Title: Reintegrating Biology in the Anthropocene

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Summary:

Novel in their scope and intensity, human-driven selective pressures such as land use change, wildlife exploitation, species introductions, and mass extinction (Brook et al. 2008; Dirzo et al. 2014, Jones et al. 2018) are combining with human-mediated impacts on genetic diversity through directed gene transfer technologies, the overuse of antibiotics, and agriculture's use of monoculture. Taken together, these human-mediated evolutionary forces are likely reorganizing the canonical mechanisms of evolution elucidated by the modern synthesis. Furthermore, the globally extensive and intensifying nature of these human-mediated evolutionary forces will impact food security and human health and so implies the need to extend evolutionary thinking into a broader range of scientific disciplines in the 21st century. Our objective is to provide a conceptual framework of evolution that explicitly incorporates human activities to better understand the evolutionary implications of the Anthropocene (*sensu* Lewis & Maislin 2015).

Introduction

The indelible influence of human activities and technologies are readily observed from the scale of genes to global biogeochemical cycles (Steffan et al. 2007). Human-mediated land-use changes in land use, wildlife exploitation, species introductions, and climate change are influencing the timing, duration, intensity, and type of evolutionary forces acting on populations (Alberti 2015; Kern & Lagerhans 2017; Otto 2018). Simultaneously, directed gene transfer technologies, the profligate use of antibiotics, and the emphasis of monocultures in agriculture are restructuring genetic diversity and therefore impinging the evolvability (e.g. mechanisms that generate, promote, and maintain genetic variation, see Schuman et al. 2015) of life as a result of distinct pressures and resulting in, possibly, unexpected outcomes. A more complete accounting of these human-mediated evolutionary forces will help us more broadly understand how humans are reshaping the tree of life.

Rapid advances in data generation with unprecedented finer resolution that have enabled to progress in our understanding of evolution and the development of new technologies to quantify and manipulate genetic makeup have revealed myriad ways genetic information is exchanged. They have also highlighted the potential for ecological and evolutionary processes to merge on similar timescales. Research has also highlighted some of the ways human activities inadvertently and intentionally change the template of genetic diversity and alter the intensity, timing, duration, and diversity of selective forces acting on biological systems. However, we do not yet have an integrated understanding of the ways in which anthropogenic activities modify evolutionary dynamics and differentially affect biological systems at multiple spatial and temporal scales.

As human populations grow and technology continues to develop, the capacity for humans to directly and indirectly influence the rate and direction of evolutionary trajectories increases. Agricultural and urban expansion (), interspecific gene transfer, and large-scale production and the subsequent escape of genetically-modified organisms are a subset of the direct ways in which humans influence selective pressures and patterns of genetic diversity within communities and across landscapes. Ocean acidification due to anthropogenically-derived increases in atmospheric carbon dioxide concentrations, and trophic cascades associated with the targeted removal of large predators from most of the world's ecosystems are ways in which human activities have influenced evolutionary processes. **Thus, it is imperative that we define and understand when will the effects of human-mediated evolutionary forces overwhelm the effects of canonical evolutionary mechanisms on the structure and function of biological systems.**

The objective of this paper is to provide a perspective of how a reintegration of biological and allied disciplines may approach how human-mediated activities have modified the balance of evolutionary forces. The evolutionary consequences of the Anthropocene may be observed across levels of biological organization and are shifting the rate of micro- and macroevolutionary changes and the feedback between them. In addition, current technology and their coming iterations will enable to define to what extent conscious and unconscious consequences have altered trajectories of evolution in the biosphere, and which patterns can be tracked through the existence of humans on earth. Even, nowadays, a relatively [large?] amount of data is available, particularly since the advent of intensification of industrialization in the second half of the 20th century.

Evolution in the Anthropocene

The proposed conceptual framework reintegrates biology by framing evolutionary biology explicitly in terms that acknowledge the dominant role of humans in the biosphere and by challenging biologists to explore the interaction and feedbacks between ecological drivers, human agency, and evolutionary processes across the hierarchy of biological organization (Steffan et al. 2007; Alberti 2015). Climate, biogeochemical cycling, disturbance, and succession are principal ecological drivers shaping evolutionary processes. In turn, drift, selection, migration, and mutation as well as speciation and extinction are the evolutionary processes that have fed back to influence Earth's environmental drivers. The advent of the Anthropocene has altered this ecological-evolutionary feedback loop by introducing the mediating effects of human activities and technologies.

Genetic editing & horizontal gene transfer

With modern molecular technologies we can now rapidly modify DNA in target organisms through gene editing technologies. Three major classes of these enzymes include meganucleases, zinc finger nucleases (ZFNs), and transcription activator-like effector nucleases

(TALENs) in increasing sequence specific order, followed most recently by CRISPR/Cas that can insert, delete, or otherwise modify DNA strands in a highly targeted manner. Prime editing is the latest iteration of the CRISPR/Cas method and can replace entire sections of DNA without disruptive breaks or donor DNA. This is especially useful for correcting disease causing mutations. Additionally, mutations are induced by treating organisms or cell cultures with mutagens. For example, to increase insect resistance BT toxin genes from a bacterium have been inserted into a variety of bioengineered crop species to reduce utilization of chemical pesticides. Similarly, crops have been transformed with genes imparting resistance to herbicides like glyphosate or 2,4-D so the crop can be treated to kill competing weeds without harm to the crop itself. In addition to these intentional changes at the genetic level, inadvertent transfers have occured when agricultural animals are treated with high levels of antibiotics, which selects for antibiotic resistance in their resident bacteria. When animal waste gets released into water or soil, antibiotic resistance plasmids can be transferred into resident bacteria rendering them resistant as well, creating potential problems for livestock health and human well-being. Likewise, antibiotic resistance in human pathogenic microbes can arise in response to overuse of antibiotics.

Organelles can now be directly transferred among individual organisms and species (Rogers and Bhattacharya 2013, Stegemann et al. 2012). For example, chloroplasts with genes coding for cold resistance can be moved to novel crop species to enhance their cold tolerance. Likewise, the frequency of newborn humans with “three parents” is increasing where mothers with mitochondrial disease can avoid passing metabolic disorders onto their offspring by incorporating the nucleus of the mother into a healthy, denucleated donor egg containing unaffected mitochondria, followed by fertilization by sperm from the male parent. The resulting baby contains one set of nuclear chromosomes from the mother and one set from the father and mitochondria from a third individual. The potential for this technology is high given that many important traits are coded by organelles.

We are just beginning to understand the ecological and fitness implications of human-mediated gene transfers between domesticated and wild populations. At the same time, research is revealing that horizontal gene transfer may be more common in nature than we realized, but human activities are likely increasing the rate and diversity of these events well above background. For example, it is estimated that by 2016 there were at least 185 million hectares planted with GMO crops worldwide (ISAAA 2016). Crop-weed hybridization is common mechanism of transfer of novel genetic material from domesticated species into wild species or weedy relatives of the crop species itself. Rice, sorghum, maize, bentgrass, sunflower, squash, canola and cotton are well studied examples (Cruz-Reyes et al. 2015, Ellstrand 2018, Zhang et al. 2018). Given that all modern crop species are derived from wild relatives, and that many crops give rise to feral forms, the potential of hybridization and introgression leading to transfer of transgenes encoding insect resistance, virus resistance and herbicide resistance from GMO crops into wild species or races is high.

Transgenic pigs, goats, sheep, cattle, dogs, mice, chickens and more have been developed over recent years. Domestic animals that spawn feral lineages (pigs, goats), or mate with wild relatives (dog-coyote) also offer the potential for movement of novel genetic material into wild species or races. While movement of novel genetic materials into wild populations of animals does not appear to be as widespread as in plants, the domestication genomic signatures of cultivated triploid Atlantic salmon has appeared in sympatric wild populations of salmon in the rivers of the Pacific northwest, and in other genetically modified fishes (Oke et al. 2013, Devlin et al. 2015). The resulting fitness impacts and changes in interspecific interactions suggests the potential for unanticipated evolutionary consequences of marine aquaculture.

Land-use, species introductions, harvest, and exploitation

Human activities are reorganizing biotic communities through land-use change, wildlife exploitation, and species introductions. Land-use intensification and extensification have wide-ranging implications for wildlife metapopulation dynamics (Mendenhall et al. 2014; Gossner et al. 2016). Polyploidization and resulting speciation associated with the *Tragopon* triangle illustrates the potential for human-mediated species introductions to influence the evolutionary trajectory of a taxa (Soltis et al. 2004).

Habitat loss and degradation caused by human activities as well as overexploitation are leading causes of extinction, where the pattern of extinction is not randomly distributed across taxa (Otto 2018). Rather, a global pattern of has emerged based on which species benefit from human activities are which are harmed (McKinney & Lockwood 1999). In a human-dominated biosphere, a small number of species benefit while large numbers of species decline. The consequence of these changes are a spatial homogenization of the biosphere favoring species with broad ecological niches, rapid dispersal, and high rates of reproduction (McKinney & Lockwood 1999).

Human-mediated eco-evolutionary feedbacks

Intentional and inadvertent manipulations of the type and strength of selective forces and the genetic makeup of organisms may also have important consequences for ecosystem-level processes including primary production, ecosystem respiration, and elemental cycling. For example, personal care products and pharmaceuticals entering the environment through aging and obsolete water infrastructure, often have constituents that can alter the diversity of genetic traits of the microbial community through selection and mutation. Microbes, especially fungi and bacteria, play fundamental roles in energy and nutrient dynamics in systems; thus, changes in microbial diversity can alter aquatic biogeochemistry. Humans have also genetically engineered individuals the functional capabilities of individuals to access energy and nutrients. Chloroplasts have been transferred among species to promote more effective carbon acquisition. Scientists have introduced genes from bacteria into crops that allow organisms to use phosphite, instead of phosphate. As phosphorus acquisition is essential for growth and reproduction, and phosphorus availability often limited ecosystem productivity, changes in the ability for a species to access new sources of phosphorus could confer competitive advantage that influences community structure and ecosystem processes.

Conclusions

For more than 150 years, evolutionary theory has integrated the thinking of scientists across biological subdisciplines (Mayr 2000). The proposed conceptual framework reintegrates biology by framing evolutionary biology explicitly in terms that acknowledge the dominant role of humans in the biosphere and by challenging biologists to explore the interaction and feedbacks between ecological drivers, human agency, and evolutionary processes across the hierarchy of biological organization (Steffan et al. 2007; Alberti 2015). Furthermore, this framework suggests lines of inquiry that can leverage existing and emerging technologies and methodologies drawn from a broad spectrum of biological subdisciplines and allied sciences.

Future research inspired by this conceptual framework might include, (a) exploring an expanded definition of fitness to include human utility; (b) predicting the consequences of biological homogenization across scales; (c) integrating additive and interactive effects of human activities on evolutionary systems (genes to biomes).

The proposed framework suggests the importance and relevance of extending evolutionary thinking to a broader range of scientific and engineering disciplines. For example, the implications of evolution in the Anthropocene suggest the importance of a renewed emphasis on evolutionary training for agronomists, sanitation engineers, public health professionals, and natural resource managers. The integration into the discussion of experts in social sciences, particularly in aspects related to risk assessment, policy development may be of great relevance.

What disciplines might be needed?

The modern synthesis of biology in the first half of the 20th century achieved the convergence of evolutionary theory with principles of genetics fed by the cumulative data coming from disciplines like botany, zoology, paleontology, and cell biology. In the criticism towards the modern synthesis, developmental systems theory has contributed to add into the discussion concepts generated under the umbrella of behavioural and developmental sciences, with considerations to extend the concept of inheritance and embrace discoveries related to gene transfer (in natural processes or human-mediated), and transgenerational epigenetic gene modifiers, as well as cultural and behavioral shaped traits (Walsh and Huneman, 2017). Recently, at the advent of the 21st century the contribution of disciplines such as ecology, developmental and molecular biology, microbiology and the addition of technologies derived from genomics have opened doors to extend perspectives to address the role of human activity on evolutionary forces during the Anthropocene. Regardless of the position taken in the way to address the evolution of life, whether is a harcore position or ecumenical, today, it is imperative to integrate tools and approaches coming from established and emerging disciplines addressing complexity, such as human dynamics, to interrogate how the balance of the dynamics of evolutionary forces has modified been modified during the Anthropocene and define casualties and enable the forecasting of evolutionary trajectories in the biosphere in which *Homo sapiens* is agent and subject (Powell 2010). In addition those fields focusing on providing services to humanity from the perspective of the reengineering of life, through genetic or metabolic engineering, and z-allied fields.

Intended audience of the paper.

The scientific community that is addressing topics on the impact of human activity on the biosphere, whom may be interested in adding/exploring how human-mediated reorganization of human forces is altering the trajectories or evolutionary process and their consequences for human existence and the biosphere.

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