

**Workshop 4****General abstract:****DNA barcoding of nematodes.**

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In this workshop we address one main question: “How to ensure that nematode biodiversity is accurately represented in global assessment of diversity? The problem: Technological advances in nucleotide sequencing are increasingly outstripping our ability to store, retrieve, and analyze taxonomic data. On projects that focus on nematode diagnosis or assessment of nematode diversity, it is common to encounter reference database deficiencies that prohibit an accurate description of the taxonomic composition of nematode communities. As stated by Waeyenberge et al., (2019) “The need of a larger, high quality, taxon-specific, reference database cannot be overstated”. For DNA barcoding process perspective, we need to:

1. Evaluate the current status of taxonomic data repositories for nematodes.
2. Identify deficiencies or blockages that compromises our nematode databasing workflow.
3. Determine what functionality we want for our databases.
4. Evaluate collaborative strategies to address these inefficiencies.

We recognize that while nematodes are among the most abundant and diverse multicellular animals on the planet, the community of Nematologists is small compared to other taxon-oriented societies. We suggest that a collaborative effort is necessary to move DNA barcoding into the future. A major goal of this workshop would be for interested parties to contribute to a white paper that would be the basis of a proposal for grant funding.