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Plant mutations: slaying beautiful hypotheses by surprising evidence

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Resilient Forests for the Future

EVOLTREE Conference 2023

12 – 15 September 2023

UNITBV, Braşov, Romania

Book of Abstracts



Transilvania University of Braşov

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:**
Plant mutations: slaying beautiful hypotheses by surprising evidence
- 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

Plant mutations: slaying beautiful hypotheses by surprising evidence

Contribution ID: 141

Tysklind, Niklas; Schmitt, Sylvain; Heuret, Patrick; Troispoux, Valérie; Beraud, Mélanie; Cazal, Jocelyn; Chancerel, Émilie; Cravero, Charlotte; Guichoux, Erwan; Lepais, Olivier; Loureiro, João; Marande, William; Martin, Olivier; Vincent, Gregoire; Chave, Jérôme; Plomion, Christophe; Leroy, Thibault; Heuertz, Myriam

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