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► To cite this version:

Eva H Stukenbrock, Mareike Moeller, Klaas Schotanus, Jessica L. Soyer, Michael Freitag. Genome dynamic and accessory elements in the plant pathogenic fungus *Zymoseptoria tritici*. 9. International symposium on Septoria diseases of cereals, Apr 2016, Paris, France. p.12. hal-02793895

HAL Id: hal-02793895

<https://hal.inrae.fr/hal-02793895>

Submitted on 5 Jun 2020

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Thursday 7 April
9:40 – 10:10

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Genome dynamic and accessory elements in the plant pathogenic fungus
Zymoseptoria tritici

Accessory chromosomes are present in the genomes of many organisms. In fungi these chromosomes are present at different frequencies in populations and usually characterized by higher repetitive DNA content and lower gene density. In the fungal pathogen *Zymoseptoria tritici*, as many as eight discrete accessory chromosomes occur in different strains comprising up to 12% of the total genome. So far no functional role has been assigned to these chromosomes. Comparative genome analyses show that genes on accessory chromosomes accumulate considerably more mutations compared to genes on core chromosomes consistent with a relaxation of selective constraints. Yet, accessory chromosomes have existed as separate entities in the karyotypes of *Zymoseptoria* species over longer evolutionary time. We have set out to investigate the properties of accessory chromosomes underlying their rapid evolution and sequence dynamics. We used ChIP-seq with antibodies against the centromere specific histone CenH3, as well as the euchromatic mark H3K4me2 and the heterochromatic marks H3K9me3 and H3K27me3 to identify centromeres and determine the distribution and proportion of euchromatin and heterochromatin in the *Z. tritici* genome. Next, we conducted a detailed computational analysis of subtelomeric repeats to compare telomeres of core and accessory chromosomes. We show that accessory chromosomes have centromeres and telomeres identical to those of core chromosomes. However, accessory chromosomes of *Z. tritici* have dramatically higher enrichment of heterochromatin, consistent with a higher proportion of repetitive DNA and an overall silencing of transcription. The overall heterochromatic state of accessory chromosomes may also contribute to their instability. We find that rearrangements and loss of accessory chromosomes not only occur, as previously described during meiosis, but also to a high extent during mitosis. Together our results suggest a central role of chromatin modifications in the maintenance of chromosome stability in *Z. tritici*. Dynamic changes of chromatin structures can thereby contribute to karyotypic variation and chromosome evolution in this important pathogen.