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International agreement for DNA barcoding the world's plants

An international team of 52 scientists working in 10 countries has concluded a four-year effort to agree on a standard 'plant DNA barcode' to provide the foundation for the widespread use of DNA technologies to identify plants. The results of their efforts will be released in a much-awaited paper in the Proceedings of the National Academy of Sciences (PNAS) during the week of 27 July 2009.

DNA barcoding, the use of a short standardised region of DNA for identifying species, has been used successfully to distinguish among animal species since 2003. A barcode library of approximately 60,000 animal species has been amassed already, based on the standard region selected in 2003. However, botanical barcoding has been more challenging. Although numerous strategies have been proposed, finding the right stretch of plant DNA has been difficult. Until now, no consensus has emerged among research groups as to which DNA region, or indeed how many regions, to use.

For the first time, the botanists involved in evaluating plant barcoding regions have pooled their data to agree on a standardised approach. This involved comparing the performance of the seven leading candidate DNA barcoding regions on a common set of samples. As a result of this research, two regions of DNA have been chosen to form the plant barcode (portions of the genes *rbcL* and *matK*).

The technique will work on minute amounts of tissue and can be used on fragments of plant material. Applications include identifying illegal trade in endangered species, identifying invasive organisms, poisonous species and fragmentary material in forensic investigations. But, potentially, the main application will be assessment of the diversity of species in the world's biodiversity hotspots where a shortage of specialist skills hampers conservation efforts.

Dr Peter Hollingsworth, Head of Genetics and Conservation at the Royal Botanic Garden Edinburgh, who has chaired the group, explained: "Identification is important - it is the link between a given plant and the accumulated information available for that species. It is not possible to know if a plant is common or rare, poisonous or edible, being traded legally or illegally etc., unless it can be identified. Conservation prioritisation, in particular, can be impeded by a lack of knowledge of what species grow where. But identifications can be

difficult: there are a large number of plant species and some look very similar. Juvenile, non-flowering or fragmentary materials are notoriously difficult to identify.”

DNA barcoding is one way round the problem – the principle of the approach is to identify a stretch of DNA which is suitable for telling most species apart and to use this to build a massive and easily accessible database to provide a universal system for identifying the world’s biodiversity.

In a companion commentary, Dr. Jesse Ausubel of Rockefeller University and the Alfred P. Sloan Foundation observed: “Building sequence libraries for multitudes of species and specimens is part of a larger revolution. Genomics began as a vertical endeavor to know the entire genome of a single species, such as the 3 billion base pairs of *Homo sapiens*. Now we are entering a companion era of horizontal genomics in which discovery comes from panoramic views of short sequences of many specimens and species.”

Dr David Schindel, Executive Secretary of Washington DC based Consortium for the Barcode of Life (CBOL) which instigated the formation of the plant working group, commented: “The selection of standard barcode regions has been a slow and difficult process because of the complex nature of plant genetics. Dr Hollingsworth and the Plant Working Group are to be congratulated for the careful and collaborative way in which they have approached their difficult task. Having an agreed upon barcode region will enable plant barcoding to accelerate rapidly. There are researchers around the world and diverse users of plant identification who are eager to get started”.

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EDITOR’S NOTES

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Background to plant barcoding

- Scientists estimate there are around 400,000 species of land plants.
- The agreement on a standard approach for plant barcoding enables the global plant biodiversity community to start the process of building a shared resource for plant identifications.

- The methodology will be used immediately in global projects such as Tree-BOL which aims to build the DNA barcodes database for the world's 100,000 tree species, many of which are of economic and conservation importance.

Details on the plant barcode

- The seven candidate barcode regions were assessed against three criteria. (1) Ease of obtaining DNA sequences, (2) Quality of the DNA sequences, (3) Ability to tell species apart.
- The selected plant barcode involves portions of two genes (rbcL and matK) from the plastid genome.
- Plastids are structures that are found in most plant cells and among other things, are involved in the process of photosynthesis.

Future challenges

- Where groups of species have evolved recently and/or hybridise, the approach may not allow all samples to be uniquely identified. However, even in these cases the barcode will massively narrow down the range of possibilities to a small group of species. Future technological innovations will undoubtedly increase the number of species than can be uniquely identified.

Publication

- The study will be published during the week of 27 July 2009 in the Proceedings of the National Academy of Sciences of the USA

Scientific team

- The research was published under the group authorship of the *CBOL Plant Working Group*.
- The scientific team involves 52 researchers working in 10 countries representing the following institutions: Royal Botanic Garden Edinburgh; National Center for Biotechnology Information; University of Guelph, Guelph; University of Johannesburg; Royal Botanic Gardens, Kew; Smithsonian Institution; UBC Botanical Garden & Centre for Plant Research and University of British Columbia; Natural History Museum, London; Korea University; University of Toronto; Universidade Estadual de Feira de Santana; Universidad de Costa Rica; Columbus State University; University of Wisconsin; Universidad de los Andes; South African National Biodiversity Institute; Aberystwyth

University; University of Cape Town; Hallym University; Seoul National University;
Natural History Museum of Denmark and University of Copenhagen; Universidad
Nacional Autónoma de México; Imperial College London; New York Botanical Garden.