ROSBREED

Combining disease resistance with horticultural quality in new rosaceous cultivars

Heritability and phenotypic correlations among bloom, flower density, and fruit set in peach (*Prunus persica*)



The peach breeding program at Texas A&M University has been working on the development of peach and nectarine cultivars adapted to the low and medium chill zones. As the major emphasis of the program is to introgress the superior horticultural traits from poorly adapted high chill germplasm into the marginal quality but well adapted low and medium chill germplasm, adaptation traits of bloom time, flower density and fruit set are essential to ensure consistent productivity. In conjunction with the RosBREED SCRI program, nine F_1 peach populations resulting from low- by high-sugar crosses from eight parents (Table 1) and characterized for bloom date (2 years, CA and TX), flower density (2 years, TX) and fruit density (1 year, TX). The characteristics of parents are listed in Table 2.

Table 1. Nine F1 populations and their crossing parents

	Population								
	1	2	3	4	5	6	7	8	9
Female Parent	TX2B136	TX2B136	Victor	Victor	Victor	TX2B136	TX3E213LW	TXW1490-1	TXW1490-1
Male Parent	Y434-40	Y435-246	Y426-371	Y435-246	Galaxy	Galaxy	Y434-40	Y434-40	Y435-246

Table 2. Fruit type, blush, chilling units, and ripe date of eight peach and nectarine genotypes in Fowler, CA and College Station, TX (2013-2014)

Genotype	Fruit Type	Blush (%)	Chilling units	Ripe date	Peach/ Nectarine	Full bloom (day)	Flower density	Fruit density
Y426-371	Ne-Yel	90	650	16 Jun	Nectarine	54.2	10.3	4.2
Y434-40	Ne-Yel	70-90	650	28 May	Nectarine	54.7	11.2	5.3
Y435-246	Ne-Yel	20-50	650	29 May	Nectarine	55.7	11.5	4.7
Galaxy	Pch-Wh	40-70	550	11 Jun	Heteroz.	56.3	14.6	5.8
Victor	Pch-Yel	50-70	450	20 May	Peach	51.5	10	3.8
TX2B136	Pch-Yel	60-80	150	25 May	Heteroz.	48.3	13.3	5.2
TX3E213LW	Pch-Wh	70-80	500	15 Jun	Peach	54.2	11.3	6.8
TXW1490-1	Pch-Yel	30-40	150	05 Jun	Peach	47.2	12.6	7.9
***Peach is comple	telv dominar	nt over necta	rine					

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Heritability and correlations

An all random effects model (REML) was used to estimate variance components and a multivariate model was used to estimate phenotypic correlations between traits. All three traits showed high broad sense heritability (0.995, 0.819, and 0.558 for bloom time, flower density, and fruit density, respectively) as has been previously reported with other populations. Narrow sense heritability estimates for bloom date (0.485) and fruit density (0.397) were moderate to high whereas the narrow sense heritability estimate for flower density (0.171) was low indicating a large non additive genetic variance (Table 3). Correlation analysis indicates that there is a good correlation (r=0.533) between flower and fruit density (Table 4) and that could be used to help select for a moderate fruit density.

sense (h²) for bloom time, flower density, and fruit density in nine F1 peach and nectarine populations in Fowler, CA and College Station, TX (2013-2014)

	Heritability (Broad sense H ²)	F (Nar
Bloom time	0.995 (n=735)	C
Flower density	0.819 (n=622)	C
Fruit density	0.558 (n=324)	C

Table 4. Phenotypic correlation coefficient among bloom time, flower density, and fruit density for nine F1 peach and nectarine populations Fowler, CA and College Station, TX (2013-2014)

	Bloom time	Flower density				
Bloom time		.044 (n=284)				
Flower density	.044 (n=284)					
Fruit density	.110* (n=324)	.533** (n=281)				
 Correlation is significant at the 0.05 level. ** Correlation is significant at the 0.01 level. 						

Correlation is significant at the 0.01 level.



Future studies

The next step in this study is to subject this data to a FlexQTL analysis to identify trait-marker associations.

Table 3. Heritability on broad sense (H²) and narrow

Heritability rrow sense h²) 0.485 (n=735) 0.171 (n=622) 0.397 (n=324)



