Conference: 12th Rosaceae Genomic Conference (RGC12)

Name: Deborah Babalola, PhD candidate, NIAB/University of Reading, UK

Location: Eden Roc hotel, Sant Feliu de Guíxols, Spain

Date: 6-9 May 2025

Travel Grant: GCRI Trust

1. **Background:**

The Rosaceae Genomics Conference is a biennial scientific meeting that dates back to 2003 and provides a communication hub for Rosaceae researchers. Over time, including this year's meeting, it has enabled the development of new collaborative research projects, allowing scientists to focus on cross-species investigations and interdisciplinary approaches. RGC12 brought together over 200 leading researchers, breeders, bioinformaticians, industry representatives, and PhD students from countries around the world, who presented and discussed recent advances in the genetics and genomics of Rosaceae species. Presentations covered comparative, functional, and structural genomics of Rosaceae, showcasing how genomic research is conducted, interpreted, and applied across economically important species, including apple, peach, strawberry, raspberry, almond, and their wild relatives. Invited talks from researchers in other areas (e.g., blueberries) showcased trends and successes in their respective fields.

During the inaugural session, Maria José Aranzana's (Head of Genomics and Biotechnology at IRTA, Spain) opening keynote presentation, highlighted the major shifts in Rosaceae genomics in the last decade and emphasised the significant improvements to current knowledge arising from the development of pangenomes, taking the Rosaceae genomics beyond single references for economically important Rosaceae species.

Presentations during RGC12 were categorized into five topics and nine sessions:

1. Genomes, pangenomes, genome variability, and crop evolution (Sessions I&II)
2. Genomics of biotic and abiotic stresses (Sessions I&II)
3. Genomics of flower, phenology, architecture, and other traits

4. Genomics and phenomics-informed breeding and new breeding tools (Sessions I&II)
5. Genomics of fruit and nut quality and other traits (Sessions I&II)

Among these topics, pangenome research stood out as a transformative tool for unravelling the genetic diversity among cultivated varieties and wild relatives of Rosaceae species, and for better understanding genome evolution and reorganisations, especially in highly heterozygous crops, moving away from reliance on single reference genomes. Pangenomics is providing a more comprehensive framework to capture and elucidate the effect of copy number variations (CNV), gene presence-absence variation (PAV), and transposable elements (TE), which can be significant for understanding evolutionary adaptation and novel alleles of importance to growers, consumers, and other stakeholders. The assembly of high-contiguity genomes across multiple cultivars and their wild relatives has been very helpful for pangenome analysis and is facilitated by the evolution of sequencing technologies and a shift towards long-read sequencing.

2. Key messages from the Conference:

i. Pangenomics is redefining Rosaceae genomics research, expediting breeding and trait discovery

Novel and more affordable sequencing technologies are enabling the development of high-quality whole-genome assemblies for multiple cultivars of crop species and their wild relatives, thereby providing researchers with additional resources to work with. The pangenomic approach addresses the limitations of single reference genomes by capturing a much wider representation of the full genetic diversity within and across species, improving our understanding of the genetic control of key agronomic traits, especially in highly heterozygous species such as apples and raspberries. Pangenomics enables more precise trait mapping and helps uncover variations, such as large indels and structural variations, that have significant effects on phenotypes but are often missed by SNP-based approaches. Efforts should be directed at leveraging the various ways genomic insights can be translated into practical tools for marker-assisted breeding of improved cultivars. Overall, the timeframe for developing new and more robust crop varieties will become shorter than when these resources were scarce. Breeders are starting to utilise pangenome-informed markers in genomic selection models.

ii. **Multidisciplinary/collaborative approach to crop improvement:**

The establishment and continued support of research groups, as well as a coordinated Rosaceae network, can significantly impact the time to variety release through interdisciplinary research collaboration, data sharing, and standardization. The use of imaging technology and machine learning approaches is becoming commonplace.

iii. **Multi-omics data integration:**

Combining genomic, transcriptomic, and epigenomic results can facilitate significant discoveries and help elucidate the control and expression of complex traits. Therefore, researchers are working towards building pantranscriptomes for a more refined representation of gene expression variations and considering pan-epigenomes to help link structural variations to gene expression and phenotype.

iv. **Bottlenecks to fully utilizing opportunities provided by the omics approach can be addressed through capacity building.**

Although there have been major advances, the assembly and analysis of polyploid genomes and highly heterozygous genomes still require improved tools and tailored pipelines. Investment in the development of these invaluable resources for genomic analysis (e.g., computational tools) and training of researchers (especially early-career researchers) is essential to addressing these challenges.

v. **Gene/genome-edited crops**

While various regulatory measures are continually rolled out and differ across countries, it is essential for breeders to ensure the safety of the cultivars they develop as they strive to meet the demands of the horticulture or food industry using biotechnologies such as the CRISPR-Cas system.

3. Advancements in Rosaceae Pangenomes

The opening keynote by Professor Zhangjun Fei of Boyce Thompson Institute for Plant Research showcased the team’s work on haplotype-resolved genome assemblies of apples and roses, as well as the pangenome analyses of wild and domesticated apples. The comprehensive pangenome analysis aids deeper insights into crop origin, domestication, genetic diversity, and functional variation. Sequencing and analysing multiple rose varieties provided a useful resource for comparative and evolutionary genomic studies, which will advance breeding efforts and help to identify novel genes and alleles associated with important agronomic traits, including double flowering and disease resistance. Similarly, Marinus Smulders from Wageningen University presented a genus-level pangenome constructed from the high-quality genomes of R. sericea and Rosa rugosa, alongside publicly available genomes, which differentiated between wild roses and cultivated roses based on their gene content and transposable elements. Sharing his results, Yong Li (Institute of Chinese Academy of Agricultural Sciences, Zhengzhou, Henan) highlighted the genetic gains achieved during domestication and improvement, as revealed by pangenome analysis of 1,020 peach accessions.

Multiple presentations emphasized the shift toward long-read sequencing, enabling the production of high-contiguity genomes across cultivars and their wild relatives. Notably, the conference showcased multiple recently completed, high-quality genomes, pangenome analysis pipelines, and analyses using both published and newly assembled genomes.

4. Plant Breeding Applications: Trait discovery, Genome editing, Evolutionary genomics, and Germplasm conservation

Genomics has played an integral role in how crops are developed in modern plant breeding programs to meet the demands of climate resilience, food security, and sustainable agriculture. The conference featured several studies demonstrating how pangenomes and other novel genomic approaches can enhance trait mapping, including traits that are missed by linear reference-based approaches, as well as an improved understanding of evolutionary pathways. Genomics-assisted breeding using key approaches, including molecular markers, Genotype-by-Sequencing (GbS), Genome-Wide association Studies (GWAS), Quantitative Trait loci (QTL) mapping, Genomic Selection (GS), Pangenome-guided selection, epigenomics, and transcriptomics, was showcased during the conference to have enhanced the various trait discovery and overall crop improvement in the Rosacea family.

Apparently, genomics is becoming an integral component of every modern breeding program as sequencing is becoming more affordable, and bioinformatics is becoming more powerful. The UK Department for Environment, Food & Rural Affairs (Defra)'s establishment of a supportive framework and providing useful resources to support soft fruit breeding through the Genetic Improvement Network (GIN) platform is a crucial step in advancing soft fruit breeding. As presented by Felicidad Fernandez, the platform will enhance breeding efforts for multiple berry crops, including the development of tools for molecular selection.

An interesting presentation by Professor Patricio R. Muñoz del Valle provided insights into the University of Florida's blueberry breeding program activities over a six-year period. While acknowledging the effectiveness of traditional breeding, the program is leveraging advances in genomics to help address the time to varietal release, which is often a bottleneck in traditional breeding methods. With consumers' preferences at the centre of decision-making, integrating genomics tools has enhanced the decision-making process for crosses to be made and what to carry forward in the breeding pipeline, while narrowing down to improved marketable varieties. He highlighted logistics in the breeding stages as a very (*most*) effective factor in increasing the time to varietal release, and this is enhanced by integrating genomic tools.

In a presentation that is of particular interest to me as it offers useful information related to my research, Dr. Mohammed Bendahmane of INRAe talked on how the researchers at the institute have employed genomics, including high-quality genome assemblies, in understanding how floral organs initiate on the meristem during flower bud development, determining their copy number, and how colour pigments are produced. The team identified key genes involved, including those related to double flowering, how a miR172-resistant RcAP2L variant controls AGAMOUS expression, and that a knockdown of the AP2 gene (through mutation) reverses double to simple flowering in roses. In another study that provided further insights into evolution, the team fine-mapped the *prickleless* locus and identified a gene (LOG) associated with prickle formation in *Solanum,* revealing the independent mutations associated with prickle loss in cultivated and wild Solanum species. These mutations were identified in other plants, including roses.

During the poster session 2, I had the opportunity to share my research on the genetics of primocane-fruiting raspberries with interested participants, including those who had worked or are working on flower initiation in Rosaceae species. Most of the discussions centred on phenotyping the complex primocane fruiting habit in raspberry and ordering candidate genes with flowering-related roles identified from my QTL mapping. It was pleasant to learn about another recently assembled high-quality reference genome of the cultivar 'Wake®Field' from the New Zealand Institute for Plant and Food Research Ltd. The team, which also has a research focus on understanding the genetic regulation of annual fruiting in raspberries, shared their preliminary results and is employing a multi-omics approach.

New genomic techniques (NGTs), including the CRISPR-Cas system, are transforming plant breeding by enabling precise and more efficient modification of the plant genome. Although these technologies are promising for improving yield and other important end-user characteristics, their adoption and commercialisation are influenced by national and international regulatory frameworks with regulations that differ across countries based on varying definitions, approval processes, and risk assessments, which are not purely science-driven. Presenters, including those from the UK, shared their findings on the application of these techniques to understanding traits such as the everbearing trait in strawberry and the DNA-free CRISPR genome editing in raspberry.

Dr Agnes Ricroch from AgroParisTech, France, talked about the current status of the regulation of the new genomic techniques (NGT), including the CRISPR-Cas system and their applications for crop genome editing in various countries, including the EU proposal on *New Genomic Techniques and Plant Reproductive Material*, specifying the different regulations for 'category 1 NGT plants' (conventional-like with targeted mutagenesis and cisgenesis) and 'category 2 NGT plants' (transgenic-like). Overall, emphasis was laid on ensuring safety and transparency while making efforts to impact agriculture and food security.

A session during RGC12 featured researchers extensively discussing genomics service providers, comparing data output types and costs.

Conference conclusion and future directions

The central role of pangenomics in understanding complex traits, guiding marker-assisted breeding, gene mining from wild relatives, and conserving genetic resources was evident from the presentations and discussions during the 12th Rosaceae Genomics conference. The major considerations for future directions are:

1. Unlocking a more dynamic and deeper understanding of genome diversity across the Rosaceae family, laying the foundation for developing resilient, high-quality, and consumer-preferred cultivars, pangenome assemblies need to be expanded to include wild species, landraces, and underutilized cultivars.
2. There is a need to develop reproducible pipelines for pangenome analysis in polyploids and highly heterozygous members of the Rosaceae family and move towards graph-based references for QTL mapping and genome-wide association studies (GWAS).
3. The (informal) collaborative network of researchers in Rosaceae genomics has produced many successful outcomes and needs to continue to build relationships between a new generation of researchers.

Overall, many thanks to the organizing committee of the Rosaceae Genomics Conference 2025. I want to thank the GCRI Trust for providing the financial support that enabled me to attend this conference.