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## Detecting molecular footprint of local adaptation in *Zymoseptoria tritici*

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**POSTER SESSION ABSTRACTS**  
**Session CS6 Ecological and population genomics**  
**CS6W38**

**Wednesday 6th April**  
**14:00 - 16:00**

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**Detecting molecular footprint of local adaptation in *Zymoseptoria tritici***

*Zymoseptoria tritici* (Zt) is one of the most common pathogen of wheat and yet the genetic basis of adaptation in this species is largely unknown. Population genetics studies using neutral markers suggest for the most part that there is a low level of genetic differentiation between natural population samples in Zt. Using new generation sequencing data, now we can provide an in depth analysis of the genetic variation segregating in natural populations, and better understand the mode and tempo of genome evolution at the intraspecific level. The aim of this work was to identify the genes / genome regions that are under extreme genetic differentiation between two French population samples that differ in environment, collected in the North and South of France. To reach this goal, we used new generation sequencing data from 30 isolates. We found a large genetic diversity for both single nucleotide polymorphisms and structural variants within and between population samples. Many polymorphic sites throughout the genome were highly differentiated between the population samples, especially we discovered a large inversion on chromosome 7. We detailed the nature of genetic variants in this specific region. We also described the pattern of linkage disequilibrium and quantify the skew in allele frequency spectrum across inverted regions to understand the nature of the selection in action. Last, we discuss the potential role of inversions in local adaptation.

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