Identifcation of *Herbaspirillum seropedicae* Genes Involved With Degradation of Naringenin

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An operon coding for 10 proteins potentially involved with degradation of flavonoids was identified in the *H. seropedicae* genome (Program GENOPAR), and named *fde* (*f*lavonoid *de*gradation). Upstream from this operon was found a *nodD*-like gene whose product belongs to LysR family of transcriptional regulators. Mutant strains of both the *nodD*-like gene and the first gene (*fdeA*) of the *fde* operon were obtained and named *H. seropedicae* DR2 and AMM1, respectively. The intergenic region *nodD*-like/*orf1* was cloned into the fusion vector pMP220, yielding pSU1. To study the regulation of the expression of the putative flavonoid degradation operon plasmid pSU1 (*fdeA::lacZ*) was introduced into *H. seropedicae* SmR1 (wild type), DR2 (*nodD*-like$^-$) and AMM1 (*fdeA*$^-$), and ß-galactosidase activity was determined. The results showed that the transcription of *fdeA* is activated by the NodD-like protein in the presence of the flavonoids naringenin or crysin. The strains SmR1 (wild type), DR2 (*nodD*-like$^-$) and AMM1 (*fdeA*$^-$) were cultivated in medium NFb containing 2 mmol/L of naringenin either in the presence or absence of malate (0.5%). Aliquots were collected at 6 hours intervals, centrifuged and the supernatant analyzed by HPLC. After 24 hours of growth only the wild type strain was capable to degrade naringenin, both in the presence or absence of malate, the preferred carbon source. These results suggest that the products of these genes are involved in naringenin degradation in *H. seropedicae* and that the LysR-type protein activates the expression of the *fde* operon in response to naringenin.

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