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The genomics of insecticide resistance: insights from recent studies in African malaria vectors

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Highlights

- 80% of the world's population is at risk from arthropod-vector-borne diseases
- 450 million clinical cases of malaria were averted via insecticide treated bednets
- Some populations of malaria mosquitoes are resistant to multiple insecticide classes
- Genomics reveals how insecticide resistance evolves and spreads
- Genomics can facilitate adaptive management of future vector control campaigns

Abstract

Over 80% of the world's population is at risk from arthropod-vector-borne diseases, and arthropod crop pests are a significant threat to food security. Insecticides are our front-line response for controlling these disease vectors and pests, and consequently the increasing prevalence of insecticide resistance is of global concern. Here we provide a brief overview of how genomics can be used to implement effective insecticide resistance management (IRM), with a focus on recent advances in the study of *Anopheles gambiae*, the major vector of malaria in Africa. These advances unlock the potential for a predictive form of IRM, allowing tractable feedback for stakeholders, where the latest field data and well parameterised models can maximise the lifetime and effectiveness of available insecticides.

Introduction

Almost 82% of the world's population is at risk from at least one arthropod-vector-borne disease, accounting for over 10% of the global disease burden [1]. Crop pests also exact a heavy toll, costing

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