

## PLENARY 7

### Regulation of Redox-Related Genes in *Hevea Brasiliensis* and Their Role in Latex Production

Pascal Montoro<sup>1,2</sup>, Yi Zhang<sup>1,2</sup>, Florence Martin<sup>1,2</sup>, Kuswanhadi<sup>3</sup>, Riza Putranto<sup>4</sup>,  
Julie Leclercq<sup>1,2</sup>

<sup>1</sup>CIRAD, UMR AGAP, F-34398 Montpellier, France

<sup>2</sup>AGAP, Univ Montpellier, CIRAD, INRA, Montpellier SupAgro, Montpellier,  
France

<sup>3</sup>Indonesian Research Institute for Biotechnology and Bio-industry

<sup>4</sup>Indonesian Rubber Research Institute, Sembawa Research Centre, Palembang,  
Indonesia

Corresponding author: pascal.montoro@cirad.fr

---

*Hevea brasiliensis* is the main source of natural rubber accounting for 42% of the worldwide rubber consumption. Natural rubber is synthesized in rubber particles of latex cells, which are differentiated from the vascular cambia and localized in the secondary phloem. Latex is collected by tapping the soft bark of rubber trees. Ethephon, an ethylene releaser, is applied on bark to stimulate latex flow and regeneration between two tappings. Above a certain threshold, environmental and harvesting stresses are known to induce an oxidative stress triggering Tapping Panel Dryness (TPD). TPD is a physiological syndrome affecting latex production through the agglutination of rubber particles. Four hundred and seven genes from 30 gene families related to reactive oxygen species (ROS) production and scavenging, and antioxidants biosynthesis were identified in the *Hevea* genome sequence. Based on a transcriptome analysis, 161 ROS-related genes were found expressed in latex cells. Small RNA and degradome analysis revealed 13 genes targeted by 11 microRNAs and 15 genes targeted by 16 transacting-siRNA in latex. These post-transcriptional regulations dramatically affect their gene expression profile. HbRBOH2 was identified as the main source gene of ROS in latex, while HbCuZnSOD4 might be the most important ROS scavenging enzyme for ROS detoxification in latex. Overexpression of genes encoding a superoxide dismutase (HbCuZnSOD) and an enzyme of the glutathione biosynthetic pathway (EcGSH1) were successfully obtained in transgenic rubber plants. These later showed an increase in plant growth and their tolerance to abiotic stress. This study revealed the crucial role of antioxidant in *Hevea brasiliensis* laticifers and suggests seeking genetic variability for antioxidant capacity in order to improve rubber tree for the tolerance to abiotic stress and TPD occurrence.