

# Comprehensive Study of Instable Regions in *Pseudomonas aeruginosa*

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**VENUE** CS Seminar Room, Y6405, 6th Floor  
Yellow Zone, Academic 1  
City University of Hong Kong  
83 Tat Chee Avenue  
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## ABSTRACT

*Pseudomonas aeruginosa* is recognized for its intrinsically advanced antibiotic resistance mechanisms. Dispensable genome which includes sequences shared by a subset of strains in a species is important to the study of a species' evolution, antibiotic resistance and infectious potential. By using a multiple sequence aligner, we segmented the genomes of 25 *Pseudomonas aeruginosa* strains into core blocks (shared by all the 25 genomes) and dispensable blocks (shared by a subset of the 25 genomes). We use the term instable blocks to refer dispensable blocks since blocks shared by a subset of the 25 genomes may be vitally important. We then built 25 scaffolds which consisted of core and instable blocks sorted by blocks' starting positions in the chromosomes for each of the 25 strains. In these scaffolds, consecutive instable blocks formed instable regions. We conducted a comprehensive study on these instable regions and found three characteristics of instable regions: instable regions were short, site specific and varied in different strains. We then studied three DNA elements which may contribute to the variation of instable regions: directed repeats (DRs), transposons and integrons. Past studies have shown that sequences flanked by a pair of DRs can be deleted from their host chromosomes or be inserted into new host chromosomes. We developed a pipeline to search for DR pairs on the flank of every instable sequence and found 27 pairs of DRs existing in the instable regions between 21 distinct pairs of core blocks. We also found that in the average, 14% and 12% of instable regions in the 25 scaffolds covered transposase genes and integrase genes, respectively.

This paper will be presented at 5th International Work-Conference on Bioinformatics and Biomedical Engineering (IWBBIO 2017), April 26-28, Granada, Spain

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Research Interests: Bioinformatics, Genome Analysis, Mechanisms for Insertions and Deletions

**All are welcome!**



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