



**CIP Learning and Knowledge Sharing Seminars  
Capacity Strengthening Department**

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**Elucidating the sweet potato evolutionary history with  
molecular markers: from domestication in America to  
diffusion in Oceania**

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**Summary**

Since ten thousand years, the domestication of crop plants and their dispersal from centres of origin, associated with the spread of agriculture and societies, have shaped the distribution of genetic diversity of cultivated plants. Despite its importance as a staple food, sweet potato (*Ipomoea batatas* (L.) Lam., Convolvulaceae) has been relatively neglected in such studies and many points of its evolutionary history from domestication to dispersal remain unsolved.

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, but how, where and how many times remains opened questions.

Even if no races have been described for sweet potato, analysis of genetic diversity using polymorphic markers has identified two genepools (Zhang et al., 2000, 2001; Gichuki et al, 2003). Are these genepools the results of domestication history (single vs multiple independent domestication events) or do they reflect the history of diffusion from a single domestication event, with isolation by distance and local adaptation? So far, all genetic studies that have been conducted on population structure and genetic diversity in American sweet potatoes have suffered from restricted sampling and the use of markers that are inadequate for solving this question. To investigate genetic diversity in American sweet potato and examine the contributions of domestication and post-domestication dispersal in explaining the patterns observed, we analyzed a comprehensive sample of landraces using adequate markers (cp and nuclear

SSRs). Our sample included 329 sweet potato landraces from an area extending from Mexico to Peru, the entire pre-Columbian range of sweet potato cultivation. Our results support the hypothesis that sweet potato was domesticated at least two times, one time in the Andean lowlands from Peru-Ecuador, and the other time in lowlands of central and Caribbean America. We are now recovering wild putative ancestors' samples and testing chloroplast and nuclear sequences to identify sweet potato botanical origin and validate this scenario.

Although sweetpotato is recognized as an important staple food for Pacific Islanders, its genetic diversity has been little studied. We are characterizing genetic diversity distribution of Pacific sweetpotatoes by sampling both present-day material and herbarium specimens. We would like retrace ancient introduction routes of the plant and test the famous tripartite hypothesis proposed by Barrau and Yen: this hypothesis proposes that sweetpotato was introduced into the Pacific Islands by three routes, 1) the kumara line, a prehistoric introduction of clones from South American coastal areas by Polynesian travellers; 2) the batatas line, whereby Portuguese explorers transferred West Indian cultivars to Africa, India and the East Indies; and 3) The kamote line, where Spanish galleons spread sweetpotato clones from Mexico to the Philippines while trading across the Pacific. Therefore, we aim to study the contribution of the both American genepools to diversification processes and evaluate the importance of recombination versus clonality in the evolutionary dynamic of Pacific genetic diversity.

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