Genetic mapping of organic acids in a F1 white wine population with high variation in acidity and maturity date

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Abstract

A balanced level of organic acids is of high relevance for wine production. New grapevine cultivars need acidity levels adjusted for the different growing regions and within a proper range to cushion the annual variations, especially under cool climate viticultural conditions as well as in the context of global warming. Organic acids protect berries from spoilage in the vineyard, stabilize the vinification process and play an important role in sensory perception of wines. The development of reliable molecular markers for organic acids to be used in marker-assisted selection (MAS) would increase breeding efficiency by early negative selection of poorly perfoming genotypes. Marker development needs a detailed long-term data acquisition to estimate the environmental factors. A white wine F1 population ‘Calardis Musqué’ x ‘Villard Blanc’ differing in acidity levels and ripening was investigated over ten years. The acidity profile was recorded by FTIR analysis between veraison and harvest under cool climate field conditions at Geilweilerhof (Palatinate, Germany). Genetic mapping of haplotype-based markers (HBMs) extracted from a genotyping-by-sequencing (GBS) approach resulted in a high-density genetic map with 2,260 mainly full-informative markers for QTL analysis. Investigated traits include total acidity, tartaric and malic acid levels as well as pH. Tartaric and malic acid are the two most important organic acids in grapes with major impact on acidity perception in wines. Best linear unbiased predictors (BLUP) were calculated over ten-year-data for maturity date. Major QTLs for total acidity were identified on chromosomes 4 and 14 explaining each 22 % of the variance when veraison was taken into account as covariant. Both loci are co-located with major malic acid QTLs having comparable values. The most pronounced tartaric acid QTLs were identified on chromosomes 7 and 13 (19 % and 18% of explained variance). They are co-located with QTLs for pH value. Thanks to a long examination period and a high-density genetic map, it is now possible to reliably identify functional genomic regions influencing acidity. This provides new insights and opens up new possibilites to increase efficiency in grapevine breeding by early selection for stable acidity level. This will lead to new cultivars well adapted to future climate conditions and combining resistance to pathogens with high quality potential.

Keywords: wine quality, climate change, tartaric acid, malic acid, QTL mapping, metabolic quality potential, genetic quality potential, cool climate