Allelic variation in a putative gene related to pungency in pepper (Capsicum spp.)

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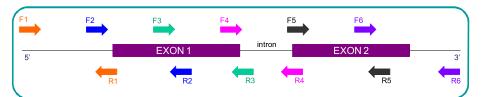


INTRODUCTION

The capsaicinoids, responsible for pungency in peppers (*Capsicum* spp.), exhibit a wide genetic and environmental control variation. Pungency in pepper is one of the most interesting quality traits and it requires a greater knowledge about its genetic control. At this moment, not all the genes involved in the capsaicinoid biosynthesis pathway have been characterized. From a previous work, a partial DNA sequence, possibly related to pungency was identified (Garcés-Claver et al., 2007). The aim of this work was to obtain and analyze variation of the complete DNA sequence in several pepper genotypes from different species.

MATERIAL AND METHODS

To obtain the full DNA sequence from a model genotype, *C. annuum* 'Yolo Wonder' the Genome Walking technique was used and several pairs of primers were designed along that sequence.



Those primers were used to obtain the full DNA sequence in the following selected genotypes:

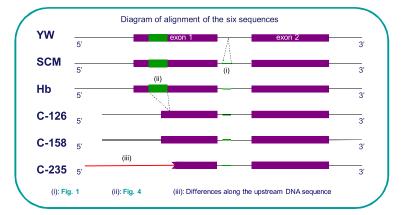
Three model pepper genotypes:

- C. annuum 'Yolo Wonder' (YW), non-pungent.
- C. annuum 'SCM-334' (SCM), pungent.
- C. chinense 'Habanero' (Hb), pungent.

Three genotypes due to their particularities concerning to pungency trait:

- C. chinense 'C-158', pungent.
- C. frutescens 'C-126', pungent.
- C. baccatum 'C-235', pungent.

RESULTS



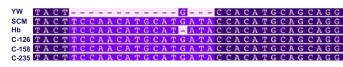


Fig.1. 15 bp deletion on C. annuum YW.



Fig. 2. Example of SNP specific to C. annuum YW and SCM.

Alignment of the six sequences showed allelic variability:

A 15 bp deletion was found only in the non pungent genotype (Fig. 1). This result was confirmed when more non-pungent genotypes were studied.

Several Single Nucleotide Polymorphisms (SNPs) were identified, ones distinctive of species (Fig. 2) and others pungent-specific (Fig. 3).

A 51 bp deletion was found on C-158 (*C. chinense*) and C-126 (*C. frutescens*) (Fig. 4).

Differences along the upstream DNA sequence region in C-235 (*C. baccatum*) were observed (iii).



Fig. 3. Example of SNP related to pungency trait



Fig. 4. 51 bp deletion on C. baccatum C-235.

Sequence polymorphisms may be involved in phenotypic trait variation concerning capsaicinoids composition and/or content. The detected allelic variation has to be further investigated, to better know how it could affect at the phenotypic level of the pungency trait.

References: Garcés-Claver A, Moore Fellman S, Gil Ortega R, Jahn MM, Arnedo Andrés MS. 2007. Identification, validation and genotyping of a single nucleotide polymorphism SNP associated with pungency in Capsicum spp. Theoretical and Applied Genetics 115, 7: 907-916.