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**Genotypes at the BoCAL-a Locus in B. oleracea do not predict Broccoli, Cauliflower, and Purple Cauliflower phenotype**

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Broccoli and cauliflower are different botanical varieties of *Brassica oleracea*, with very different phenotypes. A commonly found mutant allele at the locus BoCAL has been implicated in causing arrest at curding that is characteristic of the cauliflower phenotype. We surveyed the USDA collection of broccoli to test the correlation between the BoCAL-a genotype (homozygous wild-type, ww; heterozygous, wm; or homozygous mutant, mm) and phenotype (broccoli, intermediate (purple cauliflower), or cauliflower) of 19 accessions and 8 F1 hybrids of *B. oleracea*. The genotype at the BoCAL locus was significantly correlated with phenotype ($r^2 = 0.202$, d.f. = 161, $P < 0.01$). Numbers of (broccoli, purple cauliflower, cauliflower) plants were distributed as follows ww (46, 13, 32), wm (4, 5, 9), and mm (5, 4, 45). All three genotypic classes contained all three phenotypes. We tested 3 lines with a recessive (cauliflower) allele that included individuals with a broccoli appearance. Two lines showed a high environmental sensitivity for phenotype, one was consistently broccoli. In addition, we are testing the genotype of 3 accessions that appeared to segregate for the locus and to vary in phenotype. The mutant bocal-a allele was neither necessary nor sufficient to generate the cauliflower phenotype. There was no evidence that the gene action of the wild-type allele was dominant. Redundant function among gene products at 2 additional loci of CAL and 3 loci of AP1 could explain our findings. It is also possible that this BoCAL mutant allele is at a relatively high frequency in cauliflower but is not a causative agent of curding phenotype.
Genotypes at the BoCAL-a locus do not predict Broccoli, Cauliflower, and Purple Cauliflower phenotype

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ABSTRACT

INTRODUCTION

Broccoli and cauliflower are different botanical varieties of the same species (Brassica oleracea), with very different phenotypes. A commonly found mutant allele at the locus BoCAL-a has been implicated in causing arrest at curding that is characteristic of the cauliflower phenotype. The nonsense mutation stops production of a transcription factor that is involved in flower organ specification. This mutation causes a cauliflower-like phenotype in Arabidopsis thaliana (Kempin et al., 1995) and is present in many cauliflower accessions (Purugganan et al., 2000).

Does in reality explain the variation seen among broccoli accessions in the US germplasm system?

OBJECTIVES

1. Determine whether the CAULIFLOWER gene is diagnostic for the cauliflower form of Brassica oleracea.
2. Determine whether variation between and among lines is affected by the allele at the BoCAL-a locus.

MATERIALS AND METHODS

We surveyed the USDA collection of broccoli to test the correlation between the BoCAL-a genotype (homozygous wild-type, CC; heterozygous, Cc; or homozygous mutant, cc) and phenotype (Fig. 1) in 19 accessions and 8 F1 hybrids of B. oleracea. The genotype was determined by amplifying a region of the BoCAL-a gene containing the mutation sequencing the amplicon to determine whether base 483 was a G (wt) or a T (mutant). All the lines were planted in the field and evaluated for the stage of inflorescence arrest at harvest maturity.

RESULTS

PREDICTING PHENOTYPE FROM GENOTYPE

VARIATION AMONG LINES: The genotype at the BoCAL-a locus was significantly correlated with phenotype ($r^2 = 0.202$, d.f. = 161, $P < 0.01$). However, all three genotypic classes contained all three phenotypes (Fig. 2).

We also tested 3 lines fixed for the recessive (cauliflower) allele that included individuals with a broccoli appearance. Two lines showed a high environmental sensitivity (Fig. 3), one (High Sierra F1) was consistently broccoli.

GENETIC VARIATION WITHIN LINES: Within one mapping population, the genotype at BoCAL-a and API-a consistently predicts broccoli, cauliflower and intermediate phenotypes (Smith and King, 2000). We tested whether that was true in any of the accessions that varied both in genotype and phenotype. In these three accession, no such association was found (Table 1).

PHYSIOLOGICAL VARIATION WITHIN LINES: When the two accessions of tropical cauliflower were grown in Geneva, their phenotype changed as seasonal temperature declined (Fig. 4). That result is not entirely unexpected in that cauliflower from South Asia requires high temperatures for good cauliflower quality (Fig. 4).

The variation that is revealed in the Geneva climate could be due to promotion of flowering (broccoli-like) in individuals with the wild-type allele. However, both of these accessions had the mutant allele.

DISCUSSION

The mutant bocal-a allele was neither necessary nor sufficient to generate the cauliflower phenotype. There was no evidence that the gene action of the wild-type allele was dominant in this group of accession. Redundant function among gene products at 2 additional loci of BoCAL and 3 loci of BoAPI could explain our findings. Alternatively, the BoCAL genotype may have the effect predicted from its function only when it is not masked by other genes that are as yet unidentified. Finally, it is also possible that this BoCAL mutant allele is at a relatively high frequency in cauliflower but is not a causative agent of curding phenotype.

The mutant allele at the BoCAL locus is more common in cauliflower than in broccoli, but it is not diagnostic for classifying Brassica oleracea accessions as cauliflower.