

ARCHAEOBOTANY

Madagascar crops up

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Madagascar is only 500 km from continental Africa, yet linguistic, ethnographic and genetic evidence point to the island's colonization sometime in the first millennium AD by groups from Southeast Asia, 6,000 km away. A new study by Alison Crowther of the University of Queensland, Australia and colleagues provides the first archaeological evidence in support of this colonization, using analysis of ancient crop remains.

Malagasy, the language spoken in Madagascar, is most similar to Austronesian languages such as Hawaiian, Māori and Malay, rather than East African languages, and now it seems that early Malagasy crops also reflect a Southeast Asian origin. Crowther and her team collected archaeobotanical samples at settlements in Madagascar and contemporaneous sites

on the African mainland, dated to between 650–1200 AD. They found a distinctive signature of Asian crops (Asian rice, mung bean and cotton) at the Malagasy sites, and few of the African crops (sorghum, cowpea, baobab and African millets) common at sites in Kenya and Tanzania.

Crowther and her team also found Asian crops in the Comoros islands 300 km off the coast of Madagascar, in earlier deposits. This suggests that the Comoros islands could have paved the way for the colonization of Madagascar by Southeast Asian peoples. *LNE*

PHLOEM TRANSPORT

Pressure vessel

eLife <http://doi.org/10.1101/062124> (2016)

While the movement of water through xylem tissue is relatively well understood, the movement of solute-laden sap through phloem is not. One possibility is the 'pressure flow hypothesis' proposed by the German plant physiologist Ernst Münch in 1930. By making careful measurements of the physical properties of morning glory (*Ipomoea nil*), Michael Knoblauch at Washington State University, USA and colleagues have shown that Münch's hypothesis is physically plausible even for large plants measuring tens of metres or more.

Münch proposed that high concentrations of solutes, especially sugars, in the phloem of source tissues such as leaves would draw water into those vessels from surrounding cells by osmosis, producing large turgor pressures. Conversely, sinks,

where sugars were in demand, would have lower osmosis-sustained turgors. Material would flow from source to sink by mass transport.

Knoblauch *et al.* used *I. nil* vines from which lateral shoots were removed daily, leaving a very long plant with only two major sinks at the roots and shoot tip. These could be rolled up and carried from lab to lab: a 'portable tree'. They measured physical and anatomical properties such as turgor pressure, conductance and sap flow with a sophisticated toolkit including tiny pressure meters dubbed 'pico-gauges'. Both changes in anatomy and flow parameters scaled with the length of the vines, as Münch's hypothesis predicts. *CS*

IMMUNITY

Mossy byways

Plant Cell <http://doi.org/10.1105/PC.115.11.1999> (2016)

The basal land plant model *Physcomitrella patens* is a powerful tool for understanding the evolution of plant biological processes. Simon Bressendorff and colleagues from Copenhagen University, Denmark, studied innate immunity pathways in the non-vascular moss, and found them to be surprisingly similar to those in angiosperms, confirming that the ability to detect and fight pathogens efficiently evolved very early in plants.

Recognition of generic non-self patterns such as bacterial flagellin or fungal chitin by membrane receptors induces a cascade of molecular events often mediated by protein kinases, leading to immunity. The authors showed that chitin, unlike flagellin, activates moss MAP kinases. They identify a homologue of the *Arabidopsis* chitin receptor CERK1, which is essential for this response and other chitin-induced phenotypes. From a slightly simplified repertoire of kinases, they also implicated redundant MEKK1, MKK1 and MPK4 homologues, similar to one branch of *Arabidopsis* defence pathways. They found that moss mutated in one MPK4 is less resistant to necrotrophic fungi, confirming its role in immunity.

The role of other MAP kinases in moss remains to be elucidated. But, by discovering strong similarities (and also significant specificity differences), this work provides evidence that fully formed immunity pathways were already present before the separation between bryophytes and angiosperms 500 million years ago. *GT*

Written by Chris Surridge, Luiseach Nic Eoin and Guillaume Tena

COTTON DEVELOPMENT

Branching out

New Phytol. <http://doi.org/10.1111/nph.13444> (2016)

The architecture of a plant has a large influence on its value as a commercial crop. Ancestral cotton (*Gossypium hirsutum*) is a tall shrub that flowers on its upper branches, triggered by shortening days — but domestication has created squat bushes producing copious flowers and fruits independent of day length. Roisin McGarry at the University of North Texas, USA and colleagues show that this structural change is controlled by the relative amounts of two antagonistic gene products, SINGLE FLOWER TRUSS (GhSFT) and SELF-PRUNING (GhSP).

The role of SFT and SP in determining architecture has already been explored in tomato, and the two genes are orthologues of genes known to control meristem identity in *Arabidopsis*. The researchers identified the cotton genes through sequence similarity with their equivalents in tomato, and showed that they were differently expressed in ancestral and domesticated varieties. They then proceeded to specifically manipulate the expression of *GhSFT* and *GhSP* in cotton, both silencing and overexpressing the genes.

GhSFT stimulates a bushy growth pattern with flowers arising from multiple side branches. However, it could not override the influence of *GhSP* to produce monopodial, unbranching growth. In addition, *GhSFT* and *GhSP* are active in growth of all shoots, not just apical and axillary meristems. For example, *GhSP* is needed for cambium initiation and maintenance, and is thus an important determinant in wood production. *CS*