Detection of novel mariner like elements in two closely related species of Cecidomyiidae: Mayetiola destructor and Mayetiola hordei

Wiem Ben Amara*[1], Wafa Ben Lazhar[1], Hanem Makni[1], Mohamed Makni[1], Nathalie Choisne[2], Véronique Jamilloux[2], Timothée Chaumier[2], Hadi Quesneville[2], and Maha Mezghani-Khemakhem[1]

[1]Unité de Recherche GIRC (UR11ES10); Faculté des Sciences de Tunis; Université de Tunis El Manar;Tunis-Tunisie – campus universitaire Tunis el Manar, Tunisie

[2]URGI INRA de Versailles – Institut National de la Recherche Agronomique - INRA – France

Résumé

Mariner-like elements (MLEs), a group of Class II transposons are thought to be the most diverse and widespread transposable elements (TE) in many organisms especially in insects. In this study we aimed to characterize MLEs in two cereal pests: the Hessian fly Mayetiola destructor and the barley stem gall midge Mayetiola hordei
First, MLEs were amplified using a primer designed from TIRs of the potentially active element Desmar1. Eleven MLEs were detected in both species and exhibited similarity higher than 90% with Desmar1 suggesting the presence of a mariner ancestor element for the two studied species. A consensus was established from the alignment of these MLEs. It showed the same characteristics of Desmar1 suggesting the presence of a potentially active sequence in M. hordei. Using this consensus for in silico detection in M. destructor genome allowed the identification of 18 MLEs belonging to mauritiana sub-family that diverge into two groups. The first group contains 13 MLEs similar to Desmar1 and the second one contains 5 new MLEs that share only 50% of protein similarity with Desmar1 like elements.

Secondly, to check for the presence of these new detected elements in M. hordei genome, two primers (cons1 and cons2) were designed from TIRs and 6 MLEs were amplified. These elements exhibited 55% of protein similarity to Desmar1. None of these elements appeared to be functional, as all the open reading frames (ORF) were disrupted by the presence of frameshifts or stop codons and Indel mutations. Interestingly, phylogenetic analysis revealed that although all these elements belong to the mauritiana subfamily, they diverge in 3 clusters: the first one included MLEs amplified by cons1 in the two species whereas the two other clusters included the MLEs amplified by cons2 in M. destructor and M. hordei respectively. This study highlighted the diversity of MLEs in Mayetiola genome and showed that these different clusters reflect different evolutionary trajectories of MLEs between the two species. This requires a deeper annotation of other possible variants of MLEs but also of the other TE families to understand their contribution to Mayetiola's genome evolution. Accordingly, we are currently annotating TEs in M. destructor genome using REPET pipelines as de novo based strategy of TEs detection. Preliminary analysis will be shown.

*Intervenant