Plant mutations: slaying beautiful hypotheses by surprising evidence

Niklas Tysklind, Sylvain Schmitt, Patrick Heuret, Valérie Troispoux, Mélanie Beraud, Jocelyn Cazal, Emilie Chancerel, Charlotte Cravero, Erwan Guichoux, Olivier Lepais, et al.

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Session 3:

Evolutionary genomics

Wednesday 13 September 16:20 - 18:55

Chair: Dr. Annika Perry, UK Centre for Ecology & Hydrology, UK

Oral presentations

16:20 **Keynote**
Lind, Brandon M.:
The limits of predicting maladaptation to future climate using genomic data

17:05 **Gonzalez-Martinez, Santiago C.:**
Genetic variation within and among populations underlies adaptation to climate in a Mediterranean pine species

17:25 **Tysklind, Niklas:**
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17:45 ***Short Break***

17:55 **Păun, Ovidiu:**
The drivers of the adaptive radiation of persimmon trees on New Caledonia, a biodiversity hotspot

18:15 **Gathercole, Louise:**
Genomic evidence for extensive introgression amongst British oaks and assessment of mal-adaptation

18:35 **Paulo, Octávio S.:**
A landscape genomic approach on the cork oak and holm oak in the Western Mediterranean: insights into the species’ capacity to respond to climate change

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Contribution ID: 141

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Mutation is the source of all genetic diversity, on which selection can act allowing adaptation. Early differentiation between soma and the germline in animal development protects the germline, and thus the offspring, from the accumulation of somatic mutations. In plants, somatic mutations are expected to occur and accumulate along the branches and the differentiation between soma and germline is debated. There are several predictions on the fate of somatic mutations occurring in plant tissues: exposure to UV radiation increases mutagenesis; mutations have generally low frequency in plant tissues; branching topology of the tree dictates mutation distribution; and mutations at high frequency have a higher chance of being transmitted to the next generation. We produced a unique plant dataset of 60 high-coverage whole-genome sequences of two tropical tree species (*Dicorynia guianensis* and *Sextonia rubra*) and identified 18,274 de novo somatic mutations on branches exposed to high and low light, almost all at low frequency in tissues. We demonstrate that: 1) mutation rates and mutation spectra are not demonstrably affected by differences in UV exposure; 2) mutation phylogenies deviate from the branching topology of the tree; and 3) low-frequency mutations are transmitted to the next generation. Altogether, our results suggest far more complex links between plant growth, ageing, UV exposure, and mutation rates than commonly thought. Specially, the transmissibility of low frequency mutations, which are the most abundant, indicates a non-negligible role of low frequency somatic mutations as heritable mutations fuelling plant evolution.

Keywords: mutation, tropical trees, genomics, evolution, heritability