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**Poster Abstract – A.53**

# EVOLUTION OF MICROSATELLITES WITHIN LTR RETROTRANSPOSONS IN THE RICE GENOME

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*Gypsy and Copia like LTR-retrotransposon, microsatellite evolution, plant genomics, Oryza sativa.*

The aim of this study was to investigate microsatellite evolution in *gypsy*-like and *copia*-like LTR retroelements in *Oryza sativa* L. var. *japonica*. We screened a collection of 2807 members of the Ty-3-gypsy group and 776 members of the Ty-1-copia group, isolated from the draft genome sequence of rice, for a total amount of almost 35 Mb, searching for microsatellites in their LTR and internal domains. We characterised the microsatellites present in the gypsy-like and copia-like retroelement populations, in terms of motif class distributions and length class distributions; we estimated the abundance and distribution of the identified microsatellites in LTR retroelements grouped according to their time of insertion; finally, we investigated the mutability of microsatellites residing within the LTR regions.

We found similar microsatellite frequencies in copia and gypsy elements, according with the coeval major waves of propagation inferred for the two groups on the basis of sequence divergence between LTRs of every retroelement. Moreover our estimates confirmed the relative paucity of microsatellites in the repetitive fraction of the rice genome, in comparison to more ancient compartments, such as genes. We observed a sharp difference in the microsatellite frequencies between different structural retroelement domains, with LTRs displaying more than doubled concentration of microsatellites compared to the internal domains. Moreover, microsatellites appear more frequent in internal regions of ancient retroelements than recent ones, while reach very high frequencies in LTRs of the youngest elements. We investigated the kind of mutations responsible for length differences between pairs of microsatellites belonging to the two LTRs of the same retroelement and we observed a predominance of stepwise events followed by point mutations and other rearrangements.

We discuss these features under the hypothesis that in grasses microsatellites residing in recently amplified LTR-retrotransposon DNA are still reaching an equilibrium state.