Invasive species cause considerable ecological and economic damage but the studies discussed within this special column highlight the advantages of studying these species. Several of the articles in this special column discuss how genetic studies of invasive species add to our ability to predict invasive potential but also increase our understanding of native species’ response to climate change (Liebl et al., 2015; Rius et al., 2015). It is now well-recognised that invasions represent “experiments in evolution” and that rapid evolution is common during introduction (Rollins et al., 2013), allowing us to use invasive species as models for understanding evolutionary processes at large.

Genetic approaches have been used extensively to identify the origin of invasive populations and understand the dynamics of spread in introduced ranges. However, as summarized in this special column, our knowledge of temporal genetic changes in invasive populations remains poorly understood (reviewed in Moule et al., 2015). Temporal studies are especially important when studying populations that are unlikely to be at genetic equilibrium (such as newly established invasive populations). Using temporal data from invasive populations of the delicate skink Lampropholis delicata, Moule et al. (2015) showed that no new successful introductions of this species had occurred in their study sites over a five year period but that local allele frequencies shifted significantly, perhaps due to spread of primary introductions. Such data can be used to improve management plans and focus preventative efforts to avoid unintentional introductions; novel alleles indicate a need for greater surveillance and control.

Perhaps one of our greatest advances in this field has been the development of ecological models for invasion, which afford us a better understanding of the myriad ecological and evolutionary forces acting on invasive species following introduction. These bodies of work include genetic studies but, importantly, also provide information about ecological differences between native and introduced populations of these species. In this special column, Leibl et al. (2015) describe the wealth of information known about house sparrow Passer domesticus invasion genetics and ecology. Perhaps most importantly, studies of this species have pioneered our understanding of the role of epigenetics in animal invasions (Schrey et al., 2012; Liebl et al., 2013), which promises to be one of the most exciting new directions in invasion genetics. This may solve the “invasion paradox”, which questions how introduced species with low genetic diversity can rapidly adapt in novel environments.

While the studies reviewed in Leibl et al. (2015) focus on a single species, Sherwin et al. (2015) describe a collection of studies on a species complex that serves as an excellent model for the study of invasion. Three congeneric tephritid fruit flies (Bactrocera tryoni, B. neohumeralis, and B. jarvisi) are sympatric over much of their endemic Australian range and have strikingly similar genomes, yet display varying levels of invasiveness. Because of this, these Bactrocera species offer a unique opportunity to understand genetic drivers of invasiveness. However, this also highlights the importance of marrying ecological and genetic data to understand the forces governing invasion. Genomic resources for these species are currently under development, which will increase the power of this system with respect to studies of invasiveness (Sherwin et al., 2015).

Advances in next-generation sequencing (NGS) technologies have revolutionized our ability to study the genetic basis of traits and, specifically, to identify genes underlying adaptation to novel environments. NGS techniques are underutilised in invasion genetics but are predicted to become common as associated costs decrease (Rius et al., 2015). Approaches to understanding adaptation during invasion through the use of NGS are described by Rius et al. (2015) in this special column, with a particular emphasis on the utility of studying gene expression changes associated with invasion. In conjunction with these studies, common-garden experiments can distinguish selective changes occurring over
the scale of generations from phenotypic plasticity occurring within an individual’s lifetime. Through these studies, we are beginning to identify genes that may be important to invasiveness across taxa (Rius et al., 2015). The increasing accessibility of NGS approaches is likely to have profound impacts on the field of invasion genetics over the next decade.

The importance of understanding selection on functional genes during invasion has been highlighted by several of the contributions to this special column (Liebl et al., 2015; Rius et al., 2015; Sherwin et al., 2015). One functional gene of particular interest to invasion biologists is the dopamine receptor D4 (DRD4) gene, which has been linked to exploratory and novelty-seeking behavior in a wide range of taxa (Rollins et al., 2015). Although DRD4 has previously been associated with exploratory behavior in avian systems (Fidler et al., 2008; Mueller et al., 2014), this result is not consistent across populations (Mueller et al., 2013). In this issue, Rollins et al. (2015) investigates evidence for selection at this locus in invasive Australian populations of starlings Sturnus vulgaris. Although little evidence for selection on DRD4 was detected in Australian starling populations, the data presented by Rollins et al. (2015) support the idea that functional genes (subject to selection) may be more useful in identifying between-population variation than neutral markers (Allendorf et al., 2008), especially where genetic diversity is expected to be low, such as in recently established invasive populations.

Fifty years ago, the Genetics of Colonizing Species (Baker and Stebbins, 1965) recognized the value of investigating genetic changes associated with exotic introductions. Over the past half century, our curiosity about how invasive species establish and adapt to novel environments has grown; studies of “invasion genetics” have increased almost by an order of magnitude in the past 15 years (Rius et al., 2015). However, despite our 50 years of progress, we still have many unanswered questions regarding the nature of invasive species genetics (reviewed in Bock et al., 2015). The special column in this issue documents some of the significant progress that has been made in this field and highlights promising future research directions.

References


