Histone modifications affect the mutation rate in a plant pathogenic fungus

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Histone modifications are key regulators of many aspects of chromatin biology including transcription. DNA repair, recombination and chromosome segregation. Fungal plant pathogens often contain supernumerary or accessory chromosomes which can show a markedly different histone modification pattern. In addition, these accessory chromosomes often show higher mitotic or meiotic instability and appear to have a higher substitution rate. Whether the different histone modification patterns are causal to the observed differences in transmission fidelity and increased substitution rate of accessory chromosomes is currently unknown. Here, we conducted a mutation accumulation experiment including approx. 244800 mitotic cell divisions of the fungal pathogen Zymoseptoria tritici to assess chromosome stability and mutation rates across the genome and in different genomic compartments. In our experiment we show that the accessory chromosomes of Z. tritici, in the absence of selection, are frequently lost during mitotic cell divisions and furthermore show a higher mutation rate compared to the core chromosomes. In addition, histone modification H3K27me3 is correlated with both an increased chromosome loss rate and an increased mutation rate. This contrasts with another heterochromatin mark H3K9me3, which reduces both chromosome loss rate and mutation rate. We conclude that the histone modifications H3K9me3 and H3K27me3 directly affect both transmission of chromosomes during mitotic cell divisions and the rate of spontaneous mutations.