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Uncovering key genes and networks regulating root growth using systems genetics

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Wolfgang Busch is a Junior Group Leader of Gregor Mendor Institute of Molecular Plant Biology, Austrian Academy of Sciences. He has won the 2015 President's Medal of the Society for Experimental Biology (SEB) in the Plant section, in recognition of his outstanding work on comprehending how plant growth and development are quantitatively regulated at the molecular level

Despite their inability to move, vascular plants have colonized the vast majority of the earth's land surface. Key to this colonization was the evolution of root systems that enable plants to forage their environment for both nutrients and water and to tightly anchor themselves in the soil substrate. Soils are very heterogeneous environments, and due to the constant need to optimize root distribution in the soil according to sometimes conflicting parameters, root growth and development are some of the most plastic traits in plants. While this modulation of growth and development occurs in response to environmental conditions, both its onset and extent are genetically determined. In recent years, the genetic and molecular basis underlying root growth regulation has been approached and many genes and pathways have been uncovered that play key roles for root growth processes. However, only very recently is light being shed on the genes and genetic and molecular mechanisms that determine differences in root growth in natural populations. To approach this question, we use an approach combining custom large-scale phenotyping pipelines that enable us to capture quantitative root phenotypes of a very large number of genetically distinct individuals of the model plant Arabidopsis thaliana, genome wide association studies to identify the associated loci in the genome, and systems-biology driven approaches to identify the gene networks and pathways that quantitatively regulate root growth. Using these approaches, we have recently identified and experimentally verified multiple novel regulators that underlie a significant proportion of natural variation in root growth. One of these, a component of the exocyst complex, is a novel auxin signaling component which exclusively regulates root system architecture by modulating lateral root density and root growth direction. We show that this exocyst gene regulates the dynamic localization of a specific PIN auxin efflux carrier in root cap cells. We further show that allelic variation of the exocyst gene switches between two root system architecture types and can increase resistance to drought conditions indicating an adaptive value of root system architecture. Moreover, using these approaches, we were able to identify modules of interacting genes that, through their interaction, strongly modulate root growth. Notably, we identified a regulatory module of leucine-rich repeat receptor-like kinase (LRR-RLK) genes that regulates root growth in an epistatic manner. We are currently investigating the interaction of these genes at the molecular level and have found that at least two of these LRR-RLKs act in the same protein complex. Overall, our results demonstrate that, using a systems-genetics approach that combines large-scale phenotyping, genome wide association studies and functional genomics, it is possible to identify key genes and genetic networks that quantitatively regulate root growth and development and have potential adaptive value.

Artwork by Ann Nee, DBS, NUS