

## S7-7

### DOMESTICATION HISTORY OF A HEXAPLOID, THE SWEET POTATO (*IPOMOEA BATATAS* (L.) LAM.)

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Despite the importance of sweet potato as a food crop, its evolutionary history has been poorly investigated. The geographical and botanical origins of sweet potato remain unclear. Sweet potato is in the section *Batatas* of the genus, which also includes 13 wild relatives, almost all endemic to the Americas. *I. batatas* is not known in the wild state. Morphological and genetic analyses indicate that *I. trifida* is sweet potato's closest wild relative, but the genomic composition of *I. batatas* is still debated. It is still unclear whether this hexaploid is auto-, allo- or auto-allopolyploid. The range of *I. trifida* extends from northern Peru to Mexico, and the assumed region of origin of *I. batatas* is somewhere within this vast geographical area. *I. trifida* forms a complex of ecotypes of differing ploidy levels (diploids to hexaploids), but the distribution and origin of populations of varying ploidy levels are not documented. Moreover, no genetic studies have been conducted to determine the relationships between different wild populations of *I. trifida* and the cultivated *I. batatas*, which could allow inference of sweet potato's region(s) of origin. Finally, a major domesticated trait of *I. batatas* is its capacity to produce edible storage roots. Some *I. trifida* are known to form small tuberous roots, but these have not been studied in any depth. The purpose of our study is to investigate the origin of sweet potato and particularly the role of polyploidization in its domestication history. A set of 180 *I. trifida* populations and 450 sweet potato landraces, distributed from Peru to Mexico, were chosen from the collection of the International Potato Center (CIP, Lima, Peru). Morphological characterisation of these plants is in progress, as well as genetic analyses using neutral chloroplast markers. We plan to evaluate ploidy levels of these different wild and cultivated samples by flow cytometry and study the genome composition of representatives of ploidy groups by genomic in situ hybridization. These analyses should lead to advances in the reconstruction of sweet potato's evolutionary history.

Keywords: *Ipomoea Batatas*, domestication, origin of polyploidy