***Supplementary Material***

**Of buds and bits: a meta-QTL study identifies stable QTL for berry quality and yield traits in cranberry mapping populations (*Vaccinium macrocarpon* Ait.)**

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# Supplementary Figures and Tables

## Supplementary Figures

## Supplementary Tables

Supplementary Table S1. Summary of traditional (upright and berry) and plot traits collected from cranberry (*Vaccinium macrocarpon* Ait*.*) populations *CNJ02* and *CNJ04* in years 2011-2014.

| **Traita** | **Abbvb** | **Description** |
| --- | --- | --- |
| **Berry Shape Chimera Parameters** |  |  |
| UMCC - X-axis\* | *UKUX*\* | log of Unsigned Manhattan Chain Code - X-axis. Larger values indicate more change in berry curvature. |
| UMCC - Y-axis\* | *UKUY*\* | log of Unsigned Manhattan Chain Code - Y-axis. Larger values indicate more change in berry curvature. |
| Eccentricity\* | *UKEC*\* | Mathematical eccentricity of derived berry chimera shape. Circular berries have 0 eccentricity, elliptical berries have larger eccentricities the more oblong the berry is, but less than 1. |
| Length:Width Ratio\* | *UKLvW*\* | The derived berry chimera shape length versus width ratio. |
| Tortuosity\* | *UKTO*\* | The derived berry chimera shape tortuosity. Larger values indicate increased ‘waviness’ in the berry contour. Smoother/rounder berries will have lower values. |
| Solidity\* | *UKSO*\* | The derived berry chimera shape density relative to its convex hull. Lower values indicate more ‘waviness’ in the berry contour, while higher values have smoother contour curvature. |
| **Largest Berry Traits** |  |  |
| Length () | *UBL* |  |
| Width () | *UBW* |  |
| Mass () | *UBM* |  |
| Calyx Diameter () | *UCD* |  |
| Calyx Lobe Fold Pattern () | *UCLP* |  |
| Calyx Lobe Size () | *UCLS* |  |
| Calyx End Shape () | *UCES* |  |
| Berry Pedicel End Shape () | *UBES* |  |
| Berry Skin Bloom Level () | *UBBL* | Assesses the amount of wax on the berry surface. |
| Berry Shape (  ) | *UBS* |  |
| Number Developed Seeds | *UNS* |  |
| Length:Width Ratio\* | *ULvW*\* | Derived from UBL / UBW |
| **Plot Traits** |  |  |
| Total Yield () | *TY* |  |
| Sound Fruit Yield () | *SFY* |  |
| Mean Fruit Mass () | *MFM* | Calculated based on random sample of 100 berries. |
| Percent Fruit Rot (**)** | *PFR* |  |
| Total Anthocyanins () | *Tacy* |  |
| °Brix (*Soluble Solids* ) | *Brix* |  |
| Titratable Acidity () | *TA* |  |
| Proanthocyanins () | *PAC* |  |
| **Upright Traits** |  |  |
| Total Berry Mass () | *UTBM* |  |
| Upright Length () | *UL* |  |
| Upright Secondary Length | *USL* | Secondary vegetative growth on upright. |
| Dry Mass of Leaves () | *UDM* |  |
| Rebud () | *URB* | Evidence for rebud behavior, where a fruiting upright has a larger bud than a vegetative upright. |
| Number of Pedicels | *UNP* |  |
| Number Pedicels without Fruit | *UN0* |  |
| Number Pedicels with Mature Berries | *UNB* |  |
| Number Pedicels with Aborted Flowers | *UNAF* |  |
| Number Pedicels with Aborted Berries | *UNAB* |  |
| Upright Mean Fruit Mass\* () | *UMFM*\* | Derived from UTBM / UNB |
| **Biennial Bearing Traits†** |  |  |
| Biennial Bearing Index – Upright Total Berry Mass\* | *BBIUTBM*\* |  |
| Bienniel Bearing Index – Total Yield\* | *BBITY*\* |  |
| Bienniel Bearing Index – Sound Fruit Yield\* | *BBISFY*\* |  |
| aUpright Traits were measured on 10 fruiting-uprights. Largest berry traits represent phenotypic values of the largest berry on a given fruiting upright. Plot traits were collected by harvesting berries from a 0.09 m2 plot sample and running appropriate assays onsite at Marucci Center. Upright Traits and Largest Berry Traits were collected at Rutgers and assayed at UW-Madison. Trait abbreviations are used to label subsequent figures. Berry Shape Chimera Parameters were derived from canonical representations of berry shapes. Expressions between parentheses indicate trait units or categorical values. | | |
| bTrait abbreviations are used to label subsequent figures. | | |
| \*Trait is derived, or calculated, from other measured traits. | | |
| **†**Measure of yield stability over successive years, as described in Schlautman *et al.* (2015). | | |

Supplementary Table S2. Abbreviations and descriptions for relevant cranberry (*Vaccinium macrocarpon* Ait*.*) digital and plot traits referenced from Diaz-Garcia *et al.* (2018a), Diaz-Garcia *et al.* (2018b), and Schlautman *et al.* (2015).

| **Traita** | **Abbv** | **Description** |
| --- | --- | --- |
| ***Diaz-Garcia et al. (2018a)*** |  |  |
| Berry Area | *BA* | Berry Area |
| Berry Length | *BL* | Berry length digital measure (major axis diameter of berry contour) |
| Berry Width | *BW* | Berry width digital measure (minor axis diameter of berry contour) |
| Eccentricity | *EC* | A value of 0 represents a perfect circle and a value of 1 represents an ellipse stretched infinitely long (straight line). |
| Berry Length vs. Width | *LvW* | Ratio of berry length to width (major/minor axis lengths). |
| Persistent Homology -  Principal Component 1 | *PH\_PC1* | Moderate-to-high correlation with LvW and EC. |
| Persistent Homology -  Principal Component 2 | *PH\_PC2* | Moderate-to-low correlation with LvW and EC. |
| ***Diaz-Garcia et al. (2018b)* and *Schlautman et al. (2015)*** |  |  |
| Berry Color | *BCOLOR* | Digital mean of berry color. |
| Berry Color Variance | *BCOLORVAR* | Digital variance of berry color. |
| September Brix | *BRIX\_SEP* | Percent soluble solids for September. |
| October Brix | *BRIX\_OCT* | Percent soluble solids for October. |
| September Mean Fruit Mass | *MFM\_SEP* | Mean fruit mass for September. |
| October Mean Fruit Mass | *MFM\_OCT* | Mean fruit mass for October. |
| October Titratable Acidity | *TA\_OCT* | Titratable acidity for October. |
| September Total Anthocyanins | *TACY\_SEP* | Total Anthocyanins for September. |
| October Total Anthocyanins | *TACY\_OCT* | Total Anthocyanins for October. |
| ***Schlautman et al. (2015)*** |  |  |
| Mean Fruit Mass  () | *MFM* | Mean fruit mass on 100 randomly sampled berries. |
| Total Yield () | *TY* | Total yield. |
| Biennial Bearing Index | *BBITY* | Biennial Bearing Index of total yield.  is the difference in *TY* between successive years, and is sum of *TY* in successive years. |
| aBold italic text indicates the study of origin. Entries between parentheses indicate the units of measurement. | | |

Supplementary Table S3.List of categorical traits and their mapped numeric values. Generally, numeric values were chosen such that larger values represented more desirable breeding attributes.

|  |  |  |
| --- | --- | --- |
| **Trait** | **Categorical Value** | **Numeric Value** |
| Calyx Lobe Form | open (strongly folded back) | 0 |
|  | medium | 1 |
|  | closed (folded over calyx) | 2 |
| Calyx Lobe Size | large | 0 |
|  | medium | 1 |
|  | small | 2 |
| Rebud | no | 0 |
|  | yes | 1 |
| Berry Skin Bloom Level | shiny | 1 |
|  | moderate | 2 |
|  | heavy (waxy) | 3 |

Supplementary Table S4.Comprehensive list of significant QTL, including pairwise interactive QTL, for cranberry (*Vaccinium macrocarpon* Ait*.*) population *CNJ02*. Table fields are as follows:

* *method:* r/QTL package (RRID:SCR\_009085) function used to map QTL.
* *model:* Mixed model used to generate BLUPs used as inputs to r/QTL package. Can be one of *2011*, *2012*, *2013*, or *all-years*.
* *trait:* Abbreviated trait name.
* *chr:* Chromosome number for QTL.
* *position:* Genetic position (cM) for QTL.
* *chr2:* Chromosome number for pairwise interaction QTL. *NA* if QTL is additive.
* *position2:* Genetic position (cM) for pairwise interaction QTL. *NA* if QTL is additive.
* *nearest\_marker:* Nearest marker on genetic map to QTL.
* *qtl\_lod:*QTL LOD score.
* *marker\_variance:* PVE of QTL.
* *qtl\_pvalue:* p-value of QTL under 1000 permutation.
* *model\_variance:* PVE of all QTL found for this trait and model.
* *interval\_left:* Smaller genetic position (cM) where LOD profile intersects with 1.5 × LOD below LOD of QTL position.
* *interval:* Width (cM) of interval between *interval\_left* and *interval\_right*.
* *interval\_right:* Larger genetic position (cM) where LOD profile intersects with 1.5 × LOD below LOD of QTL position.

Supplementary Table 5.Comprehensive list of effect sizes for additive QTL in cranberry (*Vaccinium macrocarpon* Ait*.*)population *CNJ02*.

* *method:* r/QTL package (RRID:SCR\_009085) function used to map QTL.
* *model:* Mixed model used to generate BLUPs used as inputs to r/QTL package. Can be one of *2011*, *2012*, *2013*, or *all-years*.
* *trait:* Abbreviated trait name.
* *chr:* Chromosome number for QTL.
* *position:* Genetic position (cM) for QTL.
* *genotype:* One of four possible genotypes derived from four-way cross – AC,AD,BC,BD
* *effect\_mean:* Mean effect size of QTL for given genotype.
* *effect\_se:* Standard error of effect size of QTL for given genotype.
* *AvB:* Maternal effect size - (AC+AD)-(BC+BD).
* *CvD:* Paternal effect size - (AC+BC)–(AD+BD.
* *Int:* Interaction effect size - (AC+BD)-(AD+BC).

Supplementary Table 6. Comprehensive list of significant QTL, including pairwise interactive QTL, for cranberry (*Vaccinium macrocarpon* Ait*.*) population *CNJ04*. Table fields are as follows:

* *method:* r/QTL package (RRID:SCR\_009085) function used to map QTL.
* *model:* Mixed model used to generate BLUPs used as inputs to r/QTL package. Can be one of *2011*, *2012*, *2014*, or *all-years*.
* *trait:* Abbreviated trait name.
* *chr:* Chromosome number for QTL.
* *position:* Genetic position (cM) for QTL.
* *chr2:* Chromosome number for pairwise interaction QTL. *NA* if QTL is additive.
* *position2:* Genetic position (cM) for pairwise interaction QTL. *NA* if QTL is additive.
* *nearest\_marker:* Nearest marker on genetic map to QTL.
* *qtl\_lod:*QTL LOD score.
* *marker\_variance:* PVE of QTL.
* *qtl\_pvalue:* p-value of QTL under 1000 permutation.
* *model\_variance:* PVE of all QTL found for this trait and model.
* *interval\_left:* Smaller genetic position (cM) where LOD profile intersects with 1.5 × LOD below LOD of QTL position.
* *interval:* Width (cM) of interval between *interval\_left* and *interval\_right*.
* *interval\_right:* Larger genetic position (cM) where LOD profile intersects with 1.5 × LOD below LOD of QTL position.

Supplementary Table 7. Comprehensive list of effect sizes for additive QTL in cranberry (*Vaccinium macrocarpon* Ait*.*) population *CNJ04*.

* *method:* r/QTL package (RRID:SCR\_009085) function used to map QTL.
* *model:* Mixed model used to generate BLUPs used as inputs to r/QTL package. Can be one of *2011*, *2012*, *2014*, or *all-years*.
* *trait:* Abbreviated trait name.
* *chr:* Chromosome number for QTL.
* *position:* Genetic position (cM) for QTL.
* *genotype:* One of four possible genotypes derived from four-way cross – AC,AD,BC,BD
* *effect\_mean:* Mean effect size of QTL for given genotype.
* *effect\_se:* Standard error of effect size of QTL for given genotype.
* *AvB:* Maternal effect size - (AC+AD)-(BC+BD).
* *CvD:* Paternal effect size - (AC+BC)–(AD+BD.
* *Int:* Interaction effect size - (AC+BD)-(AD+BC).

Supplementary Table 8. Inter-trait Pearson correlation coefficients for cranberry (*Vaccinium macrocarpon* Ait*.*) population *CNJ02*.

Supplementary Table 9.Inter-trait Pearson correlation coefficients for cranberry (*Vaccinium macrocarpon* Ait*.*) population *CNJ04*.