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Identification of Proteomics Changes Associated with Epigenetics for Aluminum Stress in Tomato

Abstract

Aluminum (Al) is the most abundant metal in the earth's crust, accounting for around 7% of the total mass. In acid soil, Al toxicity is a significant factor limiting crop yield. Aluminum toxicity is an ongoing issue for many cultivators of crops. Toxicity of Al is a key restriction for agricultural productivity in acidic soils across the world. When the pH of the soil falls below 5, Al^{3+} is released into the soil and enters the root tip cell, stopping the plant's root growth. So, in turn, researchers are now looking at various tolerance strategies of plants when put under heavy Al toxicity stress. There is also research that shows that the tomato plant shows the capability of certain avoidance mechanisms that can protect itself from the effects of Al toxicity. However, there is not enough significant research that tests this adaptive mechanism, proteomics changes associated with epigenetics or identifies how it works over long periods of Al stress. As there could be tolerance instilled against Al toxicity in tomato, research will be done to further test if this tolerance can be bred naturally over a longer span of generations. Using a specific cultivar of tomato plant, a procedure developed to examine how multiple generations of the same species will build Al tolerance over time will be useful. In this study, tomato plants were grown in a hydroponic system supplemented with Al during the reproductive stages (from flowering until fruit ripening). Tomato seeds produced by these plants were considered to be Al-enriched as they contained a higher Al content than those harvested from plants growing in a solution without added Al. Subsequently, the Al-enriched seeds were germinated in an Al solution, and a proteomics analysis of their radicles was performed to identify proteome changes in response to the Al treatment as a means to identify candidate proteins that could play a key role in acquiring Al tolerance