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**The genome of *Chenopodium quinoa* provides insights into saponin biosynthesis and salinity tolerance mechanisms**

**Thursday, September 14, 14.00, Seminar Room B2**

*Chenopodium quinoa* (quinoa) is a highly nutritious grain crop identified as an important crop to improve world food security; unfortunately, few resources are available to facilitate its genetic improvement. The assembly of a high-quality, chromosome-scale reference genome sequence for quinoa was produced using single-molecule real-time sequencing in combination with optical, chromosome contact, and genetic maps. We also report the sequencing of two diploids from the ancestral gene pools of quinoa – which enabled the identification of sub-genomes in quinoa – and reduced-coverage genome sequences for 22 other accessions of the allotetraploid goosefoot complex. The genome sequence facilitated the identification of the transcription factor likely to control the production of anti-nutritional triterpenoid saponins found in quinoa seeds, including a mutation that appears to cause alternative splicing and a premature stop codon in sweet quinoa accessions. By integrating physiological data with RNAseq and SNP analyses we are also starting to unravel salinity tolerance mechanisms in quinoa.

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