

Supplementary materials

Benzimidazole Derivatives Suppress Fusarium Wilt Disease via Interaction with *ERG6* of *Fusarium equiseti* and Activation of the Antioxidant Defense System of Pepper Plants

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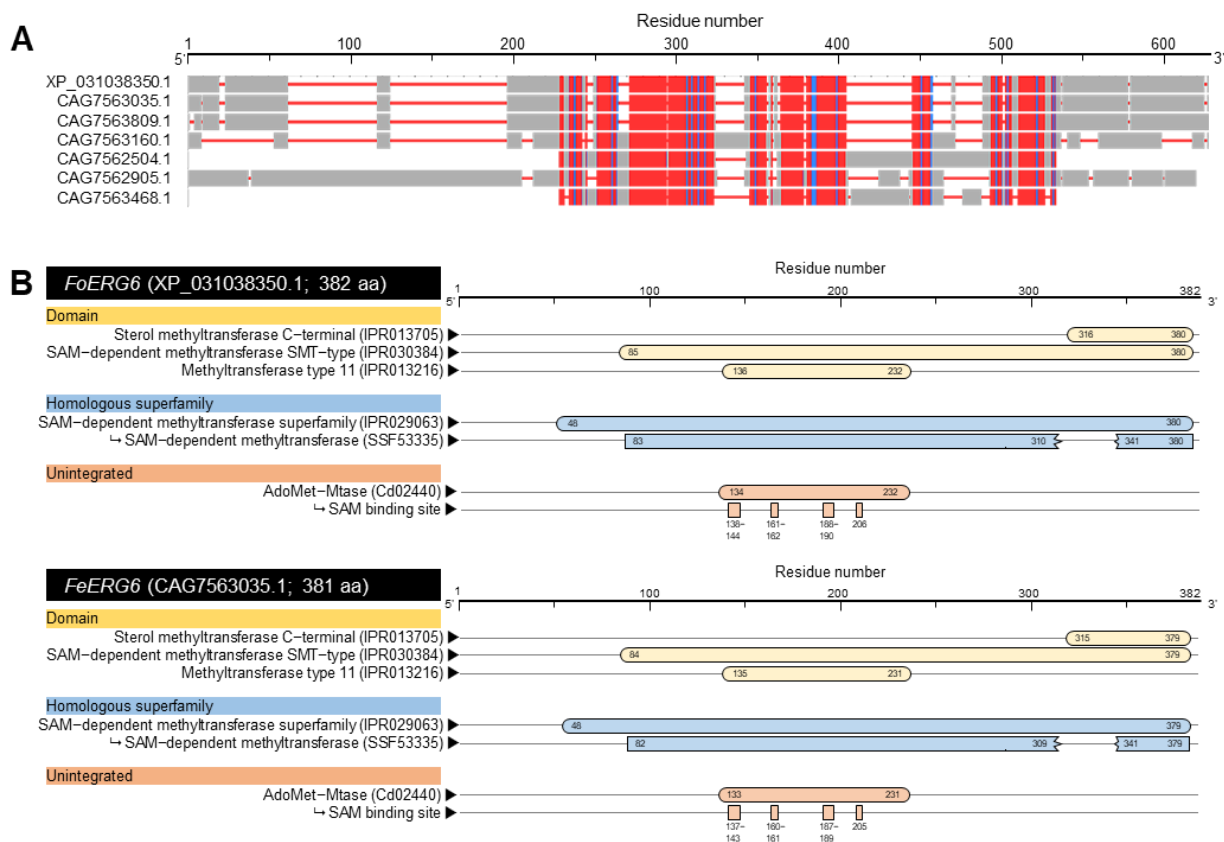
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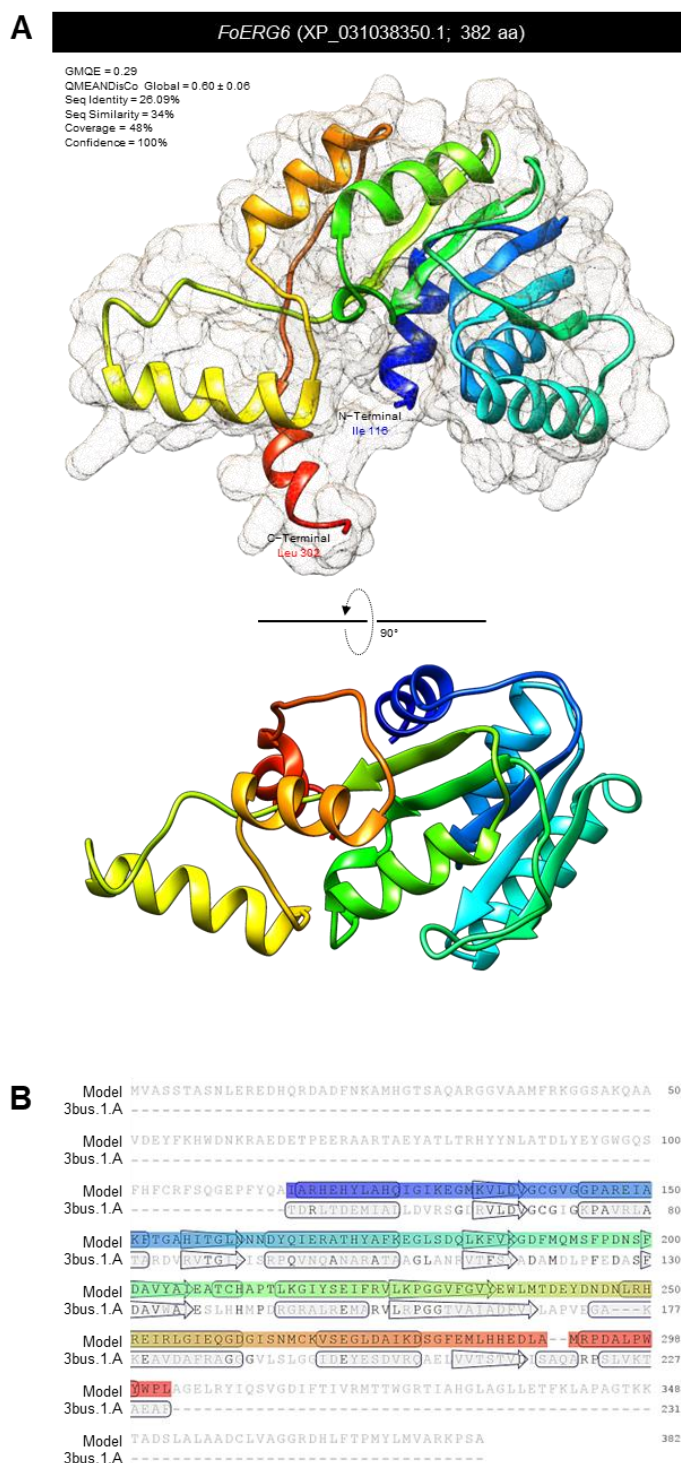
Supplementary Table S1. Sequences from *Fusarium equiseti* that produce significant Alignment with sterol 24-C-methyltransferase (ERG6) gene from *Fusarium oxysporum* NRRL 32931 ^a.

Gene Description	Protein				Protein-Protein Alignment statistics				
	GenBank Accession	aa	Theoretical isoelectric point (pI)	Molecular weight (MW)	Max Score	Total Score	Query Cover (%)	Identity (%)	E value
Unnamed Protein Product	CAG7563035.1	381	5.93	42536.94	715	715	100	95.03	0.0
Unnamed Protein Product	CAG7563809.1	381	5.57	43083.56	498	498	96	67.12	1e-177
Unnamed Protein Product	CAG7563160.1	345	5.55	38171.43	76.6	76.6	52	27.98	9e-16
Unnamed Protein Product	CAG7562504.1	279	6.22	30823.11	64.7	64.7	27	32.38	5e-12
Unnamed Protein Product	CAG7562905.1	521	6.06	59867.38	47.0	47.0	46	22.16	6e-06
Unnamed Protein Product	CAG7563468.1	246	5.49	27835.68	39.7	39.7	26	22.12	7e-04

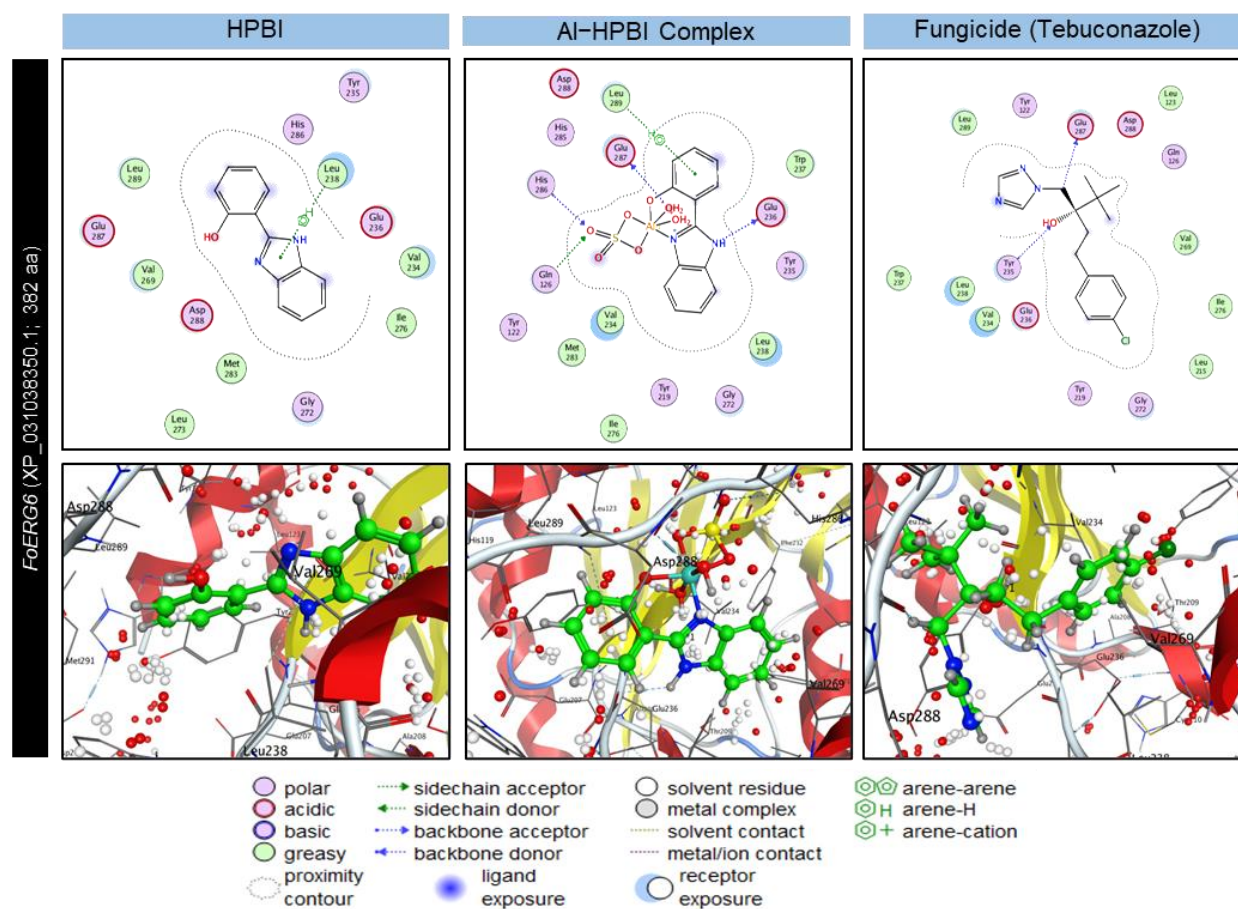
^a The listed putative gene candidates were identified using the protein-protein BLAST (BLASTp) using sterol 24-C-methyltransferase (*FoEGR6*; GenBank accession no. XP_031038350.1; 382 aa) from *Fusarium oxysporum* NRRL 32931 as a query sequence against *F. equiseti* genome available in GenBank, national center for biotechnology information website (NCBI, <http://www.ncbi.nlm.nih.gov/gene/>), using the compositionally adjusted substitution matrices [44,57].



Supplementary Figure S1. *In silico* analysis of Sterol 24-C-methyltransferase (EGR6) of *Fusarium equiseti*. (A) Multiple protein sequence alignments of EGR6 from *F. oxysporum* and its homologs from *F. equiseti* using the Constraint-Based Alignment tool (COBALT). (B) The protein functional and conserved domains analysis of FoEGR6 (XP_031038350.1) and FeEGR6 (CAG7563035.1) using the InterPro Scan tool.



Supplementary Figure S2. The crystallographic three-dimensional (3D) modeling of 24-C-methyltransferase from *F. oxysporum* (*FoERG6*). (A) The predicted 3D structure model and its associated mesh surface of *FoERG6* (XP_031038350.1) from *F. oxysporum*. (B) Model–template alignment of *FoERG6* from *F. oxysporum*. GMQE: Global model quality.



Supplementary Figure S3. Two-dimensional (2D) and three-dimensional (3D) docking interaction of HPBI, AI-HPBI Complex, and Fungicide (Tebuconazole) with 24-C-methyltransferase from *F. oxysporum* (FoERG6; XP_031038350.1).