**Improving the power and efficiency of biodiversity assessment through the use of DNA metasystematics and next-generation sequencing**

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Conventional biodiversity research via individual identification is costly and slow. To draw conclusions about changes in communities in response to natural and anthropogenic effects, biodiversity analysis needs to become more rapid, comprehensive, and cost-effective. High-throughput next-generation sequencing (NGS) technology (e.g. 454, Illumina MiSeq) allows the biodiversity of a given locale at a given time to be determined rapidly, accurately, and at a much lower cost per sample. We will present research that employs NGS and a metasystematic approach to better assess the biodiversity contained within mixed environmental samples. Samples include soil cores, water samples, benthic samples, and terrestrial Malaise trap samples. Each NGS sequencing run generates over a million DNA sequences from the organisms contained in each sample. Multiple target gene regions have been chosen for each kingdom of life, from bacteria, to plants, to fungi, to invertebrates, to vertebrates. By facilitating greater biodiversity recovery in a shorter amount of time, DNA-based massively-parallel sequencing approaches will greatly multiply the force of human impact on assessing, and improving, the status of pristine and impacted ecosystems.