Genome wide associations for metabolic traits in tomato

Guillaume Bauchet, S. Grenier, N. Samson, J. Bonnet, L. Grivet, E. Bolygo, C. Baxter, Mathilde M. Causse

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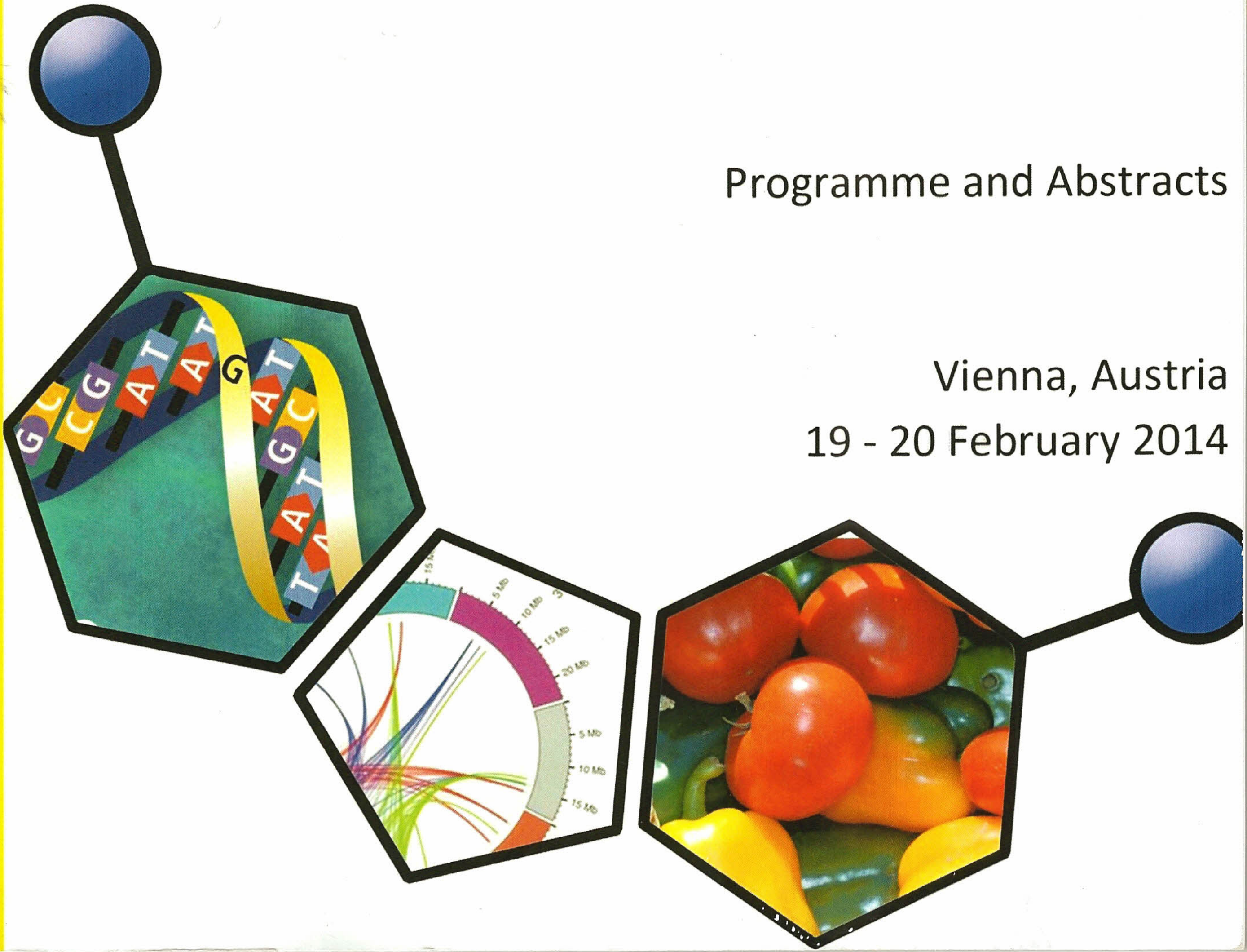

Programme and Abstracts

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N 4. Genome Wide Associations for Metabolic Traits in Tomato

G. Bauchet [1, 2], S. Grenier [2], N. Samson [2], J. Bonnet [2], L. Grivet [2], E. Bolygo [3], C. Baxter [3], M. Causse [1]

[1] INRA GAFL, Montfavet, France, [2] Syngenta Seeds, 12 chemin de l'hobit, Saint-Sauveur, France, [3] Syngenta, Jealott's Hill, Bracknell, Berkshire, United Kingdom

Modern breeding has impacted fruit composition, inducing low volatile content and therefore low organoleptic quality. Genome-wide association studies (GWAS) have been successful in identifying genes involved in polygenic traits notably in tomato, and can be used for crop improvement. We used an association panel including 70 wild relative (S. pimpinellifollium), 170 admixed (S.l. cerasiforme) and 50 domesticated (S. lycopersicum) accessions, to perform GWAS with 12000 SNPs and a set of metabolic traits including a range of volatile compounds. We found significant associations for 84 loci with a total of 17 traits. Identified loci were consistent with QTL previously discovered (for guaiacol and sugars), while new loci were identified (for example for phenylacetaldehyde). These results present (1) a list of candidate loci to be validated and (2) a powerful analytical approach for finding genetic variants to be used for crop improvement and deciphering the genetic architecture of complex traits.