RECONSTRUCTION OF REGULATORY NETWORKS IN *FUSARIUM GRAMINEARUM* USING A SYSTEMS BIOLOGY APPROACH

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Regulatory networks (RN) function as information centers that transform signals into coherent cellular responses. The network plasticity achieved through evolutionary rewiring of regulatory networks is an important source of diversity among species. This study employs *Fusarium graminearum*, a mycotoxigenic filamentous fungus and causal agent of head blight diseases in cereal crops, as a model system. A robust searching algorithm using Bayesian networks model was developed and we tested the algorithm on a collection of *F. graminearum* transcriptomic datasets to infer the relationship between candidate regulators and their target genes. Preliminary validation of the inferred network using prior biological knowledge proofs the effectiveness of the program. Using a heuristic greedy approach, the program predicted in the network a set of top regulators, which interestingly control specialized and modularized gene regulation and cellular functions, providing exciting insights into the dynamics of transcriptional regulatory mechanisms orchestrating the fungal biology and pathogenesis. Combining comparative studies of sequenced *Fusarium* genomes with the network inference, the conservation of the regulatory modules will be identified and allow us to transfer the network knowledge gained from *F. graminearum* to other *Fusarium* species. The reconstruction of the regulatory networks will enable a comprehensive understanding of the complex biological processes related to pathogenesis and will have broad implications in disease controls.