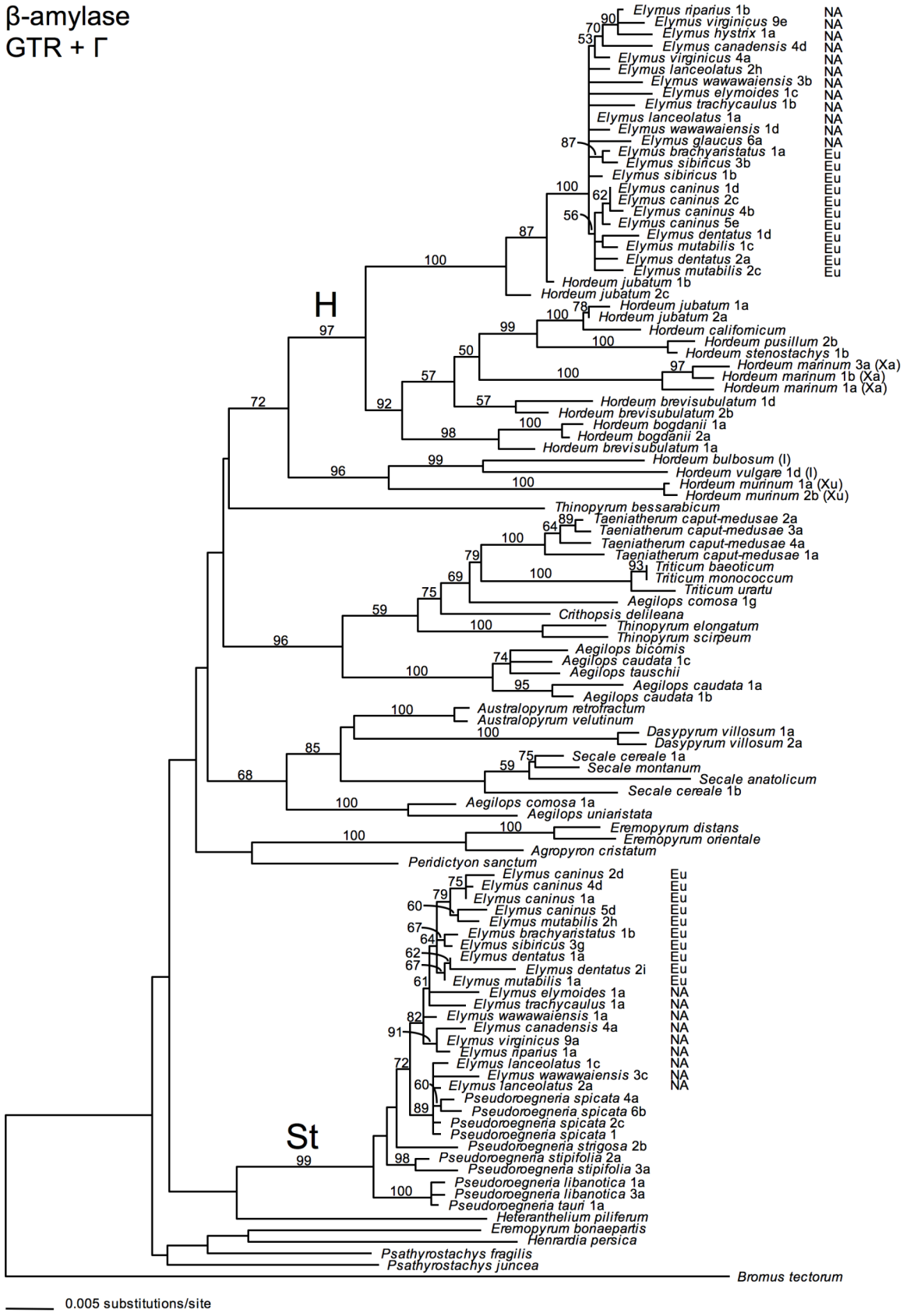

β-amylase gene tree. The best-scoring ML tree was selected from 30 GARLI analyses of the β-amylase sequence data set under a GTR+Γ model of sequence evolution. Numbers above branches show ML bootstrap support >50%. ‘‘NA’’ and ‘‘Eu’’ distinguish North American and Eurasian *Elymus* species, respectively. Where applicable, numbers following taxon names distinguish individuals within species. Letters following these numbers designate cloned sequences from within individuals.