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Recentering evolution for sustainability science

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Abstract

Non-technical summary. Evolutionary biology considers how organisms and populations change over multiple generations, and so is naturally focused on issues of sustainability through time. Yet, sustainability science rarely incorporates evolutionary thinking and most scientists and policy makers do not account for how evolutionary processes contribute to sustainability. Understanding the interplay between evolutionary processes and nature's contribution to people is key to sustaining life on Earth.

Technical summary. Evolution, the change in gene frequencies within populations, is a process of genetically based modification by descent, providing the raw material essential for adaptation to environmental change. Therefore, it is crucial that we understand evolutionary processes if we aim for a sustainable planet. We here contribute to this development by describing examples of contemporary, rapid evolutionary changes of concern for sustainability, specifically highlighting the global spread of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) and how the evolutionary toolbox allowed tracking the origins and evolution of SARS-CoV-2 in real time and predicting potential future outbreaks. We also consider how urban development accelerates evolutionary processes such as altered phenotypic and physiological changes and the spread of infectious and zoonotic diseases. We show the importance of evolutionary concepts and techniques for public-health decision making. Many examples of the potential of evolutionary insights contributing to crucial sustainability challenges exist, including infectious and zoonotic diseases, ecosystem and human health, and conservation of natural resources. We thus join recent calls advocating for a stronger collaboration between evolutionary biologists and the sustainability community, increasing interdisciplinarity and the awareness about the knowledge of evolutionary processes for decision making and policies.

Social media summary. Evolution is fundamental to sustaining life on Earth and should be incorporated in sustainability measures and policies.

1. Introduction

Evolution is the process of genetically based modification by descent across generations, with genetic variation providing the raw material essential for evolution by natural selection, allowing populations to adapt to environmental change. If genetic diversity is lost, the resilience of ecosystems and their associated services are reduced. Therefore, it is crucial that we understand evolutionary processes if we aim for a sustainable planet (Exposito et al., 2022).

Sustainability science studies the interactions between natural and social systems, and how those interactions impact the central goal of sustainability: meeting the needs of present and future generations while substantially increasing human well-being and maintaining the planet's life support systems (Clark & Dickson, 2003). This emphasis in human and environmental health through time means sustainability science and evolution share a common conceptual lens focused on change across generations. Yet, despite sustainability science being an interdisciplinary subject spanning natural, social, economic, and technological sciences, most scientists and policy makers do not make a direct connection to evolutionary biology (Díaz et al., 2020; Messerli et al., 2019).

We acknowledge the importance of macroevolutionary processes, where evolutionary change driven by selection, gene flow, drift, or mutation can lead to populations with unique combinations of traits and to the origin of new species. But although speciation is often a slow process, trait evolution within populations can be rapid, occurring on contemporary timescales that impact sustainability. Here, we show how evolutionary insights and the evolutionary toolbox – the suite of analytical tools and techniques used to study contemporary evolution – contribute to meeting crucial sustainability challenges. We specifically describe the global spread of

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severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), the virus that causes coronavirus disease-2019, as an example that underscores the importance of evolutionary concepts and techniques for public-health decision making. We emphasize how evolutionary tools for comparative genomic analyses and phylogenetic reconstruction provide insight into the genetic changes responsible for the origin and spread of virus variants and play a central role in identifying genetic targets for vaccine development and anti-viral medication. We also underline how urban environments have accelerated contemporary evolutionary processes, often with negative consequences, briefly discussing some examples including the spread of diseases and the evolution of invasive species and impacts on wildlife and human health. We conclude that evolutionary principles, combined with insights from other disciplines including ecology, virology, geography, and economics allow us to address the role of evolution in the provision of ecosystem services and hence, ultimately informing efforts to achieve sustainability measures and policies that are key to sustaining life on Earth.

2. Tracking the origins and evolution of SARS-CoV-2 in real time

SARS-CoV-2, like all RNA viruses, evolves rapidly due to its high mutation rate (spontaneous mutation rate of 1.3×10^{-6} ; Amicone *et al.*, 2022). Rapid genome sequencing of viral isolates shared through public repositories allows tracking the evolution of the virus in near real time (Singh & Yi, 2021), providing insight into emerging variants of concern that can be used to support public-health decision making (see, e.g. <https://covarr-net.github.io/duotang/duotang.html#Introduction>). The result has been an explosion of genomic data since the first sequence was published in early January 2020, with over 15,389,037 genome sequence submissions now available and more being published every day. These genomic resources have provided unprecedented insight into important aspects of the origins of SARS-CoV-2, such as the key genetic changes thought to allow the virus to cross the species barrier from animals into humans (Andersen *et al.*, 2020).

Phylogenetic analyses, part of the evolutionary toolbox contributing to genomic epidemiology (Grubaugh *et al.*, 2019), reveal the date of the first human infection sometime between late November and mid-December 2019 (Hill & Rambaut, 2020; Li *et al.*, 2020). Such methods continue to provide insight into the transmission dynamics and spread of viral strains regionally and globally. Genomic analyses also reveal highly conserved regions where mutations are rare. These can assist in the development of vaccines and antiviral interventions. Ongoing research focuses on specific sites in genome showing evidence of selection that impact transmission or virulence, as well as analytical strategies needed to identify strains bearing these mutations as early as possible (Cyrus *et al.*, 2022; Obermeyer *et al.*, 2022).

The repeated spread of variants of concern – viral genotypes that have a demonstrated impact on human health either because they are more transmissible or more virulent (or both) – is driven by the high mutation rates and extremely large viral population sizes resulting from rapid transmission (Visher *et al.*, 2021). Competition among genetically distinct viral variants has led to the spread of ever more transmissible forms of the virus, an evolutionary dynamic that closely resembles that seen both in laboratory evolution experiments with microbes (Good *et al.*, 2017) and in theoretical models (e.g. Gandon *et al.*, 2016). The role of selection within and among patients in generating variants of concern,

especially in the context of a changing immunity landscape for the virus, remains an active area of investigation. Knowing when and where a zoonotic outbreak is likely to occur, namely when a virus whose normal host is an animal species gains the ability to cross the species barrier and causes infection in humans, remains an enormous challenge (Hernandez-Castro *et al.*, 2022). Notably, evolutionary tools have enabled analyses of the transmission of SARS-CoV-2 between human and non-human species and to identify mutations associated with each species (Naderi *et al.*, 2023), where for instance animal-to-human transmission from minks was detected to be higher compared with lower transmission from other species (cats, dogs, and deer). Hence, continuous molecular surveillance of SARS-CoV-2 from animals is paramount to reveal new insights into SARS-CoV-2 host range and adaptation, contributing to our understanding of the risk of reinfection from animal reservoirs back into humans (Naderi *et al.*, 2023).

3. Zoonotic outbreaks and vector dispersal

Not only coronaviruses but a myriad of other viruses, bacteria, parasites, and fungi can cause zoonoses, infectious diseases that are transmitted between species from animals to humans, or from humans to animals, for which forecasting spillover risk and outbreaks is crucial. Zoonotic outbreaks should be unusual because a virus that thrives in one animal species may not possess the mechanism allowing it to establish (i.e. replicate) in a human cell and transmit from person-to-person (Randolph & Rogers, 2010). Multiple genetic changes are often required, though we do not typically know a priori how many or which specific environmental conditions promote their evolution (Naderi *et al.*, 2023; Visher *et al.*, 2021). The principles governing the evolution of novelty suggest that any factor which increase the likelihood of a rare mutation contributing to a novel trait, either through genetic mechanisms like gene amplification or ecological ones like increased population size, can enhance the chance that novelty will evolve (Kassen, 2019). While only a small fraction of the thousands of animal viruses with zoonotic potential have led to public health emergencies (Albery *et al.*, 2021), evidence suggests a growing number of viruses are spilling over into human hosts (Smith *et al.*, 2014). The more often spillover happens, the more chances the right combination of mutations allowing infection within and transmission among human hosts will evolve (Visher *et al.*, 2021), making zoonotic infectious diseases a major sustainability challenge.

Effective tools for forecasting the occurrence and dynamics of outbreaks and the evolution of variants requiring public health attention after an outbreak are being developed (Campbell *et al.*, 2022; Polonsky *et al.*, 2019). A novel approach proposed by Campbell *et al.* (2022) involves defining a lineage by phylogenetic methods for tracking virus spread and comparing sequences across geographic areas, which they demonstrated with the globally distributed cosmopolitan clade of rabies virus, defining 96 total lineages within the clade. Integrating this tool with a new rabies virus sequence data resource (RABV-GLUE; <http://rabv-gluе.cvr.gla.ac.uk/#/home>) enabled highlighting lineage dynamics relevant to control and elimination programs. In addition, ‘Outbreak analytics’ is an emerging data science focused on the technological and methodological aspects of the outbreak data. It has aided field epidemiologists in collection, visualization, and data analyses, providing decision makers with insightful information and improving our understanding of and response to outbreaks of emerging pathogens (Polonsky *et al.*, 2019).

Landscape genomics is a discipline that evaluates drivers of population structure, gene flow, and potential local adaptation and selection across the landscape. It is an approach that has been successfully used to determine dispersal in disease vectors at fine spatial scales. As an example, a study of the triatomine bug *Rhodnius ecuadoriensis*, a Chagas disease vector, found high-directional dispersal from forest to urban environments, as well as genomic regions likely linked to adaptations to the built environment (Hernandez-Castro et al., 2022). These findings evidenced that this triatomine bug has high capabilities to geographically disperse across multiple human communities, which jeopardizes sustainable control of Chagas disease. Importantly, readiness to predict future outbreaks and dispersal will require integration of evolutionary and epidemiological models in the context of climate, habitat, and socioeconomic modification. Among such modifications, anthropogenic perturbation and urban development prompt rapid contemporary evolutionary changes which, among others, can significantly impact transmission and the opportunity for establishment of pathogens in novel hosts (Ahmed et al., 2019; Szulkin et al., 2020).

4. Contemporary evolutionary change: how urban development accelerates evolutionary processes

Anthropogenic perturbation and urbanization drastically transform landscapes, resulting in habitat fragmentation, degradation, and isolation, which can markedly alter dispersal and have detrimental effects on the long-term survival of populations (Mimura et al., 2017). Evolutionary change can be driven, among others, by gene flow, which is the exchange of genetic material among populations linked to the dispersal of individuals or gametes and reflecting landscape connectivity. Gene flow can impact evolutionary dynamics by fostering the maintenance of genetic diversity within populations and thus their potential to adapt to changing environments (Lambert & Donihue, 2020; Richardson et al., 2014; Tigano & Friesen, 2016).

Although evolutionary change is commonly thought of as a long-term process, it is now clear that it can occur on short, ecological timescales, rendering significant changes in evolutionary traits and leading to genetic and phenotypic shifts in just a few generations (Kinnison & Hendry, 2001; Koch et al., 2014). It is now also recognized that contemporary evolution shapes ecological communities and ecosystem functions (Hendry, 2017; Leibold et al., 2022). The rapid development and growth of cities around the world can be an important driver of species' evolution (Santangelo et al., 2022). Indeed, urban evolution, the heritable genetic changes of populations as a response to anthropogenic activities in urban ecosystems, is one of the best and earliest examples of rapid contemporary adaptation and evolution (Kettlewell, 1955; van't Hof et al., 2016). Such evolutionary change can have both short- and long-term effects on the health and fitness of organisms (Diamond & Martin, 2021; Johnson & Munshi-South, 2017; Miles et al., 2021; Szulkin et al., 2020), impact ecological dynamics of populations (Des Roches et al., 2020; Lambert & Donihue, 2020), and yield positive outcomes for key ecosystem services like pest control and enhancement of pollination (Lambert & Donihue, 2020).

Evolution in urban environments can also have many significant negative consequences, including altered responses and spread of infectious and zoonotic diseases (Hassell et al., 2017), and the rapid evolution of invasive species (Baxter-Gilbert et al., 2022; Touchard et al., 2023). Notably, genetic exchange can

occur between species or between genotypes or lineages coming from different populations, and such introgressive hybridization can provide a boost in evolutionary potential (Chaturvedi et al., 2020; Pacheco-Sierra et al., 2018). Conversely, when exotic species are introduced outside their native range and become invasive they can lead to population declines or extinction, either due to displacement resulting from interspecific interactions (e.g. competition, predation) or through hybridization with the native species (Quilodr an et al., 2020). The evolution of different behavioral or reproductive traits, as well as competitive ability of invasive species, has been documented as factors facilitating range expansion and spread. For instance, the dwarf spider *Mermessus trilobatus* is native to North America and one of the most invasive spiders in Europe. Interestingly, dispersal behavior is highly heritable in these invasive spiders, via recessively inherited and phenotypically expressed genotypes only in offspring of two high-dispersive parents. The accumulation of dispersive genotypes in newly colonized areas and spatial selection resulting in an increase in dispersal ability has contributed to the accelerated spread of *M. trilobatus* in Europe (Narimanov et al., 2022). Evolution of such traits can play a key role in numerous arthropod invasions worldwide, with potential devastating consequences particularly in species like invasive crop pests (Nyamukondiwa et al., 2022).

Cities are associated with increased air, water, and soil pollution, and while some species can adapt to these pollutant stressors (Oziolor et al., 2019), others are driven to local extinction (Knapp et al., 2021). As such, another example of concern for sustainability is that many chemical pollutants are carcinogenic, and there is mounting evidence that multiple forms of pollution elevate cancer in humans and wild animals (Hamede et al., 2020; IARC, 2016). Evolutionary concepts have been recently integrated into different forms of wildlife disease management like cancer (Hamede et al., 2020), and also to understand for instance host–pathogen dynamics in non-primate humans (Sol rzano-Garc a et al., 2021). Hence, understanding the interplay between evolutionary processes and urbanization impacts and effects is key to achieve good health and well-being, along with sustainable cities and communities.

5. Contemporary evolution and ecosystem services

Ecosystem services encompass the properties and processes through which natural ecosystems, and their constituent species, sustain human life (Daily, 1997; Des Roches et al., 2020). Ecosystem services are defined as 'all the uses or services to humans that are produced from the evolutionary process' (Faith et al., 2010), coined to capture the importance of evolution for the myriad of services nature renders to people (Norgaard, 2010). Given that all living organisms, and hence all ecosystem services derived from them, stem from evolution, this definition includes all ecosystem services as ecosystem services (Norgaard, 2010; Rudman et al., 2017). More recently, Rudman et al. (2017) introduced the term *contemporary ecosystem services* to explicitly address the importance of contemporary evolution to the provisioning of ecosystem services, resulting from evolution occurring quickly enough to alter ecological processes. For instance, evolutionary principles offer a novel and complementary perspective on services to humans like pollination. By considering synergies among fundamental evolutionary research, genetic engineering, and agro-ecological science, van der Niet et al. (2023) highlight how principles of evolutionary history of wild plant species can be applied to deal with the present pollination

crisis, using technological advances to adapt crop flowers for optimal pollination by local wild pollinators, particularly by increasing generalization in pollination systems. Evolutionary concepts and tools have also been applied to control pathogens using numerical simulations of eco-evolutionary dynamics (Bargués-Ribera & Gokhale, 2020), as well as for biocontrol of pest insects (Páez & Fleming-Davies, 2020).

Genetic diversity is positively associated with the provision of ecosystem services, as demonstrated by experimental restoration studies. For instance, seagrass plots with a small increase in genetic diversity harbor plants that survive longer, increase in density more quickly, and provide more services including invertebrate habitat, increased primary productivity, and nutrient retention (Reynolds et al., 2012). Seagrasses are key productive ecosystems engineering the maintenance of coastlines, where genetic diversity is crucial for seagrass local acclimation and adaptation in the face of climate changes (Pazzaglia et al., 2021). A decrease in species diversity and evolutionary potential, the latter caused by the loss of genetic diversity because of urbanization, habitat destruction, and habitat fragmentation, among others, strongly and negatively impact ecosystems and their associated services (Lambert & Donihue, 2020). Hence, to protect and enhance the functioning of ecosystems we need to maintain the within-species genetic diversity that fuels contemporary evolution (Díaz et al., 2018, 2020; Hughes et al., 2008; Molina-Venegas, 2021). The capacity of evolutionary processes to buffer environmental change and enhance the resilience of ecosystems also needs to be fully incorporated into sustainability science.

6. Evolution in natural and social sciences

Applied evolutionary biology and cultural evolution are key interdisciplinary approaches that intersect the natural and social sciences. Applied evolutionary biology provides a suite of strategies, from common policies that promote medicine and public health (Natterson-Horowitz et al., 2023), or preserve habitat for threatened species, to the engineering of new genomes, which help address global challenges that threaten human health, food security, and biodiversity (Carroll et al., 2011, 2014). Some examples include manipulation of genetic, developmental, and environmental factors, like the genetic engineering of crops to enhance drought- and flood-tolerance. However, such strategies are easily overlooked as having an evolutionary rationale (Carroll et al., 2014). Cultural evolution integrates cultural change and variation into the theoretical framework of evolutionary science, in which cultural change and adaptation are viewed as evolutionary processes that share, but also differ in, key characteristics of genetic evolution (Boyd & Richerson, 1985; Mesoudi, 2017; Pisor et al., 2023). Notably, recent developments about theories of cultural evolution, niche construction, and gene-culture co-evolution are helping to bridge the gap between the study of biology, culture, and social-ecological systems (SEs) (i.e. the intersection of natural and social sciences), of which agriculture is a leading example (Altman & Mesoudi, 2019). Moreover, Currie et al. (2024) advise that formal evolutionary theory has rarely been applied as a dynamic theory of change of complex phenomena in SEs and propose a framework on how to integrate such dynamics of evolutionary theory into SEs. We thus fully embrace the importance of considering cultural/social evolution in furthering sustainability science, and although a more thorough consideration of these ideas is beyond the scope of our Briefing, we nonetheless encourage further readings in relevant

literature (see Carroll et al., 2011, 2014; Currie et al., 2024; Pisor et al., 2023).

7. Conclusion

There are many examples of the potential of evolutionary insights to contribute to key sustainability challenges like those detailed here – spread of infectious and zoonotic diseases, epidemics, ecosystem, and human health. Additionally, other contributions include food production via evolution of pesticide resistance, crop improvement by selection, genetic diversity of crop-wild relatives, water purification and soil fertility (evolution of micro-organisms to efficiently remove pollutants from water bodies and to enhance nutrient cycling and soil fertility, respectively), and conservation of natural resources. Hence, as these examples show, application of evolutionary principles and tools should be integrated into crucial research for sustainability and the future of life on Earth. EvolvES, one of the Global Research Networks within Future Earth (<https://futureearth.org/networks/global-researchprojects/evolves>), aims to connect evolutionary biology and diversity to human well-being, stimulating collaboration between evolutionary biologists and scientists engaged in sustainability research, while raising awareness on the added value of evolutionary insights for the sustainability goals. Furthermore, among EvolvES goals is to inspire future research that explores how evolutionary expertise can be applied to find solutions that help us to achieve a sustainable future. With this Briefing we provide some insights and arguments furthering the call for a stronger collaboration between evolutionary biologists and the sustainability community. The former by increasing interdisciplinarity with sustainability research and being more active to study implications of evolutionary biology for sustainability measures and policies; and the latter by being more amenable to include natural evolutionary processes and evolutionary toolbox for decision making and development of new policies.

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