

maize transposable element database

Welcome to the Maize transposable element (TE) database.

Get data from database

[Download the FASTa](#)

Show the TE classes (in [list format](#) or [table format](#)) and sub-classes, etc.

List of the number of TEs associated with [annotators](#), [organisms](#), [TE classifications \(list\)](#), [TE classifications \(table\)](#). The latter two are the same as above only with a count of the classes, etc.

[User guide](#) (documentation). PDF format. Revised July 2009.

[Curator-related links and information.](#)

Do a [BLAST search](#) against the database.

Project Summary

[Susan R. Wessler](#) (PI, University of California - Riverside)

[Jeffrey L. Bennetzen](#) (Co-PI, University of Georgia)

[R. Kelly Dawe](#) (Co-PI, University of Georgia)

[Ning Jiang](#) (Co-PI, Michigan State University)

[Phillip SanMiguel](#) (Co-PI, Purdue University)

[Byron Freeman](#) (Collaborator, University of Georgia, Georgia Museum of Natural History)

Transposable elements (TEs) are the most abundant component of all characterized genomes of higher eukaryotes and the genome of maize is recognized as having the most dynamic TE component. As such, it is the organism of choice for understanding how TEs contribute to gene and genome evolution. In addition to identifying all TEs in maize, this project will pay particular attention to the characterization of TEs such as Pack-MULEs and Helitrons that routinely capture and amplify gene fragments and thereby confound gene annotation. This project will generate a comprehensive and rigorously annotated TE database that will greatly assist all future maize genome annotations. Computational analysis will serve to identify candidate active TEs whose mobility will be validated using the transposon display technique in conjunction with a wide spectrum of maize genomic DNAs. This project will, for the first time, extend the analysis of TEs to the pericentromere, a region that in other sequenced genomes has been unfinished and/or unannotated.

The scientific goals of this project and the familiarity of maize provide outstanding opportunities for student training and for connections between the research community and the broader public. This project dedicates over 10% of its resources to this mission with the centerpiece being the development of web-based and traveling museum exhibits that describe the history of maize as a crop, as a model organism for genome research, and as a key component of many Native American cultures. To this end, collaborations have been established with the University of Georgia Museum of Natural History, the Smithsonian Institution and the U.S. Botanic Garden.

Acknowledgment and Disclaimer

This material is based upon work supported by the [National Science Foundation](#) under Grant No. 1118550.

Any opinions, findings, conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the National Science Foundation.

