This third issue of *Evolutionary Applications* features a wide range of topics, including evolutionary causes of invasiveness (Lee and Gelembiuk 2008), human sexual dimorphism (Crespi 2008), estimation of effective population size (Nomura 2008), genetic connectivity and habitat restoration (Raeymaekers et al. 2008), maize adaptation (Mercer et al. 2008), fitness consequences of wild-farm salmon hybridization (Fraser et al. 2008), adaptation to environmental stress (Gilchrist et al. 2008), and Darwinian perspectives on fisheries management (Olsen et al. 2008). Similar to the first two issues in this inaugural year, once again we see that evolutionary biology greatly contributes to our understanding of a wide array of practical issues. Below we highlight just a few of the articles representing the breadth of topics covered in this month’s issue.

**Evolutionary origins of invasive populations (Lee and Gelembiuk 2008)**

Why are some populations particularly invasive? Do invasive species become widespread merely due to transport opportunity, or might some common evolutionary mechanism also contribute to the origins of invasive populations? This perspective discusses mechanisms that might lead to the evolutionary origins of invasive populations. Lee and Gelembiuk synthesize a large body of literature from diverse disciplines, including theoretical population genetics and evolutionary ecology, to hypothesize on the evolutionary forces that might promote invasive potential. In particular, they focus on the role of disturbance in the native range. The authors note that populations within species frequently vary in their invasibility, and that the invasive populations often arise from habitats prone to disturbance. They argue that the particular selection regime in the native source range of invasive populations might be a critical factor in shaping invasive potential. For example, disturbance in the form of fluctuating selection in the native range might lead to the evolution of generalist strategies or the evolution of evolvability, depending on the rate of fluctuations relative to generation time. Thus distinct strategies, such as phenotypic plasticity or evolvability, might result from a continuum of the same evolutionary processes, and seemingly disjoint phenomena are interrelated. In their concluding remarks, the authors advocate elevating invasion biology to a predictive science, where hypotheses are based on fundamental evolutionary principles. Such a comprehensive treatise on the potential impact of disturbance on the evolution of invasive populations is unprecedented, and will hopefully stimulate much discussion and future research.

**Turner syndrome and the evolution of human sexual dimorphism (Crespi 2008)**

Turner syndrome is caused by loss of all or part of an X chromosome in females. A series of recent studies has characterized phenotypic differences between Turner females retaining the intact maternally inherited versus paternally inherited X chromosome, which have been interpreted as evidence for effects of X-linked imprinted genes. In this study, Crespi demonstrates that the differences between Turner females with a maternal X and a paternal X broadly parallel the differences between males and normal females for a large suite of traits, including lipid profile and visceral fat, response to growth hormone, sensorineural hearing loss, congenital heart and kidney malformations, neuroanatomy (sizes of the cerebellum, hippocampus, caudate nuclei and superior temporal gyrus) and aspects of cognition. This pattern indicates that diverse aspects of human sex differences are mediated in part by X-linked genes, via genomic imprinting of such genes, higher rates of mosaicism in Turner females with an intact X chromosome of paternal origin, karyotypic differences between Turner females with a maternal versus paternal X chromosome or some combination of these phenomena. Determining the relative contributions of genomic imprinting, karyotype and mosaicism to variation in Turner syndrome phenotypes has important implications for both clinical treatment of individuals with this syndrome, and hypotheses for the evolution and development of human sexual dimorphism.

**Modeling genetic connectivity in sticklebacks as a guideline for river restoration (Raeymaekers et al. 2008)**

River systems around the world are being highly impacted, namely by habitat fragmentation caused by human-made structures such as dams, tunnels, water mills and sluices. These barriers greatly influence migration and mating behavior of the organisms inhabiting...
these rivers, potentially resulting in decreased gene flow and decreased genetic diversity within populations. This in turn may lead to evolutionary change in population characteristics such as reproductive success, and survival. To better understand how these artificial structures affect genetic connectivity of riverine organisms, Raeymaekers et al. performed a detailed landscape genetics analysis based on an extensive sampling of 20 populations of the threespined stickleback (*Gasterosteus aculeatus* L.) in the Scheldt River basin in Belgium. In particular, Raeymaekers et al. adapted a method to detect the geographical factors causing genetic drift. These models allowed the authors to examine the relative contribution of various environmental features to patterns of allelic variation within and among stickleback populations. Anthropogenic structures dominated population structure, affecting not only genetic diversity, but also the balance between gene flow and genetic drift (migration–drift equilibrium). This study thus nicely illustrates the usefulness of a rigorous landscape genetics framework for quantifying the significant impact of artificial barriers to the genetic health of riverine organisms.

**Clinal patterns of desiccation and starvation resistance in ancestral and invading populations of *Drosophila subobscura* (Gilchrist et al. 2008)**

Physiological tolerance to environmental sources of stress, such as extreme temperature and aridity, influences the geographic range of many organisms and can limit an organisms’ rate of spread. Today, climate change is altering the physical environment at a rapid rate, frequently shifting the geographic distribution of many species. To better understand how environmental stresses have influenced the worldwide distribution of *Drosophila subobscura*, Gilchrist et al. compared desiccation and starvation tolerance along approximately 1500 km latitudinal gradients in three *D. subobscura* populations: ancestral populations from Europe (EU) and ‘replicate’ invasive South (SA) and North American (NA) populations. The authors expected that flies from low-latitude (hot, dry) regions should have increased stress resistance. Interestingly, they found that although starvation tolerance did not vary with latitude in any continent, desiccation tolerance varied with latitude and climate on all three continents, but curiously, not always as predicted. In NA and EU, the pattern for desiccation tolerance was as expected, with higher tolerance at low latitudes, but in SA, tolerance actually increased slightly with latitude. The authors speculate that the presence of closely related competitors in EU and NA, and the absence of such competitors in SA could help explain these patterns of desiccation tolerance. Overall, these data provide grounding for the theoretical study of how evolving stress tolerance affects population ranges in changing environments, and also suggest that more study is needed on how biotic interactions such as competition can mediate adaptation to environmental stress.

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