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POSTER ABSTRACT

Novel enzymes required for pigment production in Fusarium graminearum

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Abstract

The plant pathogenic fungus *Fusarium graminearum* produces large quantities of the red mycelium pigment aurofusarin. This dimeric polyketide is produced under both natural growth conditions and in artificial environments (on media). The enzymes which catalyze the biosynthesis are encoded by a gene cluster consisting of 10 genes located on chromosome 1. The gene cluster covers 22 kb and includes *aurR1*, *aurO*, *aurR2*, *aurT*, *PKS12*, *aurC*, *aurJ*, *aurF*, *gip1* and *aurS*. We have previously reported the targeted replacement of seven of the ten genes and the resulting pheno- and chemotypes. Based on these results we presented a hypothesis for the aurofusarin biosynthesis pathways consisting of five enzyme catalyzed steps.

In the present study we report the targeted replacement of the remaining three genes in the cluster: *aurT*, *aurC* and *aurS*. Replacement vectors were constructed using Xi-cloning (*in vivo* bacterial homologous recombination) based on the available *F. graminearum* PH-1 genome sequence. The verified vectors were transformed into *F. graminearum* PH-1 by *Agrobacterium tumefaciens* mediated transformation. AurT shows significant similarity to the major facilitator superfamily of efflux pumps, while AurC and AurS do not show homology to any characterized enzymes.