DIAGNOSTICS OF PLANT-PARASITIC NEMATODES IN THE ERA OF HIGH-THROUGHPUT SEQUENCING

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Identification of nematodes, including plant parasites, has been traditionally reliant on the use of microscopy and morphology. Although the technique can still provide accurate diagnosis at a species level, it has many well-recognized problems: it requires specialized knowledge, it is slow and laborious, and accuracy can be affected by life stages, sexes, or the presence of cryptic species. Over the last 20 years, nematode identification has been increasingly augmented by single organism high-resolution molecular approaches. Selective molecular markers (e.g. mtDNA, 18s rDNA, RFLP) have been successfully applied to detect and diagnose nematode species of agricultural importance (e.g., *M. incognita*, *G. pallida*) in known situations where species are already known or suspected to exist. However, this approach falls short when a potential nematode parasite is unknown, unexpected, or in untested environment (e.g. new agricultural commodity). To overcome the limitations of both traditional morphological and molecular diagnostics, the new approach of metabarcoding—a one-step high-throughput amplicon sequence analysis of all the members of the community simultaneously—offers tremendous potential for advance. It is now possible to apply the approach to large-scale studies involving not only intense sampling collections but also identification of all the individuals in all samples at a fine level of taxonomic resolution.

Could this approach be successful in nematode parasite diagnostics? I will discuss the approach using a test-case study involving substrates of a gradient of nematode community complexity to illustrate that a simple answer is an "Overwhelming Yes", despite the presence of many technical problems, which I will acknowledge as well.