

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

Figure 1 displays the phylogenetic tree of the 30 Japanese species of the genus *Stenobothrus*, based on a combined analysis of 18S and 28S rDNA sequences. The tree is rooted with *Stenobothrus* sp. 1 as the outgroup. The scale bar represents 0.1 substitutions per site. The tree is divided into two main clades, 27 and 28, which are further subdivided into smaller groups. The species names and their corresponding institutions are listed on the left and right sides of the tree. The tree shows a clear separation between the two main clades, with clade 27 containing 15 species and clade 28 containing 15 species. The tree is rooted with *Stenobothrus* sp. 1 as the outgroup. The scale bar represents 0.1 substitutions per site. The tree is divided into two main clades, 27 and 28, which are further subdivided into smaller groups. The species names and their corresponding institutions are listed on the left and right sides of the tree. The tree shows a clear separation between the two main clades, with clade 27 containing 15 species and clade 28 containing 15 species.