

# Integration Of Meta-QTL Analysis With Transcriptomic Data Identifies Candidate-Genes Controlling Veraison Time In Grapevine

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## Introduction

In grapevine, the genetic and molecular knowledge of phenology-related processes like flowering, veraison and ripening is a key step towards the breeding of varieties that are adapted to a world affected by severe climate change. Different quantitative trait loci (QTL) studies are available in literature attempting the dissection of the genetic control of phenology-related traits. However, the identified genomic regions often span very large portions of the genome where thousands of candidate-genes are present. Transcriptomic studies have identified different sets of genes modulated along ripening, including direct regulators (switch) and indirectly modulated genes (Palumbo et al., 2014). Also in this case, the number of genes is still too large for a functional characterization.



Figure 1. Marzemino cultivar during veraison.

## Aims

With the aim of identifying among this big number the most promising candidate-genes involved in the regulation of grapevine phenology, we developed a candidate-gene prioritization strategy based on two steps. In the first step we performed a meta-QTL analysis in order to narrow down the QTL intervals available in literature obtained from studies investigating the traits flowering, veraison and ripening. In the second step we checked the co-localization of genes identified from transcriptomic studies (Zenoni et al., 2010 and Fasoli et al., 2012) with the genes underlying the newly generated mQTLs. In this way, the number of candidate genes putatively modulating grapevine phenology was reduced by several orders of magnitude.

## Experimental procedure

### Step 1 – Meta-QTL analysis

- Grapevine genetic linkage maps were collected from literature
- The individual maps were integrated into a consensus map using Biomercator v4.2 (Arcade et al., 2004)
- Phenology-related QTLs were projected onto the consensus map
- Meta-QTL analysis was performed

### Step 2 – Transcriptomic data integration

- The grapevine consensus map was anchored to the grapevine genome
- Genes below the meta-QTLs intervals were identified
- Co-localization of the positional meta-QTL genes with transcriptional candidates was assessed

## Results

Table 1. List of all the genetic linkage maps used in the construction of the consensus map.

Reference	Cross Name	Pop Size	Mapped Loci	Map Length
Bon et al. 2014	Pinot Noir	228	214	931.4
Boysen et al. 2015	Pinot Noir	228	228	1,274.0
Bellin et al. 2009	Chardonnay	116	116	948 (Ch); 957 (B)
Roy et al. 2011	CS x RDA1995-1	138	132	1,274.0
Bon et al. 2011	V. amurensis x Ruprecht 51	232	130	975.0
Correia et al. 2006	RS x S	128	128	1,030.0
Correia et al. 2006	RS x S	78	235	1,144.0
Correia et al. 2012	RS x S	137	272	1,334.0
Correia et al. 2015	RS x S	137	272	1,334.0
Correia et al. 2016	RS x S	137	272	1,334.0
Costantini et al. 2008	RS x S	137	272	1,334.0
Costantini et al. 2010	RS x S	137	272	1,334.0
Costantini et al. 2012	RS x S	137	272	1,334.0
Costantini et al. 2014	RS x S	137	272	1,334.0
Costantini et al. 2016	RS x S	137	272	1,334.0
Costantini et al. 2018	RS x S	137	272	1,334.0
Costantini et al. 2020	RS x S	137	272	1,334.0
Costantini et al. 2022	RS x S	137	272	1,334.0
Costantini et al. 2024	RS x S	137	272	1,334.0
Costantini et al. 2026	RS x S	137	272	1,334.0
Costantini et al. 2028	RS x S	137	272	1,334.0
Costantini et al. 2030	RS x S	137	272	1,334.0
Costantini et al. 2032	RS x S	137	272	1,334.0
Costantini et al. 2034	RS x S	137	272	1,334.0
Costantini et al. 2036	RS x S	137	272	1,334.0
Costantini et al. 2038	RS x S	137	272	1,334.0
Costantini et al. 2040	RS x S	137	272	1,334.0
Costantini et al. 2042	RS x S	137	272	1,334.0
Costantini et al. 2044	RS x S	137	272	1,334.0
Costantini et al. 2046	RS x S	137	272	1,334.0
Costantini et al. 2048	RS x S	137	272	1,334.0
Costantini et al. 2050	RS x S	137	272	1,334.0
Costantini et al. 2052	RS x S	137	272	1,334.0
Costantini et al. 2054	RS x S	137	272	1,334.0
Costantini et al. 2056	RS x S	137	272	1,334.0
Costantini et al. 2058	RS x S	137	272	1,334.0
Costantini et al. 2060	RS x S	137	272	1,334.0
Costantini et al. 2062	RS x S	137	272	1,334.0
Costantini et al. 2064	RS x S	137	272	1,334.0
Costantini et al. 2066	RS x S	137	272	1,334.0
Costantini et al. 2068	RS x S	137	272	1,334.0
Costantini et al. 2070	RS x S	137	272	1,334.0
Costantini et al. 2072	RS x S	137	272	1,334.0
Costantini et al. 2074	RS x S	137	272	1,334.0
Costantini et al. 2076	RS x S	137	272	1,334.0
Costantini et al. 2078	RS x S	137	272	1,334.0
Costantini et al. 2080	RS x S	137	272	1,334.0
Costantini et al. 2082	RS x S	137	272	1,334.0
Costantini et al. 2084	RS x S	137	272	1,334.0
Costantini et al. 2086	RS x S	137	272	1,334.0
Costantini et al. 2088	RS x S	137	272	1,334.0
Costantini et al. 2090	RS x S	137	272	1,334.0
Costantini et al. 2092	RS x S	137	272	1,334.0
Costantini et al. 2094	RS x S	137	272	1,334.0
Costantini et al. 2096	RS x S	137	272	1,334.0
Costantini et al. 2098	RS x S	137	272	1,334.0
Costantini et al. 2100	RS x S	137	272	1,334.0
Costantini et al. 2102	RS x S	137	272	1,334.0
Costantini et al. 2104	RS x S	137	272	1,334.0
Costantini et al. 2106	RS x S	137	272	1,334.0
Costantini et al. 2108	RS x S	137	272	1,334.0
Costantini et al. 2110	RS x S	137	272	1,334.0
Costantini et al. 2112	RS x S	137	272	1,334.0
Costantini et al. 2114	RS x S	137	272	1,334.0
Costantini et al. 2116	RS x S	137	272	1,334.0
Costantini et al. 2118	RS x S	137	272	1,334.0
Costantini et al. 2120	RS x S	137	272	1,334.0
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Costantini et al. 2128	RS x S	137	272	1,334.0
Costantini et al. 2130	RS x S	137	272	1,334.0
Costantini et al. 2132	RS x S	137	272	1,334.0
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Costantini et al. 2142	RS x S	137	272	1,334.0
Costantini et al. 2144	RS x S	137	272	1,334.0
Costantini et al. 2146	RS x S	137	272	1,334.0
Costantini et al. 2148	RS x S	137	272	1,334.0
Costantini et al. 2150	RS x S	137	272	1,334.0
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