**BioProject**

NR

**Data type**

RAD-sequencing

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**Grants**

*ID:* CIFRE 2019/0608

*Title:* Specificity and durability of quantitative resistance of wheat to Septoria tritici blotch

*Agency:* Association Nationale de la Recherche et de la Technologie (ANRT)

**Title**

RAD-sequencing of 167 offspring individuals of *Zymoseptoria tritici* obtained from the cross I05×I07

**Abstract**

The two *Zymoseptoria tritici* strains “I05” (INRA09-FS0813, Mat1-1) and “I07” (INRA09-FS0732, Mat1-2), sampled in 2010 from STB lesions on wheat cv. Soissons in Grignon, France (48510 N, 1580 E), were crossed by co-inoculating adult plants with an equiproportional suspension of parental blastospores. After ascosporogenesis, 167 offspring individuals were collected from yeast-like colonies on Petri dishes placed upside down above wheat debris fragments to collect discharged ascospores. The population of the 167 individuals resulting from the cross is referred to as “I05×I07”. Each offspring individual was grown over 7 days in a 250mL Erlenmeyer flask containing 100mL of YPD (Yeast extract Peptone Dextrose) with constant agitation at 160rpm. At the end of the seven-day growth period, a maximum of culture medium was separated from the spores, which were then transferred into 50mL Falcon tubes to be lyophilized for 24 to 30 hours. After lyophilisation, the completely dry samples were ground in liquid nitrogen with a mortar and pestle. DNA was extracted from each sample following a phenol/chloroform-based protocol. Due to the size of the population and the extraction protocol, the DNA was extracted in two sets, one in 2018 with 83 individuals plus both parents as controls, one in 2019 with 84 individuals with both parents as controls. Samples were sequenced following the RADseq (Restriction site Associated DNA sequencing) strategy, on the Platform MGX (MGX-Montpellier GenomiX) on a HiSeq 2500 (Illumina) in paired end 2\*125nt mode. This type of sequencing enables one to target 1 to 10% of the genome via the use of a restriction enzyme and tagging of digested strands. The restriction enzyme used was *Pst*1, following a previous study in *Z. tritici*.