

International Conference on

Plant Physiology & Pathology

June 09-10, 2016 Dallas, USA

Response of Swingle citrumelo (*Citrus paradisi* Macf. x *Poncirus trifoliata* (L.) Raf.) seedlings to salt stress in four different soils of the Gharb region (Morocco)

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Salinity, affecting 35% of Moroccan irrigated land, often results in poor stand establishment, reduced plant growth and reduced yield of many horticultural crops. It is also known that salinity rarely occurs alone under natural conditions, but usually in combination with other abiotic factors which can influence plant response to stress. In the present study, we investigated the effect of substratum type and the interaction salinity x substratum on emergence, growth and chloride uptake of Swingle citrumelo, a citrus hybrid rootstock recently introduced to INRA (Morocco). 4 soil samples were collected from different citrus orchards located in the Gharb region (Morocco), analyzed for texture, pH, CE and CaCO₃ content, then used as substratum for germination of Swingle citrumelo seeds. Saline treatments were carried out for 2 months and consisted of the addition of NaCl to the irrigation solution at 3 different levels: 0 (control), 40 and 80 mM. The experiment was conducted in a split-plot design with salt levels as whole plots and soil types as subplots. The results showed variation of soil texture and CaCO₃ content but no variation regarding CE and pH within the soil samples tested. Under non saline conditions, the highest emergence rate and seedling height were observed in clay and slightly calcareous samples collected from Belksiri and Souq Tlat orchards. However, when subjected to salt stress, seedlings growing in a silty clay soil collected from Sidi Slimane showed the highest tolerance resulting in higher biomass and lower chloride accumulation in shoots. These differences as well as the relationships between soil properties and salinity responses of Swingle citrumelo seedlings are discussed.

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Analysis of the Auxin response factor gene family in soybean and common bean: Identification, dynamic and expression patterns

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Auxin response factors (ARFs) encode one of the most abundant groups of auxin mediated response transcription factors in higher plants and play a major role in different biological process. The success of whole genome sequencing allow to analyze more comprehensive phylogenetic analysis of the *ARF* genes in plants. In the present study, we identified 80 *ARF* genes belonging to 5 different groups in legume species, soybean (55) and common bean (25) based on phylogenetic analysis and supported by motif analysis. The duplication events among two species also observed by using Ka/Ks ratio. In soybean, a majority of *ARF* genes (40%; 22 of 55) were segmentally duplicated and 3.6% (2 of 55) of the genes were tandemly duplicated. This pattern was higher apparent in other plants. In addition, expression profiling indicated that *ARF* genes in soybean and common bean suggest its various functions in plant growth and development. Furthermore, Sp-1 and Skn-1 motif, which stable promoter involved in biotic and abiotic stresses and developmental processes, were highly detected in all of GmARF. Together, our work contribute to a molecular evolution of the *ARF* gene family in legume species and is useful for future study.

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