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Exploring the Zoonotic Potential of *Strongyloides stercoralis*: Insights from Population Genetics

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DESCRIPTION

Strongyloides stercoralis is a parasitic nematode that primarily infects humans but has a complex life cycle that involves both humans and various animal species, including dogs. The question of whether *S. stercoralis* constitutes a zoonotic threat from dogs to humans has been an area of ongoing research, particularly in the context of population genetics. Zoonoses are diseases that are transmitted from animals to humans, and the possibility of *S. stercoralis* being transmitted between dogs and humans has raised concerns, especially in areas where both species interact closely, such as in households and animal shelters. To explore this potential zoonotic transmission, a population genetics approach can be a useful tool to trace the genetic similarities and differences of *S. stercoralis* strains found in both humans and dogs, providing insights into the potential overlap and the risk of cross-species transmission. The life cycle of *S. stercoralis* involves several stages, with the infective larvae being the key element for transmission. These larvae can either develop directly in the environment or inside a host. In humans, the larvae penetrate the skin and migrate to the intestines, where they mature into adult worms. The nematodes reproduce and release eggs that hatch into larvae, which can either exit the host through feces or complete their lifecycle within the human host. In dogs, the cycle is similar, with the larvae infecting the animal through skin penetration or ingestion of contaminated soil or water. Both dogs and humans can act as hosts, but the environmental factors and the specific interactions between the species raise the question of whether *S. stercoralis* strains from dogs could pose a zoonotic risk to humans. Population genetics studies provide a valuable framework for investigating the genetic diversity of a parasite population and assessing the potential for zoonotic transmission. By comparing the genetic profiles of *S. stercoralis* strains from different hosts, including humans and dogs, researchers can identify whether the same or closely related strains circulate in both species. Molecular markers, such as microsatellites or single nucleotide polymorphisms (SNPs), can be used to analyze the genetic diversity and phylogenetic relationships of *S. stercoralis* populations. If strains from humans and dogs share high genetic similarity, it would suggest that transmission between species might occur. Conversely, if the genetic profiles are significantly different, it would indicate that *S. stercoralis* strains from humans and dogs are distinct, thereby reducing the likelihood of zoonotic transmission. Several studies have investigated the genetic diversity of *S. stercoralis* through population genetics, but the results have been mixed. In some regions, researchers have found evidence of genetic similarities between *S. stercoralis* strains from humans and dogs, suggesting the possibility of zoonotic transmission. For example, in areas where humans and dogs live in close proximity, there may be an increased chance of shared environmental contamination with the larvae, potentially facilitating the transmission of the parasite between the two species. However, other studies have shown distinct genetic profiles for *S. stercoralis* strains in humans and dogs, indicating that while both species may be infected by the parasite, they may represent separate evolutionary lineages or subpopulations of the nematode. These findings highlight the complexity of zoonotic transmission and the need for further research to better understand the dynamics of *S. stercoralis* transmission in different environments One of the challenges in using a population genetics approach to assess zoonotic potential is the variability in the parasite's genetic material.

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CONFLICT OF INTEREST

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