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IN SITU HYBRIDISATION OF RIBOSOMAL DNA TO WHOLE CHROMOSOMES OF THE PARASITIC PROTOZOAN, TRICHOMONAS VAGINALIS

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Trichomonas vaginalis is an anaerobic protozoan parasite of the human genitourinary tract. It infects approximately 1 billion people worldwide and is associated with birth complications, cervical cancer and predisposition to other STIs including HIV. The T.vaginalis genome was sequenced by The Institute for Genomic Research in 2003 and a primary annotation database is now available. Preliminary genome analysis reveals a 36% GC rich genome with an estimated size of 180Mb. Previous studies indicate a haploid genome of 6 chromosomes. However, due to the unexpected large size and highly repetitive nature of the genome, no genome map has been established. Protozoan genomes are typically plastic with a variety of species exhibiting chromosome size and number polymorphism, aneuploidy and polyploidy. In this study, comparison of chromosome numbers of seven metaphase-arrested T.vaginalis isolates was undertaken. The results confirm previous data identifying 6 chromosomes per nucleus, with some anomalies including the loss or gain of chromosomes and polyploidy. Karyotypes were identified based on conserved chromosome morphology displaying a single large chromosome, 2 smaller chromosomes, a single heavily constricted chromosome and 2 mini chromosomes. Ribosomal DNA is arranged in tandem arrays as shown by Southern blot analysis, and for the first time the localisation of rDNA on whole chromosomes is demonstrated by fluorescent in situ hybridisation (FISH). A primary rDNA site, containing the rDNA tandem array, was located on a single mini chromosome. In addition, multiple smaller paired sites on each of the other metaphase chromosomes may indicate single copy rRNA genes in addition to the major array. Further FISH studies with a variety of gene probes will identify strain to strain variability and enable the assembly of a complete genome map to complement the T.vaginalis genome project.