



# Editorial: The Genomics of Biological Invasion

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## Editorial on the Research Topic

### The Genomics of Biological Invasion

Understanding how invasive species rapidly infiltrate and establish in new areas is critically relevant for ecological management, pest control, climate change adaptation, and evolution (Doherty et al., 2016; Maxwell et al., 2016). Invasive species are almost always detrimental to native flora and fauna: they may out-compete natives in the race for resources, introduce parasites and diseases, and cause immense environmental damage (Clavero and García-Berthou, 2005; Hulme, 2014; Vilcinskis, 2015).

Invasion success often reflects a life history trade-off for the invading organism. Free from predators (i.e., enemy release) or toxins in the new environment, the invasive species can limit investment in defense or tolerance traits and allocate more energy toward growth and reproduction (Heger and Jeschke, 2018). Therefore, invasion is often seen as a fundamentally demographic process (National Research Council, 2002; Duncan et al., 2014). However, for a species to become invasive, it must tolerate or adapt to the environmental and ecological characteristics of the invaded habitat, in which it did not evolve and to which it may be poorly matched (Prentis et al., 2008). Thus, the success of invasive populations is likely also underpinned by adaptive genomic characteristics, such as those leading to insecticide resistance (Franck et al., 2007) or expansions in host breadth (Pearce et al., 2017).

Advances in genomic technologies allow us to better understand the role of the genome in invasion. The present special topic, entitled The Genomics of Biological Invasion, aimed to include research papers that used genomic data to understand various aspects of invasion success. With this broad scope, our special issue features research on a number of different study systems (the green crab, *Carcinus maenas*; the knapweed, *Centaurea diffusa*; the Pacific oyster, *Crassostrea gigas*; and the “pavement” ant, *Tetramorium immigrans*), and includes a simulation-based study, an opinion, and a review.

Burgess et al. focus their review on invasive mammalian species in island systems, which have experienced particularly high rates of invasive-driven biodiversity loss (Bellard et al., 2016). They evaluate current management of invasive mammals on islands and comprehensively summarize the role genomic methods can play. Of particular note, Burgess et al. identify the utility of genomics in eradication and biosecurity protocols, noting environmental DNA (eDNA) and genome editing as important emerging tools. Focusing on analytical tools, Rius and Turon assess the assumptions and applicability of phylogeography to invasion genomics. This is important because phylogeography research aims to understand the relationship between geography and genotype, and invasive species distributions are changing as they undergo geographic range expansion in the face of increased global trade and movement, and warming temperatures (Hulme, 2017, 2021; Robinson et al., 2020; Nerva et al., 2021). However, in the case of recent

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introductions yet to achieve mutation-migration-drift equilibrium, phylogeographic analyses may not be appropriate. Instead, Rius and Turon champion the use of temporal samples (e.g., museum collections) in invasion research, alongside a careful application of phylogeographic approaches and interpretation of results.

Genetic tools have been used to answer a variety of questions related to biological invasions in new habitats, spanning the invasion sequence from pre- to post-introduction to obtain insights into incursion pathways, adaptation, and demography (Barrett, 2015; North et al., 2021). Using spatially explicit simulations to examine structured populations with a low to moderate amount of hybridization, Quilodr an et al. show that the distance of the invasive taxon from the source of the original invasion influences the degree of introgression at neutral loci. This spatial heterogeneity is consistent with empirical data (Nussberger et al., 2018; Oswald et al., 2019) and may explain spatial patterns of Neanderthal introgression into modern humans following their out-of-Africa expansion (Quilodr an et al.). Zhang et al. further demonstrate the utility of genomic data in understanding the population structure and incursion pathways associated with a biological invasion. They use a citizen-science approach to analyse the invasion of the urban “pavement” ant (*T. immigrans*), which is ubiquitous in pavement and other human-modified habitats. Using 78 samples and a reduced representation sequencing approach (ddRADseq), Zhang et al. find weak population structure and low genetic diversity consistent with the original incursion including one, or a few, genetically similar colonies.

Focusing on post-introduction adaptation, Tepolt and Palumbi collected samples of a widespread invasive marine crab (*C. maena*) from six populations, which provided parallel thermal gradients in invasive and native ranges. Using a combination of genomic and phenotypic data, they identify candidate genetic markers that align with differences in thermal phenotypes across populations. Around 70% of these markers fall into a genomic cluster, exemplifying the putative role of genomic islands of divergence in facilitating rapid temperature adaptation in invasive species. Turner et al. also take a combined genomic and phenotypic approach to examine differences between invasive

and native populations. They generate genomic resources (a draft reference genome and a plastome assembly) in the non-model knapweed (*C. diffusa*), and phenotype 372 individuals from invasive/native populations in a common environment. Identifying differences in leaf width that correlate with fitness and that vary between invasive and native counterparts, Turner et al. demonstrate a mechanistic pathway for adaptation in this invasive plant, while also identifying candidate genes underlying the genetic architecture of the leaf width trait. Finally, Wegner et al. combine genomic and transcriptomic data to identify both plastic (i.e., immediate physiological) and selective (i.e., longer-term adaptation) aspects of survival in novel invaded environments in the Pacific oyster (*C. gigas*). Their approach shows that different candidate loci are generally important across the two time-scales. However, in a small number of cases, they identify overlaps between the temporal datasets that provide new insights into the mechanisms underlying rapid environmental tolerance and adaptation during invasion.

Collectively, our special topic highlights the applicability of genomic tools to a variety of study systems and analytical approaches in both basic and applied aspects of invasion. It further demonstrates the specific utility of combining genomic data with other data types to elucidate mechanistic processes that facilitate invasion success.

## AUTHOR CONTRIBUTIONS

AM proposed the special topic and wrote the first draft of the manuscript. All authors contributed to manuscript revision and read and approved the submitted version.

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