DNA fingerprinting in *C. elegans* and related species

Mark Benecke and Einhard Schierenberg

Zoologisches Institut der Universität, D-50923 Köln

We are interested in phylogenetic relationships among nematodes and related taxa. Conventional multilocus fingerprinting and the PCR-based RAPD technology of DNA fingerprinting appear to be promising tools for a molecular phylogenetic approach: They allow strain- up to genus-specific characterization of nematodes.

a. **Multilocus fingerprinting** Using short synthetic oligonucleotides, we hybridized against Southern blots of digested genomic DNA. The oligonucleotide probes we selected detect a set of tandem repeated non-coding sequences of variable length.

b. **PCR fingerprinting** Genomic DNA from the *C. elegans* wildtype and a *C. elegans* isolate from Australia, from another nematode genus *(Rhabditis)* and from a turbellarian species were subjected to PCR using several short synthetic oligonucleotides. Only a single oligonucleotide primer is employed per PCR reaction. These short primers, like short oligonucleotides in multilocus fingerprinting, visualize DNA sites which are located close to one another in inverted orientation. The technique essentially scans a genome for these small inverted repeats and amplifies intervening DNA segments of variable length (**R**andom **A**mplified **P**olymorphic **D**NA). This technique requires an extremely low amount of DNA (DNA of a single *C. elegans* individual appears to be sufficient for several RAPD experiments).

Depending on the degree of variability, probes and primers should be useful for studies on different taxonomic levels. One advantage of DNA fingerprinting over sequencing of specific RNA´s or genes is that information spread over the entire genome is obtaines in one working step.

Our fingerprints indicate that individual strains can be distinguished by their defined banding patterns. In conjunction with developmental studies we plan to use this assay to analyze phylogenetic relationships among nematodes. In addition, we would like to explore to which extent the RAPD technology is suitable for comparative studies on higher taxonomic levels.