute Trust***

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8th International Rosaceae Genomics Conference, Angers 2016

The 8th International Rosaceae Genomics Conference (RGC8) held in France this year brought together researchers and breeders with the common goal of deciphering the genetics of Rosaceous crops. The conference covered a broad range of topics including cross-disciplinary research on flower initiation, plant development, fruit quality, and abiotic and biotic stresses alongside descriptions of domestication, evolutionary genetics and marker development in Rosaceous plants.

As a molecular breeder, I found four of the presentations during the conference particularly noteworthy. The first described an effective strategy for the selection of desirable breeding material, whereas the second presentation provided an excellent example of fundamental research conducted on a model organism translating into applied science. The final two talks demonstrated the use of two non-conventional methods used to unravel causative mechanisms behind desirable crop traits.

One particular highlight of the conference was the presentation by Luis Osorio, reporting on the successful integration of genomic selection (GS) into the Florida strawberry-breeding program. Desirable strawberry (*Fragaria x ananassa*) parents were selected using predictive models for traits including high fruit quality and total marketable yield. After compatible crosses were undertaken, progeny were phenotyped and the resulting data determined that prediction accuracy was greater than 60 % for all traits of interest, with the highest genetic gain observed in the average weight of fruit. Prior to the incorporation of GS into the breeding program, two successive selection trials were required before the incorporation of material into advanced selection lines. However, the integration of GS has allowed a single seedling selection trial to be conducted for each cohort, speeding up selection by a year. The successful integration of GS into the Florida strawberry-breeding program acts as strong promotion for incorporating this strategy into breeding programs.

Fundamental science can underpin an applied technical question. An elegant example of this can be seen in the presentation given by Chris Dardick on the molecular basis behind Peach (*Prunus persica*) tree architecture. Dardick’s study identified the alleles responsible for both the columnar and weeping phenotypes of tree architecture. This research used branching mutants in the model weed species *Arabidopsis thaliana* to identify conserved genes modulating branching in both species. Such a discovery can directly assist the molecular guided optimization of tree shape, leading to a reduction in labor cost associated with tree management.

A multitude of studies were presented on the conventional strategies used to identify quantitative trait loci associated with desirable alleles through the development of linkage maps and mapping. In contrast, alternative strategies for trait loci identification were presented and may be used to support more traditional methods. The most notable example was seen in the use of comparative transcriptomics to identify genes associated with resistance to plant pathogens. Larisa Garkava-Gustavsson presented an RNA sequencing study, which investigated Apple (*Malus x domestica*) gene expression after inoculation with apple canker (*Neonectria ditissima*). Differentially expressed transcripts were identified between resistant and susceptible cultivars at multiple time points post infection. The researchers identified that resistance is associated with specific gene ontology terms, indicating that the resistance mechanism prolongs the restriction of the fungus to extracellular regions.

Further to this, Etienne Buchner described another method that may be used to unravel causative genetic mechanisms behind desirable Apple fruit traits; namely, through the creation of double haploid individuals. Comparative analysis of methylation and transcripts in double haploid apples allowed the study of the epigenetic impacts on the expression of genes controlling fruit size in apple. Buchner highlighted the potential uses of these two techniques in studying the causative mechanisms behind clonal variation. Both apple and strawberry are clonally propagated and so can serve as an excellent model species to study the stability of clonal variation through sexual and asexual propagation.

The conference promoted the Field Book application developed to assist data collection through the use of android tablets. Exposure to this information has led to the embracement of recording technology within the field and thus the optimization of recording of data. The improved phenotyping processes has led to greater reliability and reduced time requirements. The Genome Database for Rosaceae (GDR) promoted the database storage provision: Breeding Information Management System, a storage method that links into Field Book and allows sharing of data.

After the congress closed, members were invited to tour around the International Fruit Obtention Seedling production systems. We toured apple-breeding programs for white and red-fleshed apples and observed large-scale evaluation plots for apple rootstocks. Of particular note, was the primary screening of seedlings for scab and subsequent removal of all susceptible seedlings from the crossing program.

The RGC8 provided a diverse and stimulating platform for researchers and breeders looking to exchange knowledge on the most recent discoveries in Rosaceous crop research. The horticultural industry can benefit in many ways from the information conveyed at the conference. Embracing the improvements in several areas including optimizing phenotyping, genomic selection in breeding programs and implementing alternative strategies for allele identification can enhance research strategies. Furthermore, the knowledge assimilated at the RGC8 conference will directly support the research undertaken within NIAB- EMR, the primary UK research institute for soft and top fruit Rosaceae research.