GENETIC VARIABILITY IN MELON RESEQUENCED VARIETIES

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The recent completion of the Melon (Cucumis melo) reference genome sequence opens the possibility of cataloguing sequence variations between individuals, and identifying these as well as understanding their biological impact has become one of our major research goals. Resequencing the genome of several individuals for which there is a reference genome permits the investigation of relationships between sequence variation, specific biological processes and phenotypes.

In this study seven melon accessions, coming from both melo (cultivated) and agrestis (wild) subspecies, have been resequenced to a 20X coverage and mapped to the reference genome, allowing the wide-scale identification of short and large structural variations.

Three different bioinformatics pipelines have been established in order to characterize SNPs, DIPs, Large InDELs, CNVs and transposon movements.

In summary, global comparisons of the polymorphisms between resequenced lines show the same order of magnitude for SNPs and indels for all the lines, however when we consider large structural variations we see a different trend, with the melo subspecies displaying a full order of magnitude less variations than the agrestis lines. Variations have been associated with gene and transposon annotations as well as with important metabolic pathways and highlight differences in domesticated and wild characters. A subset of the in silico results have been tested by different wet lab experiments, confirming our predictions and aiding in validating this global view of the variations within the melon family.