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Expression of the translocator protein (TSPO) from *Pseudomonas fluorescens* Pf0-1 requires the stress regulatory sigma factors AlgU and RpoH.

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The translocator protein (TSPO), previously designated as peripheral-type benzodiazepine receptor, is an evolutionarily conserved protein that is found in many Eukarya, Archae and Bacteria, in which it plays several important functions including membrane biogenesis, signaling and stress response. A tspo homologue gene has been identified in several members of the *Pseudomonas* genus, among which the soil bacterium *P. fluorescens* Pf0-1. In this bacterium, the tspo gene is located in the vicinity of a putative hybrid histidine kinase-encoding gene.

Since tspo has been involved in water stress related response in plants, we explored the effects of hyperosmolarity and temperature on *P. fluorescens* Pf0-1 tspo expression using a strategy based on lux-reporter fusions.

The tspo gene (Pf01_2811) of *P. fluorescens* Pf0-1 forms an operonic structure with Pf01_2810 and is expressed transiently during the bacterial growth.

*Expression of tspo is increased in response to hyperosmolarity at least partly via the extracytoplasmic function sigma factor AlgU activity.*

A putative RpoH-consensus binding site is located in Pf01_2810-tspo promoter region: effect of temperature on growth and TSPO expression.

Conclusions

We show that the two genes Pf01_2810 and tspo are co-transcribed forming a transcription unit. The expression of this operon is growth phase-dependent and is increased in response to high concentrations of NaCl, sucrose and to a D-cycloserine treatment, which are conditions leading to activity of the major cell wall stress responsive extracytoplasmic sigma factor AlgU. The promoter region activity is strongly lowered in a *P. aeruginosa* algU mutant, suggesting that AlgU may be involved at least partly in the molecular mechanism leading to Pf01_2810-tspo expression. *In silico* analysis of this promoter region failed to detect an AlgU consensus binding site; however, we detect a putative binding site that may participate to the transcriptional regulation of this operon.