FAPESP Fundação de Amparo à Pesquisa do Estado de São Paulo

Revista Pesquisa FAPESP Ciência e Tecnologia no Brasil

Ciência e Tecnologia no Brasil

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Molecular Signature

Method uses a small fragment of DNA to identify animal species

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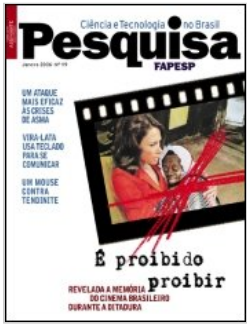
Print Edition 110 - April 2005

In the supermarket there is not a single product without a barcode, a form of identification composed in truth of a combination of eleven digits. But every kind of good a specific numerical sequence, unique and distinct from that found with all of the others. Two types of articles, even though they are very alike, display different series of algorithms. The system recognizes accurately and rapidly, any genre of the item present in the store. In nature there is no animal that does not have the cytochrome gene named C-oxidase I (COI), one of the ones most studied through genetics and located in the genome of the mitochondria, the cell's energy unit. But, according to some biologists, each species has a small fragment of COI that is characteristic, particular and diverse from that found in all of the others. Two varieties of an organism, although they may be extremely similar, exhibit, in this gene, distinct sequences of nucleotides, the chemical unit that makes up the DNA. Such a piece of COI, of around six hundred and fifty (650) nucleotides say these researchers, contains the molecular signature of each species and can serve as the base for the creation of a barcode of life: a rapid system, precise and (relatively) cheap of identifying species on a large scale, above all of animals.

The idea of implementing genetic taxonomy was proposed around two years ago by the biologist Paul Hebert, from the University of Guelph, in Canada. Since then the new form of characterization and of cataloguing organisms has gained followers within the scientific community. In February, the Natural History Museum of London served as the location for the first international conference sponsored by the Consortium for the Barcode of Life (CBOL), founded last year to spread the methodology. Close to two hundred (200) researchers from museums, zoos, herbaria, universities and research institutes from the five continents, including representatives from Brazil, participated in the event. The meeting served to gear up two international projects of weight for the next five years: the initiative that is going to determine the genetic signature of the 10,000 known species of birds and plants and the effort that is aimed at determining the life bar code of 23,000 species of fish, 15,000 from the sea and 8,000 coming from fresh waters. There are as well local initiatives, such as the project for the genetic characterization of species of trees in Costa Rica. "We estimate that it will cost around US$ 1 billion to implement a digital library with the barcode of the 10 million animal species that must exist, of which today we know only 10%", says Hebert. "It would be premature to calculate the costs of mounting a similar system with the data of organisms of other kingdoms."

1 2 Next



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Policies
Science
Technology
Humanities

Sections

Letters
Memory
Interview
Editorial
Strategies
Laboratory
Scielo Notícias
Production Line
Books

Issues

January 2006
Past Issues

Science :: GENETICS

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(Page 2 of 2)

Although it is part of the Consortium of the Barcode of Life (CBOL), Brazil as yet is not formally involved in any large scale project that makes use of molecular taxonomy. “We have only initial points, such as studies that we can carry out in our own laboratory with bats and Brazilian birds”, commented the geneticist Fabrício Santos, from the Federal University of Minas Gerais (UFMG), which is integrated into the consortium and had been present at the conference in London. “But we need a national network, as occurred in the Genome Projects, which stimulates the participation of various institutions in a wider range of work about certain groups of animals, plants and microorganisms.”

Birds and butterflies – The geneticist Ana Maria de Lima Azeredo Espin, the director of the Molecular Biology and Genetic Engineering Center of the State University of Campinas (CBMEG/Unicamp), who also participated in the meeting in England, is equally favorable to the formulation of initiatives in the area of molecular taxonomy. “We are thinking about proposing a project that uses the barcodes of DNA, perhaps within FAPESP’s Biota Program”, says Ana Maria, who makes use of the technique in genetic-evolution studies with species of flies.

The new methodology is showing itself to be useful on two major fronts: to generate a molecular signature for animals already identified by science and to discover new species that have not up until now been detailed out by traditional taxonomy. In a study published last October in the scientific magazine PLoS Biology, Dr. Hebert and his Canadian colleagues, along with North American researchers showed that the sequencing of only six hundred and forty eight (648) nucleotides of the COI gene were sufficient to correctly discriminate the two hundred and sixty (260) known species of North American birds. Each animal has a barcode in its own mitochondrial DNA, different from the sequence present in the others. The distinctions in the analyzed region of the COI gene were eighteen (18) greater among birds of two close species than between two examples of the same species. Evidence that only with the genetic information, without recurring to anatomic and environmental data, is it possible to discriminate all species. Also during October, in an article published in the American magazine Proceedings of the National Academy of Sciences, Hebert and Daniel Janzen, from Pennsylvania State University in the United States, presented ten new species of tropical butterflies, all of them derived from the Astraptes fulgerator. In this case the scientists made use of information generated by the DNA barcode technique in order to confirm an ancient suspicion developed through years of field studies with this butterfly in Costa Rica: that the A. fulgerator was not the only species, but in reality a complex of at least tem occult species. Although they generated practically identical adult butterflies, each species exhibited colors and physical traits different in their

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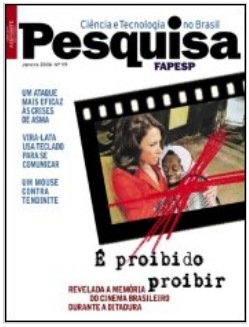

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larvae form and fed themselves from distinctly different plants – as well, clearly, of presenting a particular sequence in the COI gene.

Some biologists, accustomed to classifying organisms by way of the comparison of anatomical traits and of the study of their habitats, have turned up their noses towards the molecular signature approach. And they question: how can a piece of a single gene identify all of the animals? In spite of criticism, the new technique did not spring up to combat conventional taxonomy. On the contrary. I would be used as a tool in order to give dynamism to the work of the species professionals. “The barcode is not going to substitute classical taxonomy”, explained Dr. Santos. “It’s only the incorporation of more taxonomic information, only in the form of DNA characters.” Like every technique, it has its limitations. The COI gene, for example, may not be the best to identify certain animals. In the case of plants, there is almost a consensus of opinion that the chloroplast gene, and organelle involved in photosynthesis, should be chosen as the molecular signature of vegetables.

Previous 1 **2**