Assessment of Genetic Resistance to Crown Gall in Roots of Apricot Hybrid Descents

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Abstract

Plants from five inter-varietal crosses of the apricot cultivars Bergeron, Stark Early Orange and Stella were tested for their resistance to Crown Gall in field conditions at Velestino, Greece. One-year-old plants were inoculated by immersing the roots in a suspension of a mixture of local strains of *Agrobacterium tumefaciens* immediately before they were planted. Resistance was evaluated by the weight of the galls eight months after inoculation. Segregation of characters was observed in all the descents, demonstrating the heterozygotic nature of the parent cultivars. The distributions of gall weights obtained in the five hybrid families indicate that at least two allele pairs are involved in the determination of the level of resistance to the disease.

Keywords: *Agrobacterium tumefaciens*; apricot genotypes; resistance to crown gall

INTRODUCTION

The identification of the genetic determinism of resistance to Crown Gall is one of the components of the European research project *Optimization of the apricot genetic improvement by a joint conventional and molecular approach applied to the main agronomic traits* (FAIR CT98 4345).

This study is being conducted through the evaluation of descents obtained by crossing sensitive and resistant apricot varieties. Targeted diseases are Sharka, Bacterial Canker, Crown Gall, and Bacterial Leaf and Fruit Spot. The work is done in parallel with the search of molecular markers for the genes involved in the process of resistance.

MATERIALS AND METHODS

Plants from five inter-varietal crosses were tested for crown gall formation on roots in field conditions at Velestino, Greece. Resistant parents were Stark Early Orange (SEO) and Stella, sensitive was Bergeron (Table 1).

One-year-old plants were inoculated by immersing the roots in a suspension of a mixture of local strains of *Agrobacterium tumefaciens* immediately before they were planted. Severity was evaluated by the weight of the galls eight months after inoculation.

All statistical analyses were performed as described by SOKAL and ROHLF (1994).

RESULTS

The observed severity of galls is represented in Figure 1. A summary of the results can be found in Table 1.

Table 1. Apricot descents tested for susceptibility to Crown Gall by root inoculation

	Genotypes	Not infected	Gall weight (g) on infected	
			average	s.d.
Bergeron × Bergeron	19	1	123.1	53.3
Bergeron × Stella	43	6	105.7	37.2
Stella × Bergeron	56	11	91.1	35.1
Bergeron × SEO	21	6	81.2	16.8
Stella × SEO	10	3	76.7	27.4

Table 2. Results of a chi-square analysis of the frequencies of genotypes showing no galls against the expected Mendelian frequencies under the hypotheses of resistance being controlled by one or two genes

	One gene		Two genes							
Theoretical segregation	1:3	2:2	1:15	2:14	3:13	4:12	5:11	6:10	7:9	8:8
Bergeron×Bergeron	A	na	A	A	A	R	R	R	R	na
Bergeron×Stella	A	R	R	A	A	A	R	R	R	R
Bergeron×SEO	A	A	R	R	A	A	A	A	A	R
Stella×SEO	A	A	R	A	A	A	A	A	A	A

A – accept, R – reject H_0 ($P = 0.05$); na – not applicable

Theoretically, the two families Stella × Bergeron and Bergeron × Stella should be similar, as they are reciprocal crosses between the same genitors. This seems to be the case, as both Mann-Whitney and Kruskal-Wallis tests indicate that there are no significant differences between them (11% probability). These two descents were therefore pooled together in the following analyses. The hypothesis of the four groups belonging to the same population can be rejected (Kruskal-Wallis $H = 12.69$, probability $= 0.005$).

In order to assess how many genes are involved in the determinism of resistance to Crown Gall, a chi-square test was performed with the frequencies of genotypes that did not develop galls after experimental inoculation (resistant) against the expected Mendelian proportions, under the assumptions of resistance being determined by one and by two genes (Table 2). Under the one-gene hypothesis, the three varieties would be heterozygotic, thus having the same genetic constitution with respect to this trait. This is in contradiction with other evidence: on one hand, Bergeron has been demonstrated to be less resistant than the other two (J.M. Audergon, INRA-Avignon, France, pers. commun.); on the other hand, the galls obtained on each of the hybrid descents have a weight distribution that is statistically different from the others.

The two-genes hypothesis is compatible with several genetic configurations of the three cultivars. These were evaluated after distributing the gall weights observed in each descent by the appropriate number of frequency classes. The results of the goodness of fit chi-square tests of the various hypotheses are summarized in Table 3.

Conclusions

Segregation of characters was observed in all of the descents, demonstrating the heterozygotic nature of the parent cultivars. The distributions of gall weights obtained in the five hybrid families indicate that at least two allele pairs are involved in the determination of the level of resistance to the disease.

The results here reported seem to indicate that, if two genes (here referred to as A and B) are involved

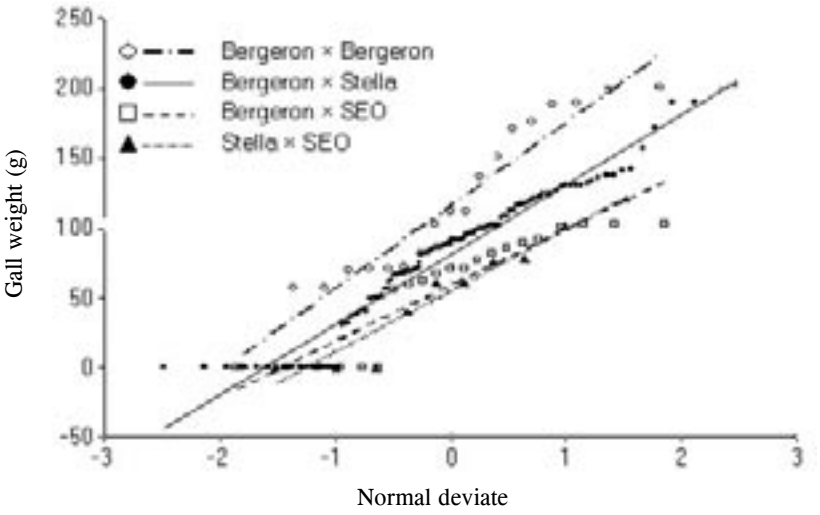

Figure 1. Severity of root galls in five descents of apricot varietal crosses (Bergeron × Stella and Stella × Bergeron pooled together)

Table 3. Analysis of the several hypothetical genetic constitutions of the parent apricot cultivars with respect to resistance to Crown Gall

Hypothetical genetic constitutions	Criteria
Reject Bergeron homozygotic in both loci	1:1 segregation not acceptable except with SEO
Bergeron heterozygotic in one locus (aaBb)	Bergeron × Bergeron = 1:2:1 ($P = 0.212$)
Stella heterozygotic in the same locus (AABb)	Bergeron × Stella = 1:2:1 ($P = 0.174$)
Reject Stella being homozygotic on both loci (AABB, AAbb, aaBB)	Bergeron × Stella = 1:1 ($P = 0$)
Reject Stella being homozygotic on the other locus (AaBB)	Bergeron × Stella = 1:1:1:1 ($P = 0$)
SEO heterozygotic in the other locus (AaBB)	Bergeron × SEO = 1:1:1:1 ($P = 0.707$) Stella × SEO = 1:1:1:1 ($P = 0.946$)
SEO homozygotic in both loci (AABB, AAbb, aaBB)	Bergeron × SEO = 1:1 ($P = 0.05$) Stella × SEO = 1:1 ($P = 0.206$)
Bergeron heterozygotic in both loci (AaBb)	Bergeron × Bergeron = 4:2:2:2:2:1:1:1:1 ($P = 0.928$)
Stella heterozygotic in one locus (AABb)	Bergeron × Stella = 2:2:1:1:1:1 ($P = 0.509$)
Reject Stella being homozygotic on both loci (AABB, AAbb, aaBB)	Bergeron × Stella = 1:1:1:1 ($P = 0$)
SEO heterozygotic in the other locus (AaBB)	Bergeron × SEO = 2:2:1:1:1:1 ($P = 0.733$) Stella × SEO = 1:1:1:1 ($P = 0.946$)
SEO homozygotic in both loci (AABB, AAbb, aaBB)	Bergeron × SEO = 1:1:1:1 ($P = 0.707$) Stella × SEO = 1:1 ($P = 0.206$)

in the resistance to Crown Gall, they have an additive effect, different hybrid constitutions showing different degrees of resistance to the disease.

Under this hypothesis, the constitution of Bergeron would be either aaBb or AaBb; that of Stella would be AABb; and that of SEO could be AaBB or homozygotic (AABB, AAbb or aaBB). However, the comparison of the descents of Bergeron with Stella and SEO seems to indicate that determinants carried by this last cultivar (locus B) induce a somewhat stronger resistance to Crown Gall.

References

SOKAL R.R., ROHLF F.J. (1994): Biometry: The Principles and Practice of Statistics in Biological Research. W.H. Freeman & Co., New York.