What can genetics bring to the concept of ecological sustainability?

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Background

The study of biodiversity, from identifying living creatures to decoding their genomes, is an important asset for Agenda 2030. Sustainable Development Goals 2 (Zero hunger) and 15 (Preserve and restore terrestrial ecosystems) both include targets which mention the importance of genetic diversity for sustainability: "Maintain the genetic diversity of seeds, cultivated plants and farmed and domesticated animals and their related wild species" (Target 2.5); "Promote fair and equitable sharing of the benefits arising from the use of genetic resources and promote appropriate access to such resources, as internationally agreed" (Target 15.6). In light of this, the development and transfer of genome analysis methods should be a major priority in order to ensure the sustainable management of resources and keep us on track to hit the Agenda 2030 targets.

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Further reading https://www.ird.fr/psf-bioandes-2021-2023

Genomics for sustainability

Human activities have already led to a considerable deterioration in the genomic diversity of life on earth (the shrinking diversity of cultivated plants, the extinction of isolated populations etc.), to the detriment of the biosphere, our own living conditions and those of all other forms of life. By emphasising the interconnections between social, economic and environmental systems, sustainability science promotes practices which preserve natural resources, protect biodiversity and maintain the equilibrium of ecosystems for present and future generations. Profiling the biodiversity of ecosystems by identifying their constituent species, genes and biomolecules is a prerequisite to understanding the way they work and are organised. This is an ambitious undertaking, especially when it comes to profiling regions identified as global biodiversity reserves, such as the Amazon rainforest. Recent technological advances in DNA sequencing have brought such studies into the realm of feasibility, thanks in particular to a new generation of sequencing techniques which are of considerable genetic, microbiological and ecological interest for biodiversity studies. This technology allows for direct, precise and rapid identification of nucleic acid sequences in very long stretches of DNA (tens of thousands of nucleotides) using protein pores with a diameter of just one nanometre (also known as nanopores). As well as driving down costs and making sequencing technology more broadly accessible, the compact size of the sequencing tools allows for analyses to be conducted in the field, thus facilitating the study of diversity in remote and inaccessible environments, and raising the prospect of real time monitoring. This technology has the power to reinforce the principles of justice, fairness and inclusiveness in the development of the latest scientific techniques and knowledge for genome research in the Global South.

Making ecosystems sustainable

The acquisition of genetic data has become key to our comprehension, monitoring and management of natural environments. One of the most recent, and most spectacular, developments has been the possibility of acquiring genetic data from environmental DNA (or eDNA), extracted from samples of water, air or soil rather than directly from living organisms. Faster, non-invasive and often more efficient than traditional sampling methods, over the past decade eDNA nucleotide sequencing has been very widely used to track the colonisation patterns of invasive species, detect pathogens, cryptospecies and elusive species, and to identify communities of species and profile their spatial and temporal variation. Last but not least, cataloguing biodiversity at the molecular level allows us to establish connections between anthropic activities - urbanisation, pollution, introduction of exotic species etc. - and climate change, as well as observedoranticipated ecological disturbances. On a general level, eDNA data are essential for steering conservation efforts and the sustainable management of ecosystems, and ultimately in order to safequard their sustainability.

Developing teaching and training in bioinformatics

Over the past decade, the development of new genomic analysis techniques has considerably reduced the cost of sequencing and led to the creation of vast databases of genetic sequences which continue to grow exponentially. The increasingly common use of big data applications highlights the fact that the use of new genomic techniques for sustainable resource management is ever more dependent on the computing power and bioinformatic capacities at laboratories' disposal. Utilised by scientists from a highly diverse array of academic disciplines, with strong interdisciplinary credentials, bioinformatics has a considerable and growing influence on health, environment sciences and society at large. Effective teaching of bioinformatics thus requires us to develop vital skills pertaining to interdisciplinary collaboration, communication, ethics and critical analysis of research practices, as well as the relevant technical capabilities. Launched in 2021, the structural training project (PSF) Bio_Andes now running in Ecuador aims to boost capacities for analysing genetic and bioinformatic data, in collaboration with partners from Colombia's LMI Bi-Inca unit. In 2023, the first training course on nanopore sequencing techniques was held in Quito, attracting teachers and students from various disciplines (zoologists, botanists, medical scientists, computing experts and bioinformatics specialists). Among other things, the knowledge acquired during this programme will equip them to better understand the genetic diversity of the ivory palm, an endemic species now at risk of extinction which was previously intensively harvested for its seeds. This



Training session on nanopore sequencing techniques, Quito (Puce, November 2023).

enhanced understanding of genetic diversity, combined with practices honed in the field, will be put to use to identify female seedlings capable of producing fruit and seeds, contributing to sustainable reforestation efforts. Moreover, work in the field of bioinformatics is of central importance to interdisciplinary research programmes devoted to managing palm trees in Ecuador, encompassing everything from environmental expertise and understanding genetic diversity to the comprehension of cultural practices by means of interactions with local communities. These new skills make the project partners more autonomous when it comes to gathering and analysing bioinformatic data, enhancing their knowledge of local biodiversity and nurturing the development of sustainable agriculture, conducive to better management of genetic resources.

KEY POINTS

The massive acquisition of genetic data constitutes an excellent opportunity to further our understanding of ecosystems and their diversity, allowing for more nuanced assessments of environmental sustainability. Teaching and knowledge transfer by means of strategic training programmes are key actions which are well-received by our partners, educating participants about cutting-edge techniques such as nanopore genome sequencing and data analysis. Finally, ensuring that these techniques and associated instruments are accessible at a reasonable cost is of utmost importance, enabling partners to retain control over biodiversity data collection and analysis within their own laboratories, advancing genome analysis in the Global South in the interests of fairness and inclusiveness.

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