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Peroxidase gene family in *Prunus persica* (L.)

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Motivation and Aim: Peroxidase (POD) is the key antioxidant enzyme, which involved in cell response to different negative factors (cold, drought, infection, heavy metal, atmospheric and soil pollutants, etc.). This gene family includes a lot of genes. At the same time, in studies that aim to assess the impact of various negative factors on peaches usually one or two genes are analyzed only [1]. It should be noted that another key enzyme, catalase, is encoded by 2 genes in peach with low nucleotide differences, but they have tissue-specific expression [2]. The aim of this study, therefore, was to evaluate the expression of all genes encoding peroxidase in peach using transcriptomics techniques and determine the possible correlation between the individual gene expression and specific organ.

Methods and Algorithms: The peach genome assembly (accession number GCA_000346465.2) contains 60 annotated genes encoding POD. The nucleotide diversity for all genes were analyzed. Phylogenetic tree analysis of all PODs was constructed with Maximum Parsimony method. The expression of genes encoding peroxidase in different tissues was analyzed using transcriptomic data available from NCBI. All genes expression was calculated using tpm method (transcripts per million) by Kallisto. The transcripts with tpm < 1 were excluded from analyses. Normalized counts by the relative log expression method implemented in DESeq2.

Results: Expression profiles of peroxidase encoding genes in different tissues were obtained. Phylogenetic analysis performed did not reveal a clear clustering of peroxidases. The exon-intron structure also varies greatly: some genes are intronless, while others have several long introns. The high nucleotide variability detected made it impossible to develop a single primer to estimate the total expression of the genes encoding a given protein.

Conclusion: Incorrect primer design and evaluation of the expression of not all genes encoding the target protein can lead to incorrect results. This needs to be taken into account during primer design as gene selection can play a significant role in studying the molecular mechanisms of adaptation of peach varieties to stress conditions.

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