

Expression of an *ampG* like gene in *Herbaspirillum seropedicae* strain SmR1 is regulated by naringenin and its product appears to be involved in the determination of LPS structure

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Herbaspirillum seropedicae is a diazotrophic bacterium belonging to the β Proteobacteria. This bacterium is found in endophytic association with maize (*Zea mays*), rice (*Oryza sativa*), sorghum (*Sorghum bicolor*) and sugar cane (*Saccharum officinarum*). Such associations probably involve molecular communication between the host plant and bacteria, with expected modification in gene expression in both partners. A library of twelve thousand random insertion mutants was constructed by introducing an artificial transposon (plasposon) (pTnMod-OGmKmlacZ) carrying a promoter-less *lacZ* and the kanamycin resistance gene, into the wild type *H. seropedicae* SmR1. Five thousand mutant strains were screened for differential expression in the presence or absence of naringenin and twenty two strains responded to naringenin. One mutant (13C4) lost the wild type capacity to grow in 0,1% SDS, and the site of plasposon insertion in the chromosome was sequenced and the inactivated gene identified as *ampG* (GENOPAR HS 249.0052), a major facilitator superfamily. This gene probably codes a muropeptide permease whose expression is induced by naringenin in the mutant 13C4. The lipopolysaccharide (LPS) profile and the fine structure of Lipid A of both the SmR1 and 13C4 strains were analyzed by SDS-page and mass spectrometry. The LPS profile and the fine structure of Lipid A of the 13C4

mutant differed significantly from those of the wild-type strain SmR1. Further biochemical and physiological characterizations of the mutant will be presented.

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