NEWS AND COMMENTARY

Invasion Biology Resolving the genetic paradox in invasive species

R Frankham

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recent paper in Nature helps to solve a genetic dilemma in invasion biology. That is, how bottlenecked populations that typically have low genetic diversity, low evolutionary potential and perhaps low reproductive fitness can become invasive.

Potential solutions to the dilemma include being asexual or self-fertilising, having high reproductive rates, purging deleterious alleles that cause inbreeding depression, or having high migration rates where repeated introductions occur to overcome low genetic diversity and inbreeding. New work by Kolbe et al (2004) provides evidence for the latter scenario with an invasive lizard species.

Many invasive species are asexual or self-fertilising and may escape inbreeding depression (Sakai et al, 2001) and invasive species may have higher than normal reproductive rates. Purging of deleterious alleles by natural selection in small populations does not remove the problem, as two recent studies in birds and Drosophila have demonstrated that bottlenecked populations typically suffer lowered reproductive fitness (Reed et al, 2003; Briskie and MacIntosh, 2004).

Kolbe et al (2004) investigated this genetic dilemma by surveying mtDNA diversity in 71 native and 59 introduced populations of the invasive brown inole lizard (Anolis sagrei) from Cuba. They found that the populations that had established in Florida from the sources in Cuba had higher genetic diversity than individual populations, due to at least eight migration events. Further, these Florida populations seem to have been the main source for other recent introductions of the lizard to Hawaii and Taiwan.

Related evidence of multiple introductions being associated with invasiveness exists for European starlings (Sturnus vulgaris) and house sparrows (Passer domesticus) in North America, and for a range of plants (Sakai et al, 2001). A similar situation has also been

found in some house mouse (Mus musculus) populations (Frankham, 1997). Several subspecies of mice exist, and island populations with genetic diversity higher than mainland populations occur on major trade routes. Further, fire ants around Brisbane, Australia have been founded by multiple introductions before they were discovered and eradication efforts begun (Henshaw et al, 2004). Thus, at least some invasive species have elevated genetic diversity and enhanced ability to evolve when they invade new places. It is important that follow-up studies be carried out in such cases to establish whether greater evolutionary changes have actually occurred in invasive populations than in noninvasive ones.

Not all introduced populations of brown anole have low genetic diversity. Of 57 introduced populations worldwide, 27 have reduced genetic diversity compared with the average level found in native Cuban populations, and 11 have lower genetic diversity than any of the Cuban populations (Kolbe et al, 2004). Information on multiple nuclear loci, such as microsatellites, would improve the precision of such comparisons.

Population bottlenecks do not stop evolution or necessarily doom populations (Frankham et al, 2002). Even a single pair bottleneck in an outbreeding species only reduces heterozygosity by 25%, provided the population then grows rapidly in numbers. The inbreeding effect of such a bottleneck in a natural outbreeding species is likely to reduce the population growth rate, but as long as it remains positive the population will still grow.

Many introduced species exhibit a lag before undergoing rapid expansion. This may be due to the early stage of exponential growth, stochastic extinctions of propagules, or genetic adaptation to the new environment (Sakai et al, 2001). The Kolbe et al (2004) study provides evidence that genetic adapta-

tion may well be involved in invasiveness, but it remains to be seen whether this is generally true. Genotypes of introduced populations certainly influence introduction and reintroduction success in fish, plants, rabbits, starlings and invertebrates; in particular, populations adapted to captivity do poorly (Frankham et al, 2002).

The Kolbe et al (2004) work has implications for controlling invasive species and for predicting the risk of introducing species that become invasive. It is clearly desirable to eliminate invasive species as soon as possible after the invasion, before they adapt to the local environment and before additional invasions occur. Unfortunately, this is rarely the case. With free trade agreements, increased trade is likely to both increase the number of introduction sites and the number of multiple introductions at individual sites. If the Kolbe et al (2004) story is general, then we are likely to face increased risks of invasive outbreaks from introduced populations in the future, both from multiple introductions to a site and from source populations being from trade centres with multiple source populations.

R Frankham is at the Department of Biological Sciences, Key Centre for Biodiversity and Bioresources, Macquarie University, New South Wales 2109, Australia.

e-mail: rfrankha@els.mq.edu.au

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Further Reading

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- Chapman H, Robson B, Pearson ML (2004). Population genetic structure of a colonising, triploid weed, Hieracium lepidulum. Heredity 92: 182–188.
- Milne RI, Abbott RJ (2004). Geographic origin and taxonomic status of the invasive Privet, Ligustrum robustum (Oleaceae), in the Mascarene Islands, determined by chloroplast DNA and RAPDs. Heredity 92: 78-87.
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