Biotechnology, Biodiversity, and Conservation

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"Biodiversity" is an issue high on the political agenda that molecular biology could help to address. Decisions concerning the environment and industrial exploitation are being made in the name of "biodiversity," but in the absence of efficient methods of evaluation and assessment. What we know is that some 1.4 million species have been identified so far and the final count may be anywhere from 1-100 million. Below the species level, diversity is so complex as to be virtually impossible to estimate. However, the term "conservation strategy" implies that conservation can be not only active but also a rational.

DNA extraction, DNA sequencing, and polymerase chain reaction (PCR)—all combined with software and data analysis—would allow the identification and classification of plants, animals, and microbes with speed and precision. But before this happens, we need to bridge gaps in knowledge and understanding between the molecular biologists who develop the tools and the conservationists who need to use them. Molecular biologists and conservationists rarely meet and, if they do, they do not speak the same language. With the project "Molecular Genetic Screening Tools," funded under the European Union's Framework III program, we have been trying to make a "marriage of necessity" between molecular biologists and conservationists work.

Conservationists should recognize the utility and limitations of molecular techniques with respect to the two stages in the conservation decision-making processes: data collection and data evaluation. Knowing how and why to select the right tool(s) and then how to analyze and interpret the data will provide a means of quantifying genetic diversity accurately.

Molecular techniques are available for resolving genetic diversity at all taxonomic levels, but it is in their ability to reveal diversity at the intraspecific level that they are having the biggest impact. PCR-based techniques are so sensitive that data can be obtained from just traces of the organism—hair, for instance, or even fecal remains. Nevertheless, while it may be possible to identify DNA markers that are diagnostic for a particular species, it is debatable whether molecular techniques will speed up the counting of higher plant and animal species identified by traditional taxonomic methods, although they can help resolve identity and phylogeny problems that will speed the inventory process.

Molecular genetic screening techniques are most often used as arbitrary indicators of diversity and, as such, will not help determine which parts of the diverse world are important, or even just economically important. Even if it was possible to design molecular screens for all traits of current economic importance, it would be impossible to predict which might be important in the future. Second, there may be little or even no correlation between the differences detected at the molecular level and phenotypic variation exhibited by organisms.

The real task for conservation, and thus for molecular biology, is to ensure that as wide, or as representative, a sample of diversity as possible is conserved.

Molecular biology can help develop methods to determine what is representative. None of the existing molecular genetic screening techniques really provides data that is either statistically representative or biologically meaningful (in characterizing a whole organism). Different tools target different regions of the genome, and it is unclear how the different molecular data relate to one another. Some techniques target expressed sequences, others "junk DNA." The input of molecular biologists is needed to determine which of these gives a more accurate assessment of organismal variation.

Molecular biologists' help is also required in developing genome sampling methods that provide meaningful assays. In extensively mapped species, one could choose markers that are spread around the map, covering as much of the genome as possible. Synteny—shared genome organization between genera—would strengthen the broad-range use of such an approach. Even so, basing the distribution of markers on existing genetic maps would mean that large parts of the genome might not be sampled.

A completely different approach would be to consider gene expression patterns. Comparisons of homoeotic genes and genes encoding intracellular signaling molecules, for example, can reveal intriguing insights into relationships between different phyla.

Another possibility would be to seek out those regions of the genome involved in response to environmental stress or that endow the organism with genome plasticity. Growing cells in culture would be a way of revealing variation in these sequences. These regions may well be eroded by breeding and would, therefore, be unlikely to emerge from studies on domesticated species. In addition, many genes that are activated under stress have been cloned and sequenced. Many of these are highly conserved, even between animals and plants, and could thus provide useful universal markers.

Without a meeting of minds between conservation and molecular biology, molecular advances will remain underexploited, tools will be blunted and open to misuse, and the data that accrues on biodiversity will be open to misinterpretation. ///