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Bacterial insecticides

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One means of controlling the spread of human pathogens and parasites that are spread by insect vectors - for example, malaria - is the [use of insecticides](#). This approach is frequently compromised by the acquisition of resistance to the chemicals by the target insects, and novel, efficacious compounds are difficult to identify and expensive to develop. In the October 5 [Nature Biotechnology](#) Eric Duchaud and colleagues at the [Institut Pasteur](#) report the whole genome sequence of the bacterium *Photorhabdus luminescens* and describe two loci-encoding proteins that are lethal to the mosquitoes *Anopheles gambiae*, *Culex pipiens*, and *Aedes aegyptae*. Further sequences encoding a number of toxins and antibiotics were identified that may provide biotechnological leads in other areas (*Nature Biotechnology*, DOI:10.1038/nbt886, October 5, 2003).

Duchaud *et al.* determined the genome sequence of *P. luminescens* subspecies *laumondii* strain TT01 from its single 5.7 megabase-pair long circular chromosome and identified 4839 predicted protein-coding sequences and 157 pseudogenes. Their investigation into the life history of this nematode symbiont revealed, in addition to the insect and bacterial toxins, a range of hemolysins, proteases, adhesions, and lipases that function in the bacterium's interaction with its host and destruction of the nematode insect prey. Comparison with related bacterial genomes demonstrated acquisition of virulence factors by horizontal gene transfer.

"The availability and the functional analysis of the genome sequence of *P. luminescens* TT01 should lead to several useful applications, such as the development of new entomotoxins for crop protection and the genetic engineering of the bacterium-nematode pair for use as biological control agents. The identification of new antibiotic biosynthetic genes, which could be manipulated to generate new biological activities by domain shuffling, provides a promising resource for fighting microbial infections in the future," the authors conclude.

References

1. Insect immunity and its implication in mosquito-malaria interactions
2. *Nature Biotechnology*, [<http://www.nature.com/nbt>]
3. Institut Pasteur, [<http://www.pasteur.fr/english.html>]