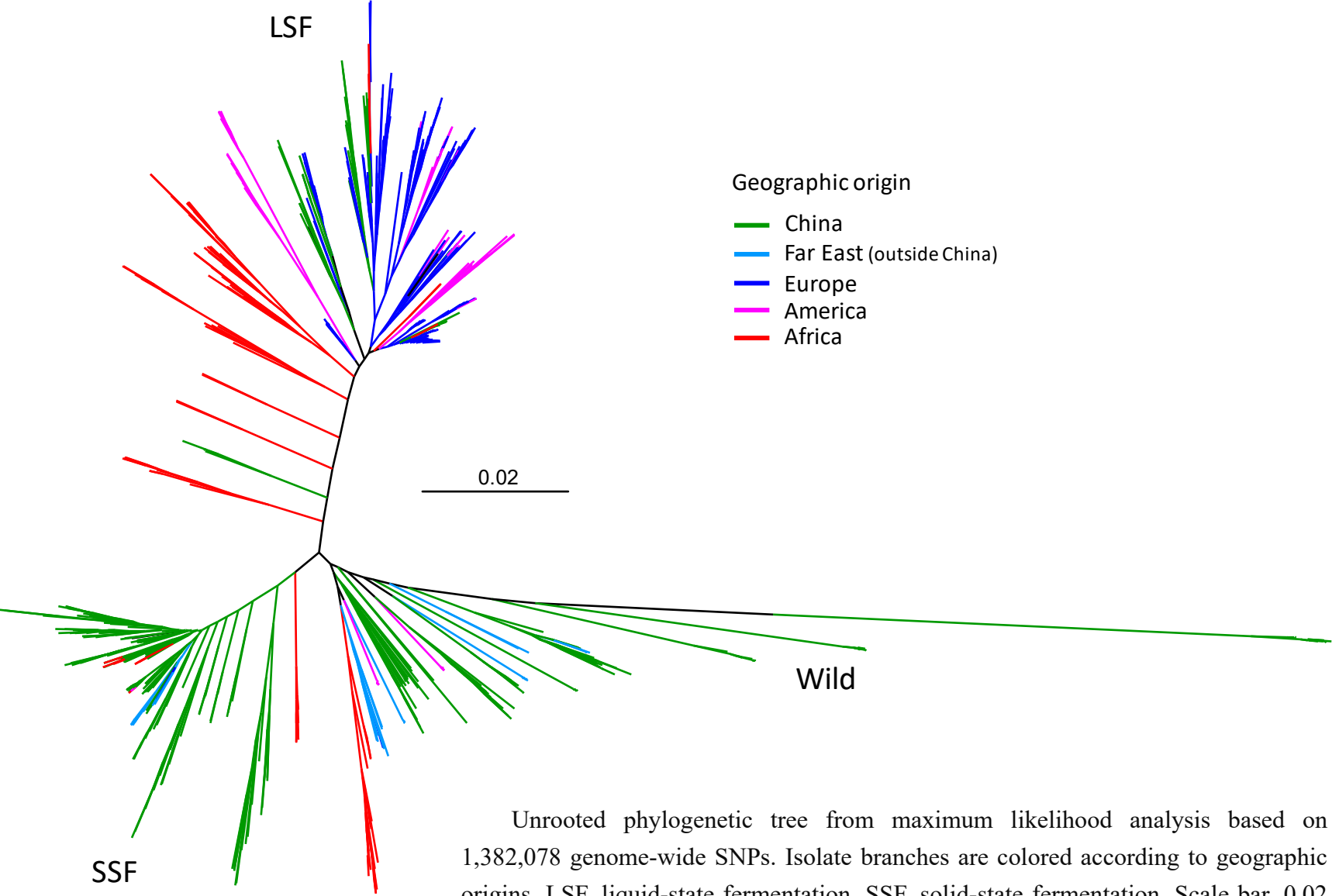


Figure S1



Unrooted phylogenetic tree from maximum likelihood analysis based on 1,382,078 genome-wide SNPs. Isolate branches are colored according to geographic origins. LSF, liquid-state fermentation. SSF, solid-state fermentation. Scale bar, 0.02 substitutions per site.