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OVEREXPRESSION OF MAIZE ROOTLESS CONCERNING CROWN AND SEMINAL ROOTS (RTCS) GENE IN TOBACCO

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The phosphorus (P) availability is one of the most limiting factors for agricultural productivity in tropical soils, since this nutrient has the lowest efficiency use by plants. Roots play essential functions such as water and nutrient uptake to plant growth, storage, anchorage in the soil and are sites for plant-microorganism interactions. The root system is complex and formed by different root types. During embryogenesis, a primary root is deposited in the basal nucleus of the embryo, while a variable number of seminal roots are formed in the scutellum, which are relevant only in the early stages of development. In more advanced stages of development, an extensive post-embryonic root system form most of the root system. The maize rtcs (rootless concerning crown and seminal roots) mutant was identified by its complete lack of embryonic and post-embryonic roots. Subsequently, it was demonstrated that RTCS encodes a transcription factor responsible for the regulation of these root types in maize. In addition, RTCS was more expressed in a P-efficient maize genotype. The aim of this work was to overexpress the RTCS gene in tobacco plants to increase root surface area. For this, the RTCS gene was amplified from a P-efficient maize line (L3) and cloned in the binary vector pMCG1005. Tobacco plants were transformed via Agrobacterium tumefaciens, selected, regenerated and the insertion was confirmed by PCR with specific primers for RTCS and BAR genes. Three transgenic events were obtained and presented high copy number and low gene expression. However, all events presented superior vegetative growth and higher root surface area compared with the control. The *RTCS* gene encodes a transcription factor, that binds to auxin responsive factors, that could be stimulating root growth, even with low expression. The information generated in this work contribute for a better understating of root system genetic mechanism and production of genotypes resistant to abiotic stresses.

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