

## **Genetic characterization of salinity tolerance traits to increase salinity tolerance in crops**

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One-third of the world's food is produced under irrigation and this is directly threatened by over-exploitation of water resources and global environmental change. This talk will focus on the use of forward genetics to discover genes affecting salinity tolerance in barley, rice, and tomatoes, along with some recent genomics in quinoa, a partially domesticated crop with high salinity tolerance. Rather than studying salinity tolerance as a trait in itself, we dissect salinity tolerance into a series of components that are hypothesised to contribute to overall salinity tolerance.

For barley, two consecutive years of field trials were conducted at a site with sandy soil and very low precipitation. Drip irrigation systems allowed the control of salinity. A barley nested association mapping (NAM) population developed by Klaus Pillen has been used to dissect physiologically and genetically complex traits in response to salt stress. Ten traits related to yield and yield components (e.g., days to flowering, harvest index, 100-seed mass) were recorded and we identified two significant loci located on the long arms of chromosomes 1H and 5H, which are both associated with several traits contributing to salinity tolerance - days to flowering, days to maturity, harvest index, and yield.

For tomatoes, the focus is on the genetics of tolerance in wild tomatoes, specifically *Solanum galapagense*, *Solanum cheesmaniae*, and *Solanum pimpinellifolium*. An association genetic approach is being taken. High-quality genome sequences have been made and genotyping-by-sequencing undertaken. Tomatoes have been phenotyped in The Plant Accelerator® and in the field, and analyses are currently in progress.

The application of this approach provides opportunities to significantly increase abiotic stress tolerance in crops and thus contribute to increasing agricultural production in many regions.