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**Unexpected Diversity and Differential Success of DNA Transposons in Four Species of Entamoeba protozoans.**

Pritham EJ, Feschotte C, Wessler SR  
*Mol Biol Evol* 2005 May 18 [[abstract on PubMed](#)] [[related articles](#)]

- New Finding
- Tech Advance

**Selected by** I Nitaya Thammalard / C. Graham Clark  
First evaluation 20 Jun 2005 | Latest evaluation 29 Jun 2005

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#### Faculty Comments

##### Faculty Member

**Nitaya Thammalard**  
Mahidol University,  
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MICROBIOLOGY

##### Comments

**This is the first exciting report to show the comparative presence and fate of transposable elements (TEs) in 4 different Entamoeba species, found by utilising a**



New Finding



Tech Advance

**computer-based approach using the known sequences of the ~20 Mb genomes of *Entamoeba histolytica* (12 fold coverage), *E. dispar* (2-2.8 fold coverage), *E. invadens*, (2-2.8 fold coverage) and 20,000 unassembled shotgun reads for *E. moskovskii*. The authors also identify 4 Class 2 DNA transposase (T<sub>p</sub>ase) superfamilies (hAT, Mutator, piggyBac, and Tc1/mariner) in these protozoan species for the first time.**

The diversity of DNA transposons and their differential amplification among these amoebae may have an important impact on species identification, along with biomarkers responsible for the pathogenicity and invasiveness of *E. histolytica*. Recently, Srivastava et al {1} first reported (using "Transposon display" techniques) the retrotransposon EhSINE1 as a potential marker to study strain variation in *E. histolytica*. Both pathogenic *E. histolytica* and the commensal *E. dispar* have numerous retrotransposons but few DNA transposons, whereas *E. invadens* and *E. moskovskii* have diverse DNA transposon populations but few LINES. At present, no LTR retrotransposons have been reported in these amoebae. The DNA transposase superfamily Tc1/mariner was previously reported in 3 ciliates and *Trichomonas vaginalis*. In contrast, the 22.8 Mb genome of *Plasmodium falciparum* appears completely devoid of TEs. I would also like to mention briefly the history behind the discovery of the transposons, which were first identified in maize (*Zea mays* aka corn) in 1940 {2} by Barbara McClintock, who was awarded a [http://nobelprize.org/medicine/laureates/1983/ Nobel Prize in Physiology or Medicine in 1983]. Since that time, various transposons have been reported and found to cause many plant diseases and tropical diseases, as well as haemophilia A and B, SCID, porphyria, predisposition to cancer, and Duchenne's muscular dystrophy. References: {1} Srivastava et al. *Exp Parasitol* 2005, 110:303-8 [PMID:15955328]; {2} McClintock *Genetics* 1940, 26:542-571.

Evaluated 29 Jun 2005

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**C. Graham Clark**

London School of Hygiene and Tropical Medicine, United Kingdom  
MICROBIOLOGY



New Finding

**The authors report a dramatic difference in the representation of different types of transposable elements among species of the genus *Entamoeba*.** While the genomes of the sibling species *E. histolytica* and *E. dispar* contain numerous retrotransposon-like elements (making up ca 5% of the genome), those of *E. moskovskii* and *E. invadens* contain very few; in contrast, the latter two species have many DNA transposons belonging to several families (making up ca. 5% of their genomes), while *E. histolytica* and *E. dispar* have very few. The underlying reasons for this apparent replacement of DNA transposons by retrotransposons since the

divergence of *E. histolytica*/*E. dispar* from the other *Entamoeba* species remains to be explained.

Evaluated 20 Jun 2005

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### Faculty Comments

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Faculty of 1000: evaluations for Pritham EJ et al *Mol Biol Evol* 2005 May 18 :  
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Nitaya Thammapalerd: Faculty of 1000, 29 Jun 2005  
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