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**MOLECULAR GENETIC MARKERS OF TOXOCARA CANIS AS A TOOL FOR DIFFERENTIAL DIAGNOSIS AND PHYLOGENETIC ANALYSIS**

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Toxocara canis, a zoonotic ascarid parasite prevalent in canids, causes human toxocariasis, which often presents diagnostic challenges due to nonspecific symptoms mimicking other helminthiases. Conventional methods like serology and microscopy lack sensitivity and specificity, especially in low-burden infections. Molecular genetic markers, such as ITS regions of rDNA and cox1 of mtDNA, offer high-resolution tools for species identification, strain differentiation, and phylogenetic mapping. This approach is critical for accurate differential diagnosis, epidemiological surveillance, and understanding parasite evolution amid rising global migration and pet ownership.

To evaluate the utility of selected molecular genetic markers (ITS-1/ITS-2, cox1, nad1) of Toxocara canis for differential diagnosis and phylogenetic analysis in clinical and research settings.Bioinformatic analysis of publicly available sequences from GenBank (n=150 T. canis isolates); PCR amplification and Sanger sequencing of cox1 and ITS regions from 50 fecal/tissue samples (dogs and human cases); phylogenetic reconstruction using MEGA X (neighbor-joining, maximum-likelihood methods with 1000 bootstraps); comparative assessment of marker polymorphism via pairwise distances and haplotype networks in DnaSP software.

Diagnostic performance evaluated by qPCR sensitivity/specificity against ELISA controls. Cox1 exhibited 2.5% intraspecific variation, outperforming ITS (0.8%), enabling distinction of T. canis from T. cati (divergence >5%). Phylogenetic trees revealed three major clades linked to geographic origins (Europe, Asia, Americas), supporting host-mediated dispersal. qPCR assays achieved 98% specificity and 95% sensitivity for differential diagnosis in mixed infections. Markers correlated with anthelmintic resistance mutations, highlighting prognostic value. Limitations include regional sequence bias; future NGS integration could enhance resolution. Molecular markers like cox1 and ITS provide robust tools for precise T. canis identification, improving differential diagnosis accuracy by 40-50% over traditional methods. Phylogenetic applications elucidate parasite diversity and zoonotic risk, informing targeted interventions in medical biology and genetics.