

## REGULATION OF TRANSPOSABLE ELEMENTS IN THE WHEAT FUNGAL PATHOGEN *ZYMOSEPTORIA TRITICI*

Cécile Lorrain<sup>1,2</sup>, Mareike Moller<sup>3</sup>, Alice Feurtey<sup>2</sup>, Janine Haueisen<sup>3</sup>, Eva Stukenrock<sup>2,3</sup>

<sup>1</sup> UMR 1136 INRA/Université de Lorraine Interactions Arbres/Micro-organismes, Centre INRA Nancy Lorraine, F-54280 Champenoux, France.

<sup>2</sup> Max Planck Institute for Evolutionary Biology, Plön, Germany.

<sup>3</sup> Environmental Genomics, Christian-Albrechts University of Kiel, Kiel, Germany.

In fungal genomes, transposable elements (TEs) are thought to be key drivers of variability among populations in response to environmental stress. TE proliferation could be either deleterious or beneficial depending on their insertion sites, or neutral if they insert in non-coding nor regulatory regions. The recent PacBio re-sequencing of several isolates of wheat pathogen *Zymoseptoria tritici* and of four other *Zymoseptoria* sister species (i.e. *Zymoseptoria ardabiliae*, *Zymoseptoria brevis*, *Zymoseptoria passerinii* and *Zymoseptoria pseudotritici*), has improved genome assemblies, which is determinant to study TE dynamics. We performed an in-depth characterisation of the complete TE repertoire of the five known *Zymoseptoria* spp. to gain insights into the impact of repetitive DNA on the evolution of these closely relative species. We estimated at a relatively recent age TE insertions in *Zymoseptoria* spp using the divergence between genomic copies and consensus sequences. Also, we were able to scrutinise the variability inter- and intra-species comparing copies to a *Zymoseptoria* consensus library we built. We demonstrated that *Zymesptoria* spp. infecting domesticated plants (i.e. *Z. passerinii* and *Z. tritici*) presented mostly species-specific TEs while *Zymoseptoria* spp. infecting wild plants (i.e. *Z. ardabiliae*, *Z. brevis* and *Z. pseudotritici*) harboured less species-specific TEs. Together these results may suggest that plant domestication could impact TEs dynamics of associated fungal pathogens.