**RosBREED-enabled use of “Jewels in the Genome”: Sweet Cherry Fruit Size**

**Trait**: Sweet cherry fruit size – weight, dimensions, mesocarp cell number

**Locus**: Quantitative trait locus about a third of the way down the linkage group of sweet cherry chromosome 2 (Zhang et al. 2009), equivalent to the middle of the TxE *Prunus* reference map and peach chromosome 2.

**Markers**: Two QTL-flanking SSRs, CPSCT038 and BPPCT034, which are 10-20 cM apart (Olmstead et al. 2008).

***Table of functional haplotypes at the G2 fruit size* *locus for sweet cherry cultivars*** *[color-blind version on next page]*

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Cultivar | Haplotype1 | | Source2 | Cultivar | Haplotype1 | | Source2 |
| 1st | 2nd | 1st | 2nd |
|  |  |  |  |  |  |  |  |
| Ambrunes | 190-255 | 190-223 | a,b,c | Rainier | 190-255 | 204-235 | a,b,c |
| Benton | 190-223 | 192-223 | a,b,c | Regina | 190-255 | 204-223 | a,b,c |
| Bing | 190-255 | 204-235 | a,b,c | Sam | 190-255 | 190-255 | a,b,c |
| Black Republican | 204-235 | 190-225 | c | Sato Nishiki | 190-255 | 204-235 | c |
| Brooks | 190-255 | 190-223 | a,b,c | Schmidt | 190-255 | 192-250 | a,b,c |
| Cashmere | 190-223 | 190-223 | c | Schneiders | 190-255 | 190-257 | a,b,c |
| Chelan | 190-223 | 192-223 | a,b | Selah | 190-255 | 190-223 | a,b,c |
| Chinook | 190-255 | 204-235 | a,b,c | Selection AA | 190-255 | 190-255 | c |
| Cowiche | 190-223 | 190-223 | b,c | Selection BB | 190-255 | 192-223 | a,b,c |
| Early Burlat | 190-223 | 190-237 | b,c | Selection CC | 190-255 | 190-255 | a,b,c |
| Emperor Francis | 190-255 | 204-235 | a,b,c | Selection DD | 190-255 | 190-255 | a,b,c |
| Gil-Peck | 190-255 | 192-223 | b,c | Selection EE | 190-255 | 204-235 | a,b,c |
| Glacier | 190-223 | 190-237 | a,b,c | Selection GG | 190-255 | 190-235 | a,b,c |
| Kiona | 190-223 | 190-237 | b,c | Selection JJ | 190-255 | 190-255 | c |
| Lambert | 190-255 | 192-223 | a,b,c | Stella | 204-235 | 190-223 | a,b,c |
| Lapins | 204-235 | 204-255 | a,b,c | Summit | 190-255 | 204-255 | a,b,c |
| MIM 17 | 190-255 | 202-250 | c | Sweetheart | 190-255 | 204-235 | b,c |
| MIM 23 | 192-223 | 202-250 | c | Tieton | 190-223 | 190-237 | a,b,c |
| Napoleon | 190-255 | 204-235 | a,b,c | Ulster | 190-255 | 192-250 | a,b,c |
| Newstar | 190-255 | 190-223 | b | Van | 190-255 | 204-235 | a,b,c |
| NY54 | 190-255 | 192-225 | a,b,c | Vic | 190-255 | 190-255 | a,b,c |
| PMR-1 | 190-255 | 192-223 | a,b,c | Windsor | 190-255 | 190-225 | a,b,c |
|  |  |  |  |  |  |  |  |

1 Colors indicate whether the haplotype is associated with large, small, or presumed small fruit size – e.g., the 1st haplotype of Ambrunes, 190-255, is associated with large fruit size. Haplotypes not assigned a fruit size effect represent those intermediate or neutral for fruit size. Recombined haplotypes are not assigned a functional association unless they are a recombination between two large-fruit haplotypes or two small-fruit haplotypes. The logic behind haplotype assignment to a presumed small fruit size effect is that the cultivars known to carry such haplotypes have small fruit and these haplotypes are very rare in the cultivated germplasm pool (with presumed selection against them during domestication).

2 Information sources are:

a = unpublished data from USDA CSREES NRI project (grant no. 2005-35300-15454) led by A. Iezzoni, Michigan State University

b = unpublished data from WTFRC project led by C. Peace, Washington State University

c = RosBREED results (genotyped cultivars of the sweet cherry Crop Reference Set)

**References**

Olmstead JW, Sebolt AM, Cabrera A, Sooriyapathirana SS, Hammar S, Iriarte G, Wang D, Chen CY, van der Knaap E, Iezzoni AF (2008). Construction of an intra-specific sweet cherry (*Prunus avium* L.) genetic linkage map and synteny analysis with the *Prunus* reference map. Tree Genetics & Genomes 4:897-910.

Zhang G, Sebolt AM, Sooriyapathirana SS, Wang D, Bink MCAM, Olmstead JW, Iezzoni AF (2009). Fruit size QTL analysis of an F1 population derived from a cross between a domesticated sweet cherry cultivar and a wild forest sweet cherry. Tree Genetics & Genomes 6:25-36

***Table of functional haplotypes at the G2 fruit size* *locus for sweet cherry cultivars*** *[color-blind version]*

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Cultivar | Haplotype1 | | Source | Cultivar | Haplotype1 | | Source |
| 1st | 2nd | 1st | 2nd |
|  |  |  |  |  |  |  |  |
| Ambrunes | **190-255** | 190-223 | a,b,c | Rainier | **190-255** | *204-235* | a,b,c |
| Benton | 190-223 | *192-223* | a,b,c | Regina | **190-255** | 204-223 | a,b,c |
| Bing | **190-255** | *204-235* | a,b,c | Sam | **190-255** | **190-255** | a,b,c |
| Black Republican | *204-235* | *(190-225)* | c | Sato Nishiki | **190-255** | *204-235* | c |
| Brooks | **190-255** | 190-223 | a,b,c | Schmidt | **190-255** | *(192-250)* | a,b,c |
| Cashmere | 190-223 | 190-223 | c | Schneiders | **190-255** | *(190-257)* | a,b,c |
| Chelan | 190-223 | *192-223* | a,b | Selah | **190-255** | 190-223 | a,b,c |
| Chinook | **190-255** | *204-235* | a,b,c | Selection AA | **190-255** | **190-255** | c |
| Cowiche | 190-223 | 190-223 | b,c | Selection BB | **190-255** | *192-223* | a,b,c |
| Early Burlat | 190-223 | **190-237** | b,c | Selection CC | **190-255** | **190-255** | a,b,c |
| Emperor Francis | **190-255** | *204-235* | a,b,c | Selection DD | **190-255** | **190-255** | a,b,c |
| Gil-Peck | **190-255** | *192-223* | b,c | Selection EE | **190-255** | *204-235* | a,b,c |
| Glacier | 190-223 | **190-237** | a,b,c | Selection GG | **190-255** | 190-235 | a,b,c |
| Kiona | 190-223 | **190-237** | b,c | Selection JJ | **190-255** | **190-255** | c |
| Lambert | **190-255** | *192-223* | a,b,c | Stella | *204-235* | 190-223 | a,b,c |
| Lapins | *204-235* | 204-255 | a,b,c | Summit | **190-255** | 204-255 | a,b,c |
| MIM 17 | **190-255** | *(202-250)* | c | Sweetheart | **190-255** | *204-235* | b,c |
| MIM 23 | *192-223* | *(202-250)* | c | Tieton | 190-223 | **190-237** | a,b,c |
| Napoleon | **190-255** | *204-235* | a,b,c | Ulster | **190-255** | *(192-250)* | a,b,c |
| Newstar | **190-255** | 190-223 | b | Van | **190-255** | *204-235* | a,b,c |
| NY54 | **190-255** | *192-225* | a,b,c | Vic | **190-255** | **190-255** | a,b,c |
| PMR-1 | **190-255** | *192-223* | a,b,c | Windsor | **190-255** | *190-225* | a,b,c |
|  |  |  |  |  |  |  |  |

1 Colors indicate whether the haplotype is associated with **large**, *small*, or (*presumed small)* fruit size

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***How to run these predictive markers***

Details to be provided here soon. In the meantime, contact Dr. C. Peace (cpeace@wsu.edu) or Dr. Nahla Bassil (nahla.bassil@ars.usda.gov)