

Reply: A universal classification of eukaryotic transposable elements implemented in Repbase

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In response to the correspondence by Vladimir V. Kapitonov and Jerzy Jurka (A universal classification of eukaryotic transposable elements implemented in Repbase. *Nature Rev. Genet.* **9** (2008), doi:10.1038/nrg2165-c1)¹ on our Review (A unified classification system for eukaryotic transposable elements. *Nature Rev. Genet.* **8**, 973–982 (2007))², Repbase is a useful tool, alongside RetrOryza, the *Triticeae* repeat database (TREP), The Institute for Genomic Research (TIGR) repeat databases and other such resources, for organizing and accessing the complexity and commonalities of the transposable elements. Any apparent under-exposure of Repbase or other tools in our paper was unintentional. The hierarchical classification system of Repbase is consistent

with that of Finnegan³ from 1989 as well those of others^{4,5}. We have endeavored to conserve the areas of agreement within the transposable element community on transposable element taxonomy, while adding features (including a full hierarchical nomenclature) and application rules that will benefit annotators and non-experts.

1. A universal classification of eukaryotic transposable elements implemented in Repbase. *Nature Rev. Genet.* **9** (2008), doi:10.1038/nrg2165-c1.
2. A unified classification system for eukaryotic transposable elements. *Nature Rev. Genet.* **8**, 973–982 (2007).
3. Finnegan, D. J. Eukaryotic transposable elements and genome evolution. *Trends Genet.* **5**, 103–107 (1989).
4. Kumar, A. & Bennetzen, J. Plant retrotransposons. *Ann. Rev. Genet.* **33**, 479–532 (1999).
5. Capy, P., Bazin, C., Higuier, D. & Langin, T. (eds) Dynamics and evolution of transposable elements (Library of Congress, Austin, Texas, 1998).