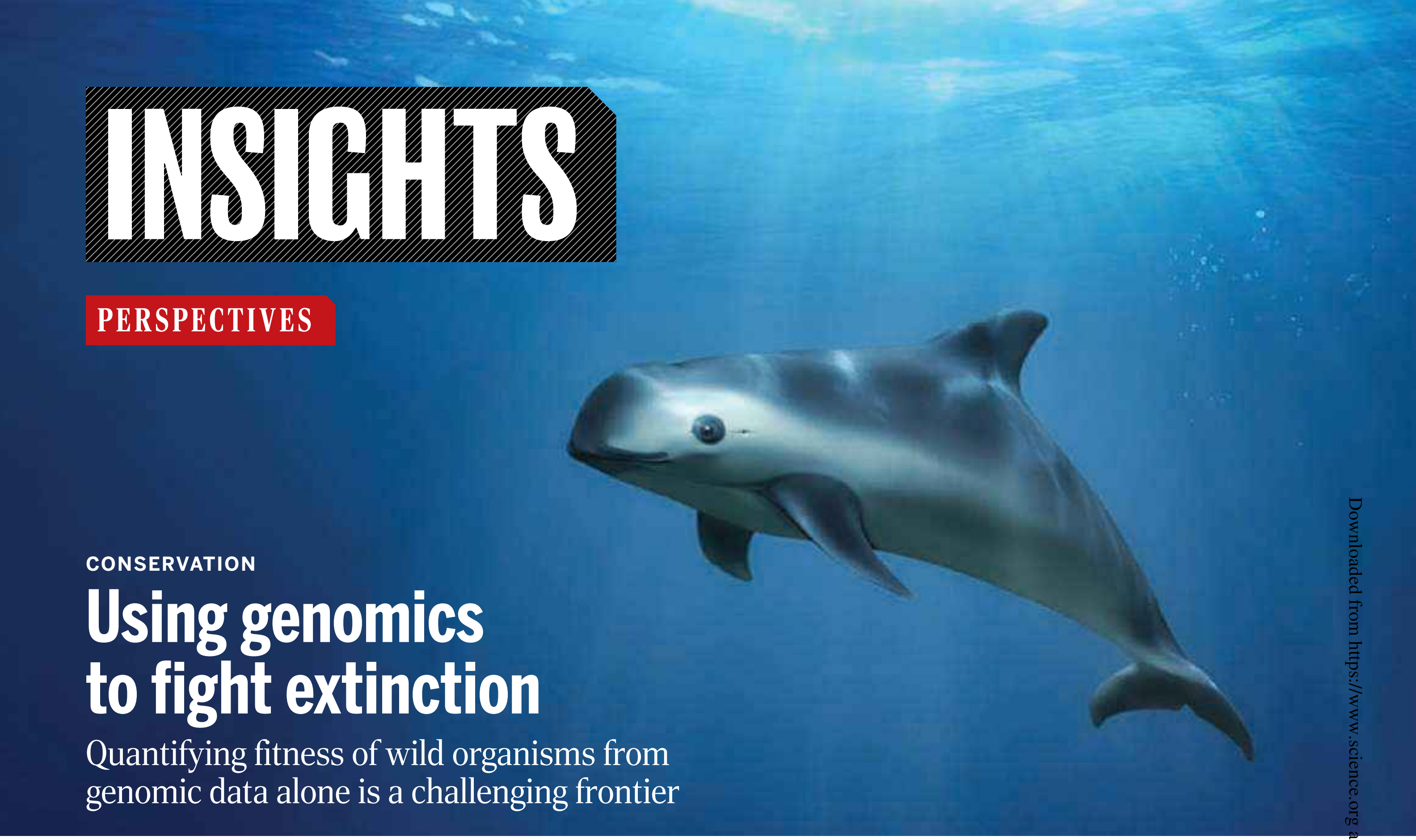

CONSERVATION

Using genomics to fight extinction

Quantifying fitness of wild organisms from genomic data alone is a challenging frontier

By **Catherine E. Grueber**[1] *and* **Paul Sunnucks**[2]

Global biodiversity is being lost rapidly, and the recovery of threatened species faces many challenges. Looming large are the anthropogenic causes of population declines, including habitat loss, invasive species, and overexploitation. Genetic threats exacerbate the problem: Population declines erode genetic variation and mating of close relatives in small populations causes inbreeding, together harming the long- and short-term viability of a population. On page 635 of this issue, Robinson *et al.* (*1*) report using genomic data from the vaquita porpoise (*Phocoena sinus*) from Mexico—which has suffered a recent severe population decline as a result of incidental mortality through fishery operations (bycatch)—to examine genetic diversity and anticipate its likely effects on future population trends. They conclude that, provided bycatch is reduced, the species shows promising potential to overcome genetic threats. The analysis exemplifies some of the ways that genomics can inform conservation policy and practice.

Genomic data are increasingly being used to tackle long-standing questions around the genetics of small populations. Because genetic processes affect survival and reproduction of individuals (i.e., fitness) and therefore the viability of populations, the results of such studies inform population futures and so should inform biodiversity policy and planning (*2*). Conservation genetics is an application of population genetics with important idiosyncrasies. Small populations fail to meet the theoretical idealized Wright-Fisher assumptions about processes that drive genetic change within populations. In particular, genetic drift plays a greatly enlarged role in small populations, the rate of inbreeding is increased, purging of harmful variation may occur (selection against harmful recessive variants expressed in inbred individuals), and even genomic associations among loci and their relationship to fitness are influenced by these processes (*3*). Empirical genomic observations of threatened species, such as that of Robinson *et al.*, are being used to discover how these genetic processes play out in real-world small populations of threatened species. Yet, formidable questions persist around the mechanistic bases of inbreeding, natural selection, allelic diversity loss, and ultimately fitness.

Inbreeding depression is fitness loss caused by increased homozygosity in the offspring of related parents (*3*). It is plausible that the severity of inbreeding depression is reduced in some small populations through two processes: removal of the most harmful genetic variants because of their exposure to selection in homozygotes (purging) (*3*) and retention of fewer harmful variants in small populations because of an overall loss of diversity (*4*). However, the relevance of these processes for the viability of real populations is poorly understood, and even less clear is how the information informs conservation decision-making. There are many reasons that these mechanisms are challenging to quantify, particularly a lack of data linking specific genomic variants with fitness variation in natural populations. The fitness impact of inbreeding is best determined using genome-wide diversity and direct measurement of lifetime reproductive success of individuals, but the latter is extremely challenging to obtain from field surveys. Hence, Robinson *et al.* and others have ventured to quantify the effect of inbreeding by using genomic data alone to estimate the genomic distribution of selection effects, also known as the distribution of fitness effects (DFE).

Although an important concept, the DFE is problematic to estimate reliably for several reasons (*5*, *6*). The DFE is controlled by a multitude of complex interacting factors that are currently largely intractable (*6*). The effects of balancing selection might not be represented in the DFE because they are transient (*7*). Most current DFE estimation methods focus on detrimental coding vari-

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The vaquita porpoise from Mexico, illustrated here, has suffered population decline. Genetic analyses suggest that the population could thrive again if bycatch is reduced.

ants; however, coding variation contributes only a small fraction to overall fitness (*8*), and ignoring beneficial variants may further bias inferences (*6*). Moreover, experimental evolution studies indicate that mutation of even a single amino acid can have a range of fitness consequences (*9*).

To resolve these issues, what population genetics in general—and conservation biology in particular—needs is to quantify empirically how well genome-based approaches predict variation in individual lifetime reproductive success in real populations (*10*). A central part of the solution lies in combining population genomics with quantitative genetics, through detailed observational and experimental data (*6*, *8*). This dual approach is powerful for understanding the genomic basis of fitness but has rarely been applied (*8*). The results of such endeavors could validate fitness inferences from genomic variant data, or at least quantify the fraction of fitness variation detectable using DFE (*7*). Doing so will be important to improve the reliability of conservation inferences based on DFE, such as those presented by Robinson *et al.*, and to facilitate wider and more-confident use of these methods.

A genetic bottleneck, caused by small population size, influences the relationships between drift, selection, individual fitness, and population viability—central considerations in conservation genetics. Genetic drift in small populations may reduce the number of fitness-reducing variants (genetic load), but the harmful variants that remain may become more problematic at the population level. This is because the frequencies of detrimental alleles in a small population may increase (even to the extinction of their alternatives) by chance, despite selection against them. Increased inbreeding in such populations further exposes harmful recessive variants, with negative impacts on individuals (*11*).

The negative effects of inbreeding have been quantified traditionally from pedigrees, or estimated using genomics (*12*), in combination with individual fitness data. A classic, extreme example is the Chatham Island black robin (*Petroica traversi*), which declined to a single breeding pair in the 1980s and has since recovered to hundreds of individuals, owing to intensive conservation efforts (*13*). Pedigree-based inbreeding studies generated from two decades of intensive field research since the single-pair decline showed that subsequent inbreeding still had measurable impacts on individual fitness, indicating that considerable genetic load persisted despite the potential for purging (*13*, *14*). Genetic threats in such populations can be reduced by removing or minimizing other threatening processes (e.g., reducing bycatch for the vaquita); this enables population growth, thereby slowing the rate of inbreeding accumulation and reducing drift effects. In turn, these activities lessen the fitness impact of inbreeding and mitigate its negative influences on population viability.

Opportunities are emerging to harness genomic insights for biodiversity monitoring and preservation, but the specific genetic drivers of variation in individual and population outcomes in model organisms, let alone in threatened species, are only beginning to be uncovered. Although genetic variation has fitness consequences, reliably connecting the distribution of genomic variants with the reproduction and survival of individuals in wild populations is at the frontier of current capabilities.

Empirically, genome-wide diversity overall is a good indicator of individual fitness and fuels the evolutionary potential of populations. Efforts to increase genomic variation in inbred and small populations will almost ubiquitously increase fitness and resilience in the face of changing threats (*4*). Robinson *et al.* conclude their work with the unassailable opinion that extrinsic causes of decline must be reduced if the vaquita is to have any chance of recovery. Active conservation efforts can reduce the extinction risk of perhaps every threatened species (*15*), and genomic advances are another tool that, when used thoughtfully, enable that effort to be deployed effectively. ■

REFERENCES AND NOTES

1. J. A. Robinson *et al.*, *Science* **376**, 635 (2022).
2. S. Hoban *et al.*, *Biol. Conserv.* **248**, 108654 (2020).
3. D. Charlesworth, J. H. Willis, *Nat. Rev. Genet.* **10**, 783 (2009).
4. M. Kardos *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **118**, e2104642118 (2021).
5. K. Ralls, P. Sunnucks, R. C. Lacy, R. Frankham, *Biol. Conserv.* **251**, 108784 (2020).
6. B. M. Henn, L. R. Botigué, C. D. Bustamante, A. G. Clark, S. Gravel, *Nat. Rev. Genet.* **16**, 333 (2015).
7. A. Fijarczyk, W. Babik, *Mol. Ecol.* **24**, 3529 (2015).
8. B. Charlesworth, *Proc. Natl. Acad. Sci. U.S.A.* **112**, 1662 (2015).
9. V. Koufopanou, S. Lomas, I. J. Tsai, A. Burt, *Genome Biol. Evol.* **7**, 1887 (2015).
10. K. A. Harrisson *et al.*, *Curr. Biol.* **29**, 2711 (2019).
11. S. Mathur, J. A. DeWoody, *Evol. Appl.* **14**, 1540 (2021).
12. A. Caballero, B. Villanueva, T. Druet, *Evol. Appl.* **14**, 416 (2020).
13. E. S. Kennedy, C. E. Grueber, R. P. Duncan, I. G. Jamieson, *Evolution* **68**, 987 (2014).
14. E. L. Weiser, C. E. Grueber, E. S. Kennedy, I. G. Jamieson, *Evolution* **70**, 154 (2016).
15. D. A. Wiedenfeld *et al.*, *Conserv. Biol.* **35**, 1388 (2021).

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QUANTUM OPTICS

Giving entangled photons new colors

A fiber-based modulator shifts photon frequency while preserving quantum correlations

By **Alexei V. Sokolov**

To narrow the distance between theory and practical applications of quantum information science, researchers must make big technological leaps in hardware development. For example, quantum communication networks, designed to facilitate the transmission of quantum bits of information, may require interfacing several separate optical devices operating in widely different spectral regions. On page 621 of this issue, Tyumenev *et al.* (*1*) offer an operation principle for such an interface and demonstrate how a specially prepared delicate quantum state of light can be transposed from one frequency region to another. In their proof-of-principle experiment, the frequency conversion is achieved through the use of a hollow-core optical fiber filled with hydrogen molecules that are vibrating in unison.

The true nature of light, and electromagnetism in general, remains a subject of advanced studies and developments pertaining to a wide range of technologies. For many applications, a simplified “classical” description of the electromagnetic field would often suffice for an adequate understanding of inner workings of the system, from high-speed fiber-optic internet to space telescopes. However, the more complete “quantum” description becomes necessary for the development of a growing number of devices and techniques, such as quantum encryption and quantum communication satellites. Processes that utilize the quantum aspects of electromagnetism are increasingly being considered for practi-

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