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Sequence of a big bug

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William Wells

Email: wells@biotext.com

The 6.3 Mbp sequence of *Pseudomonas aeruginosa*, the bug responsible for most cystic fibrosis deaths, reveals lots of pumps and lots of regulation. As reported in the 31 August [Nature](#), this, the largest bacterial genome sequenced thus far, is available thanks to an [effort](#) that used the shotgun sequencing capabilities of the [University of Washington in Seattle](#) and funding provided by the [Cystic Fibrosis Foundation](#) and [Pathogenesis Corporation](#) (Stover *et al.*, *Nature* 2000, **406**:959-964). The Foundation's next effort will be to make *P. aeruginosa* arrays available at a reasonable cost. With 5,570 predicted genes, *P. aeruginosa* has almost as many genes as budding yeast. This complexity is particularly apparent in regulation: a full 8-10% of the genes encode proteins with sequences similar to known regulators of gene expression. This may explain the bacteria's ability to live just about anywhere on just about anything. The sequence also unveiled a reason why *P. aeruginosa* is so troublesome for cystic fibrosis patients. The bacterium has six additional 'RND' multi-drug efflux pumps to add to the four that were already known.

References

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