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*Phylogenetic Relationships in the Festuca-Lolium Complex (Loliinae; Poaceae):  
New Insights from Chloroplast Sequences*

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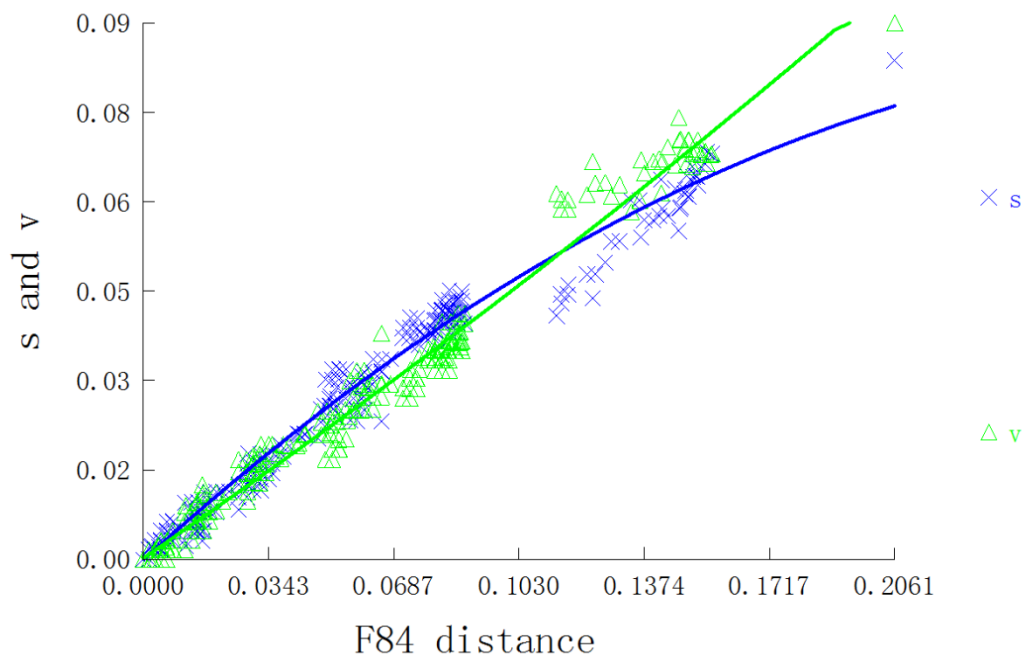
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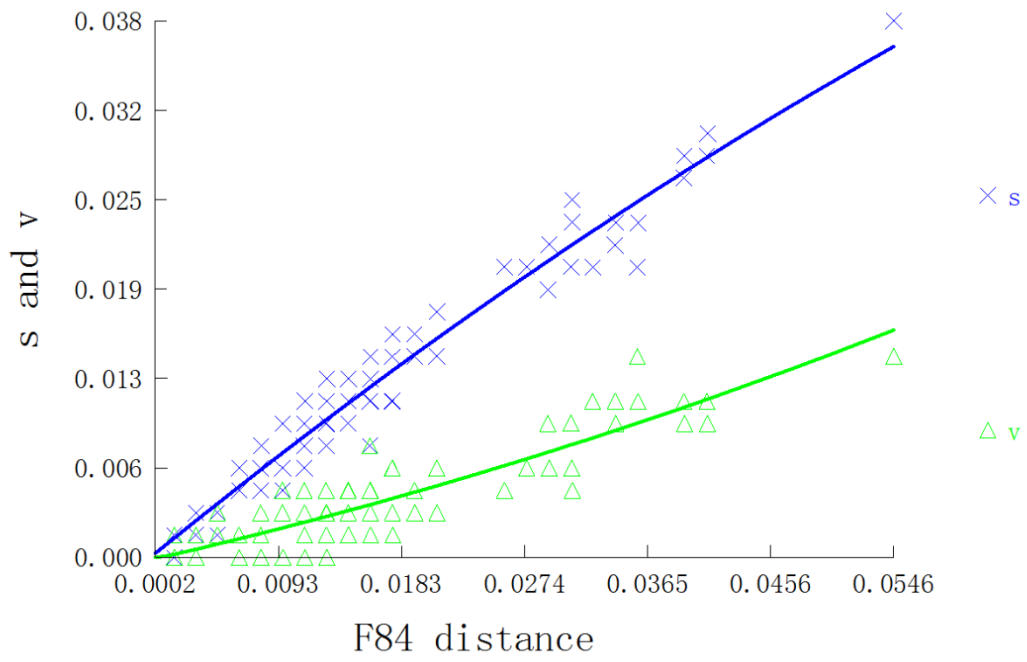
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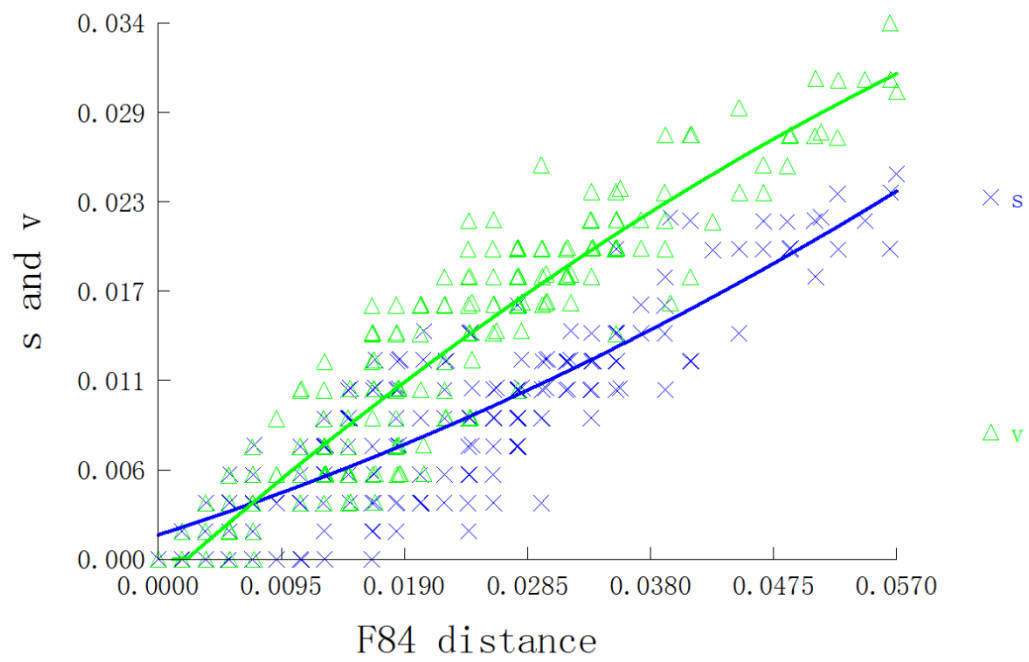
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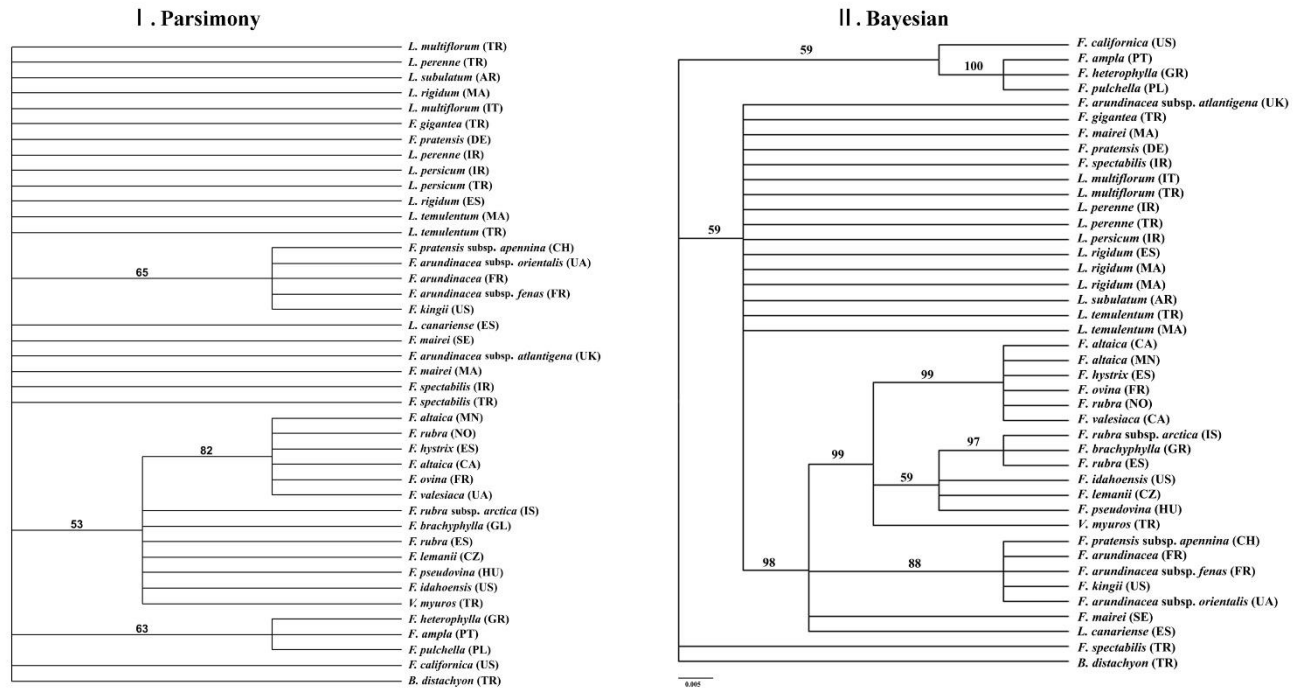
**Supplementary Figure 1 Substitution saturation test of the *trnQ-rps16* gene sequences. The letters s and v represent transition and transversion, respectively.**



**Supplementary Figure 2** Substitution saturation test of the *rbcL* gene sequences. The letters **s** and **v** represent transition and transversion, respectively.



**Supplementary Figure 3 Substitution saturation test of the *trnH-psbA* gene sequences. The letters s and v represent transition and transversion, respectively.**



**Supplementary Figure 4** Phylogenies inferred from chloroplast noncoding intergenic spacer *trnH-psbA* sequences of *Festuca/Lolium* exemplars using maximum parsimony and Bayesian inference. (I) The MP majority rule consensus tree with the numbers at nodes indicating bootstrap values  $\geq 50\%$ . (II) The 50% majority rule consensus tree from the Bayesian inference with the numbers at nodes indicating Bayesian posterior probability values  $\geq 80\%$ .