

Databases and ontologies

HTT-DB: Horizontally transferred transposable elements database

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Abstract

Motivation: Horizontal transfer of transposable (HTT) elements among eukaryotes was discovered in the mid-1980s. As then, >300 new cases have been described. New findings about HTT are revealing the evolutionary impact of this phenomenon on host genomes. In order to provide an up to date, interactive and expandable database for such events, we developed the HTT-DB database.

Results: HTT-DB allows easy access to most of HTT cases reported along with rich information about each case. Moreover, it allows the user to generate tables and graphs based on searches using Transposable elements and/or host species classification and export them in several formats.

Availability and implementation: This database is freely available on the web at <http://lpa.saogabriel.unipampa.edu.br:8080/httdatabase>. HTT-DB was developed based on Java and MySQL with all major browsers supported. Tools and software packages used are free for personal or non-profit projects.

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1 Introduction

Transposable elements (TEs) are ‘mobile genes’ that replicate inside the host genome moving from one genomic location to another. TEs are known as genomic parasites, since they do not contribute to host fitness and exploit the host’s molecular machinery for their replication. However, an increasing amount of evidence suggests that TEs can also act as evolutionary engine of organism adaptations (González *et al.*, 2010; Mateo *et al.*, 2014).

Once these elements invade a new species, they may be vertically transmitted to the entire progeny through the host gametes (Werren, 2011). However, due to their repetitive and mobile nature, TEs can damage the host genome, through chromosome rearrangements and new insertions, hence being counter selected at the host level (Petrov *et al.*, 2011). In addition, TEs can be lost from host genomes

through stochastic loss or genetic drift (Brookfield, 2005). All of these processes contribute to the extinction of TEs from host genomes. Despite that, almost all organism analysed to date have a proportion of its genomes composed by TEs (Pritham, 2009; Hua-Van, 2011). One hypothesis suggested to explain such contradiction is that TEs are capable of invading new genomes through Horizontal transfer (HT) then escaping the natural fate of vertical extinction (Silva *et al.*, 2004).

The horizontal transfer of transposable (HTT) elements between reproductively isolated eukaryotic species has been intriguing geneticists and evolutionary biologists since it was first reported in the mid 1980s (Daniels *et al.*, 1984, 1990). Several new cases have been reported since then, highlighting the potential impact of invading TEs on host genome evolution. Such a large amount of data boosted the

conception of two reviews about this topic, where general patterns governing such events could be investigated (Schaack *et al.*, 2010; Wallau *et al.*, 2012)

Due to the ever-increasing number of HTT events reported and the impact of such events on the host genomes, we decided to create the HTT database, providing an easy way for researchers to browse the data and take knowledge based decision for future research on this topic.

2 Programming languages and databases

HTT-DB was developed using a relational database (MySQL v 5.6.12) implemented in HTML and Java, running into a Web Server (Apache Tomcat 8.0.12 Server). We used Eclipse Java EE IDE as the developing tool. As programming languages, we used Java SE—1.7, HTML, javascript, and as plugins we used JQuery, JQuery UI, JQuery Multiple Select, Highcharts JS, BattaTech JQuery Excel Export, JQuery Tablesorter 2.0 and jsPhyloSVG (Smits *et al.*, 2010). Tools and software packages used are free for personal or non-profit projects.

3 Data mining

Previously reported HTT cases were recovered from the two reviews published previously (Schaack *et al.*, 2010; Wallau *et al.*, 2012<AQ4/>) and the new cases were obtained searching in PubMed—NCBI and Google Scholar with the keywords ‘horizontal transfer’, ‘horizontal transmission’, ‘horizontal transposon transfer’ and ‘HTT elements’. This same search pattern will be performed monthly in order to find new published HTT cases.

4 HTT database features

The HTT database is organised as a table with several columns that can be filtered by ‘TEs keywords’ following the TEs classification hosted in Repbase: Class, Superfamily and Family; and/or ‘Host Organisms keywords’ following the NCBI taxonomy as:

- Organism—the higher taxonomic level before the taxonomic level where the HTT occurred. For example, if the user select ‘*Drosophila*’ in this field, all HTT events reported between species of the *Drosophila* genus will be shown.
- Taxonomic level—the taxonomic level where the HTT occurred. For instance, if the user select the ‘Family’ option, all HTT events reported between species from different families will be shown.

The next two columns contains the available data about the HTT dating in million years (Mya) and the ecological relationship between the HTT involved species, if any.

One of the main features of the HTT database is its interactive interface, allowing the user to search and filter the database based on one or a combination of several keywords, both from TEs and host taxonomy. Resulting tables can be converted into interactive graphs that can be exported in several figure formats, as shown in Figure 1.

We also linked the original published manuscript where HTT events were described. Additionally, we included a ‘How to add data’ tab that can be used by researchers publishing new cases of HTT and who want to include their data in the database. All new submitted HTT cases only will be accepted and added to the database if they were published in peer reviewed journals.

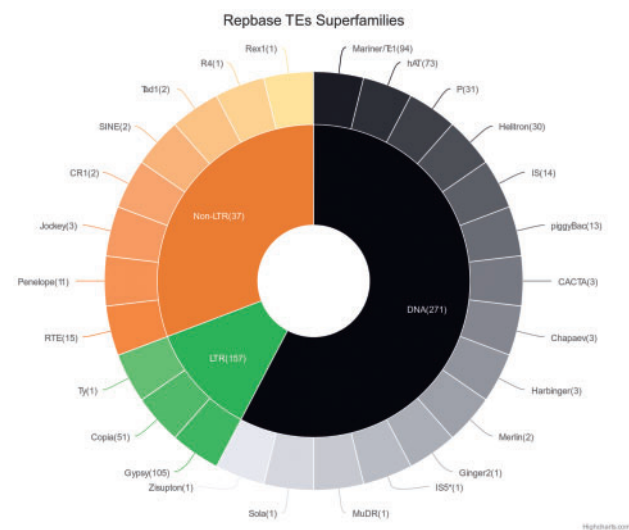


Fig. 1. Overall distribution of HTT events sorted by TE Repbase classification

5 Availability and long-term database maintenance

The database is available at the web server of the Universidade Federal do Pampa and will be maintained by this university for an unlimited time. HTT-DB is a free database, which is publicly available at (<http://lpa.saogabriel.unipampa.edu.br:8080/httdatabase>) and open for the deposition of additional data. Moreover, the database is expandable and can incorporate all new findings as our knowledge about HTT or HT in general increases.

6 Future developments

Virus-to-host and horizontal gene transfer are other interesting phenomenon that can be added to the HTT-DB in a similar fashion.

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