Mapping the Genetic Architecture of Grapevine Bud Dormancy and Chilling Fulfillment in Grapevine









Timing of dormancy induction and release are critical for sustainable grapevine production in changing climate.

Develop and use a genetic model system to identify key factors controlling

- Dormancy induction
- Chilling Fulfillment
- Budbreak timing
- Fall, winter and spring freeze tolerance





Genetic System

V. riparia

- Tolerates extreme low temperature
- Decreasing daylength induces dormancy and acclimation

Seyval

- Moderately freezing tolerant.
- Low temperature promotes dormancy.

F1 (16_9_2)

 Intermediate photoperiod and dormancy responses

F2 population

 Fruit quality, architecture, chilling fulfillment, sex, dormancy induction, freezing tolerance, fruit ripening period

Vitis riparia X Seyval

F1 population Screen for photoperiod induced dormancy (Fennell SDSU)





Phenotyping initiated prior to linkage map availability.

- 110 individuals placed in 2 field locations (SD and MN) and original vines in controlled environment.
- Photoperiod and low temperature response phenotypes measured in multiple years.
- Field conditions and controlled temperature and photoperiod conditions.



Decreasing photoperiod induces growth cessation and early dormancy promoting winter survival. F2 population segregates for photoperiod and dormancy induction responses.





Photoperiod Response QTLS identified on linkage groups 11, 12, 13 using SSR map (Garris et al. 2009)

Timing of dormancy induction influences timing of cold acclimation. F2 population segregates for acclimation responses.

Lethal bud freezing temperature determined by monitoring low temperature exotherm (LTE) using differential thermal analysis. (Mills et al., 2006).



Bud LTE measured in Nov., Dec., Jan. and Feb. in five dormant seasons.



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RESEARCH ARTICLE

Next Generation Mapping of Enological Traits in an F₂ Interspecific Grapevine Hybrid Family

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• F2 map generated with 1,449 GBS markers from 424 individuals

Publish

About

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- 2424 cM in genetic length
- Genome coverage 95%
- Average distance between markers of 1.67 cM
- Mapping protocol, YAN and malate metabolism QTLS & candidate genes

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Photoperiod response QTLs are identified in multiple years in field and controlled environment conditions.

Lateral growth cessation, tip abscission and dormancy induction QTLs explain 10 to 20% of phenotypic variation.

Trait	No. of individuals	Linkage Group	Position	LOD score	Phenotypic variation (R2)
Mean lateral cessation	87	12	60.115	3.90	17.97
Critical Photoperiod GH Mean	106	11	98.89	5.57	14.80
Mean lateral cessation	106	12	55.45	4.03	10.20
Mean tip abscission	106	11	98.890	4.17	14.70



Dormancy, chilling fulfillment and LTE QTLs on linkage groups 4, 11, 13 or 18 explain 12 to 25% of phenotypic variation.

Haplotypes associated with the QTLs indicate genotypes in common between critical photoperiod, growth cessation, and long term winter survival.

- AA V. riparia grandparent H – Heterozygote
- **BB** Seyval grandparent

Vine Winter Survival Score





Summary

- Multi-year dormancy and winter survival trait analyses identified multiple QTLs explaining 10 to 25% of phenotypic variation.
- Use of haplotype analysis provides ability to select individuals that have multiple desired traits for further breeding or functional analysis.
- F2 Population is being propagated and established in replicated planting to allow more rapid fruit, architecture and viticultural trait analyses.

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