Micalis
Microbiologie de l'Alimentation au service de la Santé

Evolution and ecology of virulence in *Bacillus thuringiensis*, from theory to application

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'Public goods' are shared products, paid for by individuals, but which benefit groups. The idea that secreted virulence factors might be shared public goods has had tremendous impact on microbiology. Numerous experiments have show that non-producer mutants can behave as cheaters and outcompete producers of virulence factors in mixed culture. Nevertheless, a possible flaw that many laboratory experiments in this field lack realism or expose conflict between cheaters and cooperators that does not exist in natural systems.
For *Bacillus thuringiensis* it is clear that the Cry toxins are a very good example of a microbial public good. We also understand a great deal about the processes maintaining investment in Cry toxins, despite possible competition from cheaters. The next most important set of virulence factors in *B. thuringiensis* are regulated by the *PlcR/papR* quorum-sensing system. Here, it is clear that both signals and QS regulated virulence are predominantly not public goods in natural infections.
I will present recent unpublished work that has had two aims. First, my lab has applied our new understanding of cooperative virulence to design selection experiments to increase the killing power of *B. thuringiensis*. Initial results suggest that this is possible, but that increased virulence in experimental evolution does not provide a simple route to the identification of new virulence factors. Second, we have investigated whether social evolution can explain the diversity of the *PlcR/papR* quorum-sensing system in *B. thuringiensis, i.e.* the persistence of different pherotypes with small variations in receptor and signal sequence. Again our results suggest that cooperation is an unlikely explanation for this diversity. However, differerent pherotypes can confer fitness benefits that vary with environment in particular with the size of infected hosts, an explanation that resonate with the diverse ecology of the *Bacillus cereus* group.

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