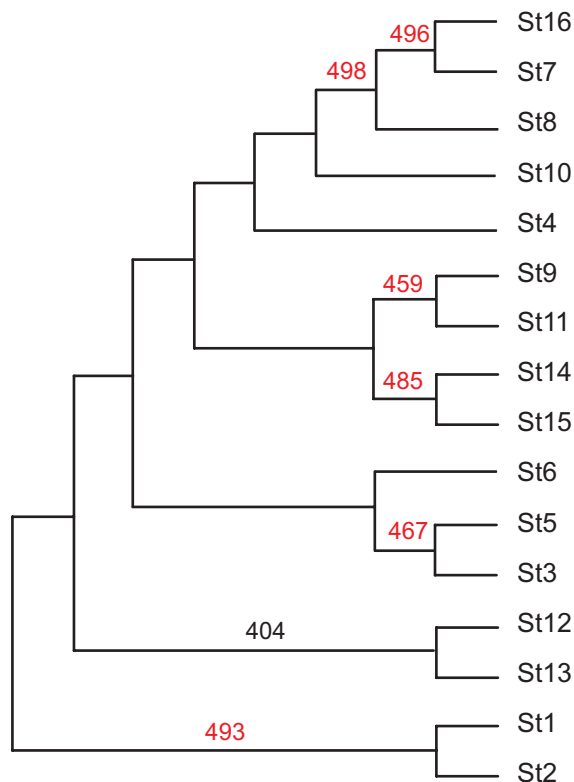
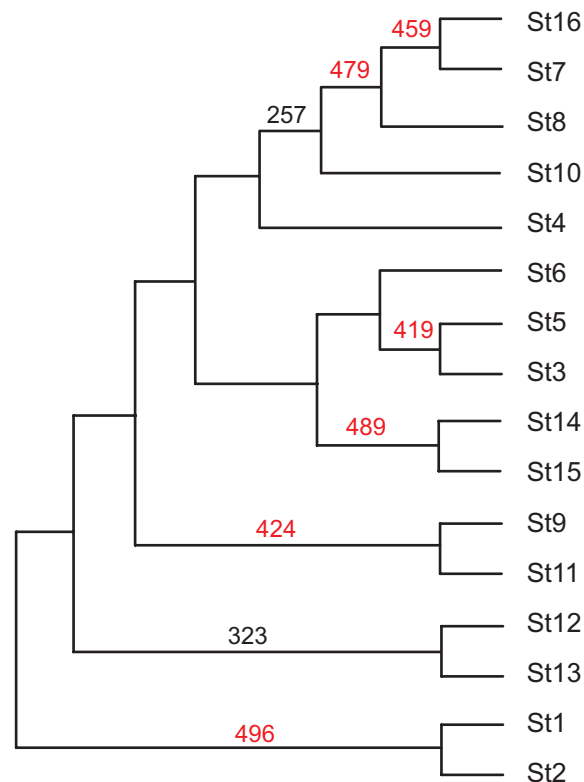


Neighbor-joining



Maximum likelihood



Cladograms of potato HyPRP protein sequences constructed using the NJ and ML methods. Both trees are unrooted, bootstrap values above 50 % (from 500 replicates) are shown above branches. Bootstrap values in red denote branches that were supported by both methods and also recovered in trees based on nucleotide sequences (see Figure 1).