

Poster presentation

Exploring Parasite Gene Space

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Funding allocation for complete genome sequencing has a severe taxonomic bias; nearly half of the completed or draft stage genomes are from vertebrates. The luxury of a full genome sequence is unlikely to be available for the vast majority of organisms, regardless of their importance in terms of evolution, health or ecology. This has led to the investigation of genomes from an increasing number of species, especially parasites, through generation of expressed sequence tags (ESTs).

Over 300,000 ESTs are available for 36 species of parasitic nematode. The species include whipworm and filarial worms, which currently infect 3 bn people, as well as a large number of plant parasites. We have constructed NEMBASE, a database and analysis suite that integrates these transcriptomes with associated annotation and meta-data www.nematodes.org. The system enables comparative transcriptomic analyses across the phylum Nematoda. At present we are focusing upon differences both between and within the parasitic and free-living species. This has led to the discovery of greatly expanded protein families and novel protein domains that will provide possible drug targets for lab verification.