

## §S5. Transposable Elements

A number of unusual features were also observed in *Aspergillus* TEs. First, in *A. fumigatus*, one subfamily of I-1\_AF non-LTR retrotransposons has a unique target-site, and was found in long terminal repeats of the Afut2 *Gypsy*-like LTR retrotransposon. Second, the *Aspergillus Helitrons* have 5'-TT and CTTG-3' termini, which differ from the canonical 5'-TC and CTRR-3' termini<sup>70</sup>. Moreover, *Aspergillus Helitrons* do not contain 3' palindromic structures, which are present in other eukaryotes<sup>70,71</sup>, indicating that 3' palindromes are not essential for rolling-circle transpositions. Third, all three genomes possess unusual *Mariners*, 7-9 kb in length, that encode a conserved protein of unknown function in addition to a transposase. Finally, we identified families of SINE elements derived from the 5'-half of 5S rRNA containing an internal pol III promoter. They are the first examples of SINE elements present in fungi. Moreover, such 5s RNA derived SINE elements have been found previously in the zebrafish genome only.

**Table §S5.1: Major superfamilies of transposable elements identified in the aspergillus genomes**

Species	Percentage of all TEs and repetitive elements in the assembly	Percentage of different classes among all transposable and repetitive elements						
		Non-LTR retrotransposons	LTR retrotransposons			DNA transposons		
		<i>I</i>	<i>Gypsy</i>	<i>Copia</i>	<i>Mariner</i>	<i>MuDR</i>	<i>hAT</i>	<i>Helitron</i>
<i>A. nidulans</i>	3.0	19	22	14	20	12 <sup>†</sup>	5 <sup>†</sup>	2
<i>A. fumigatus</i>	2.9	15	55	4	25	-	-	-
<i>A. oryzae</i>	1.4	20	31	-	49	<<1	-	-

<sup>†</sup>Putative classification based on hallmarks of nonautonomous elements DNA9-1\_AN, DNA9-2\_AN, DNA9-3\_AN, and DNA9-4\_AN (*MuDR* superfamily) and hAT-N1\_AN, and hAT-N2\_AN (*hAT* superfamily). There are no *MuDR* and *hAT* transposases detectable in the *aspergillus* genomes.