

Scientists call for gap between genomics and invasion biology to be bridged

18 June 2015

Scientists at the University of Southampton think that Next-Generation Sequencing (NGS) of invasive organisms holds the key to furthering our understanding of ecological and evolutionary processes.

In a review of recent studies published in *Current Zoology*, the researchers say the technique is underutilised in the field of invasion biology. They believe NGS has the potential to transform our understanding of why non-native species adapt and thrive in new environments, often at the expense of their indigenous competitors.

The key to the success of biological invasions may lie in the genome (the complete DNA code of an organism) and the transcriptome (the specific genes which are being expressed). While the genome of an individual is roughly fixed (altering only through mutation), the transcriptome can vary according to the environment.

"Introduced species adapt to their new environment as we speak, so rather than taking hundreds of thousands of years to evolve, we can witness how species adapt in real time," says Dr Marc Rius, Lecturer at the University of Southampton.

Co-author Dr Mark Chapman, who is also a Lecturer at the University of Southampton, says: "By comparing and contrasting an indigenous population with an introduced one, genomics allows you to separate which genetic traits are due to natural selection and which are due to neutral evolution, which occurs as a matter of course."

The output of NGS is 100 to 100,000 times higher than First-Generation, or Sanger, sequencing and has several other advantages. For example, NGS makes sequencing without a complete genome or transcriptome for reference much more cost effective and easy to do, which has led to many more 'non-model' organisms being sequenced.

"Compared to previous methods, NGS is a much more cost-effective option to sequence large portions of the genome," says co-author Harry Hornsby, a postgraduate researcher at Southampton. "It allows us to compare whole genomes and transcriptomes, giving us a much broader and more detailed picture of what is happening at a genetic level among individuals and populations, revealing patterns of selection and the genes that might underpin adaptation."

The review shows that as the cost of NGS has steadily decreased (since its inception during the mid-2000s), the number of publications looking into invasion genetics has increased, paving the way for an NGS revolution in the field. Despite this, relatively few studies have utilised the technique and much of the work that has is descriptive, rather than comprehensive analyses.

Steve Bourne, who also co-authored the study, comments: "What we have seen is there can be some really interesting insights to be gained when NGS is applied to invasion biology. It has huge potential to accelerate our understanding and help us find out what makes an [invasive species](#) successful, and more broadly how species adapt to new environments. However, there is a gap to be bridged before it becomes common practice."

As well as offering an insight into the evolutionary process, findings could have practical applications for the management of ecosystems, and the detection and control of invasive species that can negatively impact biodiversity. For example, when cane toads came to Australia, their defence mechanism proved so toxic that it depleted populations of native predators, which died from eating them.

Provided by University of Southampton

APA citation: Scientists call for gap between genomics and invasion biology to be bridged (2015, June 18) retrieved 26 September 2020 from <https://phys.org/news/2015-06-scientists-gap-genomics-invasion-biology.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.