

PEPTIDE-BASED APPROACH FOR DIFFERENTIAL IMMUNODIAGNOSIS OF *ASCARIS SUUM* INFECTIONS AND HELMINTH CROSS-REACTIVITY IN MICE

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Ascariasis, a disease of significant medical and veterinary importance, is caused by parasitic nematodes that primarily infect humans and animals (*Ascaris lumbricoides* and *Ascaris suum*). The World Health Organization classifies ascariasis as one of the most prevalent Neglected Tropical Diseases, disproportionately affecting populations in endemic regions with poor sanitation and limited healthcare access. Helminth infections caused by species such as *Toxocara canis* and *Schistosoma mansoni* share similarities with *Ascaris* spp., leading to cross-reactivity in diagnostic tests and complicating the development of specific diagnostic tools. This study adopted an unconventional approach, using peptides derived from the Tc-CTL-1 protein of *T. canis*, to evaluate the reactivity of sera from infections with different helminths, focusing on *A. suum*. Immunoblotting assays were performed with sera from mice infected and uninfected with *T. canis*, *A. suum*, and *S. mansoni*. IgG1 and IgG2a antibodies were used for detection, followed by densitometric analysis with ImageJ software and statistical evaluation. Results showed strong recognition of specific peptides by IgG2a antibodies against *A. suum*, while IgG1 antibodies exhibited lower reactivity. Peptides with optical density (OD) ratios ≥ 2.5 for IgG2a ($n = 14$) and ≥ 1.5 for IgG1 ($n = 3$) were identified as promising candidates for differential diagnosis. BLASTp analysis revealed alignment between selected peptides and proteins of *T. canis* and *S. mansoni*, indicating conserved regions among these parasite proteins. These findings suggest that this unconventional peptide selection approach may effectively identify superior targets for the differential diagnosis of *A. suum* infections. Further investigation and validation using immunoenzymatic methods are planned to confirm the diagnostic potential of these peptides, contributing to improved diagnostic tools for helminth infections in endemic regions.

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