C. R. Biologies 336 (2013) 375–383

Contents lists available at SciVerse ScienceDirect

Comptes Rendus Biologies

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Review/Revue

A bird's-eye view on the modern genetics workflow and its potential applicability to the locust problem

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A R T I C L E I N F O

Article history:
Received 10 June 2013
Accepted after revision 23 July 2013
Available online 22 August 2013

Keywords:
Orthoptera
Locusts
Grasshoppers
Genetics
Gene expression
Next generation sequencing
Microarrays
RNAi

A B S T R A C T

Genetics is an immense science and the current developments in its methods and techniques as well as the fast emerging tools make it one of the most powerful biological sciences. Indeed, from taxonomy and ecology to physiology and molecular biology, every biological science makes use of genetics techniques and methods at one time or another. In fact, development in genetics is such that it is now possible to characterize and analyze the expression of the whole set of genes of virtually every living organism, even if it is a non-model one. Locusts are notorious for the damage they cause to the ecosystems and economies of the areas affected by their recurrent population outbreaks. To prevent and deal with these outbreaks, we now count on both biological as well as chemical agents that are proving to be successful in reducing the damage that otherwise locust population outbreaks might cause. However, a better, efficient and environmentally friendly solution is still a hoped-for target. In my opinion, the ideal future pesticide should be both environmentally friendly, risk free and species-specific. To reach the knowledge needed for the development of such species-specific anti-locust agent, deep and accurate knowledge of the locusts' genetics and molecular biology is a must. Since genes and their expression levels lie at the bottom of every biological phenomenon, any species-specific solution to the locust problem requires a good knowledge of these organisms' genes as well as the quantitative and spatio-temporal dynamics of their expression. To reach such knowledge, collaborative work is needed as well as a clear workflow that, given the fast development in the genetics tools, is not always clear to all research groups. For this reason, here I describe a genetics workflow that should allow taking advantage of the most recent genetics tools and techniques to answer question relating to locust biology. My hope is that the adoption of this and other work strategies by different research groups, especially when the work is a collaborative one, would provide precious information on the biology and the biological phenomena that these economically important organisms exhibit.

1. Introduction

Among orthopterans, locusts are notorious for their population outbreaks and swarming capabilities and no continent is spared from locust outbreaks. Indeed, infamous among the species known to experience population outbreaks, we find *Schistocerca gregaria* and *Oedaleus senegalensis* in Africa and parts of Asia, *Locusta migratoria* and *Oedaleus asiaticus* in Africa and Asia, *Melanoplus sanguinipes* in North America, other *Schistocerca* species (such as *S. Cancellata* and *S. americana*) in South America and *Chortoicetes terminifera* in Australia. At the outbreak phase, each of these species can cover large geographic areas (Fig. 1), often with disastrous consequences. Indeed, millions of dollars are spent each year in order to control the population size of such species that, otherwise, might experience outbreaks and become even

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1631-0691/$ – see front matter
http://dx.doi.org/10.1016/j.crvi.2013.07.002

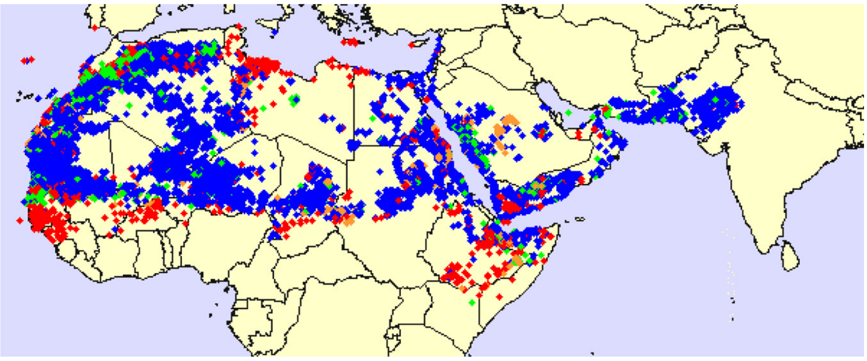

Fig. 1. Geographical distribution of *Schistocerca gregaria* populations sighted between 01-01-2000 and 01-01-2013. Green dots: solitary hoppers; blue dots: solitary adults; orange dots: gregarious hoppers; red dots: gregarious adults.
United Nations Food and Agriculture Agency (http://www.fao.org/ag/locusts/en/info/info/index.html).

more costly. For instance, a document on the benefit-cost analysis of locust control operations for 2010–2011 by the Australian Plague Locust Commission (http://www.daff.gov.au/animal-plant-health/locusts) states: "Locust control operations this season are estimated to have avoided potential losses of $963 million. Total expenditure by all parties was estimated to be $50 million. The net benefits of control are therefore $913 million, with an estimated ratio of benefits to costs of around 19.2:1."

Thus far, the solution to the outbreaks problem is largely based on prevention, with significant governmental personnel and resources dedicated to this task (e.g., the Moroccan anti-locust centre http://www.criquet-maroc.ma/, the pest research unit of the French CIRAD http://ur-bioagresseurs.cirad.fr/, and the Kenyan ICIPE http://www.icipe.org/). Coordination between countries is also needed and a section of the United Nations Food and Agriculture Organization is dedicated to this issue (see http://www.fao.org/ag/locusts/en/info/info/index.html). The strategies adopted for preventing locust outbreaks are proving helpful but, when they fail, the options are few. Although entomopathogenic fungi (such as *Metarhizium anisopliae* var. *acridum*) are currently available (e.g., http://www.lubilosa.org/) and, sometimes, used as a bio-control agents for treating the locust outbreaks, the pesticides option is still on the table and prevalent (e.g., Fipronil). No need to stress here that governments, society and local communities are increasingly aware of the dangers of the excessive use of pesticides (e.g., http://www.panna.org/). Neither it is necessary to extend on the issue of the non-specificity of the pesticides that, when used, affect the targeted locust as well as other organisms in the treated area, including humans, other mammals, bees... (e.g., [1–5]).

In my opinion, a species-specific treatment would be the ideal solution. For that, a deep knowledge of the molecular biology of the target species and its peculiarities is needed. Such knowledge would also offer precious data to many fundamental biological questions as well as to comparative studies (including the model organisms). Much is known about grasshoppers and locusts and the interest of researchers on this subject is continuously growing. In fact, a search for the word locust on the Pubmed database of the US National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/pubmed/) shows strong positive correlation between the number of published papers and the year of publication ($r = 0.871$). In fact, the numbers went from 25 papers published in 1970 to 221 in 2012, with 22 articles published just in January 2013 (Fig. 2a). However, these numbers are misleading, and their real meaning is only revealed when compared to the numbers from research on other organisms. For *Drosophila*, the number of published works on the NCBI database shows stronger correlation with the year of publication ($r = 0.957$). It grew from 331 papers published in 1970 to 3711 in 2012, with 406 papers published just in January 2013 (Fig. 2b). Strikingly, the ratio of locust articles to *Drosophila* articles per year shows that the number of publications on locusts represents just around 5% of the number of published works on *Drosophila* (Fig. 2c). Even more, the between-years increase in the number of research papers is much more irregular when it comes to locusts than it is for *Drosophila* (Fig. 2d). One might argue that comparing with a model organism may not be the right way to assess the state of the research on locusts. That is partially right, but the word locust includes several species. In addition, each of these species represents a serious (sometimes almost existential) threat to entire regions of the globe. One would thus expect research on these organisms to represent a bit more than a meager 5% of the research on *Drosophila*. Furthermore, the number of published works on locusts in 2012, for instance, is lower than that on ants (526), bees (580), and spiders (517).

The number of published articles is directly dependent on the number of research groups and on the level of financing (the first also dependent on the second in a way that the more financing a research area, the more attractive it gets it to researchers). Discussing the reasons for this near-precarious state of the research on locusts and the ways to overcome it could by itself be a theme for a manuscript and would probably be better discussed in meetings, conferences and other scientific gatherings. What matters for us now is that we are still far from reaching the level of knowledge that should allow a deep understanding of the molecular mechanisms associated with locust population outbreaks, and efficient comparative studies to determine the species-specific processes