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Evolution: Small populations, low recombination, big trouble?

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Small populations harbour less genetic diversity and more harmful mutations. They thus adapt more slowly. A new study supports these notions and suggests that reduced recombination exacerbates these effects, highlighting the impact of genome architecture on adaptability.

Today, the nearly neutral theory of molecular evolution constitutes a cornerstone of evolutionary theory. Back in the late 1960s when its foundation, the neutral theory, was formulated, however, the suggestion that most molecular variation has no effect on individual fitness and molecular evolution is dominated by genetic drift[1–3] was an antithesis to the then prevailing understanding of evolution. Selection was thought to be the major driver of evolution by which phenotypes adapt to their environment. This view, though, conflicted with the observation of significant variation at the molecular level. How were the observed levels of molecular variation maintained in natural populations, despite selection eliminating harmful or fixing beneficial mutations? None of the prevailing selectionist arguments provided a single explanation to this conundrum. Only the insight that most segregating mutations have at most a weak fitness effect and evolution must be dominated by genetic drift provided a unified framework reconciling patterns of molecular and phenotypic evolution. The impact of the nearly neutral theory, however, reaches far beyond the fields of molecular evolution and evolutionary theory. It formulates the condition under which we can have good hope for species to survive today's fast changing world: $s > 1/2N_e$. That is, only in populations of an effective size (N_e) large enough for selection (s) to dominate over genetic drift ($1/2N_e$) can harmful mutations be removed and beneficial mutations be promoted by selection — otherwise their fate is up to chance. This is bad news from a conservation perspective: small populations may not only host a high proportion of harmful mutations ('genetic load'), but also have poorer prospects to adapt to the rapidly changing environments of the Anthropocene. A paper by Thibault Leroy, Benoit Nabholz and colleagues[4] in this issue of *Current Biology* adds evidence from island songbird populations in support of the nearly neutral theory and discusses its implications in the light of conservation biology.

Island species are ideally suited to test the nearly neutral theory. Both the colonization process involved in their evolution and the limited ranges offered by islands contribute to reduced effective population size, and we can expect drift to be a major force in their evolution. With this in mind, Leroy and colleagues[4] investigated the genomic diversity of 14 island and 11 continental songbird species (Figure 1). They found that island birds are genetically less diverse than continental congeners and have smaller effective population size; they harbour a higher proportion of harmful mutations, and less beneficial mutations reached fixation over the course of their evolution. In line with the nearly neutral theory, these results demonstrate that selection is often not strong enough to remove harmful mutations and to promote beneficial mutations in island birds.

Moreover, the study highlights that features of genome architecture may play a significant role in determining the genetic load of small populations. In island birds, not all parts of the genome display an equally elevated genetic load. Leroy and colleagues[4] show that in regions of the genome presumed to recombine rarely (inferred as ones with a low proportion of G and C nucleotides at third codon positions) the genetic load is elevated compared to frequently recombining regions of the genome (Figure 2). This finding is in line with a now widely described pattern of recombination-dependent variation in genetic diversity and effective population size along the genome[5–7], and provides compelling evidence that the impact of nearly neutral evolution varies not only between species but also between genomic regions within the same species as a function of local effective population size. In rarely recombining genome regions, selection on one site reduces genetic diversity at many linked sites[8,9]. This results in a reduction of genetic diversity — and hence effective population size — compared to surrounding genome regions. The results of Leroy and colleagues[4] suggest that, besides this effect of selection and as a consequence of reduced population size, drift in rarely recombining genome regions is often too strong to be overcome by purifying selection. Consequently, their genetic load increases. From a molecular evolution perspective, this finding provides a compelling example for the interplay between selection, genetic drift, and genome architecture in shaping the distribution of genetic diversity along the genome. It consolidates the nearly neutral theory as a cornerstone of evolutionary theory.

Most remarkably, however, it appears that without the effect of rarely recombining genome regions, the genetic load of island birds would not be much higher than in continental congeners.

Figure 1. Island endemic finch species and continental congener.
The Tenerife Blue Chaffinch (*Fringilla teydae*; top) – whose range is restricted to the Teide massif of Tenerife – harbours about one order of magnitude less neutral genetic diversity but double the proportion of harmful genetic diversity compared to its congener, the Chaffinch (*Fringilla coelebs*, bottom) – whose range covers vast parts of Eurasia and northernmost Africa. (Photos: Reto Burri.)

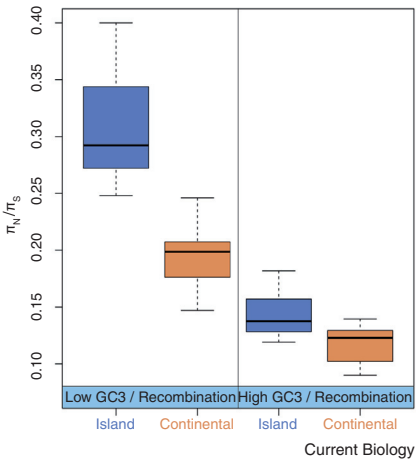

Figure 2. Genetic load in island versus continental species and in frequently versus rarely recombining regions of the genome.
The proportion of harmful mutations (π_N/π_S), the genetic load, is most elevated in the rarely recombining fraction of island species' genomes (low content of G and C nucleotides at third codon positions, GC3). In the frequently recombining fraction of the genome, the genetic load is barely (though significantly) higher in island than in continental species. Data kindly provided by Leroy and colleagues[4].

Indeed, within frequently recombining genome regions (Figure 2) the genetic load of island species is not much higher than in continental species. This limited effect of insularity by itself is rather modest when compared to the effect of recombination within continental species but between rarely and frequently recombining genome regions (Figure 2). Indeed, the highly elevated genetic loads in island species locate to the rarely recombining fractions of the genome. In these, they strongly exceed the ones of the same genomic regions in continental species as well as those of frequently recombining genome regions within island species. This finding raises the question of what role recombination and its variation along the genome, but also genome architecture more generally, has to play in the genetic erosion of small populations that may be of relevance from a conservation genomics point of view.

Genome architecture and conservation biology drive on paths that meet not all too often. The findings of Leroy and colleagues[4] now put island birds at one of their crossroads. The concentration of elevated genetic load in rarely recombining genome regions of island birds consolidates the importance of recombination in buffering potentially harmful consequences of habitat fragmentation and population declines. However, recombination not only dissociates the evolutionary trajectories of harmful from physically linked beneficial mutations[10]. As Leroy and colleagues[4] show, it also reduces the proportion of the genome most prone to accumulate harmful variation in small populations. The concentration of genetic load to rarely recombining genome regions raises additional questions: may high genetic load be particularly problematic in rarely recombining regions of the genome, given that these are often of particular relevance for the maintenance of alternative adapted phenotypes[11,12]? Might potential fitness impacts vary according to whether genetic loads are distributed heterogeneously (as in island birds) or more uniformly along genomes, and in extension of the species' karyotype (number and size of chromosomes)? Elevated genetic loads may not

necessarily lead to a swirl down the extinction vortex in all species. May this fate depend on whether genes of adaptive relevance are located in frequently or rarely recombining regions of the genome? Questions such as these take a far leap even on a broadly interpreted roadmap for conservation genomics. Nevertheless, they point out that the relationship between genetic parameters and species' decline or ultimately extinction may be highly complex. This complexity may be part of the reason why studies like the present one find no evidence for a relationship of genetic load with species' threat status, and why the translation of genomics into conservation-relevant results continues to be a substantial matter of debate[13]. In island birds, a first step forward would now be to establish not only whether, in rarely recombining regions of the genome, genetic load is elevated but also whether adaptive evolution happened at a slower rate. From there on, genomicists and conservation biologists alike may then continue following the yet stony path taken by Leroy and colleagues[4] trying to connect the threads of yet disparate fields.

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Vision: What's so special about words?

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Readers are sensitive to the statistics of written language. New research suggests that this sensitivity may be driven by the same domain-general mechanisms that enable the visual system to detect statistical regularities in the visual environment.

As you read this, you are doing something that your ancestors in 5000 BC never did. They would be fascinated at your ability to convert squiggles into sound and meaning. They were sophisticated users of language and had the same perceptual apparatus as you; no doubt they could have read perfectly well, had someone taught them, but written language had yet to be invented. If the perceptual apparatus we use for reading was inherited from our ancestors, though, what were *they* doing with it? What is the connection between our ability to read and the much older cognitive and perceptual abilities that have been selected for over the course of evolution? A new study by Vidal *et al.*[1], reported in this issue of *Current Biology*, sheds new light on the answer to this question.

Though most of us take it for granted, our ability to recognise printed words — which is the foundation of our ability to read — is rather remarkable. An adult reader of English knows tens of thousands of words[2]. To a rough approximation, the printed words of a given script all look rather similar (looking at an unfamiliar script reminds one of the difficulties that ought to be posed by this visual similarity). Nevertheless, here you are, speeding through the words on this page, effortlessly recognising each one almost instantaneously. You are still able to do this if I change the font or the size or the CASE of the words[3]. Researchers have been asking questions about the mechanisms underlying this ability for over a century. The answers may have