Probable Qualitative Inheritance of Full Red Skin Color in Peach

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Abstract. Recently observed hybrid populations of peach [Prunus persica (L.) Batsch] provide evidence for the presence of a single gene controlling full red skin color. The fruit of seedling populations of ‘UFQueen’ x ‘Springbaby’, ‘UFQueen’ x ‘Springprince’, FL93-12C x ‘Springprince’, FL92-22C x BY79P1945, and AP98-18 o.p. were rated for percent red skin color at full maturity. At this stage of development, “full red” phenotypes display red color over the entire surface of the fruit, including the stem cavity and portions of the fruit shaded by leaves or stems. Both crosses with ‘UFQueen’ yielded populations displaying a 1:1 segregation ration for partial red : full red. All other crosses produced populations that did not deviate significantly from a 3:1 segregation ratio. These data are consistent with the hypothesis that the “full red” phenotype is a single gene recessive trait. We propose the gene symbols of fr and F_r for the recessive full red and dominant partial red (wild-type) alleles, respectively.

Red skin color is a desirable trait contributing to the attractiveness of a peach. Hence, high levels of red blush are sought in most breeding programs developing cultivars for the fresh market (Scorza and Sherman, 1996). Several reports have been published on the expression and inheritance of red skin color (Blake, 1932, 1940; Hansche, 1986; Weinberger, 1944;), all of which concluded that it was under the control of multiple genes. We present evidence for the presence of qualitative gene control accounting for redness in the epidermis of peach fruit.

Table 1. Distribution of partial red skin color phenotypes and full red skin color phenotypes from crosses evaluated at Attapulgus, Ga. (2000 or 2001).

| Cross | Seedlings rated | Partial red | Full red | Test ratio | \( \chi^2 \) | P |
|-------|----------------|-------------|----------|------------|------------|---|
| ‘UFQueen’ x ‘Springbaby’ | 83 | 42 | 41 | 1:1 | 0.012 | 0.91 |
| ‘UFQueen’ x ‘Springprince’ | 14 | 7 | 7 | 1:1 | 0.000 | 1.00 |
| Pooled | 97 | 49 | 48 | 1:1 | 0.010 | 0.92 |
| FL93-12C x ‘Springprince’ | 19 | 15 | 4 | 3:1 | 0.158 | 0.69 |
| FL92-22C x BY79P1945 | 29 | 21 | 8 | 3:1 | 0.103 | 0.75 |
| AP98-18 o.p. | 35 | 26 | 9 | 3:1 | 0.010 | 0.92 |
| Pooled | 83 | 62 | 21 | 3:1 | 0.004 | 0.95 |

- Nectarine phenotype.
- Peach phenotype.
- Pooled samples were generated for the 1:1 and 3:1 segregation classes, respectively, after testing for heterogeneity.
- ‘FL93-12C’ = ‘Aztex Gold’ x ‘Honey A’.
- ‘FL92-22C’ = ‘Aztex Gold’ x ‘Oro A’.
- BY79P1945 = VP7117 o.p.
- AP98-18 = FL92-23C (= ‘Conserva’ x ‘Oro A’) x ‘Spring Baby’.
- FL95-1NW = FL88-18W (= ‘Flordiago’ o.p.) x ‘Suncoast’.
- FL94-5NW = FL84-18C (= ‘Oro A’ x ‘Summer’) o.p.

These data are consistent with the hypothesis that the “full red” phenotype is a single gene recessive trait. We propose that the recessive allele controlling full red skin development is present in the homozygous state in ‘UFQueen’ and ‘Spring Baby’, ‘Springprince’, FL93-12C, FL92-22C, BY79P1945, and AP98-18 are heterozygous. Selections FL95-1NW and FL94-5NW are evidently both homozygous for the dominant allele. We propose the gene symbols of fr and F_r for the recessive full red and dominant partial red (wild-type) alleles, respectively.

This trait should prove useful in breeding fresh market peach and nectarine cultivars, as red blush development in the full red phenotype is profoundly accelerated providing very high percent red blush at the “shipping ripe” stage, i.e., as ground color starts to change from green to yellow. Full red color development is achieved in many seedlings before any shift in ground color is observed.

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Hansche, P.E. 1986. Heritability of fruit quality traits in peach and nectarine breeding stocks dwarfed significantly from a 3:1 (partial red : full red) phenotypic segregation ratio. The phenotypic distributions for the partial red progeny from ‘UFQueen’ x ‘Spring Baby’ (Fig. 1B) and FL92-22C x BY79P1945 (Fig. 1C) indicate that quantitative segregation for percent skin color is also occurring in these populations. These data also appear to indicate that the homozygous full-red genotype may be masking the expression of the quantitative red genotypes similar to the recessive epistasis observed in conjunction with the white flower (W) locus of peach (Lammerts, 1945).

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Fig. 1. Distribution of red skin color in seedlings of three peach crosses.