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

Joanne Labate¹, Larry Robertson¹, Thomas Björkman²

¹Plant Genetic Resources Unit, USDA-ARS, Collier Dr., Geneva, NY, 14456, ²Horticultural Sciences, Cornell University, NYSAES,

630 W. North St., Geneva, NY, 14456

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

Joanne A. Labate¹, Larry D. Robertson¹, and Thomas Björkman²

ABSTRACT
233



¹Plant Genetic Resources Unit, ARS, Geneva, New York 14456.

²Department of Horticultural Sciences, NYSAES, Cornell University, Geneva, New York 14456.



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 it really 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.



Figure 1. Scale for scoring stage of arrest

LITERATURE CITED

Kempin, S.A., B. Savidge, and M.F. Yanofsky. 1995. Molecular basis of the cauliflower phenotype in *Arabidopsis*. *Science* 267: 522-525.

Purugganan, M.D., A.B. Boyles, and J.I. Suduth. 2000. Variation and selection at the CAULIFLOWER floral homeotic gene accompanying the evolution of domesticated *Brassica oleracea*. *Genetics* 155: 855-862.

Smith, L.B. and G.J. King. 2000. The distribution of *BoCAL-a* alleles in *Brassica oleracea* is consistent with a genetic model for curd development and domestication in cauliflower. *Molecular Breeding* 6:603-613

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.

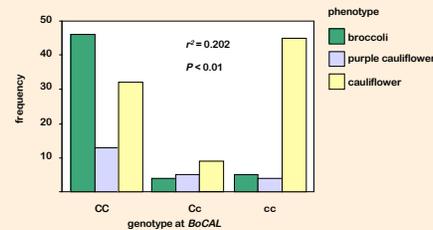


Fig. 2. Frequency of *BoCAL-a* genotypes in broccoli, cauliflower and purple cauliflower plants (C = wild-type allele, c = mutant allele).

GENETIC VARIATION WITHIN LINES: Within one mapping population, the genotype at *BoCAL-a* and *API-1a* 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 accessions, no such association was found (Table 1).

Table 1. Three accessions segregated for the <i>BoCAL</i> genotype and for phenotype. The expected effect of the mutant allele (c) is to make the phenotype more cauliflower-like (a higher score). The <i>BoCAL</i> genotype did not significantly affect the observed phenotype in any of the three accessions.					
Ramoso (PI 4411510)					
	Score				
Genotype	1	3	5	6	Mean
CC	0	1	12	0	4.8
Cc	1	1	7	2	7.7
cc	2	1	5	0	4.7
					$\chi^2=8.12, P=23\%$
Cavolo Broccolo precoce (G30928)					
	Score				
Genotype	2	4			Mean
CC	10	6	0		2.8
Cc	0	0			-
cc	4	5			3.1
					$\chi^2=0.76, P=38\%$
Indian cauliflower (PI 115881)					
	Score				
Genotype	2/3	4	5	6	Mean
CC	1	0	3	0	4.3
Cc	2	1	3	2	4.6
cc	1	2	8	6	5.1
					$\chi^2=4.48, P=61\%$

PHYSIOLOGICAL VARIATION WITHIN LINES: When the two accessions of tropical cauliflower were grown in Geneva, their phenotype changed as seasonal temperature declined (Fig. 3). 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.

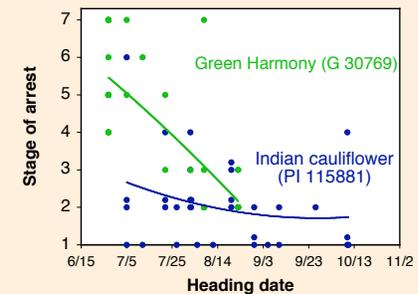


Figure 3. Two accessions of tropical cauliflower were scored as more broccoli-like as temperatures declined.



Figure 4. Effect of growth-chamber temperature on the phenotype of 'Green Harmony' inflorescences. This variety is homozygous for 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.