

The *Schistosoma* Genome Project (SGP) – a resource for studies of platyhelminth diversity, evolution and biology

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Since 1994, laboratories in both the Developed and Developing Worlds have collaborated to undertake genome analysis on the digenean *Schistosoma*. Although the rationale for the SGP is biomedical (to identify new targets for drug and vaccine development, to determine mechanisms of pathogenesis and drug resistance, and to analyse inter- and intra-specific variation), the biological and informatics resources generated by the SGP have considerable potential to reveal fundamental information on parasite biology, behaviour, diversity, and evolution, and thus to be of great value to workers in the wider platyhelminth field.

In the initial phase of the project, attention has focussed on: (a) Gene discovery. 13,000 expressed sequence tags (ESTs) representing 7,000 different genes (35% of the estimated gene content) have been generated for *S. mansoni*, and numerous stages of the life cycle examined. A smaller EST project for *S. japonicum* permits initial comparative studies. (b) Development of resources to facilitate physical mapping and genome sequencing. Markers have been mapped onto the karyotype to create a first generation chromosome map. A high quality, large fragment, genomic DNA library has been generated and is being used to develop a physical map of chromosome 3. (c) Informatics. WWW resources and a distributed database (SchistoDB) have been developed.

The quantity of data generated is now sufficient to allow meaningful “post genomics” / functional analysis. cDNA array and proteomics projects have recently been initiated to assign function to ESTs with no database homology, and to link the parasite’s protein profile with its genome. Funds have also been secured for genomic sequencing. This will generate markers for the mapping project, provide additional gene discovery, and identify microsatellites, as well as reveal fundamental information on genome organisation.

The current status of the SGP was reviewed and specific applications of its biological and informatics resources for studies of wider platyhelminth biology were described.

Results can be found in

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