Recent reactivation of a pathogenicity-associated transposable element is associated with major chromosomal rearrangements in a fungal wheat pathogen

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Abstract

Transposable elements (TEs) are key drivers of genomic variation contributing to recent adaptation in most species. Yet, the evolutionary origins and insertion dynamics within species remain poorly understood. We recapitulate the spread of the pathogenicity-associated Styx element across five species that last diverged \(-11,000\) years ago. We show that the element likely originated in the Zymoseptoria fungal pathogen genus and underwent multiple independent reactivation events. Using a global 900-genome panel of the wheat pathogen Z. tritici, we assess Styx copy number variation and identify renewed transposition activity in Oceania and South America. We show that the element can mobilize to create additional Styx copies in a four-generation pedigree. Importantly, we find that new copies of the element are not affected by genomic defenses suggesting minimal control against the element. Styx copies are preferentially located in recombination breakpoints and likely triggered multiple types of large chromosomal rearrangements. Taken together, we establish the origin, diversification, and reactivation of a highly active TE with likely major consequences for chromosomal integrity and the expression of disease.

Keywords: Transposable element, Genome evolution, Fungal pathogen, Structural rearrangement

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