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# Two-component systems of *Pseudomonas aeruginosa*: From a large-scale study to targeted approaches

## Résumé

*Pseudomonas aeruginosa* (*Pa*) has one of the most complex bacterial regulatory networks, largely responsible for the high adaptability of this pathogen, in which two-component systems (TCS) play a major role. These allow the bacteria to perceive and adapt to physico-chemical changes in their environment. TCSs generally consist of two partners communicating by phosphate transfer: a histidine kinase (HK) which detects the signal and transmits it to the response regulator (RR) which is often a transcription factor. Particularly numerous in *Pa*, TCSs are highly studied because of their importance in antibiotic resistance and virulence. However, our knowledge of the signals they detect and the genes they regulate is largely incomplete. A recent study conducted by our team used the DAP-seq (DNA Affinity Purification-sequencing) technique to determine *in vitro* the set of binding sites for 55 *Pa* RRs on the genomes of 3 strains belonging to the 3 main phylogenetic groups. This study provides the first complete determination of the TCS regulatory network in *Pa*, highlighting the great complexity of this network and the specificities between strains. Thanks to the exploitation of the DAP-seq results and the analysis of the synteny of the genes coding for the different actors of this network (RRs, HKs and targeted genes), my work consists in deciphering the functioning of some *Pa* TCSs involved in virulence and antibiotic resistance. Through our investigations, the Roc (Regulation of cup) system known for its interconnected components (2HKs and 3RRs) appear to be even more complex and intriguing.

**Mots-Clés:** *Pseudomonas aeruginosa*, Régulation, Systèmes à deux, composants, Facteurs de transcription