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Transcriptomic profiling of fruits from pepper (*Capsicum annuum* L.), variety Padrón (mild hot), at two ripening states †

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Abstract: Pepper (*Capsicum annuum* L.) fruits are one of the most consumed vegetables worldwide. This produce has a great agro-economical relevance since it is extensively cultivated. These fruits are characterized by their high vitamin C and A, and mineral contents [1]. *Capsicum annuum* has many varieties, whose fruits differ in size, shape, colour, and pungency being this last characteristic due to the presence, in different degrees, of capsaicinoids, alkaloids which are exclusive of the genus *Capsicum* [2]. The present study focuses in the transcriptomic profiling of an autochthonous Spanish variety called "Padrón" (mild hot) [3]. Pepper "Padrón" plants were grown in farms under the local conditions and fruits at both green and red ripe stages were collected. The transcriptome profiling was carried out in both types of fruits by RNA sequencing (RNA-seq) in the NextSeq550 system (Illumina®) [4]. RNA-seq analysis revealed that the expression of more than half of the 17,499 identified transcripts was modulated during ripening. Thus, comparing to green fruits, 5,626 and 5,241 genes were up- and down-regulated, respectively, in red fruits. These differentially expressed genes (DEGs) have been analyzed to determine the functional categories which orchestrate the ripening process at the genetic level of this non-climacteric fruit.

Keywords: Pepper fruits; ripening; RNAseq; transcriptome

Reference

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