

P66 – The diversity of condensed tannins in domesticated grapevine associates with an unsettled multicopy F3'5'H region on Chr6 that expanded before the allopatric speciation of the *Vitis* genus

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Abstract

Condensed tannins or proanthocyanidins (PA) are key players in oenology as they determine the colloidal stability, oxydo-reduction activity and astringency in the wine. It can therefore be hypothesized that their composition underwent selection during both domestication and modern breeding. An international network recently presented a vast phenotyping campaign on condensed tannins in the family of Vitaceae (ca 600 accessions) with emphasis on the *Vitis* genus. We therefore confirmed that the respective abundances of di, and trihydroxylated catechins as constitutive monomers in PA may vary strongly not only in this plant family but also within the *Vitis* genus (submitted).

In the present work, to investigate the impact of domestication on PA features, the diversity of PA composition was characterized throughout a representative set of more than 500 wild or domestic cultivated *V. vinifera* genotypes. This was made possible by the collaboration of a number of international partners and the contribution of the Vassal-Montpellier Grapevine Biological Resource Center (INRAE, France).

We found more EGC+EGCG in *V. sylvestris* as compared to *V. vinifera*, and globally more diversity in the East as compared to the West. For this trait, some old traditional cultivars could not be distinguished from *V. v. subsp. sylvestris*, suggesting the trihydroxylation ratio could have been counter-selected for oenological and taste reasons.

A GWAS approach was then conducted in cultivated grapevine, between these phenotypic data and 10k SNPs scattered along its genome. SNP flanking the multicopy Flavonoid 3'5' hydroxylase (F35H) region of Chr6 previously documented by Falginella et al. (2010) appeared significantly associated with the relative enrichment of condensed tannins in epigallocatechin subunits. Public DNA sequences based on long-range techniques allowed to compare the F35H copy number in this region among genotypes, together with its content in transposable elements. As it is notoriously difficult to place SNPs in such regions, present results highlight the interest in long-range sequencing to explore the impact of structural variants on the phenotype.

Keywords: Vitaceae, *Vitis vinifera*, tannin, proanthocyanidin subunits composition, domestication, genetics, diversity