

Identification of candidate long non-coding RNAs associated with host colonization processes in the wheat pathogen *Zymoseptoria tritici*

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Non-coding RNAs (ncRNAs) have been linked to a number of regulatory and signalling processes within fungal cells. Despite evidence that they may be important actors in fungal pathosystems, little is known about the presence and functions of ncRNAs in *Zymoseptoria tritici*, the fungal agent of septoria wheat blotch. In this study, we apply an individualized *in-silico* pipeline to identify intergenic long ncRNA (lincRNA) candidate regions in *Z. tritici*, and integrate different datasets to investigate the particularities of these candidates. We identify 258 candidate regions, of which 71 are differentially expressed throughout the infection cycle, mainly during the latent biotrophic phase. We find that many of these show low polymorphism density, suggesting moderate conservation in the worldwide population, and that they contain a number of potential binding sites that may imply functionality pertaining to stress response, gene expression regulation, and/or chromatin association. Additionally, we find that candidates co-locate with retrotransposon rich regions of the genome. Overall, this preliminary study suggests that functional lincRNAs exist in *Z. tritici* and that they may be involved in initial host colonization. Our study demonstrates that research on fungal ncRNAs should be an important focus going forwards in the field of pathogen genomics.

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