MOLECULAR BASIS FOR THE RESISTANCE OF *AEDES AEGYPTI* TO *BACILLUS SPHAERICUS*

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Bacillus sphaericus (Bs) is considered the most successful biological control agent available against mosquitoes. Its toxic activity depends on the interaction of the binary (Bin) toxin with receptors on the epithelium of the larvae midgut. In Culex quinquefasciatus this receptor is a 60 kDa, GPI anchored, membrane alpha-glucosidase (maltase), named Cqm1, and the toxin binding site was mapped to its N-terminus. Here, to investigate the molecular basis for the natural resistance to Bs of *Aedes aegypti*, we have studied a Cqm1 orthologue (Aam1 – 73% identical) identified within genome sequences available for this species. No features in Aam1, such as the absence of a GPI anchor, were identified which could explain the lack of binding of the Bin toxin to the larvae midgut. The gene fragment encoding the 45 kDa Aam1 N-terminal region was amplified, cloned and expressed as a recombinant His-tagged protein (Rec-Aam1). In vitro affinity assays showed that Rec-Aam1 bound specifically to the immobilized Bin toxin, similarly to Cqm1, and confirmed the presence of the toxin binding site. Nevertheless, in gel alpha-glucosidase assays using *Ae. aegypti* larvae midgut extracts demonstrated an expression profile distinct from *Culex* samples. These results suggest a lack of expression of the receptor in the larvae, which might explain the resistance to Bs.

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