Fig. S1. One of 500 most parsimonious phylogenetic trees found with a heuristic search with simple sequence addition for 22 combined chloroplast DNA trnH-psbAand trnK-rps16 spacer haplotypes (CPH) from Leymus cinereus (199 plants) and Leymus triticoides (14 plants), which displayed 25 parsimony informative and 14 parsimony uninformative characters. The tree has 42 steps with consistency index (CI)= 0.9106 and retention index (RI)= 0.9123. Bootstrap support values shown at branches were determined from 1,000 heuristic searches with simple sequence additions. The tree was rooted using Eurasian L. racemosus and L. angustus outgroups.