A147 · Interactional experimental design for the efficient demonstration of the Plasmodium inhibitory property of an endosymbiont Eα alone or in association in Anopheles mosquitoes within a context of endosymbiotic diversity for the success of biological control

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The fight against malaria has led to the development of several control strategies, among which biological control currently holds great promise. However, the remarkable performances of certain endosymbionts, particularly their Plasmodium-inhibitory properties and their ability to restore mosquito susceptibility to insecticides remain subject to debate due to the lack of a suitable experimental design specifically tailored to this type of study. Such investigations, given their high level of complexity, require approaches consistent with computational biology, which is often not considered in laboratory evaluations or in natural transmission studies. Indeed, by integrating factors such as the diversity of the mosquito microbiota, its various immune expressions, and its insecticide resistance genes, it becomes necessary to adopt a scientific methodology that embraces the interactional concept proposed by this new experimental approach, modeled on the Direct Membrane Feeding Assay (DMFA) system. The scientific relevance of the proposed interactional design, in relation to the predefined set of hypotheses, would enable the elucidation of several observed mechanisms and the identification of the specific role of each endosymbiont (whether in association or not) previously characterized as candidate symbionts. Another key outcome would be the establishment of an endosymbiotic database, supporting more informed choices by different scientific teams according to their specific objectives, thereby contributing to the overall success of biological malaria control programs. Keywords: Malaria, computational biology, inhibitory property, endosymbiont, genes, resistance, interaction, biological control, causality, correlation