

**EXPRESSION OF GENES IN THE PATHOGENICITY ISLAND PAPI-1 OF
Pseudomonas aeruginosa PA14 AND THEIR ROLE IN VIRULENCE IN THE
Dictyostelium discoideum MODEL**

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Pseudomonas aeruginosa is an ubiquitous gammaproteobacteria that infects immunocompromised individuals and causes nosocomial infections. Strain PA14 is highly virulent and the presence of pathogenicity islands may account for it. Two gene clusters transcribed in opposite directions are found between two direct repeats in the island PAPI-1. The first comprises two putative operons, *pvrSR* and *rscCB*, encoding two-component systems. The second presents five genes (*cupD1-D5*) for a putative pilus whose expression is hypothesized to be under the control of the two-component systems. In this work, we found a decrease in *cupD1* expression in strains lacking the response regulator RcsB, but no effect was seen for PvrR. We also demonstrated that *pvrRS* is indeed an operon, as a transcript comprising the *pvrR* and *pvrS* mRNA was detected by RT-PCR. The low expression levels of *rscCB* and *cupD1-D2* did not allow verifying whether they are also cotranscribed. As a second goal, the ability of strains carrying mutations in PAPI-1 genes to inhibit growth of *Dictyostelium discoideum* was evaluated in order to establish a simple infection model. Trials using control strains of *P. aeruginosa* presented consistent results with data in the literature and our preliminary results showed that *rscB* seems to be relevant in this model, as it was already demonstrated in other models.

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