Morphological and biochemical variability in two-species congruity backcross (CBC) *Phaseolus vulgaris x P. coccineus* hybrids

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Introduction

With two-species, bidirectional *P. vulgaris x P. acutifolius* CBC pedigrees, transference of economically important traits from *P. acutifolius* into *P. vulgaris* have been reported (Petersen, 1993; Anderson, et al., 1995). Transgressive, individuals surfaced with novel mechanisms of drought tolerance. More recent studies have shown that other traits were transmitted to produce CBC individuals with morphological or biochemical markers of nonparental *Phaseolus* species. While these two species differ for many important traits, they both possess many of the same "species genes" described by Lamprecht (1948). Species genes mean that all members of the same species are homozygous for alleles (usually dominant) encoding the diagnostic trait.

P. vulgaris and *P. coccineus* have been frequently employed to create interspecific hybrids. Both species differ for species genes controlling cotyledon (epigeal / hypogeal) and stigma position (introrse / intermediate / extrorse). There have been no reports of recombination for species-specific traits. We initiated a CBC crossing scheme involving these two species as parents to test the effectiveness of CBC in disrupting the species-specific traits, i.e. would CBC disrupt the tight linkages between these two species.

Materials and Methods

Two different CBC pedigrees were initiated, both involving *P. vulgaris* 'Soldier' as female and either a 2- (2WPC) or 4-way (4WPC) intraspecific *P. coccineus* as male. Genotypes in each generation were selected for fertility (pollen stainability, self or cross seed set); F_2 or later selfed generations were created (if the genotypes possessed introrse stigmas & could self). Morphological traits (germination type, stigma position, leaf length / width ratios, primary inflorescence lengths, growth habit, seed coat coloration, etc.) and biochemical markers (total seed protein & root peroxidase profiles using 1-D SDS/PAGE) were recorded for all generations.

Results and Discussion

Seed protein banding profiles showed primary F_1 hybrids to be intermediate to the parents. Later selfed or CBC generations more closely resembled the female parent, *P. vulgaris* 'Soldier'. New high and low molecular weight proteins appeared. Early generations of 'Soldier' x 4WPC resembled 'Soldier' in morphology and remained stable through the F_4. However, as CBC progressed transgressive segregants were found. CBC2 individuals possessed cross-overs for species-specific traits (determinate, self-fertile plants with introrse stigmas, red flowers, and epigeal germination). As would be expected, seed morphological traits (under maternal control and lagging one generation behind in expression) resembled 'Soldier' during the early generations. All genotypes within the 'Soldier' series are ttee

(Prakken, 1934), but segregated for minor genes (hypostatic on ttee) controlling the presence or absence of color in six color centers. However, as CBC progressed F_2 phenotypes (F_1 genotypes) appeared without the 'Soldier' phenotype. The loss of the 'Soldier' expression in 94-16 F_2 phenotype (CBC3) is due to a change in the genotypic constitution: a switch from ttee to ttEE (tt encodes white flowers & prevents pigment production in some areas of the testa). In CBC2, 93-19 F_2 phenotype the switch was from ttee to TTEE (since these seeds had 100% pigment production & colored flowers). This is the first documented change of two homozygous, recessive genes into dominants due to CBC.

The most unusual segregants occurred with 'Soldier' x 2WPC, in which the primary F_1 (92-1 individuals) possessed primarily *P. coccineus* traits. Transgressive segregants, similar to 93-18 progeny, were found that had cross-overs for species traits: a determinate, red-flowered plant with *P. coccineus* flowers and *P. vulgaris* introrse stigmas. By CBC1, all of the variation reported for three-species CBC hybrids (*P. coccineus x [P. vulgaris x P. acutifolius*]) was evident. Seed morphology showed the most dramatic change in the primary F_1 generation (F_2 phenotype). The maternal genotype of ttee was changed immediately to TTEE. Why this genetic change would occur prior to the initiation of CBC is unclear, since 4WPC was derived from 2WPC. Clearly, seed coat coloration and patterning unique to *P. vulgaris* (ttee) can be ameliorated into other *P. vulgaris* types with the addition of *P. coccineus*.

References

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