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Effects of *Xanthomonas oryzae* pv. *oryzae* gum gene mutations on xanthan biosynthesis

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Xanthomonas oryzae pv. *oryzae* (*Xoo*) is a gram-negative bacterium which is the casual agent of bacterial blight (BB) on rice and is specific in producing copious amounts of exopolysaccharides (EPS) named xanthan gum as a virulence factor. *Xoo* is also the organism for industrial production of xanthan gum, which has a variety of applications in the field of recent bioindustry. Genome sequence analysis of *Xoo* KACC 10833 provides insight into the *Xoo* gum gene cluster composed of 13 open reading frames designated *gumB*, *-C*, *-D*, *-E*, *-F*, *-G*, *-H*, *-I*, *-J*, *-K*, *-L*, *-M*, and *-N*. A cluster of 12 genes in the *Xanthomonas campestris* pv. *campestris* *gum* gene cluster has been suggested to encode proteins involved in xanthan gum biosynthesis. However, no experimental evidence supporting a similar situation in *Xoo* has been presented so far. Thus, we decided to construct a defined set of *Xoo* *gum* mutants by using a highly efficient chromosomal recombination system in order to assign molecular functions to the products of the *Xoo* *gum* genes. In this work, we present genetic and molecular biological experimental data for assessing a correlation between *gum* gene mutations and xanthan gum biosynthesis in *Xoo*.

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