Pseudomonas aeruginosa and its ability to use a plethora of siderophores produced by other microorganisms

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Bacterial genome sequencing has shown that most bacteria can produce siderophores and use siderophores produced by other bacteria. The opportunist pathogen *P. aeruginosa* is able to express (i) one ferrous (Fe^{2+}) iron-uptake pathway, (ii) three heme-acquisition pathways, (iii) two ferric (Fe^{3+}) iron-uptake pathways using the two siderophores pyoverdine and pyochelin produced by the pathogen, and (iv) at least 15 different Fe^{3+} uptake pathways using siderophores produced by other bacteria (siderophore piracy strategy). The presence of a large number of potential iron uptake pathways in the genome does not mean that they are all expressed simultaneously. The presence of such a large panel of iron-acquisition pathways in the genome involves a large panel of possible phenotypes, with various combinations of expression of these iron-uptake pathways, depending on the environmental stimuli. In our team we have investigated expression of the various iron-uptake pathways of *P. aeruginosa* in different growth media, in the presence of various siderophores produced by other microorganisms (present individually or as a mixture), using proteomic and RT-qPCR.[1–4] We observed an extremely complex phenotypic plasticity in the expression of the various iron-uptake pathways depending on the xenosiderophores present. In most of the conditions tested, catechol-type siderophores were more efficient in inducing the expression of their corresponding uptake pathways than the other siderophores, showing that bacteria opt for the use of catechol siderophores to access iron when they are present in the environment. In parallel, expression of the proteins of the pyochelin pathway was significantly repressed under most conditions tested, as well as that of proteins of the pyoverdine pathway, but to a lesser extent. Such high phenotypic plasticity concerning the various iron-uptake pathways present in *P. aeruginosa* genome indicates a high potential of adaptation to a large variety of biotopes.

References:

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(4) Normant, V. *et al.* How the Presence of Hemin Affects the Expression of the Different Iron Uptake Pathways in *Pseudomonas aeruginosa* Cells. *ACS Infect Dis* **2021**.