Resumos do GENÉTICA 2016 - 62º Congresso Brasileiro de Genética • 11 a 14 de setembro de 2016
Hotel Glória • Caxambu • MG • Brasil
www.sbg.org.br - ISBN 978-85-89109-06-2

Study of root architecture by overexpressing the maize *Rtcs* gene in tobacco

Campolino, ML.[1]; Carneiro, A.A.[2]; Lana, U.G.P.[1,2]; de Sousa, SM[1,2]

[1]Centro Universitário de Sete Lagoas (UNIFEMM), Sete Lagoas, MG; [2] Embrapa Milho e Sorgo, Sete Lagoas, MG.

Keywords: phosphorus, root, *Agrobacterium tumefaciens, Rtcs*, transcription factor

Phosphorus (P) availability is one of the most limiting factors for agricultural productivity in tropical soils, since this nutrient has the lowest use efficiency by plants. Roots perform essential functions, such as the absorption of water and nutrients for plant growth, storage, anchorage of the plants in the soil and are sites for plant-microorganism interactions. Therefore, the maize root system is complex and formed by different root types. During embryogenesis, a primary root is laid down at the basal pole of the embryo while a variable number of seminal roots are formed at the scutellar node, which are relevant only during the early stages of seedling development. At later stages of development, an extensive post-embryonic shoot-borne root system forms the major backbone of the adult root stock. The maize *rtcs* mutant (rootless concerning crown and seminal roots) was identified by its complete lack of embryonically formed seminal roots and post-embryonically formed shoot-borne roots. Later it was shown that *Rtcs* encodes a transcription factor responsible for the formation of these types of roots in maize. Furthermore, the *Rtcs* has been reported to be more expressed in P efficient maize genotypes under low P than in inefficient genotypes. The aim of this work was to better understand the increase in root surface by overexpressing the *Rtcs* gene in transgenic tobacco plants. For this, the *Rtcs* gene was amplified from two maize inbred lines contrasting for P acquisition efficiency (L3 - efficient and L22 - inefficient) and both were cloned into the binary vector pMCG1005. The construct harboring the gene of interest under the ubiquitin promoter also had the bar gene as a selective agent. The two constructs were transferred to *Agrobacterium tumefaciens* EHA101 in order to transform tobacco *Petit Havana* plants. Tobacco plants were regenerated from selected callus in shooting and rooting medium supplemented with 100 mg/ml of Tioxin and 1 mg/L of Phosphinothricin. PCR with gene specific and bar primers confirmed the presence of *Rtcs* gene in tobacco plants. Currently, putative transgenic tobacco plants are grown in the greenhouse for subsequential molecular and functional analyses of *Rtcs* regarding the enhancement of root surface, P acquisition and grain yield under low P conditions.

Fonte de financiamento: Fapemig, Embrapa e Unifemm.