Figure 1 - Counts of the number of deleterious (Del) non-synonymous sites and the total number of non-synonymous (NS) sites in selfing and outcrossing genotypes of *Eichhornia*.

Deleterious mutations were identified using the program MAPP, which uses evolutionary constraint in homologous proteins to infer the potential fitness impact of non-synonymous changes. The colours along the branches reflect the putative model of changes in mating system although the exact timing of the transition along each branch is not known. The branch lengths are not to scale.