Variation and polymorphism in helminth parasites.

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Abstract

There are strong biological, evolutionary and immunological arguments for predicting extensive polymorphism among helminth parasites, but relatively little data and few instances from which the selective forces acting on parasite diversity can be discerned. The paucity of information on intraspecific variation stands in contrast to the fine detail with which helminth species have been delineated by morphological techniques, accentuating a trend towards considering laboratory strains as representative of a relatively invariant organism. However, in the fast-moving evolutionary race between host and parasite one would predict a monomorphic species would be driven to extinction. We review the arena of intraspecific variation for the major helminth parasites, ranging from biological properties such as host or vector preference, to biochemical and immunological characteristics, as well as molecular markers such as DNA sequence variants. These data are summarized, before focusing in more detail on polymorphisms within protein-coding genes of potential relevance to the host-parasite relationship, such as vaccine candidates. In particular, we discuss the available data on a number of major antigens from the filarial nematode Brugia malayi. Information is currently too sparse to answer the question of whether there is antigenic variation in filariasis, but the indications are that proteins from the blood-borne microfilarial stage show significant intraspecific variability. Future work will define whether polymorphisms in these antigens may be driven by exposure to the host immune response or reflect some other facet of parasite biology.

PMID: 12622326 [PubMed - indexed for MEDLINE]