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## **Resolution provided by microsatellite markers in detecting population structure of the wheat pathogen *Zymoseptoria tritici***

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**POSTER SESSION ABSTRACTS**  
**Session CS6 Ecological and population genomics**  
**CS6W45**

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

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**Resolution provided by microsatellite markers in detecting population structure of the wheat pathogen *Zymoseptoria tritici***

*Zymoseptoria tritici* (Zt) causes Septoria leaf blotch, one of the most important worldwide diseases of wheat. Yield losses can reach 50% in disease-conducive climates and epidemics occur regularly on bread wheat (*Triticum aestivum*). A set of 614 isolates was sampled from naturally infected fields of main French regions during two years, and genotyped using 12 microsatellite markers. The data were analyzed with population genetic statistics and population structure analyses. The genetic structure of Zt in France is characterized by high genetic diversity (95% of unique genotypes), regular recombination (all populations were in gametic equilibrium), and gene flow. No significant genetic differentiation was found among the sampled populations. To further investigate the extent of genetic structure in Zt, we re-sequenced using Illumina technology the whole genome of 30 isolates from two geographically distant populations (sampled in the north and the southwestern regions of France). The NGS data were used to identify more than 4000 microsatellite markers and to analyze their variation across the 30 isolates. In this study, we compared the resolution of these new markers spread across the genome with the 12 microsatellites previously used in detecting genetic patterns in Zt.

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