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Poster

## Discovery of lost genes in the genome of *Acinetobacter baumannii* using AnAblast.



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### ABSTRACT

**Motivation:** Microbial resistance to antibiotics is currently one of the greatest threats in global health. Multiple outbreaks of multi-resistant *Acinetobacter baumannii* strains have been documented [1] and it is necessary to find new drugs against it, and the finding of new genes in the bacteria could help in this fighting. As *A. baumannii* is a highly studied organism, it is difficult to find new genes by homology with traditional predictors.

For this reason we have chosen the AnAblast program which is a new bioinformatics tool which has been successful in finding out new genes in eukaryotes. This program generates profiles of accumulated alignments in query amino acid sequences using a low-stringency BLAST strategy [2], which highlight regions with evolutionary meaning.

**Methods:** First, we used AnAblast to locate new coding regions in the *A. baumannii* genome. After that we analyzed the regions found by AnAblast comparing them with known sequences from the GenBank database to look for the genes found in intergenic regions and we obtain a series of candidates that we need to analyze, characterize and validate.

**Results:** We obtained nine candidates that have been characterized analyzing both its evolutionary conservation and function annotation. Eight of them were also found in other strains of *A. baumannii* and one could be a gene not found until now that needs to be validated.

**Conclusions:** Using the AnAblast program we have found nine possible coding regions not detected by other methods in the reference strain of *A. baumannii*. Although they need validation, AnAblast has proven itself useful for gene detection in prokaryotes

### REFERENCES

1. Dijkshoorn, L. et al. (2007) An increasing threat in hospitals: multidrug-resistant *Acinetobacter baumannii*. *Nature Reviews Microbiology*, 5(12), 939-952.
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