

Advances in DNA markers in cherry: from the S locus to a genome wide array

Amy Iezzoni, Elisabeth Dirlewanger

► To cite this version:

Amy Iezzoni, Elisabeth Dirlewanger. Advances in DNA markers in cherry: from the S locus to a genome wide array. 7. International Cherry Symposium, International Society for Horticultural Science (ISHS). INT., Jun 2013, Plasencia, Spain. hal-02806008

HAL Id: hal-02806008 https://hal.inrae.fr/hal-02806008

Submitted on 6 Jun2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Advances in DNA markers in cherry: From the S-locus to a genome-wide array

Amy lezzoni

Michigan State University

MICHIGAN STATE UNIVERSITY

Presented by: Elisabeth Dirlewanger

INRA - Bordeaux



DNA markers in sweet cherry

Self-incompatibility locus

- 34 S-alleles identified to date
- Within these S-alleles, 6 pollen-part mutants (SFB: S haplotype-specific F-box protein)
 - & 5 stylar part mutants (S-RNase) were identified

At the same time, polymorphic genome-wide markers for cherry were not available.



Advances in genome-wide DNA markers for cherry were possible due to the available peach genome sequence



The high-quality draft genome of peach (*Prunus persica*) identifies unique patterns of genetic diversity, domestication and genome evolution

The International Peach Genome Initiative, Ignazio Verde, Albert G Abbott, Simone Scalabrin, Sook Jung, Shengqiang Shu, Fabio Marroni, Tatyana Zhebentyayeva, Maria Teresa Dettori, Jane Grimwood, Federica Cattonaro, Andrea Zuccolo, Laura Rossini, Jerry Jenkins, Elisa Vendramin, Lee A Meisel, Veronique Decroocq, Bryon Sosinski, Simon Prochnik, Therese Mitros, Alberto Policriti, Guido Cipriani, Luca Dondini, Stephen Ficklin, David M Goodstein 🗈 *et al.*

Outline

- Rosaceae COS markers
- High Density SNP markers
- Application Why are some cherry fruit large and some small?

GDR Genome Database for Rosaceae										
	Home	Species	Projects	Maps	Search	Tools	Community	Contact		
File - Help -										
Prunus Persica: 50 kbp from scaffold_1:27,696,15327,746,152										
Browser Select Tracks Snapshots Community	Fracks Custo	m Tracks Pre	ferences							
Search										
Landmark or Region: Scaffold_1:27,696,153.27,746 Configure Go scaffold_1:27,696,153.27,746 Search Search Load Snapshot Examples: scaffold 1:12360000.12479999, ppa014948m, BU045951, CPPCT016, AG25A. Save Snapshot Load Snapshot										
Data Source Prunus Persica	~					Scroll	Zoom: <mark>« <</mark> —	Show 50 kb	p 💌 🕂 🎽 😕 🗆 Flip	

Cherry markers aligned to the peach genome sequence (www.rosaceae.org)



Conserved Ortholog Set (COS) markers

- Orthologous: common evolutionary origin, conservation in sequence
- Single copy
- <u>Strategy used for the identification</u> <u>of the Rosaceae- COS</u>
- The COS set was comprised of Rosaceae single copy genes (ESTs) that were orthologous to the single copy genes in the Arabidopsis genome.



627 RosCOS were identified

To identify RosCOS polymorphic in sweet cherry, all these RosCOS were sequenced from a diverse panel of sweet cherry cultivars.

Emperor Francis	Krupnoplodnaya
Lambert	Cristobalina
Regina	New York 54

282 polymorphic sweet cherry RosCOS were identified



Research article

Development and bin mapping of a Rosaceae Conserved Ortholog Set (COS) of markers

Antonio Cabrera¹, Alex Kozik², Werner Howad³, Pere Arus³, Amy F Iezzoni⁴ and Esther van der Knaap^{*1}



Open Acce

6

RESEARCH ARTICLE



Open Access

Comparative analysis of rosaceous genomes and the reconstruction of a putative ancestral genome for the family

Eudald Illa¹, Daniel J Sargent², Elena Lopez Girona², Jill Bushakra³, Alessandro Cestaro⁴, Ross Crowhurst⁵, Massimo Pindo⁴, Antonio Cabrera⁶, Esther van der Knaap⁶, Arny lezzoni⁷, Susan Gardiner³, Riccardo Velasco⁴, Pere Arús¹, David Chagné³, Michela Troggio^{4*}

Based on the position of 129 orthologous markers

Prunus

Malus

Hypothetical ancestral Rosaceae genome : 9 chromosomes

Figure 4 Reconstruction of a hypothetical ancestral Rosaceae genome. Syntenic regions among the genomes were elucidated

Fragaria

Gbrowse view of the peach sequence with RosCOS highlighted

Browser Select Tracks Snapshots Community Tra	cks Custom Tracks Preferences	
Search		
Landmark or Region:		Annotate Restriction Sites 🕑 Configure Go
scattold_1:27,671,15327,771, Search		Save Snapshot Load Snapshot
Data Source	500-5051, 011-01010, A025A	
Prunus Persica	▼	Scroll/Zoom: 📉 📉 👘 Show 100 kbp 🝸 🦵 🖉 🛄 Flip
🖬 Region 🗖 Details		
	20 kbp	
		<u>erzew czas</u> ty z7750k 27760k 27770k
	★ ■ 🛛 🖬 H 🖾 🖬 Rosc OS markers	RosCOS_1756
		P
		rs159238479
	Conserved Ortholog Set (RosCOS)	
		RUSC_FMLY_USR1_1/56 I
	anean ad Ortholog Sat (BacCOS)	
	onserved Ortholog Set (RosCOS)	ROSC_FMLY_CSA1_1756 I→
	t cherry Pol 27651152 Pos	sBPEFD son sweet cherry Pol 27714539
		PhsChS1756-104 shi sweet cherry Ph1 27721194
	★ 🖬 🗙 🖬 🕂 😰 🖬 Transcript Model pa017333m ppa019451m ppa020788m ppa003665m ppa019695m	ppa007348m ppa020891m ppa003024m ppa026110m ppa017249m
	pourasecant pouraset of pourase for	014966m ppa006701m ppa009847m ppa003031m
		014966m ppa005701m ppa009847m ppa003031m INT→ INT++++++++++++++++++++++++++++++++++++
	P→ ← ← ↑ ↑ ↑ ↑ ↑ ↑ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓ ↓	014966m ppa005701m ppa009847m ppa003031m
	Ppa015711n ppa006089n ppa014867n	014966m ppa005701m ppa009847m ppa003031m ppa002589m ppa005302m ppb019112m ← 111111
		014966m ppa005701m ppa009847m ppa003031m Ppa0050289m ppa006302m ppb019112m ← ppa006301m
		014966m ppa005701m ppa009847m ppa003031m ppa002589m ppa006302m ppb019112m ← ppa006301m ← ppa006301m
		014966n ppa005701n ppa009847n ppa003031n ppa005302n ppa006302n ppa005302n ctritteri ppa002589n ppa002589n ctritteri ppb019112n ctritteri ppa007348n ppa020891n ppa003024n ppa026110n ppa017249n ctritteri
	ppa015711n ppa006089m ppa014867n ★ ■ ⊠ ⊠ ⊢ / 2 ≅ Updated Transcript Model ★ ■ ⊠ ⊠ ⊢ / 2 ≅ Updated Transcripts v1.0-11 pa017333n ppa019451n ppa0020788m ppa003665m ppa019695m → ppa019351n ppa019070n ppa014594m ppa011545m ppa0	014966n ppa005701n ppa009847n ppa003031n ppa002589n ppa006302n ← ppb019112n ← ppa006301n ← ##### ppa007348n ppa020891n ppa003024n ppa026110n ppa017249n HTTTTT→ ← TTTTTTT→ ← TT+ 014966n ppa00701n ppa009847n ppa003031n HTTTTT→ ← TT+ 014966n ppa005701n ppa009847n ppa003031n
	ppa015711# ppa006089# ppa014867# ★ ■ ⊠ ⊠ ⊢ /2 ≅ Updated Transcript Model ★ ■ ⊠ ⊠ ⊢ /2 ≅ Updated Transcripts v1.0-r1 pa017333# ppa019451# ppa020788# ppa003665# ppa019695# ppa019351# ppa01970# ppa014594# ppa013655# ppa019695# ppa019351# ppa019070# ppa014594# ppa01457# ppa019751# ppa006088# ppa014867#	014966n ppa005701n ppa009847n ppa003031n ppa002589n ppa005302n ppb019112n ← ppa005301n ← ppa006301n ← ppa006301n ← ppa006301n ← ppa006301n ← ppa006301n ← ppa006301n ← ppa006302n ← Ppa006302n ←
	ppa015711# ppa006089# ppa014867# ★ ■ ⊠ 圖 H Z B Alternate Transcript Model ★ ■ ⊠ 圖 H Z B Updated Transcripts v1.0-r1 pa017333m ppa019451# ppa020788# ppa003665m ppa019695# ppa019351# ppa019070# ppa014594# ppa011545# ppa019351# ppa019070# ppa014594# ppa014867# ppa019351# ppa019070# ppa014594# ppa014867#	014966n ppa005701n ppa009847n ppa003031n ppa005302n ppa005302n ppa005302n ctiller ppa002589n ctiller ppa005302n ctiller ppa006301n ctiller ppa006301n ctiller ppa006301n ppa006302n ppa005002n ppa005002n ppa005002n ppa005002n ppa005002n ppa005002n ppa005002n ppa005002n ppa005002n ppa0050302n ctiller ppa002898n ctiller

Outline

- Rosaceae COS markers
- High Density SNP markers
- Application Why some cherry fruit are large and some fruit are small.



<u>MSU</u> Amy lezzoni (PD) Jim Hancock Dechun Wang Cholani Weebadde

Univ. of Arkansas John Clark <u>WSU</u> Cameron Peace Dorrie Main Kate Evans Karina Gallardo Ji Raymond Jussaume Vicki McCracken Nnadozie Oraguzie Mykel Taylor

Univ. of Minnesota Jim Luby Chengyan Yue

<u>Oregon State Univ.</u> Alexandra Stone USDA-ARS Nahla Bassil Gennaro Fazio Chad Finn Plant Research Intl, Notherlando

<u>Netherlands</u> Eric van de Weg Marco Bink

Enabling marker-assisted breeding in Rosaceae Enabling MSU Jezzoni (PD)

> <u>Clemson</u> Ksenija Gasic Gregory Reighard

> > <u>Texas A&M</u> Dave Byrne

Univ. of CA-Davis Tom Gradziel Carlos Crisosto

Univ. of New Hamp. Tom Davis

Genome Wide SNP arrays

 Genome-scanning SNP arrays developed and utilized for apple (8K), peach (9K) and cherry (6K) by international RosBREED-led efforts



OPEN 3 ACCESS Freedy available online

PLos one

Genome-Wide SNP Detection, Validation, and Development of an 8K SNP Array for Apple

David Chagné¹, Ross N. Crowhurst², Michela Troggio³, Mark W. Davey⁴, Barbara Gilmore³, Gindy Lawley⁶, Stijn Vanderzande⁴, Roger P. Hellens², Satish Kumar⁷, Alessandro Cestaro³, Riccardo Velasco³, Dorrie Main⁶, Jasper D. Rees⁹, Amy lezzoni¹⁰, Todd Mockler¹¹, Larry Wilhelm¹², Eric Van de Weg¹³, Susan E. Gardiner¹, Nahla Bassil⁵, Cameron Peace⁸

OPEN CACCESS Freely available online

PLoS one

Development and Evaluation of a 9K SNP Array for Peach by Internationally Coordinated SNP Detection and Validation in Breeding Germplasm

Ignazio Verde¹*⁹, Nahla Bassil²⁹, Simone Scalabrin³, Barbara Gilmore², Cynthia T. Lawley⁴, Ksenija Gasic⁵, Diego Michelett⁶, Umesh R. Rosyara⁷, Federica Cattonaro³, Elisa Vendramin¹, Dorrie Main⁸, Valeria Aramini¹, Andrea L. Blas⁶, Todd C. Mockler^{9,10}, Douglas W. Bryant^{9,11}, Larry Wilhelm¹², Michela Troggio¹³, Bryon Sosinski¹⁴, Maria José Aranzana⁶, Pere Arús⁶, Amy Iezzoni⁷, Michele Morgante^{3,15}, Cameron Peace⁸*

OPEN CACCESS Freely available online

Enabling marker-assisted breeding in Rosaceae

PLOS ONE

Development and Evaluation of a Genome-Wide 6K SNP Array for Diploid Sweet Cherry and Tetraploid Sour Cherry

Cameron Peace¹*, Nahla Bassil², Dorrie Main¹, Stephen Ficklin¹, Umesh R. Rosyara³, Travis Stegmeir³, Audrey Sebolt³, Barbara Gilmore², Cindy Lawley⁴, Todd C. Mockler⁵, Douglas W. Bryant^{5,6}, Larry Wilhelm⁷, Amy lezzoni³

1 Department of Horticulture, Washington State University, Pullman, Washington, United States of America, 2 USDA-ARS, National Clonal Germplasm Repository, Corvallis, Oregon, United States of America, 3 Department of Horticulture, Michigan State University, East Lansing, Michigan, United States of America, 4IIIurina Inc., Hayward, California, United States of America, 5 The Donald Danforth Plant Science Center, St. Louis, Missouri, United States of America, 6 Intuitive Genomics, Inc., St. Louis, Missouri, United States of America, 7 Oregon Health Sciences University, Portland, Oregon, United States of America

www.rosbreed.o







illumina

United States Department of Agriculture National Institute of Food and Agriculture

Gbrowse view of the peach sequence with the RosBREED SNPs highlighted

Browser Select Tracks Snapshots Communication	unity Tracks Custom Tracks Preferences	
Search		
Landmark or Region:		Annotate Restriction Sites 💙 Configure Go
scaffold_1:27,671,15327,771,; Search		Core Consistent Local Consistent
Examples: scaffold_1:1236000012479999, ppa01	4948m, BU045951, CPPCT016, AG25A.	Save Snapsnot Load Snapsnot
Data Source		Scrall/Zeam: 🔣 🧹 💻 Show 100 kbn 💽 🕂 🗦 ≫ 🗆 Elin
Prunus Persica	▼	
Overview		
Region Details		
Details		20 kbp
★■XIIIH 20 IRSC_6K_cherry		tart_cherry_a_Pp1_27702307
t_cherry_Pp1_27651152		RosBREED_snp_sweet_cherry_Pp1_27714539
		RosCOS1756-104_snp_sweet_cherry_Pp1_27721194
	* 🗆 🛛 H 🖓 🗈 All Calturus 💦 🖇	
	★ ■ ⊠ 🗟 H 💋 🖬 IRSC_6K_cherry_SNP_array t_cherry_Pp1_27651152	RosBREED_snp_tart_cherry_a_Pp1_27702307 I RosBREED_snp_sweet_cherry_Pp1_27714539 I RosCOS1756-104_snp_sweet_cherry_Pp1_27721194
	★ B12131 H 2121 Franscript Model pa0127333n ppa019451m ppa020788n ppa00 → fifth ← fifth ppa019351m ppa019070m ppa014594m ↔ fifth ppa015711m ppa006089m	03665m ppa019695m ppa007348m ppa002891m ppa003024m ppa0126110m ppa017249m ppa011545m ppa014966m ppa0005701m ppa009847m ppa0003031m HYH HYH HYH HYH ppa0003031m ppa014867m ppa002589m ppa006302m e ppa002589m ppa006302m e ppb019112m e
	★ 🖬 🖾 🛏 🖆 🖾 Alternate Transcript Model	ppa006301m
	★ ■ 20 10 H 22 12 Updated Transcripts v1.0.r1 pa017333n ppa019451m ppa020788n ppa00 D→ D→ HTTH→ ← HTTD ppa019351m ppa019070m ppa014594m D→ HTT ppa015711m ppa005089m ↓ HTTTH→	33665m ppa019695m ppa007348m ppa020891m ppa003024m ppa026110m ppa017249m C M1110 M11101 M11101 H Difference ppa011545m ppa014966n ppa000501m ppa009847m ppa0003031m H110 H1101 Difference Difference Difference ppa014867m ppa002589m ppa006302m 12 ppb019112m ppa006301m 12
	+ 🗆 🛛 🕞 🖵 🕅 Arabidansis Dentide Alianment	rumu⇒ u>

RosBREED Cherry 6K SNP Array v1 Quality-controlled genotypic data

Michigan State University cherry: genetics and breeding team



Enabling marker-assisted breeding in Rosaceae

www.rosbreed.org

PLOS ONE

Construction and Comparative Analyses of Highly Dense Linkage Maps of Two Sweet Cherry Intra-Specific Progenies of Commercial Cultivars

Carolina Klagges^{1®}, José Antonio Campoy^{2®}, José Quero-García², Alejandra Guzmán³, Levi Mansur³, Eduardo Gratacós³, Herman Silva⁴, Umesh R. Rosyara⁵, Amy Iezzoni⁵, Lee A. Meisel^{1,6}*, Elisabeth Dirlewanger²*

Regina x Lapins

(687 SNPs mapped)



Black Tartarian x Kordia

(723 SNPs mapped)

RNA based cherry SNPs

Koepke et al. BMC Genomics 2012, 13:18 http://www.biomedcentral.com/1471-2164/13/18



METHODOLOGY ARTICLE



Rapid gene-based SNP and haplotype marker development in non-model eukaryotes using 3'UTR sequencing

Tyson Koepke¹, Scott Schaeffer¹, Vandhana Krishnan², Derick Jiwan¹, Artemus Harper¹, Matthew Whiting³, Nnadozie Oraguzie³ and Amit Dhingra^{1*}

RNAseq Bing / Rainier



Gbrowse view of the peach sequence with the 3' UTR SNPs highlighted



Progress in sour cherry genetics

(a

(a)		Emperor	New Yor	k 54	(b)	Ujfehertoi	Surefire	
()		Francis		_	(~)	Furtos		
		1 2	3 4			1 2 3 4	4 5 6 7 8	
	ss490556201	AG	A G		ss490556207	A G A A	A G G A A	
	\$\$490550254	GG	C C C		\$\$490550254			
	ss49055026.	GG	C A		\$\$490550203 cc400556216		A G G G A	
	ss490556221		GA		ss490556220			
	ss490550220	GG	GG		ss490550220	GGGG		fr and ST
	ss490556239	AG	GA		ss490556239	GGGG		Ve Ve Win
	ss490556242	GA	AG		ss490556242	GAA	A GAAA	et la
	ss490556243	AC	CA		ss490556245	CCCC		-ta ch
	ss490556251	A G	AA		ss490556251	GGG	A G G A	er eli
	ss49055625-	A G	G G		ss490556254	u u u u	a <mark>uuuu</mark>	
	ss490556257	G A	A A		ss490556257	AAAA	A A A A	ed R
	Slocus	34	26		Slocus	1' 4 36b 3	²⁵ 13' 4 36a 35	ed (s o rg
	ss490556260	G A	🗶 🛛 🖸 🖸		ss490556260	GAA A	A 🗶 G A A A	ete ou
	ss490559322	AA	A C		ss490559322	CAAA	A A A A A	or D of
	ss49055626.	GG	A G		ss490556263	G G A C	G G G A G	F) S
	ss490550280	GG	GG		ss490550286	G G A	A G G A A	
								100
	89 a.	1	-					
	8(24) 2(34) 3	(24)	1(47) 3(5	6)	27-04-16	27-03-29	
ſ	8(24) 2(34) 3	(24)	1(47) 3(5	6)	27-04-16	27-03-29	
ss490556207	8(24) 2(1 3 A A	34) 3	(24)	1(47) 3(5 1 4 2 4 A G G	6) //3 G \$\$490556207	27-04-16 2 5 4 7 G G A A	$\begin{array}{c} 27-03-29 \\ \hline 1 & 6/5 & 3 & 7 \\ \hline A & G & A & A \end{array}$	enome: sour sour
ss490556207 ss490550254	8(24) 2(1 3 A A G G G	34) 3 4 6 6	(24) 2 3 3 3 3 3 4 3 3 6	1 (47) 3(5 1 4 2 4 A G G G G	6) //3 G ss490556207 g ss490550254	27-04-16 2 5 4 7 G G A A G G A O	27-03-29 7 A G A A 6 G G G G	enome: sweet c sour ch
ss490556207 ss490550254 ss490550263	8(24) 2(1 3 A A G G G G G G	34) 3 4 G G G	(24) 2 3 3 3 4 3 6 6 6 6	1(47) 3(5 1 4 A G G G G G G G G G G G	6) //3 G ss490556207 G ss490550254 G ss490550263	27-04-16 2 5 4 7 G G A A G G A C G G A C	27-03-29 7 A G A A 6 G G G G 7 G G G G	enome: sweet che sour cherr sour cherr
ss490556207 ss490550254 ss490550263 ss490556216	8(24) 2(1 3 2 A A 6 G G 6 G G 6 C C A	34) 3 4 G G A	(24) 2 3 3 3 A 3 G 3 G 3 G 4 C	$\begin{array}{c c} \mathbf{I}(47) & 3(5) \\ \hline 1 & 4 & 2 & 4 \\ \mathbf{A} & \mathbf{G} & \mathbf{G} \\ \mathbf{G} & \mathbf{G} & \mathbf{G} \\ \mathbf{G} & \mathbf{G} & \mathbf{G} \\ \mathbf{G} & \mathbf{G} & \mathbf{G} \\ \mathbf{C} & \mathbf{A} & \mathbf{A} \end{array}$	6) //3 G ss490556207 G ss490550254 G ss490550263 A ss490556216	27-04-16 2 5 4 7 G G A A G G A C G G A C A A C C	27-03-29 7 A G A A 6 G G G G 7 G G G G 7 A A C C	enome: sweet cherry sour cherry (
ss490556207 ss490550254 ss490550263 ss490556216 ss490556220	8(24) 2(1 3 2 A A G G G G C C A A G G G G G G G G C C C A G G	34) 3 4 G G A A	(24) : 2 3 3 A 3 G 3 G 3 G 4 C 3 G	1 4 3 (5 1 4 2 4 A G G G G G G G G C A A A A G	6) //3 G ss490556207 G ss490550254 G ss490550263 A ss490556216 A ss490556220	27-04-16 2 5 4 7 G G A A G G A C G G A C G A C G A C G A C	27-03-29 1 6/5 3 7 A G A A G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G	enome: sweet cherry, sour cherry (<i>av</i> sour cherry (<i>fru</i>
ss490556207 ss490550254 ss490550254 ss490556216 ss490556220 ss490550267	8(24) 20 1 3 2 A A G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G	34) 3 4 G G G G A A G G G G G G G G G G G G G	(24)	1 4 3 (5) 1 4 2 4 A G G G G G G G G C A A A A G G G G	6) //3 G ss490556207 G ss490550254 G ss490550263 A ss490556216 A ss490556220 G ss490550267	27-04-16 2 5 4 7 G G A A G G A C G G A C G A C G A C G A C G A C G A C	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	enome: sweet cherry, sour cherry (<i>aviur</i> sour cherry (<i>frutic</i>
ss490556207 ss490550254 ss490550254 ss490556216 ss490556220 ss490556220 ss490556239	8(24) 20 1 3 2 A A G G G G G G G C C A A G G G G G G A G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G	34) 3 4 6 6 6 6 6 7 7 8 6 9 6 9 6 9 6 9 6 9 6 9 6 9 6 9 6 9 6 9 6	(24) 2 3 3 3 4 3 6 3 6 3 6 3 6 3 6 3 6 3 6	1 4 2 4 A G G G G G G G G C A A A A G G G G A A G A A G A A G G G G	6) //3 G ss490556207 G ss490550254 G ss490550263 A ss490556216 A ss490556220 G ss490550267 G ss490556239	27-04-16 2 5 4 7 G G A A G G A C G G A C G A C G A C G G A C	27-03-29 1 6/5 3 7 A G A A G G G G G G G G G G G G G G G G G G G	enome: sweet cherry, sour cherry (<i>avium</i>) sour cherry (<i>fruticos</i>
ss490556207 ss490550254 ss490550263 ss490556216 ss490556220 ss490556220 ss490556239 ss490556242	8(24) 20 1 3 A A G G G G G G C C A G G G G G G G G G G G G G G G G G G G G G G G G G G G G G	34) 3 4 6 6 6 6 6 A 6 G 6 A 6 A 6 G 6 A 6 G 6 G 6	(24) 2 3 A 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G 4 A	1 4 2 4 A G G G G G G G G C A A A A G G G G C A A A A G G G G G G G G G G A A G G G G A A G G G A	6) //3 G ss490556207 G ss490550254 G ss490550263 A ss490556216 A ss490556220 G ss490550267 G ss490556239 A ss490556242	27-04-16 2 5 4 7 G G A A G G A C G G A C G A C G A G C G A G C G A G A A G A A	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	enome: sweet cherry, sour cherry (<i>avium</i>) sour cherry (<i>fruticosa</i>)
\$\$490556207 \$\$490550254 \$\$490550263 \$\$490556216 \$\$490556220 \$\$490556220 \$\$490556239 \$\$490556242 \$\$490556242 \$\$490556245	8(24) 20 1 3 A A G G A G G G A G G G A G G G A G G G A G G G A G G G A G G G G G G G G G G G G G G G G G G G <td< td=""><td>4 34) 3 4 6 6 6 6 6 A 6 A 6 A 6 A 6 A 6</td><td>(24) 2 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G 4 A 4 C</td><td>1 (47) 3(5 1 4 2 4 A G G G G G G G G C A A A A G G G G G G G G G G G G G G G G A A G G G G A A G G G A A A C</td><td>6) //3 G ss490556207 G ss490550254 G ss490550263 A ss490556216 A ss490556220 G ss490556220 G ss490556239 A ss490556242 C ss490556245</td><td>27-04-16 2 5 4 7 G G A A G G A C G G A C G A C G A G C G A G A G A G A A G A A C A C C C A C C C A C C C C A C C C C A C</td><td>$\begin{array}{c ccccccccccccccccccccccccccccccccccc$</td><td>enome: sweet cherry, sour cherry (<i>avium</i>) sour cherry (<i>fruticosa</i>)</td></td<>	4 34) 3 4 6 6 6 6 6 A 6 A 6 A 6 A 6 A 6	(24) 2 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G 4 A 4 C	1 (47) 3(5 1 4 2 4 A G G G G G G G G C A A A A G G G G G G G G G G G G G G G G A A G G G G A A G G G A A A C	6) //3 G ss490556207 G ss490550254 G ss490550263 A ss490556216 A ss490556220 G ss490556220 G ss490556239 A ss490556242 C ss490556245	27-04-16 2 5 4 7 G G A A G G A C G G A C G A C G A G C G A G A G A G A A G A A C A C C C A C C C A C C C C A C C C C A C	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	enome: sweet cherry, sour cherry (<i>avium</i>) sour cherry (<i>fruticosa</i>)
\$\$490556207 \$\$490550254 \$\$490550263 \$\$490556216 \$\$490556220 \$\$490556220 \$\$490556239 \$\$490556242 \$\$490556245 \$\$490556251	8(24) 20 1 3 A A G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G A A C A A	4 34) 3 4 6 6 6 6 6 6 6 6 A 6 G 6 A 6 A 6 A 6 A 6 A 6 A 6 A 6 A 6	(24) 2 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G 4 A 4 A C C 3 A	1 4 2 4 A G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G A A G G G A A A G G G A A A G A A G	6) //3 G \$\$490556207 G \$\$490550254 G \$\$490550263 A \$\$490556216 A \$\$490556220 G \$\$490556220 G \$\$490556220 G \$\$490556239 A \$\$490556242 C \$\$490556245 A \$\$490556251	27-04-16 2 5 4 7 G G A A G G A C G G A C G A C G A G A G A G A C A G A A C A C C G A A C G A A C C A C C C A C C C A C C C A C C C C C C C C C C C C C C C C C C	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	enome: sweet cherry, sour cherry (<i>avium</i>) sour cherry (<i>fruticosa</i>)
ss490556207 ss490550254 ss490550263 ss490556220 ss490556220 ss490556239 ss490556242 ss490556245 ss490556251 ss490556254	8(24) 20 1 3 A A G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G A A C A G G G	34) 3 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	(24) 2 3 A 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G	1 (47) 3(5 1 4 2 4 A G G G G G G G G G G G G G G G G G G G G G G G G G G G G G A A G G G A A A G A A G A A G A A G A G G	6) //3 G ss490556207 G ss490550254 G ss490550263 A ss490556216 A ss490556220 G ss490556220 G ss490556239 A ss490556242 C ss490556245 A ss490556251 G ss490556254	27-04-16 2 5 4 7 G G A A G G A C G G A C G G A C G A G C G A G A C A G A A C A C C G A A C G A A C C A C C G A A C C A C A C A C C C C C C A C C C C C C A C C C C C	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	enome: sweet cherry, sour cherry (<i>avium</i>) KE sour cherry (<i>fruticosa</i>)
ss490556207 ss490550254 ss490550263 ss490556216 ss490556220 ss490556239 ss490556239 ss490556245 ss490556251 ss490556251 ss490556257 ss490556257	8(24) 20 1 3 2 A A G G G G G G G C C A A G G G G G G G G G G G G G G G G G A G G A C C A A G G G A A G G G A A C C A	4 34) 3 4 6 6 6 6 6 6 6 6 7 7 7 8 7 7 9 7 7	(24) 2 3 A 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G	1 (47) 3(5) 1 4 2 4 A G G G G G G G G G G G G G G G G G G G G G G G G G G A A G G G A A A G A A G A A G G A A A G G G A A G A A	6) //3 G ss490556207 G ss490550254 G ss490550263 A ss490556216 A ss490556220 G ss490556220 G ss490556239 A ss490556242 C ss490556251 G ss490556251 G ss490556254 A ss490556257 C ss490556257	27-04-16 2 5 4 7 G G A A G G A A G G A C G G A C G A G C G A G A C A C G A A C C A C C A A C C A C C A C C A A C C A C C A A C C A C C A C C A C C A C C A A C C A C C A A C C A C C A C C A C C A A A A A A A A A C A A A A A C A C C A A A A A C A A A A A C A A A A A A C A C C A A A A A A C A C C A A A A A C A C C C C	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	enome: sweet cherry, sour cherry (<i>avium</i>) KEY sour cherry (<i>fruticosa</i>)
ss490556207 ss490550254 ss490550263 ss490556220 ss490556220 ss490556239 ss490556245 ss490556245 ss490556251 ss490556254 ss490556257 ss490556250	8(24) 20 1 3 2 A A 6 G G 6 G G 6 G G 6 G G 6 G G 6 G G 6 G G 6 G G 6 G A 6 G A 6 G A 6 G A 6 G A 7 G C 6	34) 3 4 6 6 6 6 6 6 6 6 6 6 6 6 6	(24) 2 3 A 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G	1 (47) 3(5 1 4 2 4 A G G G G G G G G G G G G G G G G G G G G G G G G G G A A G G G A A A G A A G G A A A A G G A A G A A G A A G A A G A A G A A G A A	6) //3 G ss490556207 G ss490550254 G ss490550263 A ss490556216 A ss490556220 G ss490556220 G ss490556239 A ss490556242 C ss490556245 A ss490556251 G ss490556254 A ss490556257 C slocus	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	enome: sweet cherry, sour cherry (<i>avium</i>) sour cherry (<i>fruticosa</i>)
ss490556207 ss490550254 ss490550263 ss490556220 ss490556220 ss490556239 ss490556242 ss490556242 ss490556251 ss490556254 ss490556254 ss490556254 ss490556257 ss490556260 ss490556259322	8(24) 20 1 3 2 A A 6 G G 6 G G 6 G G 6 G G 6 G G 6 G G 6 G G 6 G A 6 G A A G A A G G A G G A A A A	34) 3 4 6 6 6 6 6 A 6 A 6 A 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6	(24) 2 3 A 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G	1 (47) 3(5) 1 4 2 4 A G G G G G G G G G G G G G G G G G G G G G G G A A G G G A A A G G G A A A G G A A 3 6 4 G G A A G A	6) /3 G ss490556207 G ss490550254 G ss490550254 G ss490556216 A ss490556220 G ss490556220 G ss490556239 A ss490556242 C ss490556251 G ss490556254 A ss490556254 A ss490556254 A ss490556263 A ss490556260 A ss490556260	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	enome: sweet cherry, sour cherry (<i>avium</i>) sour cherry (<i>fruticosa</i>)
ss490556207 ss490550254 ss490550263 ss490556220 ss490556220 ss490556239 ss490556242 ss490556242 ss490556251 ss490556254 ss490556254 ss490556260 ss490556263	8(24) 20 1 3 2 A A 6 G G 6 G G 6 G G 6 G G 6 G G 6 G G 6 G G 6 G A 6 G A 6 G A 6 G G A G G A G G A G G A G G A G A A G A A G A A	34) 3 4 6 6 6 6 6 A 6 A 6 A 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6	(24) 2 3 A 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G	1 (47) 3(5) 1 4 2 4 A G G G G G G G G G G G G G G G G G G G G G G G A A G G G A A A G G G A A A G G A A G G A A C A A C A G G A A C A G G G A C A	6) /3 G ss490556207 G ss490550254 G ss490550254 G ss490550263 A ss490556216 A ss490556220 G ss490556220 G ss490556231 G ss490556251 G ss490556254 A ss490556254 A ss490556254 A ss490556263 A ss490556263 A ss490556263	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	enome: sweet cherry, sour cherry (<i>avium</i>) sour cherry (<i>fruticosa</i>)
ss490556207 ss490550254 ss490550263 ss490556216 ss490556220 ss490556239 ss490556242 ss490556245 ss490556251 ss490556254 ss490556254 ss490556260 ss490556263 ss490556263 ss490556263	8(24) 20 1 3 2 A A 6 G G 6 G G 6 G G 6 G G 6 G G 6 G G 6 G A 6 G A 6 G A 6 G A A G G A A A 6 G G A A A 6 G G 6 G G 6	34) 3 4 6 6 6 6 6 A 6 A 6 A 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6 G 6	(24) 2 3 A 3 G 3 G 3 G 3 G 3 G 3 G 3 G 3 G	1 (47) 3(5) 1 4 2 4 A G G G G G G G G G G G G G G G G G G G G G G G A A G G G A A A G G A A G G A A G G G G A A G G G G A G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G G	6) /3 G ss490556207 G ss490550254 G ss490550263 A ss490556216 A ss490556220 G ss490556220 G ss490556239 A ss490556242 C ss490556251 G ss490556251 G ss490556254 A ss490556254 A ss490556254 A ss490556263 G ss490556263 G ss490556263 G ss490556263 G ss490556263 G ss490550286	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	enome: sweet cherry, sour cherry (<i>avium</i>) sour cherry (<i>fruticosa</i>)

17





Outline

- Rosaceae COS markers
- High Density SNP markers
- <u>Application</u> Why some cherry fruit are large and some fruit are small?



Relative Contribution of Fruit Size Components (Olmstead et al. 2007)



NY54

Two fruit size QTLs were identified: LG2 and LG6

LG2 LG6 0.0 PR85 EPPCU3855-PR72 4.0 9.5 ME1-EM2-575 11.9 EMPaS01 0.0 - EAC-MCTA-260 16.5 UDP96-001 EPPCU9366-PR70 2.9 19.2 EAT-MCTC-375 BPPCT008 25.3 28.3 Ma014a 17.5 **BPPCT006** PR127 31.9 EPPCU6536-PR69 26.3 06Cel EAA-MCCC-160 33.3 29.1 EAA-MCAC-110 35.7 EAC-MCTA-225 EAC-MCTA-525 29.7 37.8 CPPCT029 30.5 EAC-MCTA-148 06FW 37.9 UDA-471 31.3 **EPPCU8702** 07FW 39.6 BPPCT006 EAT-MCCC-150 32.2 40.3 EMPA004 35.7 Ma069a CPSCT029 43.0 37.1 CPSCT038 EAT-MCTC-272 44.7 38.9 PR96 BPPCT009 44.9 39.8 UDA-059 48.5 **CPPCT023** 46.7 BPPCT034 EPPCU2828 50.1 MA005c 48.4 55.6 **PR86** EAA-MCCC-370 49.3 **EPPCU3090** 55.9 UDAp-461 51.5 57.2 EAA-MCAC-420 59.4 BPPCT002 59.6 EAA-MCCC-130 68.1 MA007a 59.7 UDAp-413 PCHGMS1 75.3 62.2 EAT-MCCC-100 UDA-005 76.4 UDP98-021 62.7 80.5 CPSCT021 EPPB4227 63.3 82.1 UCD-CH12 71.4 Ma040a 91.3 PceGA34 74.8 PrPFT 95.3 CPSCT034 PR93 EPPCU4092-PR56 75.5 76.5 EAC-MCTA-350 78.0 EAT-MCTC-142 EAC-MCTA-185 113.3 - EAA-MCCC-295 78.2 79.3 S-locus 82.4 PR121

Gbrowse view of the peach sequence for the G2 fruit size QTL region



Tomato: *fw2.2*

fw2.2: A Quantitative Trait Locus Key to the Evolution of Tomato Fruit Size

Anne Frary,¹* T. <u>Clint Nesbitt</u>,¹* <u>Amy Frary</u>,¹† Silvana Grandillo,¹<u>Esther van der Knaap</u>,¹ Bin Cong,¹ Jiping Liu,¹ Jaroslaw Meller,² Ron Elber,² Kevin B. Alpert,¹ Steven D. Tanksley¹§

Domestication of many plants has correlated with dramatic increases in fruit size. In tomato, one quantitative trait locus (QTL), fw2.2, was responsible for a large step in this process. When transformed into large-fruited cultivars, a cosmid derived from the fw2.2 region of a small-fruited wild species reduced fruit size by the predicted amount and had the gene action expected for fw2.2. The cause of the QTL effect is a single gene, ORFX, that is expressed early in floral development, controls carpel cell number, and has a sequence suggesting structural similarity to the human oncogene c-H-ras p21. Alterations in fruit size, imparted by fw2.2 alleles, are most likely due to changes in regulation rather than in the sequence and structure of the encoded protein.

Tomato and cherry fruit are both enlarged ovaries A fruit size gene was discovered in tomato that is a regulator of cell division





23 cell number regulator (CNR) genes were identified in the peach genome sequence



Three sweet cherry PavCNR12 alleles were identified that were differentiated by 14 SNPs





Three sweet cherry PavCNR12 alleles were identified that were differentiated by 14 SNPs





Mean fruit weight and cell number based on Group 2 *PavCNR12* allelic variants







Cell number regulator genes in *Prunus* provide candidate genes for the control of fruit size in sweet and sour cherry

P. De Franceschi · T. Stegmeir · A. Cabrera · E. van der Knaap · U. R. Rosyara · A. M. Sebolt · L. Dondini · E. Dirlewanger · J. Quero-Garcia · J. A. Campoy · A. F. Iezzoni

Mol Breeding 2013



Frary et al. 2000. Science



Fig. 1. (A) Fruit size extremes in the genus *Lycopersicon*. On the left is a fruit from the wild tomato species *L. pimpinellifolium*, which like all other wild tomato species, bears very small fruit. On the right is a fruit from *L. esculentum* cv Giant Red, bred to produce extremely large tomatoes. (B) Phenotypic effect of the fw2.2 transgene in the cultivar Mogeor. Fruit are from R1 progeny of fw107 segregating for the presence (+) or absence (-) of cos50 containing the small-fruit allele.

Fw2.2 – Prunus avium CNR12 & 16 have a common genetic basis, and possibly a common role in fleshy fruit growth & development

Conclusions

- Genome-wide polymorphic DNA markers are available for cherry
- The peach physical map locations for all these markers are known
- The genetic linkage map locations for many of these markers are known
- This information is publically available and "just a click away" on the Genome Database Rosaceae (<u>www.rosaceae.org</u>)
- This genetic knowledge will enable researchers to determine the genetic basis of trait variation in cherry





Acknowledgements

MICHIGAN STATE UNIVERSITY Travis Stegmeir Audrey Sebolt Umesh Rosyara

Esther van der Knaap Antonio Cabrera



Paolo De Franceschi Luca Dondini University of Bologna, Italy Jose Antonio Campoy Elisabeth Dirlewanger Jose Quero-Garcia



WASHINGTON STATE UNIVERSITY

www.rosaceae.org Dorrie Main & Sook Jung









United States Department of Agriculture National Institute of Food and Agriculture





PLOS ONE

Construction and Comparative Analyses of Highly Dense Linkage Maps of Two Sweet Cherry Intra-Specific Progenies of Commercial Cultivars

Carolina Klagges^{1®}, José Antonio Campoy^{2®}, José Quero-García², Alejandra Guzmán³, Levi Mansur³, Eduardo Gratacós³, Herman Silva⁴, Umesh R. Rosyara⁵, Amy Iezzoni⁵, Lee A. Meisel^{1,6}*, Elisabeth Dirlewanger²*



Table 1. Numbers of RosCOS and RosBREED Illumina SNP markers polymorphic in sweet cherry and average numbers of polymorphic RosBREED SNP markers based on the peach physical map (Mb) and sweet cherry genetic maps (cM). Values are presented for each of the eight *Prunus* linkage groups.

	-	۰.		
		r		
	_			
	-			
	-			

Linkage	Physical	Genetic	Number of	Number of	Average	Average
Group	length	length	polymorphic	polymorphic	physical	genetic
	(Mb)ª	(cM) ^b	<u>RosCOS^c</u>	RosBREED	distance	distance
				<u>SNPs^d</u>	between	between
					RosBREED	RosBREED
					SNPs (kb)	SNPs (cM)
1	46.88	189	71	359 (42)	130	0.53
2	26.81	90	19	204 (17)	131	0.44
3	22.02	102	29	203 (14)	108	0.50
4	30.53	78	27	222 (26)	138	0.35
5	18.50	68	29	184 (33)	101	0.37
6	28.90	120	43	228 (30)	127	0.53
7	22.79	72	24	199 (22)	114	0.36
8	21.83	91	26	226 (19)	97	0.40
TOTAL	218.26	788	268	1825 (203)	120	0.43

^a From Verde et al. (2013)

^b Sweet cherry genetic map length from <u>Klagges</u> et al. (2013). The longest <u>cM</u> length reported is presented.

^c From <u>Cabrara</u> et al. (2012)

^d From Peace et al. (2012). Numbers in parentheses are totals from <u>RosCOS</u> SNPs derived from sweet cherry and included in the first number.