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PROJECT 1 ABSTRACT
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Fusarium graminearum is a causal agent of Fusarium head blight (FHB) and a producer of deoxynivalenol (DON). *Ras2* GTPase and its potential downstream cAMP-PKA and Gpmk1 pathways all are important for regulating DON biosynthesis and plant infection. Whereas non-preferred nitrogen sources including arginine and putrescine induce DON biosynthesis, ammonium suppresses *TRI* gene expression. The global nitrogen transcriptional regulator Are1 also plays a critical role in regulating DON biosynthesis and three ammonium permease (*MEP*) genes in *F. graminearum*. Our preliminary data showed that *MEP2* functions as an ammonium sensor and its cytoplasmic tail (CT or *Mep2*-CT) is essential for functions. The *mep2* mutant was defective in ammonium repression of DON production. However, to date, it is not clear how the nitrogen availability signal recognized by a membrane protein *Mep2* is relayed to intracellular targets and what is its functional relationship with *Are1*.

The goal of this study is to understand how ammonium sensing leads to the suppression of DON production. Based on our preliminary data and phenotypes of *are1*, *ras2* and *mep2* mutants, we hypothesized that *Mep2*-CT interacts with *Ras2* and nitrogen availability signals are relayed to cAMP-PKA or Gpmk1 for regulating *Are1* activation and DON biosynthesis. Objective 1 aims to identify and characterize the amino acid sequences of *Mep2*-CT responsible for ammonium suppression of DON production. The roles of *Mep2* in regulating *Are1* and genes responsible for the uptake and utilization of arginine or putrescine also will be determined. For objective 2, besides characterizing the interaction and functional relationship between *Mep2* and *Ras2*, we will examine the roles of cAMP-PKA in ammonium repression. Objective 3 will determine the roles of *Are1* in *TRI* gene expression and *Mep2* functions. *Are1* may directly regulate *TRI* expression and phosphorylation of *Are1* by PKA/Gpmk1 may connect *Ras2-Mep2* with DON biosynthesis.

Overall, results from proposed experiments will be helpful to better understand the transcriptional regulation of *TRI* gene expression and DON biosynthesis in *F. graminearum*, and genetic mechanisms for ammonium suppression of secondary metabolism, which is a common phenomenon in fungal pathogens. Inhibiting DON biosynthesis can be used to control FHB or avoid mycotoxin contamination. Proposed study fits the research area of PBG on characterizing plant-fungal interactions to identify genes that may be useful to reduce DON contamination in barley and wheat. It is a project based on recent progresses.