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Fusarium graminearum 의 ZEB2 동형단백질에 의한 지랄레논 생합성 자가조절

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The ascomycete fungus Fusarium graminearum is the most common pathogen of Fusarium head blight (FHB), a devastating disease for major cereal crops worldwide. FHB causes significant crop losses by reducing grain yield and quality as well as contaminating cereals with trichothecenes and zearalenone (ZEA) that pose a serious threat to animal health and food safety. ZEA is a causative agent of hyperestrogenic syndrome in mammals and can result in reproductive disorders in farm animals. In F. graminearum, the ZEA biosynthetic cluster is composed of four genes, PKS4, PKS13, ZEB1, and ZEB2, which encode a reducing polyketide synthase, a nonreducing polyketide synthase, an isoamyl alcohol oxidase, and a transcription factor, respectively. Although it is known that ZEB2 primarily acts as a regulator of ZEA biosynthetic cluster genes, the mechanism underlying this regulation remains undetermined. In this study, two isoforms (ZEB2L and ZEB2S) from the ZEB2 gene in F. graminearum were characterized. It was revealed that ZEB2L contains a basic leucine zipper (bZIP) DNA-binding domain at the N-terminus, whereas ZEB2S is an N-terminally truncated form of ZEB2L that lacks the bZIP domain. Interestingly, ZEA triggered the induction of both ZEB2L and ZEB2S transcription. In ZEA producing condition, the expression of ZEB2S transcripts via alternative promoter usage was directly or indirectly initiated by ZEA. Physical interaction between ZEB2L and ZEB2L as well as between ZEB2L and ZEB2S was observed in the nucleus. The ZEB2S-ZEB2S interaction was detected in both the cytosol and the nucleus. ZEB2L-ZEB2L oligomers activated ZEA biosynthetic cluster genes, including ZEB2L. ZEB2S inhibited ZEB2L transcription by forming ZEB2L-ZEB2S heterodimers, which reduced the DNA-binding activity of ZEB2L. This study provides insight into the autoregulation of ZEB2 expression by alternative promoter usage and a feedback loop during ZEA production.