Like in many higher plants, bioinformatics analyses of coffee ESTs and gene sequences showed that around 30% of them are novel in the sense that their corresponding sequences (nucleic or putative translated protein) do not exhibit similarity with those already deposited in public databases. Recent concepts called such sequences as "no hits" or "orphan" genes, and postulate that they resulted of plant specific and adaptive responses regarding stresses and adverse environmental conditions that occurred during the evolution of species. Our work is focused on the identification and functional characterization of coffee orphan genes which may have a high potential for innovation and biotechnological applications either for coffee itself but also for other higher plants. In the frame of identifying candidate genes for drought-tolerance in coffee, several orphan genes (herein called Unk for Unknown) were previously identified. For example, this was the case of CcUNK8 gene that showed higher over-expression under drought in leaves of drought-tolerant clones of C. canephora than in those of the drought-susceptible clone. Aiming to identify the functions of CcUNK8 protein, this gene was cloned in an expression vector used to transformed embryogenic callus of Setaria viridis by Agrobacterium tumefaciens. Thirteen T₀ transformed plants of S. viridis were selected and the presence of T-DNA was confirmed by conventional PCR. For these plants, leaf CcUNK8 gene expression was analyzed by RT-qPCR and ranged from 1 to 20. In order to see if CcUNK8 over-expression enhances drought tolerance in S. viridis, physiological and phenological analyses of T₂ plants grown under irrigated and non-irrigated conditions were carried out. For all transformed events of S. viridis grown under drought stress, we observed that accumulation of fresh biomass in roots and shoot was higher than in WT (untransformed) plants. These preliminary results, suggesting that CcUNK8 could play in protecting plant against drought, should be confirmed in homozygous T₃ of S. viridis that are currently being analyzed.

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