

Evaluation of PUN1 gene and capsaicinoids content in pepper genetic resources with excellent phenotype

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ABSTRACT

Pepper (*Capsicum* spp.) is one of the main quality features of this crop because of its sense of pungency, which is due to the presence of capsaicinoids. This compound is synthesized as a secondary metabolite and found only in the placental tissue of spicy fruit (Suzuki et al., 1980). Stewart et al. (2005) concluded that Pun1 encodes for the acyltransferase AT3 and they demonstrated its involvement in capsaicinoids metabolism. It was analyzed that the capsaicinoids content and PUN1 genotype in pepper genetic resources which were selected with excellent phenotype in field evaluation. The number of pepper genetic resources analyzed was 135, and species were *C. annuum*, *C. baccatum*, *C. chinense*, *C. frutescens*. The content of capsaicinoid ranged from 0 mg/100g to 828 mg/100g. The content of 0 mg/100g was the sweet pepper type, the highest content is IT 158530, the capsaicinoid content of which was 828 mg/100g and species was *C. annuum*. PUN1 gene analysis showed 117 pungent, 5 hetero, and 13 non-pungent. PUN1 analysis showed that 5 out of 13 non-pungent accessions were detected with low levels of capsaicinoid.

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