

Supplementary Material to “Genome-wide analysis of the maize superoxide dismutase (SOD) gene family reveals important roles in drought and salt responses”

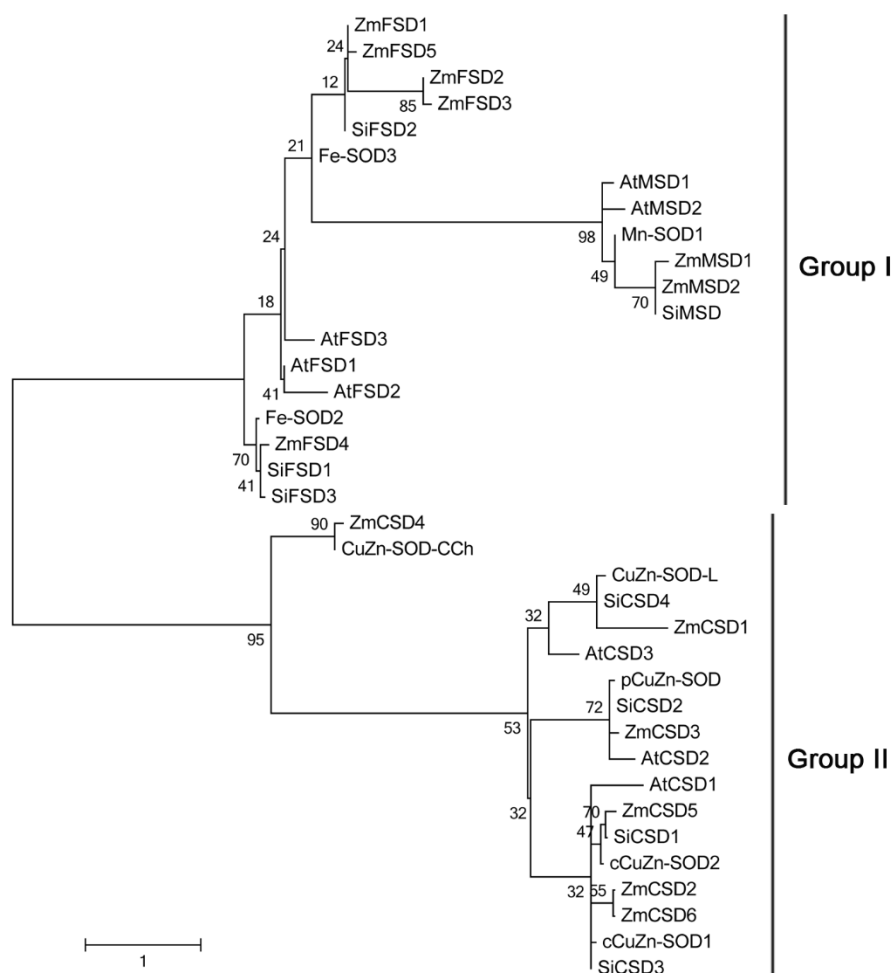


Figure S1 - Maximum likelihood phylogenetic tree of 37 SOD proteins from different plant species. The Maximum Likelihood (ML) tree was constructed using MEGA 5.05 software by alignments of the full-length sequences of the 37 SOD proteins. Bootstrap values from 1,000 replicates were shown at each branch.