



Analysis of phenology and ripening quality traits in segregating populations derived by crossing 'Corvina' with divergent varieties

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Introduction

Adaptation of varieties to changing climatic conditions is a major breeding target, which includes the selection of late ripening varieties/clones, whose bunches may escape the warmer summer condition by postponing the ripening period. However, assessment of the genetic basis of phenology and quality related traits is a prerequisite to develop breeding programs for grapevine varieties adapted for the cultivation in specific viticultural areas and/or to identify the candidate genes for the new breeding technology approaches.

The present work reports a two-season evaluation of traits segregation in populations derived from crosses of the red skinned cv. Corvina, the principal local variety of the Valpolicella wine area (Verona, Italy), with other two cultivars: the white skinned cv. Solaris (cross: **CxS**), highly divergent from Corvina for the phenology and fruit ripening traits, and the red skinned cv. Cabernet Sauvignon (cross: **CSxC**), whose bunches shows distinctive ripening and post-ripening traits from Corvina.

Methods

142 CxS and **129 CSxC** seedlings from two crosses done in 2015/2016 at University of Verona were considered for phenotyping. Genetic relationships were validated by SSR for each seedling and each plant was propagated in two copies on SO4 rootstock and is grown at Società Agricola Vivai Gozzo in Verona under standard viticultural practices. During 2020-21 seasons the main phenological stages from budbreak to berry maturation were determined for each genotype in the two populations as well as several morphological and technological parameters at ripening. The data collected have been used to evaluate the distribution of each trait across the individuals in each population. Correlations and hierarchical clustering analyses have been performed for each trait between seasons, as well as across traits.

Results

Most of the phenological phases distributions had a normal trend.

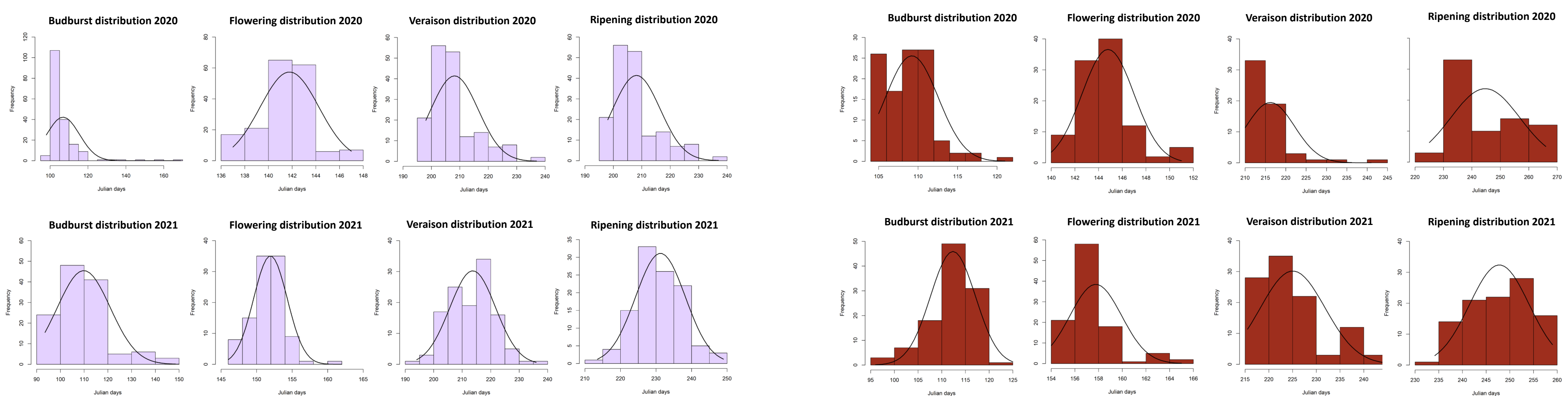


Figure 1. Distribution of phenological phases in the **CxS** (left panel) and **CSxC** (right panel) populations determined during 2020-21 seasons. Bin width was determined by Scott method. Curved line represents the probability density function for the normal distribution given the mean and sd of each parameter.

The clustering algorithm positions adjacently most of parameters measured in the two consecutive years. Notably, a rapid dehydration test (WL_simulation) applied on CSxC grape clusters is positively correlated with the polyphenolic content.

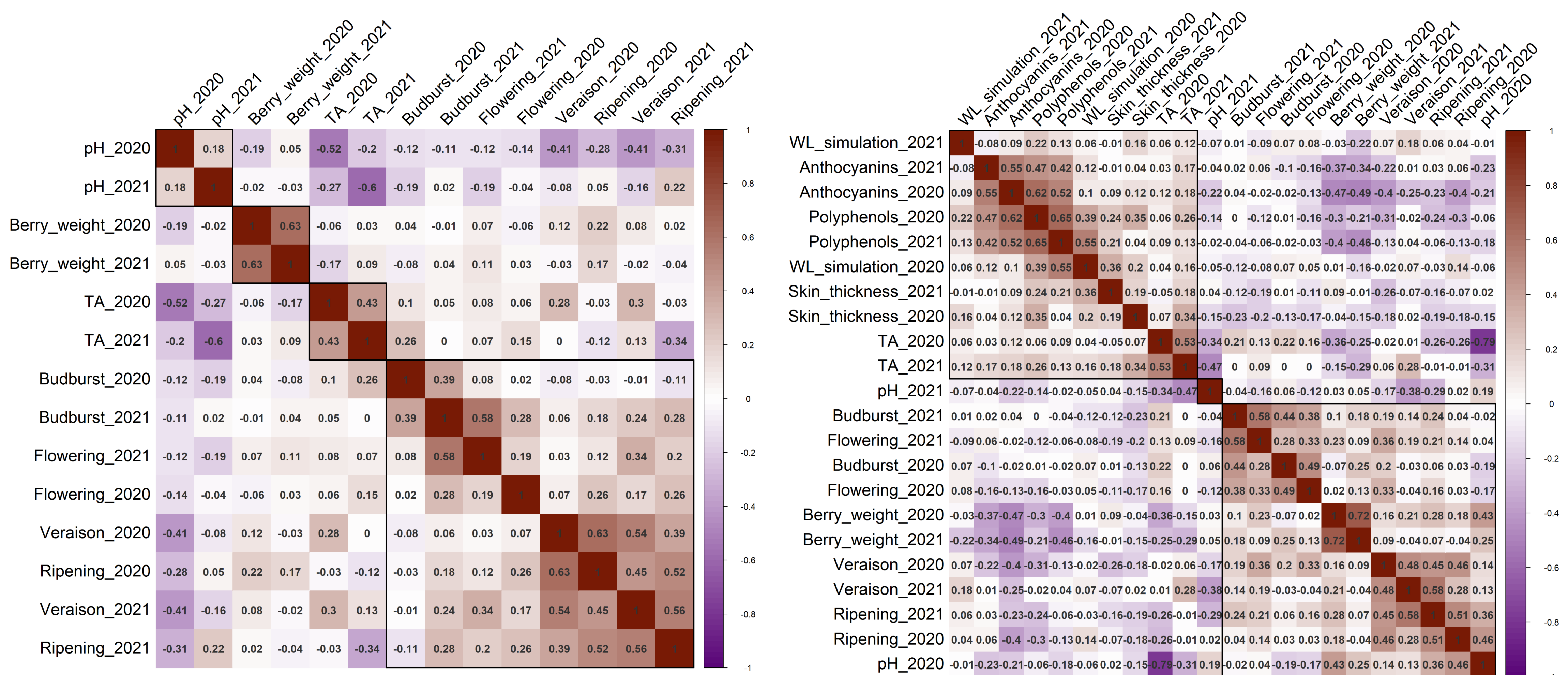


Figure 2. Spearman correlation coefficient matrix of the parameters measured in the **CxS** population (left panel) and **CSxC** population (right panel) during 2020-21 seasons. Hierarchical cluster analyze was applied on the measured parameters using average as clustering algorithm.

Conclusions

The comprehensive information obtained will be used for QTL mapping. The identification of genetic markers associated with the studied traits will help accelerating the selection of new cultivars more adapted to the changing climatic conditions. Altogether, the described approaches will finally allow to improve our current understanding of the genetic control of phenology and berry quality traits in grape, thus helping and assisting breeding.