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Poster

Genetic Regulation of Virulence Gene Clusters in U. maydis

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ABSTRACT

The regulation of virulence gene clusters in pathogenic fungi is essential for carrying out the entire infectious process. Therefore, the silencing and unsilencing of these clusters must be highly regulated when the pathogenic fungus interacts with the host. During the infection process, the genes within these clusters must be unsilenced, either by losing the necessary histone methylation or by introducing acetylation (Elías-Villalobos et al., 2019). This study aims to identify potential genetic regulators that regulate these virulence gene clusters in Ustilago maydis, a pathogenic fungus that infect maize (Zea mays). In order to do that, previously in our laboratory, a geneticine resistance marker was introduced into a virulence gene cluster in U. maydis. This marker was silenced, but numerous spontaneous mutants appeared in media with geneticine, which made difficult the mutagenesis process. Therefore, in this study, we opted to incorporate two different resistance markers, for the antibiotics geneticin (Gen) and nourseothricin (Nat), into two different virulence gene clusters. Once the resistance markers were introduced and silenced, spontaneous mutants were sought by exposing the U. maydis strain in media containing these antibiotics. In contrast to when only one antibiotic resistance was present, no spontaneous mutants were found in candidates containing resistance to both drugs in two different virulence clusters. Thus, we have decided to perform UV mutagenesis to conduct a genome-wide screening in U. maydis, aiming to find any mutants with both markers unsilenced. We are currently optimizing UV dose and drug concentrations to ensure optimal mutagenesis.

REFERENCES

Elías-Villalobos, A., Barrales, R. R., & Ibeas, J. I. (2019). Chromatin modification factors in plant pathogenic fungi: Insights from Ustilago maydis. Fungal Genetics and Biology, 129, 52–64. https://doi.org/10.1016/j.fgb.2019.04.006