

Significance: Our experiments have shown that NGS is able to overcome the drawbacks of Sanger Sequencing and real-time PCR in complex animal and microbial samples. Constantly declining costs for NGS and the ability to analyse animal and microbial components in parallel make the method attractive for routine analyses.

Use of BOLD systems in species conservation

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Background: The identification of species by short DNA sequences has been at the centre of DNA barcoding and is being adopted by all fields of biology. **Results:** Herein we represent the role of BOLD systems for species conservation especially for the fish *Anguilla bengalensis bengalensis* through uploading various data of biological and geographical importance with detailed photographs, strata of fish found, life stages of individuals, latitude and longitude of the fish's occurrence, etc. **Significance:** The documentation of fish life stage records maintained by the data base could add to the study of the status of populations. This can become a crucial part in conservation studies and adding to the world's knowledge of living systems.

DNA barcoding may aid in conservation and fare trading of ornamental fish in India

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Background: In the wake of trade liberalization under WTO agreement, international trading in agricultural products, foods, pharmaceuticals, and marine products has facilitated massive extraction of natural resources and ultimately has created potential risks to biodiversity. Practical concerns to managing the ornamental fish species under trade include the recognition of fish by their common names. Interestingly, the rapid rate of hybridization and sometimes mutations (natural or imposed) are creating variations among the same species of fish, which are recognized by different names. Besides, juvenile fish are often cumbersome to identify to the species level even for experts. Therefore, the correct identification of ornamental fish using morphological characters is often difficult and requires expert help. Also, it is challenging to judge the origin of ornamentals, such as wild, cultured, or exotic, etc., as over one billion individual fish are traded annually through more than 148 countries. **Results:** Our study covers a collection of 940 ornamental fishes collected from aquarium retailers, wholesalers, and exporters from India. Moreover, almost 673 wild ornamental fish specimens were collected from eight major rivers in India. All collected specimens were barcoded and analysed to determine species boundaries, mean genetic differences, and genetic distances to nearest neighbour species (barcode gap analysis). Several cryptic species were recorded in this study. We detected some issues with unexpectedly high intraspecific divergences, cases which were resolved using different approaches. Overall, our paper demonstrates high ambiguities in names currently used in fish trading, which may help traders to escape regulation or prosecution. **Significance:** This study highlights the misuse of common names in the trading of banned fish, which may cause potential losses to biodiversity.

High-throughput molecular approach for quantifying pest regulation services and disservices provided by farmland insect communities

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Background: Maximizing farmland biodiversity has been widely promoted through public policies as a sustainable alternative to chemical inputs. The biodiversity of naturally occurring generalist predators, such as spiders or ground-living beetles, has been positively associated with pest control in intensively managed agro-ecosystems. However, our ability to successfully predict ecological functions, such as pest regulation by natural enemies, requires more direct and mechanistic insight. Disentangling trophic interactions among service-providing organisms in agricultural landscapes will afford a direct and holistic view of the processes determining ecosystem services' achievement. In order to elucidate factors affecting biological control of pests, we built semi-quantitative trophic networks of a major group of insect generalist predators (carabid beetles) by using a molecular metabarcoding approach. **Results:** Gut contents from 500 individuals of 13 carabid species were collected in 6 intensively managed wheat and oilseed rape fields and analyzed with a combination of plant and animal universal primers. The most significant variation in carabids' trophic choice was explained by the crop type and the field identity ($p < 0.01$). This variation was mainly explained by differences in the consumption of non-pest organisms, including other natural predators (i.e., disservice). Indeed, predation on non-pest prey was two times higher in wheat crop compared to oilseed rape ($p < 0.01$). Finally, we observed a significant effect of field identity on major properties of the carabids' trophic network structure (nestedness, linkage density, and connectance, $p < 0.01$). **Significance:** The physical mosaic of the agricultural landscape plays a major role in the trophic behavior of insect generalist predators, with significant consequences for the success of biological control. This finding is important because of the urgency to identify concrete actions for sustainable crop protection. It also emphasizes the value of DNA barcoding-based approaches for tackling questions of ecological, economic, and societal relevance.

Barcoding of fresh water fishes from Pakistan

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Background: DNA barcoding is a taxonomic method to identify species. It uses a short genetic marker in an organism's mitochondrial DNA for identification. It uses the sequence diversity of a 658-bp fragment near the 5' end of the mitochondrial cytochrome c oxidase subunit I (COI) gene for identification. When compared with morphological identification DNA barcoding is more accurate and reliable. It is useful in both juvenile and adult stages of fishes. It also helps with the identification of processed or damaged fish, which is impossible by traditional methods. **Results:** A total of three COI barcodes were recovered for three species from three genera of the family Cyprinidae for the present study. Fish F1 and Fish R1 primers were used. The species were *Cyprinus carpio* (1), *Cirrhinus mrigala* (1), and *Ctenopharyngodon idella* (1). The average read length was 680 bp with 116 polymorphic sites, 109 singleton variable sites, and no parsimony-informative sites. No insertions/deletions or pseudogenes or contaminant sequences (e.g., from bacteria) were observed, which supports the view that all of the amplified sequences constituted functional mitochondrial COI sequences. **Significance:** From these findings it is concluded that the gene sequence, COI, may serve as milestone for identification