Addressing Planetary Biodiversity

Our planet is in transition; air temperatures are rising, rainfall patterns are shifting, and ice is retreating. These changes are restructuring ecosystems around the world, creating the need for approaches which can track biodiversity change at large geographic scales. Because of the exponential rise in the power of both DNA sequencers and computational technology, DNA-based identification systems can meet this need. In fact, they can do more; they can disclose the intensity, nature, and flux of interactions among the constellation of species present at each locality.

The shift to DNA-based identification systems makes it possible to ascertain the species composition of mass collections, permitting biodiversity surveys with unprecedented taxonomic resolution and at hitherto impossible temporal and spatial scales. It also enables a rapid answer to a previously intractable question – how many species share our planet? Finally, it provides a new pathway, symbiome analysis, to both reveal and investigate interactions among species. It achieves this by linking every sequence recovered from a particular specimen to its source, be it commensal, parasite or mutualist.

Outcome

By registering patterns of biodiversity across ecoregions, BIOSCAN will make it possible to forecast changes in response to anthropogenic drivers such as shifting land use, pollution, and global warming. It will also deepen our understanding of species interactions by probing the symbiome, a new approach that employs the array of mitochondrial sequences recovered from any specimen to diagnose the species associated with it. Although BIOSCAN’s initial studies will target terrestrial environments, the resultant protocols will soon see adoption in freshwater and marine ecosystems.

International Organization

The International Barcode of Life (iBOL) Consortium, an alliance of research organizations in 30+ nations, began to lay the foundational elements for a DNA-based identification system for eukaryotes in 2010. By 2015, it had completed its first project, BARCODE 500K, a $125 million effort that delivered DNA barcode coverage for 500,000 species. In June 2019, iBOL will launch BIOSCAN, a 7-year, $180 million project that will ascertain species assemblages at 2,000 sites around the planet, while also examining the interactions among the species present at these locations.

Our understanding of the physical world has been revolutionized by technology; shifts in surface features are now sensed by satellite and hyperspectral imaging. High-throughput sequencers represent the technology that will transform our understanding of the biological world by detailing species interactions and by allowing ecosystem appraisal on a planetary scale. BIOSCAN lays the foundation for this transformation. Its successor, the PLANETARY BIODIVERSITY MISSION, will complete it; all species will be registered, all ecosystems will be monitored, and all species interactions will be codified.
Tracking Ecosystems

Our planet is an island of life in the cosmos. We know its major domains, but the details are lacking, even for multi-cellular organisms. **BIOSCAN** will illuminate millions of dark species by metabarcoding assemblages from 2,500 sites, first targeting the most diverse compartment of terrestrial life, arthropods. As **BIOSCAN**'s work will involve the analysis of at least 100 million specimens, millions of new species will be encountered. Their registration will be expedited by algorithms that translate sequence arrays into understanding of species diversity and distributions. It’s not simply a matter of registering species; it’s the capacity to study their dynamics. Over its duration, **BIOSCAN** will survey at least half the world’s ecoregions, setting the stage for a subsequent push towards global coverage and the activation of a planetary biosurveillance system that will track biotic change.

Revealing Symbiomes

No organism is an island; it is a complex ecosystem where multi-cellular parasites, parasitoids, commensals, and mutualists are joined by single-celled microbes. Lured by the prospect of discovering unknown domains of prokaryotic life, researchers are now probing the microbiome in diverse taxa. Until now, much less effort has been directed towards analyzing the associations of multi-cellular organisms. **BIOSCAN** will address this gap; it will use sequence variation in the mitochondrial genome to ascertain eukaryotic associations, the symbiome. Because third generation sequencers produce high-fidelity reads from single DNA molecules, they can reveal the full diversity of mitotypes associated with any specimen. When many individuals of a particular species are analyzed, the results provide a taxon-level perspective on the symbiome. For example, perhaps 10% of specimens will carry a particular parasite, 20% a particular commensal, and 95% a mutualist. That’s the symbiome of a species.