

本試題是否可以使用計算機：可使用，不可使用（請命題老師勾選）

1. 解釋名詞（每小題 5 分）
 - a. schizogony
 - c. reservoir host
 - d. complete metamorphosis
 - e. sporocyst
2. 請簡述寄生行為對寄生蟲個體本身型態與構造所引起的影響。（20 分）
3. 藉由性接觸傳播的寄生性原蟲有哪些？並簡述之。（20 分）
4. 能引起人畜共通寄生性吸蟲病有哪些？並列舉出他們的主要動物宿主（20 分）
5. 針對下列文章回答下列問題：（20 分）
 - a. 敘述你對 expressed sequence tags 的了解，以及與 redundancy 的關係。
 - b. 請扼要描述該篇文章的主要內容與結論。

It is estimated that *S. mansoni* genome should have around 270 megabases, one tenth of human's. This large genome size discourage the genome sequencing approach and, because this, the priority is given to gene identification through the sequence of expressed sequence tags (ESTs). This approach provides important, fast and inexpensive information, but also have their problems. The sequences produced may present a great number of errors, redundancy and small size. In order to overcome this problems, sequence clustering procedure is frequently used. Since the creation of the *Schistosoma* Genome Network more than 17,000 cDNA sequences of the worm were deposited in public databases. These sequences were analyzed in groups as soon as different research teams have produced them. Nobody, however, have joined and analyzed them all within a biological perspective. This is the objective of the present work. We analyzed a total of 17,071 partial and full-length cDNA sequences and filtered 1,506 of poor quality. The other 15,565 were clustered as 6,328 non-redundant sequences by the CAP3 program. All uniques were identified by visual inspection of BLAST results and classified into functional COG categories. The percentage of genes in the main functional categories was: 32% cellular processes, 21% information storage and processing, 15% metabolism and 32% poorly characterized. After a detailed analysis of each category, we identified some new and relevant *S. mansoni* genetic information, such as the presence of the glutamate synthase gene (a putative drug target) and genes for fatty acids omega oxidation, among others. We also found molecular evidence on the lack of some biochemical pathways, such as the *de novo* synthesis of purines, fatty acids and steroids.