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Applying GIS and population genetics for managing livestock insect pests: Case studies of tsetse and screwworm flies

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ABSTRACT

The Food and Agriculture Organization of the United Nations (FAO) and the International Atomic Energy Agency (IAEA) have supported a Co-ordinated Research Project (CRP) on '*Applying GIS and population genetics for managing livestock insect pests*'. This six-year CRP (2008–2013) focused on research aimed at under-pinning the Area-Wide Integrated Pest Management (AW-IPM) of populations of tsetse and screwworm flies, and this introductory paper to the Special Issue integrates the findings of the CRP participants and discusses them in a broader context. The tools and techniques for mapping and modelling the distributions of genetically-characterised populations of tsetse and screwworm flies are increasingly used by researchers and managers for more effective decision-making in AW-IPM programmes, as illustrated by the reports in this Special Issue. Currently, the insect pests are often characterized only by neutral genetic markers suitable for recognizing spatially isolated populations that are sometimes associated with specific environments. Two challenges for those involved in AW-IPM are the standardization of best practice to permit the efficient application of GIS and genetic tools by regional teams, and the need to develop further the mapping and modelling of parasite and pest phenotypes that are epidemiologically important.

1. Introduction

A Joint Division of the Food and Agriculture Organization of the United Nations (FAO) and the International Atomic Energy Agency (IAEA), namely the Joint FAO/IAEA Division of Nuclear Techniques in Food and Agriculture, supports need-driven basic and applied research on identified shortcomings for sustainable agricultural development in Member States, including topics relevant to managing major insect pests of agricultural, medical and veterinary importance. One way of doing this is through the FAO/IAEA Co-ordinated Research Programme, which brings together scientists from developed and developing Member States to collaborate through a Co-ordinated Research Project (CRP) for a period of five to six years on an identified research theme. A CRP involves issuing research contracts and grants to participating institutions in developing countries and research agreements with scientists in developed countries; and, it also funds Research Co-ordination Meetings (RCMs) every 18 months, in order to enable all collaborating teams to exchange results and plan future research. The CRP '*Applying GIS and population genetics for managing livestock insect pests*' involved 13 research agreements, research contracts and technical contracts awarded to scientists from collaborating institutions in Australia, Brazil, Burkina Faso, Ethiopia, France, Indonesia, Iraq, Israel, Kenya, United Kingdom, United States and Yemen. The CRP ran from 2008 to 2013, and four RCMs were held, including an opening meeting at FAO/IAEA headquarters in Vienna (Austria) and subsequent meetings in Nusa Dua (Bali, Indonesia), Bobo-Dioulasso (Burkina Faso) and London (UK). A geographical information systems (GIS) specialist from the FAO Animal Health Services assisted the project officer from the Joint FAO/IAEA Division in co-ordinating the CRP. Specifically, this CRP focused on research aimed at under-pinning the Area-Wide Integrated Pest Management (AW-IPM) of populations of tsetse and screwworm flies, and this Special Issue reports the findings of the CRP participants and their collaborators from Africa, Asia, Australia, Europe as well as North and South America.

GIS are widely used to help map the detected distributions of insect pests, to develop models assessing the suitability of certain environmental conditions for sustaining specific insect

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pest species, and to predict where pest species might find suitable conditions and become established with economically important consequences (Sutherst et al., 1989; Atzeni et al., 1994; Cecchi et al., 2008, 2014). Maps illustrating pest presence or habitat suitability alone have limited operational utility for AW-IPM campaigns if a pest behaves not as one species with a single set of phenotypic traits but as several genetic populations that may differ in traits such as diurnal activity peaks, mating compatibility, or livestock preferences (Ahrens et al., 1977; Clausen et al., 1998; Bouyer et al., 2007). Predictive models can be useful complements, including those developed to predict the spatial and temporal expansion of a pest after its first introduction into suitable habitats, or to estimate increasing economic losses to the livestock sector. For the area-wide approach of managing the populations of an insect pest, population genetic methods have been developed that permit the detection of gene flow or genetic isolation between neighbouring populations, and the findings have major implications for the planning and implementation of intervention campaigns. Distinctive populations within a pest species are often first recognized by studying the population genetics of its wild populations sampled across the different regions of the geographical range (Lyra et al., 2009; Solano et al., 2010; Wardhana et al., 2012). The current Special Issue focuses on this topic, as applied to insect pests causing two sorts of livestock ailments.

Tsetse flies of the genus *Glossina* (Diptera: Glossinidae) are the vectors of several parasitic protozoans (Kinetoplastida: Trypanosomatidae): *Trypanosoma brucei gambiensis* and *T. b. rhodesiensis*, the causative agents of human trypanosomiasis (HAT or sleeping sickness) in sub-Saharan Africa; and, *T. b. brucei, T. congolense* and *T. vivax*, which are also transmitted by different tsetse flies and cause African animal trypanosomiasis (AAT or nagana) among livestock in about 8.7 million square kilometres of arable land in Africa (Maudlin et al., 2004; Stevens and Brisse, 2004; Cecchi et al., 2014). Wild game mammals serve as reservoir hosts for some of these parasites, which are transmitted between them, cattle and other livestock when tsetse flies of either sex take a blood meal. These diseases have major economic implications for rural development as well as for human and livestock health in sub-Saharan Africa (Feldmann et al., 2005). The Programme against African Trypanosomiasis (PAAT) was initiated in 1997, bringing together the efforts of FAO, the World Health Organization (WHO), the IAEA and the African Union (formerly the Organisation of African Unity) Interafrican Bureau for Animal Resources (AU-IBAR); and, the Pan-African Tsetse and Trypanosomiasis Eradication Campaign (PATTEC) was established by the Heads of State and Government of the African Union (formerly the Organisation of African Unity) in 2000–2001 (Cecchi et al., 2014).

Approaches to AAT and HAT alleviation and treatment depend mostly on old trypanocidal drugs with recorded development of resistance, while vector management attempts are dominated by insecticide-based tactics (Molyneux et al., 2010). The Joint FAO/IAEA Division has supported research for improved and up-scaled application of the Sterile Insect Technique (SIT) as part of an AW-IPM approach through applied in-house research in their laboratories in Seibersdorf, Austria, and through the Agency's CRP scheme. The SIT was effectively applied against the tsetse fly *Glossina austeni* 1994–1996 to eradicate this pest from Zanzibar (Vreysen et al., 2000), and it is currently being successfully applied against *Glossina palpalis gambiensis* in the Niayes region of Senegal (http://www.fao.org/news/story/en/item/211898/icode/).

The parasitic maggots that hatch out of eggs deposited on the skin by screwworm flies harm the flesh of all warm-blooded vertebrates, including humans and livestock (FAO, 1991). These "fleshflies" (or, more strictly, blowflies) cause economic losses by damaging hides and reducing growth rates, and the Joint FAO/IAEA Division has previously supported a CRP on '*Enabling Technologies for the expansion of screwworm SIT programmes*' (Robinson et al., 2009). Economic losses by cattle ranchers prompted the successful area-wide integration of SIT to eliminate the New World screwworm (NWS) fly, *Cochliomyia hominivorax* (Diptera: Calliphoridae), from the southern USA, Mexico and Central America (Dyck et al., 2005) and even from Libya after a human-assisted introduction (FAO, 1991). This fleshfly is widely distributed in South America, where the current CRP's activities were focused on research to support future control. SIT requires factories for the mass production of sterile males, and they have been established for the NWS fly several times. In contrast, SIT has never been used operationally to eradicate the Old World screwworm (OWS) fly, *Chrysomya bezziana* (Diptera: Calliphoridae), although there have been successful pilot control projects in Papua New Guinea (Spradbery et al., 1989) and Malaysia (Mahon, 2002). This second fleshfly is widely distributed in humid habitats in sub-Saharan Africa, the Middle East and southern Asia (Hall et al., 2014 [This issue]).

The two species of screwworm flies and some species of tsetse flies have very large geographical ranges, and population genetics has provided neutral molecular markers for some regional populations (Lyra et al., 2009; Solano et al., 2010; Wardhana et al., 2012). Such markers can permit the identification of the geographical origins of populations that have invaded an area, and also help predict and map possible re-invasion paths following establishment of a pest-free area as a result of implementing an AW-IPM programme. This provides another reason for integrating the application of GIS and population genetics. The mapping and modelling of discrete pest populations depends on efficient sampling, and so this topic was also covered by the CRP. In particular, the adults of the OWS fly are not easily trapped without the optimisation of lures.

The selection and use of GIS software to map or model pest distributions can be challenging for non-specialists, and so the Joint FAO/IAEA Division has also supported measures to make free software accessible to all. This includes support for on-line open source GIS packages (see Section 2.2), as well as the assessments of off-the-shelf modelling software reported in this Special Issue.

Some reports suggest that wing morphometric studies can be an economical, simple alternative or complementary tool to molecular phylogenetics in support of planning AW-IPM operations (Dujardin, 2011). Metric properties of insect pest species, for example of wing shapes, may vary and – over time – change under the influence of both environmental and genetic factors. Therefore, efforts were made under this CRP to assess whether comparative morphometric analyses of the wing shapes of some populations of tsetse and screwworm flies might reveal close accordance with their regional variation.

2. Results and discussion

2.1. Sampling genetic variation among pest populations

In tsetse flies the egg stage, the first and second larval instars and most of the third larval instar are located in the uterus of the adult female fly. After about five days of intra-uterine development and immediately upon release, the third instar larva buries into the ground, where it pupates and remains for about a month. Therefore, tsetse flies are mainly sampled as adults. The design of visual attractants (traps and targets), attractant lures and their optimal placement in suitable habitats have been subject to numerous research efforts (reviewed by Maudlin et al., 2004) and were also the theme of an earlier CRP (http://cra.iaea.org/cra/about-us.html), both for savannah species such as *Glossina morsitans s.l.* and for riverine species such as *G. palpalis*. Novel findings under the current CRP come from Ethiopia (Getahun et al., 2014 [This issue]).

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