



Impact of the ‘Pinot’-family on early ripening in cool climate viticulture varieties

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Abstract (250 words)

‘Pinot Precoce Noir’ (PPN) is an early ripening clone of ‘Pinot Noir’ (PN). The phenological differentiation is visible by an about two weeks earlier onset of veraison. It was found that the early veraison locus *Ver1* on chromosome 16, previously identified in ‘Calardis Musqué’, originated from PPN. A highly correlated SSR marker, namely GF16-*Ver1*, was developed and tested for its ability to molecularly differentiate between PPN and PN as well as its potential to trace individual descendants. GF16-*Ver1* shows a 2bp difference in fragment size, which is sufficiently descriptive to discriminate between the original PN allele and the mutant *Ver1* allele of PPN associated to early veraison. All screened cultivars showing the specific fragment sizes of the veraison affecting PN or PPN allele, appeared to be related to the Pinot family, demonstrating its unique character. Grouping of cultivars based on the fragment length of GF16-*Ver1* matched with known pedigrees and allowed a reliable allocation of entire family trees to their respective PN or PPN founder. Additionally, grouping of cultivars by the GF16-*Ver1* marker demonstrated the phenological significance and descriptive value. The marker enables an easy screening of genetic resources and breeding material using established SSR-based marker-assisted selection pipelines. The use of GF16-*Ver1* will help breeders to adapt their breeding programs for cool-climate viticulture to the challenges of climate change through counter-selection of *Ver1*. It will also help to elucidate all early ripening PPN descendants on a genetic basis and demonstrate the high relevance of this locus in current cool-climate varieties.

Keywords: climate change, cool climate viticulture, marker development, Frühburgunder. Spätburgunder