

059 Insights into *Pseudomonas aeruginosa* quorum sensing therapeutics through text- and network-mining

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The unceasing emergence of antibiotic-resistant strains and resilient biofilm-related infections is pressing researchers to develop novel antimicrobial strategies. Quorum sensing (QS) is a key communication mechanism that holds promise as target to control clinical pathogens. QS allows bacteria to regulate gene expression, and thus many physiological activities, such as virulence, motility, and biofilm formation. Available information about anti-QS drugs is scattered in the vast ever-growing biomedical bibliome. Therefore, bioinformatics techniques, such as text mining and network mining, can greatly assist in the condensation and organization of such information, allowing researchers to readily identify relevant drug-QS interactions and generate new hypothesis for antimicrobial research.

In this work, an automated workflow that automatically extracts key information on *P. aeruginosa* anti-QS studies from PubMed records was implemented. The workflow outputs an integrated network, capturing the effect of drugs over QS genes, QS signals and virulence factors. Moreover, these drug-QS interactions are contextualized by additional information on the experimental methods employed, details on the drugs, QS entities and strains. The public Web-based interface (<http://pcquorum.org>) enables users to navigate through the interactions and look for indirect, non-trivial associations. Currently, the *P. aeruginosa* drug-QS network contains 958 interactions encompassing 238 different drugs and 133 different QS entities; but it is in continuous, semi-automated growth. The web-based interface also has available a regulatory network for *P. aeruginosa* so users can have a comprehensive picture of emerging anti-QS findings and thus gain novel understandings and select new antimicrobial experiments.

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