Salt responsive proteins in two scion/rootstock combinations of dwarf cashew plants with salinity contrasting tolerance

Nathália Dias de Oliveira Amaral[1,3]; **Francisco Dalton Barreto de Oliveira[1],** Rafael de Souza Miranda[1], Rosilene de Oliveira Mesquita[3], Dirce Fernandes de Melo[1,2]; Enéas Gomes Filho[1,2].

[1]Departamento de Bioquímica e Biologia Molecular/UFC, Campus do Pici,Bl.907, CEP 60455-760 - Fortaleza – CE, Fone: (85) 3366 9405, e-mail: nathybio2002@yahoo.com.br, [2]Instituto Nacional de Ciência e Tecnologia em Salinidade (INCTSal/CNPq), Brasil. [3]Departamento de Agronomia/Fitotecnia/UFC .

INTRODUCTION: Cashew tree (*Anacardium occidentale* L.) is an important fruit crop in the Northeastern region of Brazil, displaying a great economic and social relevance in the arid and semiarid areas, where the low water disponiblity and/or saline soils have severely impaired the agricultural practices. Hence, particular interest exists in unraveling mechanisms leading to salt tolerance and improved crop plant performance on saline soils. This study aimed to analyse the leaf proteome profile of two scion/rootstock combinations of cashew plants irrigated with saline water in order to select salinity responsive proteins. **MATERIALS AND METHODS:** Two dwarf cashew scion/rootstock combinations, CCP 06/CCP 06 (salt sensitive) and BRS 265/CCP 06 (salt tolerance), were grown in plastic pots with 7.0 L of soil and irrigated with water of electric conductivity (ECw) of 0.8 (control) and 4.0 dS m^{-1}, during two months. The leaf proteome was analyzed based on two-dimensional gel electrophoresis (2DE) and a number of combination-specific and salinity stress-responsive proteins were identified by mass spectrometry. **RESULTS AND DISCUSSION:** Proteomic characterization by 2DE showed 489 and 360 differentially expressed spots in salt-tolerant and salt sensitive clones, respectively. In salt tolerant one, a total of 126 protein/peptides presented an altered expression by salinity; whereas only 68 protein/peptides have their expression changed by salt stress in the salt sensitive clone. In addition, under salinity, 99 spots/peptides showed differential expression between salt-tolerant and salt-sensitive clones. Mass spectrometry-based identification was successful for 151 proteins, which are associated with photosynthetic metabolism, reserve metabolism, response to stresses, carbohydrate metabolism, energy metabolism, antioxidant metabolism and structural function. **CONCLUSION:** Our data evidence a diferential modulation of protein expression in cashew tree scion/rootstock leaves affected by salinity and. Also, the results indicate some proteins responsive to salt stress, which may be used in plant breending studies.

Keywords: dwarf cashew; salt stress; proteomics.

Acknowledgements: CNPq; CAPES; INCTSal.