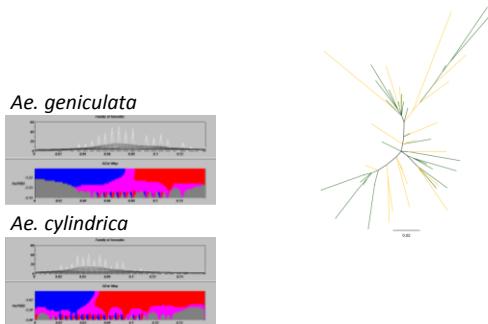
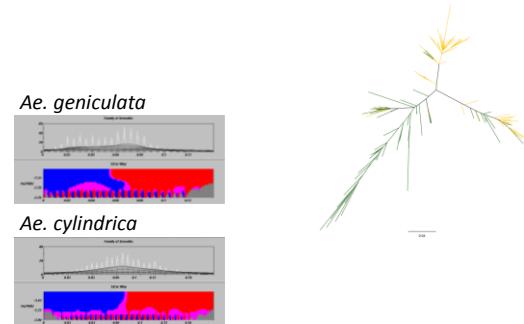


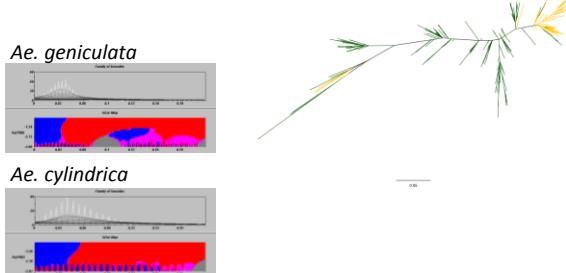
*Abia*



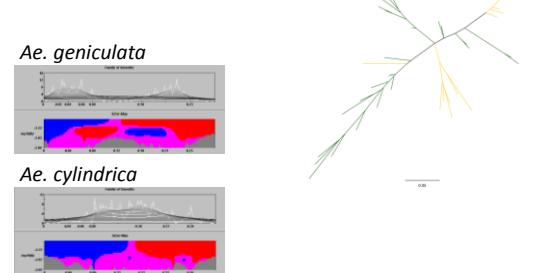
*Barbara*



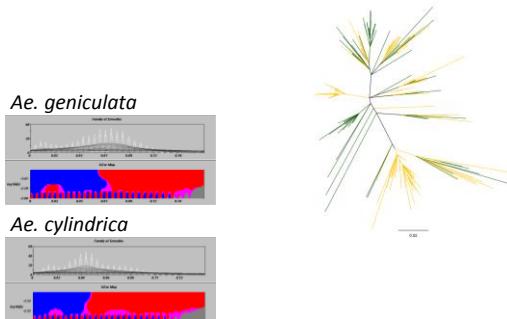
*BARE1*



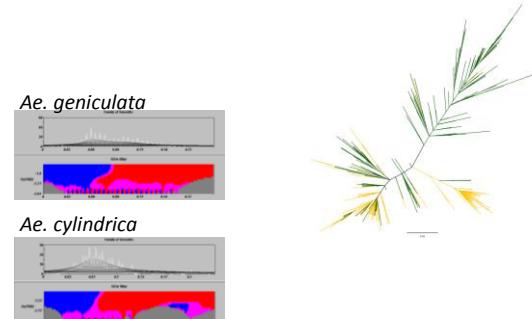
*Carmilla*



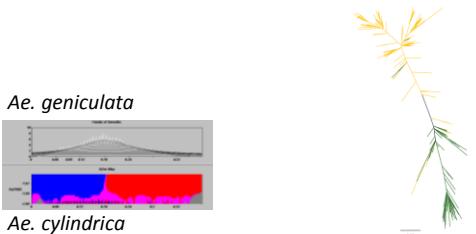
*Cereba*



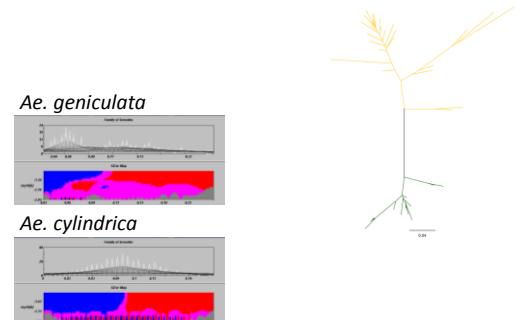
*Claudia*



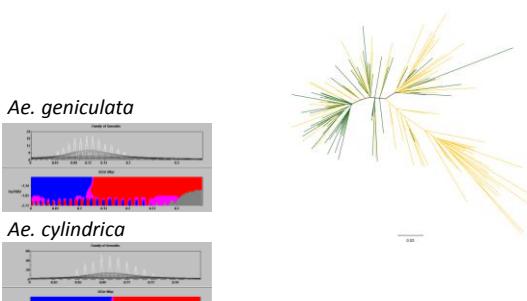
*Danae*



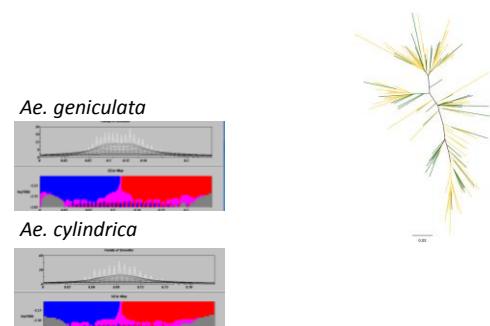
*Daniela*



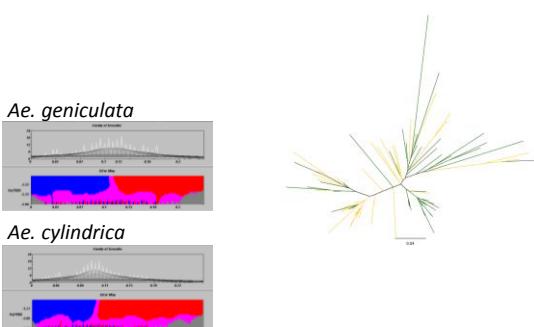
*Derami*



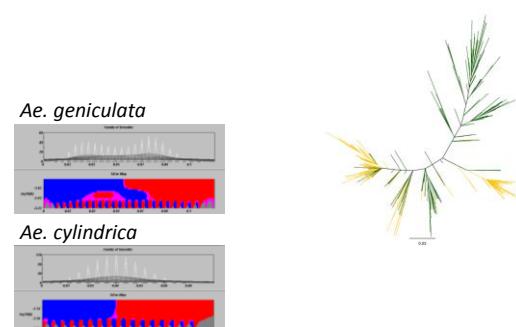
*Egug*



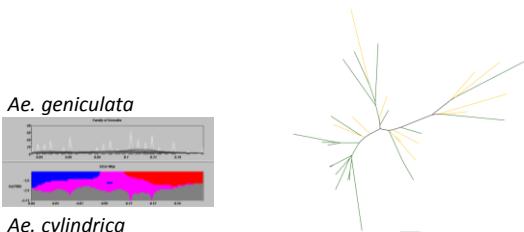
*Eugene*



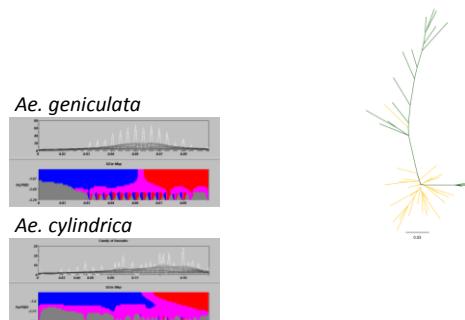
*Fatima*



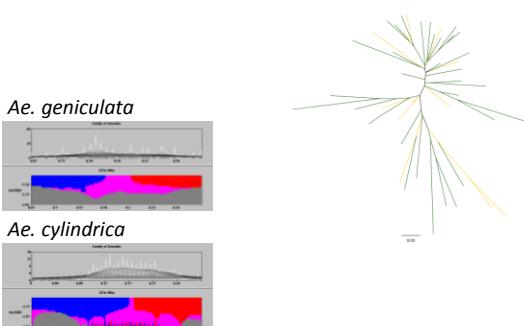
*Ginger*



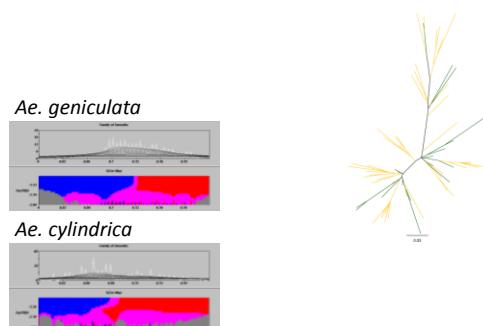
*Gujog*



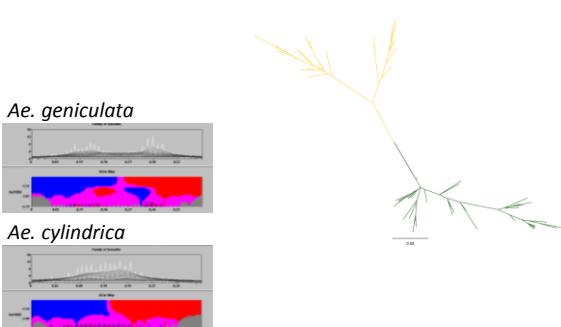
*Hawi*



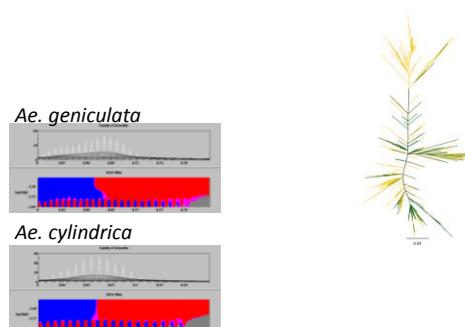
*Jeli*



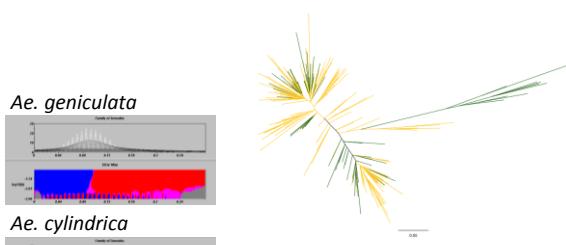
*Lila*



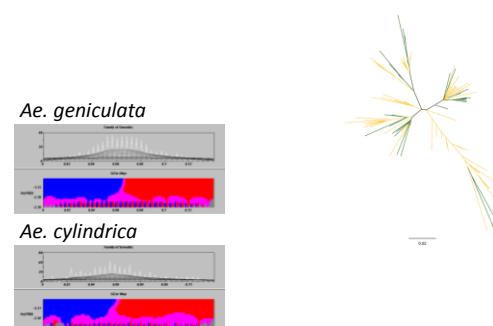
*Maximus*



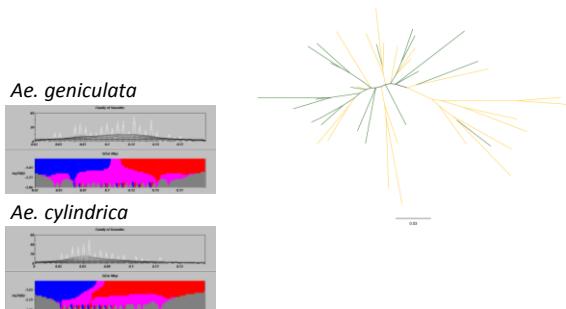
*Nusif*



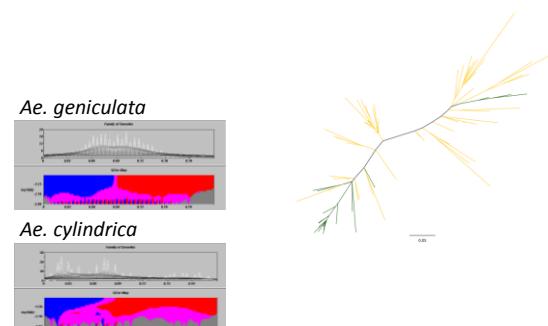
*Quinta*



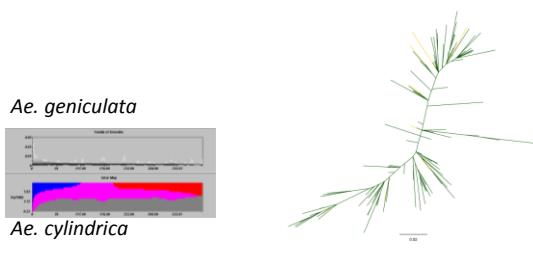
*Romana*



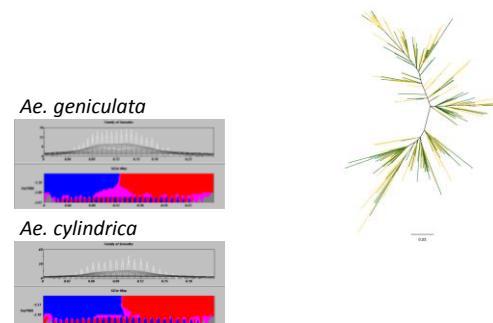
*Romani*



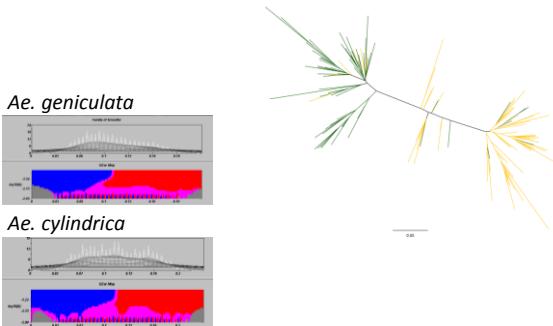
*Sabine*



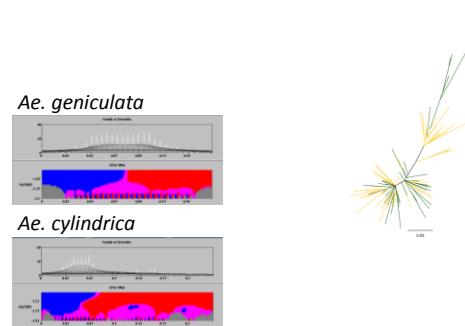
*Sabrina*



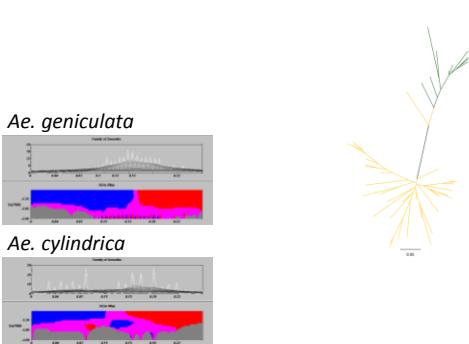
## WHAM



## Wilma



## Xalax



- Legend

For all retrotransposon family investigated by evolutionary genetics

**left** bimodal distribution of distance among sequences (i.e. mismatch distribution) done with MEGA version 5 (**above**) on species-specific alignments), and statistically visualized with the software sizer (**below**). Sizer used blue color to indicate when a 95% confidence interval for the slope is  $<0$ , thus when the slope is significantly positive, and red when the same confidence interval is  $<0$ , the slope is significantly negative.

**right** phylogenetic tree inferred with an unrooted maximum likelihood tree with high performance computing using RAXMLHPC (GTR model with gamma-distributed rate across sites; branch support assessed by 100 bootstraps).

green: *Ae. cylindrica* individual inserted copies

yellow: *Ae. geniculata* individual inserted copies.