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# TRANSCRIPTIONAL RESPONSE OF GIANT REED (*ARUNDO DONAX* L.) TO LONG TERM SALINITY STRESS BY UNIGENE-BASED RNA-SEQ

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*Arundo donax* L. is one of the most promising bioenergy crop due to its high biomass yield and low irrigation requirement, Considering that it naturally propagates by rooting of rhizome and from stem fragments, the genetic diversity among genotypes is expected to be low, but it is nevertheless detectable. Salinity is one of the extreme abiotic stress limiting growth and productivity of plants in many areas of the world, mainly because of an increasing use of brackish water for irrigation. The aim of this work was to analyze the effect of a long period of salt stress upon the whole leaf transcriptome by using a RNA-seq approach. Two genotypes (namely G2 and G34) have been selected based on their contrasting behavior under salinity stress. Two doses of NaCl (250 mM and 420 mM) were applied weekly with the irrigation water, after the emergence of the first shoot from buds, from August to November 2017. The Illumina based sequencing output was of 1073 million clean reads, which were assembled into 311960 unique sequences (unigenes) with an N50 of 1945 bp.The analysis of Differential Expressed Genes (DEGs) highlighted a different response of the genotypes either in control conditions, as a total of 9847 DEGs have been found by comparing G2 and G34 transcriptome, or under salt stress condition. In this latter case, the response of G34 genotype to both salt doses has involved a decisively smaller number of DEGs than that observed in G2 genotype.Thus,the results clearly indicate that distinct transcriptional regulation occurred, despite the low genetic diversity expected in this species. Among the most significantly enriched KEGG pathways identified by comparing G34 with G2 grown in control conditions, a crucial role is played by genes involved in plant hormone-signal transduction and in starch and sucrose metabolism. Carbon metabolism and phenylpropanoid biosynthesis are enriched KEGG pathways in salt treated G34 and G2 genotypes, respectively. In addition, 45529 SSR markers were identified, as well as a total of 1186724 SNPs, thus facilitating the future analysis of genetic diversity in this crop. This study lays the foundation to select candidate genes for genome editing with the aim to improve salt stress tolerance. Finally, the analysis of the methylation status of DEG promoters, will clarify the role of epigenetic modifications upon gene expression in such vegetative propagated specie.