

Supplementary Information

Additional file 1:

Fig. S1. Phylogenetic relationships in of *Aquilegia* obtained from an maximum likelihood analysis of the 78-protein-coding gene dataset. Numbers above branches are bootstrap values ($BS \geq 50\%$) and posterior probabilities ($PP \geq 0.50$), “-” indicates the nodes not supported.

Fig. S2. Phylogenetic relationships in of *Aquilegia* obtained from an maximum likelihood analysis of the 15-introns dataset. Numbers above branches are bootstrap values ($BS \geq 50\%$) and posterior probabilities ($PP \geq 0.50$), “-” indicates the nodes not supported.

Fig. S3. Phylogenetic relationships in of *Aquilegia* obtained from an maximum likelihood analysis of the concatenated dataset of 117 intergenic spacer regions. Numbers above branches are bootstrap values ($BS \geq 50\%$) and posterior probabilities ($PP \geq 0.50$), “-” indicates the nodes not supported.

Fig. S4. Phylogenetic relationships in of *Aquilegia* obtained from an maximum likelihood analysis of the concatenated dataset of 15 introns and 117 intergenic spacer regions. Numbers above branches are bootstrap values ($BS \geq 50\%$) and posterior probabilities ($PP \geq 0.50$), “-” indicates the nodes not supported.

Fig. S5. Phylogenetic relationships in of *Aquilegia* obtained from an maximum likelihood analysis of the large single-copy region dataset. Numbers above branches are bootstrap values ($BS \geq 50\%$) and posterior probabilities ($PP \geq 0.50$), “-” indicates the nodes not supported.

Fig. S6. Phylogenetic relationships in of *Aquilegia* obtained from an maximum likelihood analysis of the inverted repeat region dataset. Numbers above branches are bootstrap values ($BS \geq 50\%$) and posterior probabilities ($PP \geq 0.50$), “-” indicates the

nodes not supported.

Fig. S7. Phylogenetic relationships in of *Aquilegia* obtained from an maximum likelihood analysis of the small single-copy region dataset. Numbers above branches are bootstrap values ($BS \geq 50\%$) and posterior probabilities ($PP \geq 0.50$), “-” indicates the nodes not supported.

Fig. S8. Comparison of structure variations (SVs) in the large single-copy region of 21 representative species of *Aquilegia*. The left side shows the SVs of the taxa. LSC, large single-copy; sIR, short inverted repeat.

Fig. S9. Phylogenetic relationships in *Aquilegia* obtained an maximum likelihood (ML) analysis of the concatenated dataset of the ten identified hypervariable regions. Numbers above branches are bootstrap values ($BS \geq 50\%$) and posterior probabilities ($PP \geq 0.50$), “-” indicates the nodes not supported. An ML phylogram is shown in the upper left hand corner.

















