



GrTEdb: the first web-based database of transposable elements in cotton (*Gossypium raimondii*)

Although several diploid and tetraploid *Gossypium* species genomes have been sequenced, the well annotated web-based transposable elements (TEs) database is lacking. To better understand the roles of TEs in structural, functional and evolutionary dynamics of the cotton genome, a comprehensive, specific, and user-friendly web-based database, *Gossypium raimondii* transposable elements database (GrTEdb), was constructed.

Meanwhile, the web-based sequence browsing, searching, downloading and blast tool were implemented to help users easily and effectively to annotate the TEs or TE fragments in genomic sequences from *G. raimondii* and other closely related *Gossypium* species.

GrTEdb provides resources and information related with TEs in *G. raimondii*, and will facilitate gene and genome analyses within or across *Gossypium* species, evaluating the impact of TEs on their host genomes, and investigating the potential interaction between TEs and protein-coding genes in *Gossypium* species.

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Results

1. Construction and content of the database.

14 332 TEs were structurally annotated and clearly categorized in the *G. raimondii* genome, including 2929 *Copia*-like elements, 10 368 *Gypsy*-like elements, 299 *L1*, 12 *Mutators*, 435 *PIF-Harbingers*, 275 *CACTAs* and 14 *Helitrons* (Table 1).

2. User interface.

The GrTEdb database organization is navigated by six sections: Home, Browse, Search and Download, Blast, Links and Contact (Figure 1A).

3. Browse.

In the browsing interface, the classification structures of TEs deposited in GrTEdb were showed. Users can download the whole TEs sequences, and can browse any one superfamily of interest by the hyperlinks provided. The detailed information of each superfamily can be retrieved and downloaded by clicking the corresponding entry (Figure 1B).

Table 1. Summary of the identified TEs in *G. raimondii*

Class	Order	Superfamily	Copy numbers
Retrotransposons	LTR	<i>Copia</i>	2929
		<i>Gypsy</i>	10 368
DNA transposons	LINE	<i>L1</i>	299
	TIR	<i>Mutator</i>	12
		<i>PIF-Harbinger</i>	435
		<i>CACTA</i>	275
	Helitron	<i>Helitron</i>	14
Total			14 332

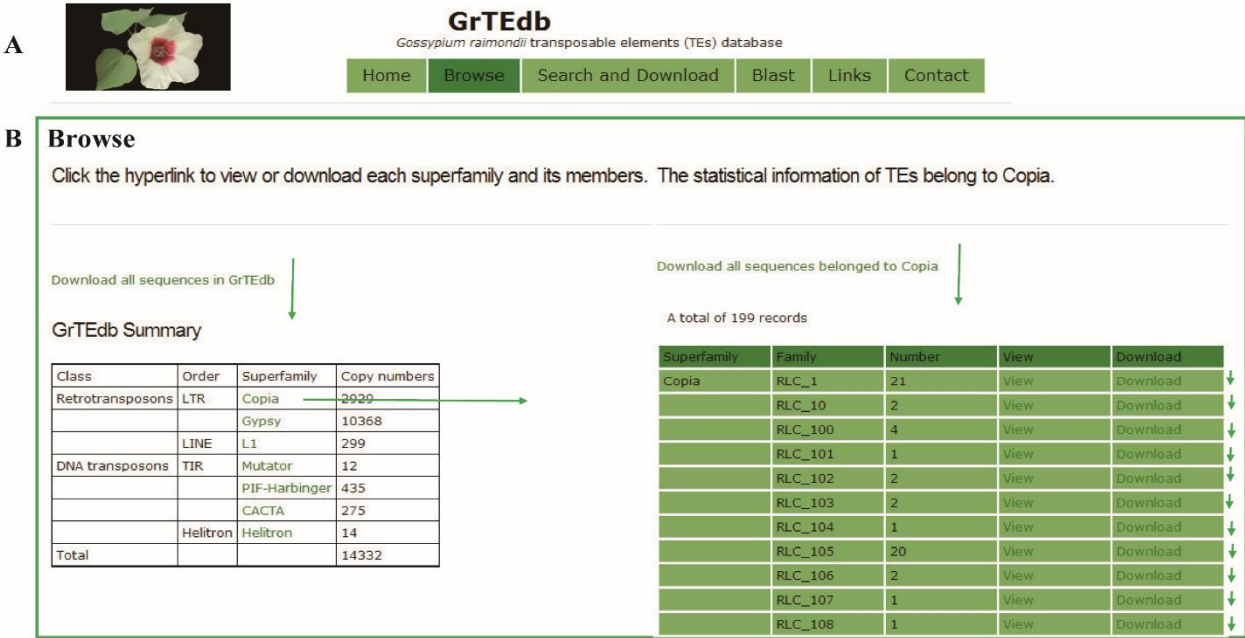


Figure 1. (A) The top menu of GrTEdb. (B) The user interface of browsing in GrTEdb.

Results

4. The searching interface of GrTEdb.

In the searching and downloading interface, users can use a keyword to search the GrTEdb (e.g. TE ID, Class, Order, Superfamily and Family) to locate specific TEs quickly. The search results can be viewed and downloaded by clicking the hyperlinks provided on the page (Figure 2).

5. The chromosomal region search page.

In the chromosomal region search page, users can retrieve the TEs for any one entire chromosome or in a defined window around either a chromosomal position or a gene model, and the detailed information of each retrieved TEs can be viewed and downloaded by clicking the hyperlinks provided on the page (Figure 3).

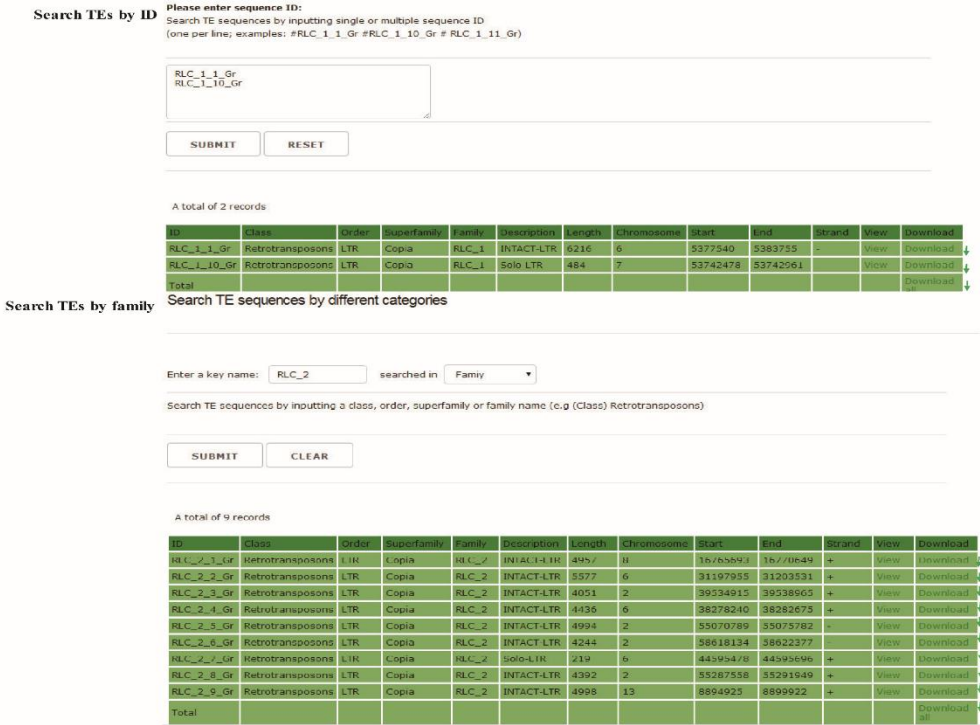


Figure 2. The searching interface of GrTEdb.

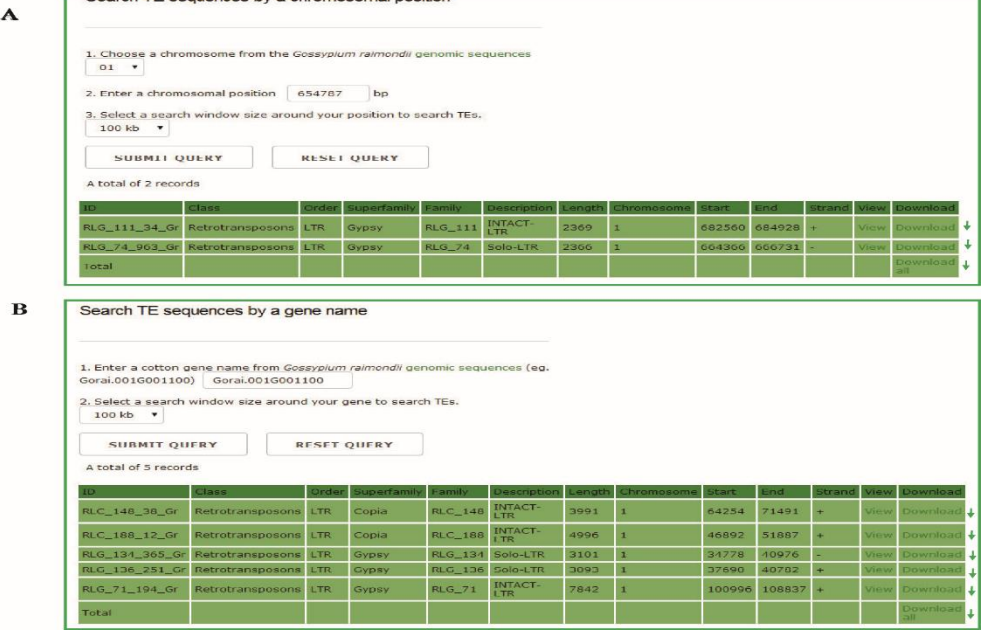


Figure 3. The chromosomal region search page.

Results

6. Blast.

In the BLAST search page, users can handy and quickly compare their sequences with the cotton TEs deposited in GrTEdb (Figure 4).

Conclusions

We have generated a web-based GrTEdb, and it provides researchers with not only resources and information related to different TEs in the cotton genome but also tools for performing data analysis.

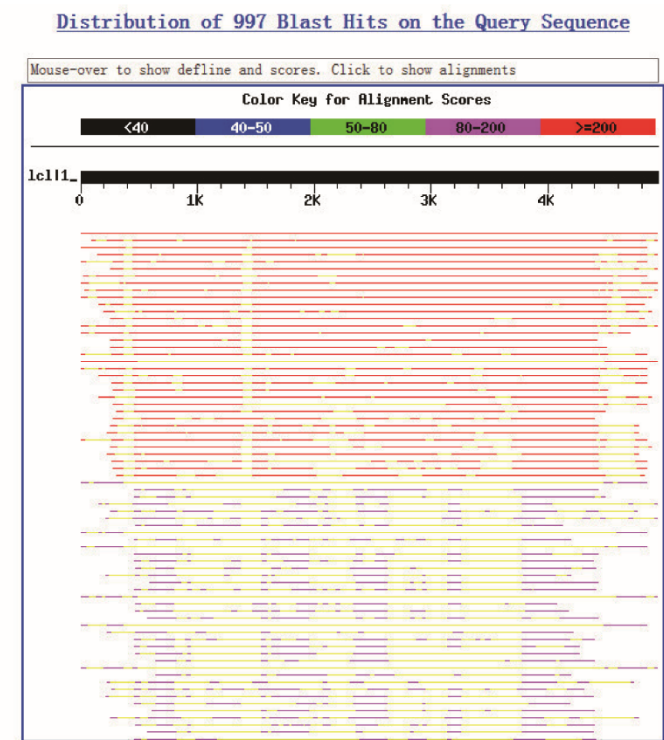


Figure 4. The BLAST interface (left) and a sample of BLASTn results (right) provided in GrTEdb.



Database tool

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