

1R    2R    3R    SF    F    SF    3R    2R    1R

Figure 1. Phylogenetic tree of the 30 Japanese taxa of the genus *Phyllanthus* based on the combined analysis of the *trnK* and *trnT-trnK* regions. The tree is rooted with *Phyllanthus* *sp.* (1) as the outgroup. The numbers at the nodes indicate the bootstrap values for the *trnK* and *trnT-trnK* regions, respectively. The taxa are listed on the left and right sides of the tree, with their corresponding numbers in parentheses. The tree is divided into two main clades, each containing 15 taxa. The left clade includes taxa 1 through 15, and the right clade includes taxa 16 through 30. The tree is rooted with *Phyllanthus* *sp.* (1) as the outgroup. The numbers at the nodes indicate the bootstrap values for the *trnK* and *trnT-trnK* regions, respectively. The taxa are listed on the left and right sides of the tree, with their corresponding numbers in parentheses. The tree is divided into two main clades, each containing 15 taxa. The left clade includes taxa 1 through 15, and the right clade includes taxa 16 through 30.