The beauty of beetles

Dr Jesús Gómez-Zurita describes his passion for studying leaf beetles, the importance of molecular methodologies and his team’s contribution to traditional theories of evolutionary processes.

Can you begin by describing the different branches of your work in evolutionary biology and how they are all connected?

As a member of the scientific community, I am an heir to the Age of Enlightenment, emphasising fact-based knowledge and the scientific method to influence society and its development. I navigate seas of facts and observations; logic and analyses. But explaining evolution is telling stories, and as a storyteller I must also draw from intuition, speculation and creativity. The discipline demands knowledge of fields as diverse as the study and description of biodiversity, molecular biology, biochemistry, phylogenetics, ecology, geology, geography, statistics and so on. Only by merging facts and ideas from all of these fields can we compose the story that we want to tell about the organisms we study from an evolutionary point of view.

What makes beetles – particularly Chrysomelidae (leaf beetles) – especially suitable for your research?

Insects are the paradigm of biological diversity. Name an evolutionary process, and there will be dozens of insect systems to test it. Given their overwhelming diversity, they provide numerous independent repetitions of the same evolutionary phenomenon, which is ideal when we, as scientists, are looking for the generalities of these processes. With well over 350,000 described species, beetles are indisputably the most diverse among the diverse, and – in part due to their intimate association with plants – Chrysomelidae beetles provide an attractive study system. Not only do they bring evolution and ecology together in well-defined study cases, they are extraordinarily beautiful creatures too!

How does DNA sequencing aid your studies of biodiversity?

Biodiversity is the diversity of life at any level of complexity, from alternative regulation mechanisms of one particular gene to differences among individuals within a species or even the manifold ways in which communities of organisms assemble across space and time. Each level of complexity has an impact on the genome, therefore DNA-based knowledge is fundamental to address most – if not all – questions related to biodiversity.

Over the course of your research in New Caledonia, were you successful in identifying the mechanisms behind leaf beetle origins and diversification on the island?

In New Caledonia we discovered that the diversity of one particular group of leaf beetles
was higher than in the whole of North America, a piece of land more than one thousand times bigger. We wanted to know how many species of these animals we could expect to live there and what caused that explosive diversity. In order to do this, we ran a modest research programme, whereby we hoped to use intense fieldwork and DNA-based approaches to shed some light on these questions. We obtained some answers, including the confirmation of high species numbers (more than 200 species in the environments that we sampled), but also the time framework for the assemble of this diversity. Some characteristics of the diversity pattern, framed with the phylogeny, then raised new working hypotheses.

What do your findings concerning beetle and host plant evolution mean for traditional theories of coevolution?

The enormous diversity of insects and plants since the Carboniferous period – when they both started their journey towards eventual dominance of terrestrial ecosystems – illustrates evolutionary interactions between herbivorous insects and plants that have taken every imaginable combination of characteristics. My contribution to this field is at most expanding our knowledge of the diversity of evolutionary possibilities by describing interactions of specific groups of leaf beetles and their host plants with a phylogenetic background. The possibilities are almost endless; as such, evolutionary biologists usually develop a creative mindset to imagine all the alternative scenarios to test for. Usually, the problem is not thinking of explanations, but restraining our imagination and simplifying the assumptions to explain a process – in this case, how the interactions of beetles and plants condition the way they evolve.

How has DNA barcoding helped to shed light on beetle-host interactions?

DNA barcoding is a simple (and by virtue of its simplicity, powerful) idea. Different species show differences in DNA sequence for each of their genes. Among the tens of thousands of genes in each species’ genome, there must be some for which the level of differentiation among individuals of the same species is lower than between individuals of different species. The DNA sequence for these genes is a species marker of sorts; a specific sequence of nucleotides that can be used to tag a particular known species, i.e. a DNA barcode. In principle, by characterising the DNA barcode of an unidentified organism and comparing to this reference, we should be able to name this organism, just as barcode scanners recognise products in shops. We characterise plant DNA barcodes from beetle DNA extractions (including whatever was in their guts – generally digested plant tissue). By comparing them with a reference database that we had previously produced in the lab – that is, correspondence tables of plant DNA barcodes and plant names – we can eventually assign a plant name to the diet of the herbivore insect.

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DESPITE PROVIDING THE foundation for modern biological science, evolution largely remains a mystery. One of the least understood aspects of the broader theory of evolution is speciation – the process by which one species diverges into two or more. Understanding such a complex process requires detailed observation of natural biological systems, and choosing a suitable system is difficult. Further complications arise from the enormous timescales over which speciation tends to operate, and the difficulty in definitively establishing that it has even taken place. As such, few organisms are consistently suitable models for this process.

One animal that bucks this trend by offering a potential window into the process of evolution and speciation is the beetle. Beetles are the most diverse group of animals in the world; their ubiquity and variety of life histories make them ideal models for such research. This is why research scientist Dr Jesús Gómez-Zurita from the Institut de Biologia Evolutiva, Spain, is focusing his efforts on beetle evolution – specifically the evolution of the Chrysomelidae, or leaf beetles.

The leaf beetles are themselves a numerous clade, consisting of more than 35,000 known species. Their most important characteristic, as their name suggests, is their relationship with plants: “They are intimately associated with plants, developing, feeding and reproducing on them, sometimes in a one-to-one species relationship,” explains Gómez-Zurita.

THE RISE OF MOLECULAR METHODOLOGIES

Since the beginning of Linnaean taxonomy, naturalists and scientists have been concerned with the classification of species. Originally based on similarities in morphology and behaviour, scientists today primarily rely on molecular analysis – most often the analysis of DNA. This classification comprises an area of evolutionary research called phylogenetic systematics: “Nowadays, the most prolific source of variable characteristics for phylogenetic inference is the genome and differences in DNA sequence between individuals, both within and among species,” Gómez-Zurita notes. By employing such methodologies, his team is currently working to gain a comprehensive understanding of the evolution of leaf beetle communities from tropical forests in Vietnam, Nicaragua and New Caledonia.

While understanding processes such as speciation is one of the more obvious applications of molecular methodology, the reality is that the majority of research into biodiversity now includes at least some molecular component, as Gómez-Zurita neatly summarises: “When our study of biodiversity focuses on fundamental aspects, DNA sequences are simultaneously the means and the goal of the research”.

Perhaps the most widely employed tool in this work is the DNA-barcode. This method uses specific regions of the genome to identify and characterise species. By comparing the structure of these specific regions between individuals, the team can identify whether a particular specimen is from a known or newly discovered species, as well as how closely related species are to each other. The researchers are even using DNA-barcoding to identify the plant material found in leaf beetles’ guts in order to build up a picture of

Leaf and let live

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INTELLIGENCE

LEAF BEETLE BIODIVERSITY

OBJECTIVES
To use extensive DNA analysis and fieldwork to elucidate a range of evolutionary processes in Chrysomelidae leaf beetles.

KEY COLLABORATORS
Consejo Superior de Investigaciones Científicas

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One of the most striking adaptations that Gómez-Zurita and his colleagues have been studying is the ability of some leaf beetles to reproduce in the absence of males.

NEW CALEDONIA
- A LIVING LABORATORY

Advances in molecular techniques have handed biologists the tools required to understand species relatedness and family evolution, but there are still major challenges to overcome, most notably the difficulty of conducting field work. Due to their interest in biodiversity, much of the team’s field work is conducted in tropical forests, where diversity is generally considerably greater than in temperate regions. In addition, the scarcity of the target species means that huge amounts of time, energy and commitment are required to find the beetles that will ultimately contribute to the group’s knowledge in a laboratory setting: “Fieldwork is fundamental: sampling is both the key and the limiting factor for relevant science,” highlights Gómez-Zurita.

The curious case of unisexuality

One of the most striking adaptations that Gómez-Zurita’s group has been studying is the ability of some leaf beetles to reproduce in the absence of males. This adaptation presents a number of fascinating questions regarding the evolutionary pressures and responses acting upon these insects. This is an area in which the researchers have made some progress: “Thanks to DNA analysis, we now have very detailed knowledge of the processes that generated this extraordinary reproductive strategy,” reveals Gómez-Zurita. The team believes that this unique approach to reproduction is the result of a series of independent species hybridisation events that took place over many thousands of years. With the foundations of their understanding laid, the researchers have now moved on to investigating the complexities of this phenomenon, particularly in terms of what happens to genes typically involved in male functions, such as sperm production, once they get trapped in an evolutionary lineage that lacks males.

While this research is crucial to furthering understanding of beetle biology and speciation, the work also has implications for the quantification of anthropogenic effects on biodiversity. “Based on our research, we understand that, during historic periods of climate change, a lifeline for survival has always been provided by organisms shifting their ranges. The problem is that this is no longer possible in most cases due to human-induced habitat destruction,” Gómez-Zurita remarks. This concerning finding highlights the fragility of the world’s biodiversity. Due to the timescale of speciation, the impact that anthropogenic change has already had and continues to have on biodiversity may never be repaired. In this context, the work conducted by Gómez-Zurita and his colleagues may not only be a window into the extraordinary evolutionary processes that take place in leaf beetles, but may also demonstrate one of the last opportunities that science has to understand the processes governing biodiversity, before the tree of life becomes markedly more stunted.