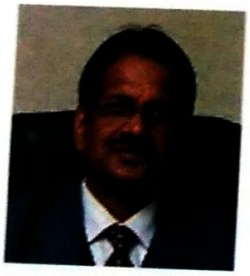
Laboratory diagnosis involves a set of tests and the choice of tests depends on the clinical history. Most commonly, CSF and blood samples are taken for the diagnosis of CNS parasitic infections. CSF samples are processed for wet mount microscopy and stained preparations. Most parasitic infections can be diagnosed by microscopy if morphologically relevant parasitic cells are found. In multiple cases, the parasite load in the CSF is low since they adhere to the blood vessel walls. In such cases serological testing of CSF and blood sample is helpful. For, neurocysticercosis, in house developed immune assays including Enzyme linked immunosorbent assay (ELISA), dot immunobinding assay (DIA) and passive haemagglutination assay (PHA) were evaluated for the detection of anticysticercal antibodies Partially against purified antigen of 64-68 kDa antigens in CSF have been evaluated by Chandramukhi et al;1991. Utility of Toxoplasma antibodies detection in CSF was also reported by Chandramukhi et al; 2004. For cases such as *Naegleria* and *Acanthameoba* which causes fulminant disease with poor prognosis, it is advisable to obtain autopsied brain sample. Brain biopsy is not followed commonly in India, though it is a more common procedure in the west. Histopathological workup is advised for such cases. Diagnostic polymerase chain reaction (PCR) is also available as a molecular method. Clinical imaging methods such as tomography is currently more relied upon to gain an idea on the extent of infection proliferation and as a diagnostic support. Satischandra et al; 2011 and Jayakumar et al; 2013 have reported that advanced MRI techniques are useful in characterizing the type, viability, and burden of the parasites and the host tissue response.

Genomics in Amoebiasis



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Amoebiasis, caused by the protozoan parasite *Entamoeba histolytica* is an important cause of morbidity and mortality world-wide. Amoebiasis has a global distribution, but more prevalent in the developing countries. Diagnosis of amoebiasis has undergone a huge transformation from the classical microscopic analysis that cannot differentiate between the pathogenic and the non-pathogenic species to molecular-based analysis. Genome information allows for better understanding of pathogenic processes and consequently helps improve the prevention, diagnosis, and treatment of the disease. In 2005, Loftus *et al.*, drafted the genome sequence of the standard strain of *Entamoeba histolytica*- HM1:IMSS, that was further re-assembled and re-annotated by Clark et al., and Lorenzi *et al.*,. According to the data generated from the whole-genome shotgun sequencing method, it was see that Entamoeba genome was ~20 Mb in size containing 1,496 scaffolds and 8,201 predicted genes. Putative function was assigned to 46% of the predicted proteome and has also identified 58 protein families that share no homology with any of the previously known proteins and thus could be *Entamoeba*- specific. Genome analysis also revealed new features such as the presence of segmental duplications flanked by inverted repeats, and the association of some gene families with transposable elements. This data has provided the scientific community with the first comprehensive view of the gene set and tools for elucidating the genetic basis of *Entamoeba* pathogenicity. With this, the molecular-based assays like PCR were employed for differential detection of the pathogen. Nested-multiplex PCR, LAMP-based assay, real-time PCR assays and also DNA microarrays are being carried out based on the available genome data. Research on the genome of *E. histolytica* is an emerging area of importance in understanding the virulence of the parasite. Recent studies have shown how the parasites genetic factors affect how infectious it is. Molecular level analysis have found high diversity in the nucleotide repeats of the tRNA genes or genes coding for Serine-rich *E. histolytica* Protein (SREHP) and chitinase. Gene copy number is diverse, suggesting that this could be an important part of the variety of virulence seen from the parasite.