

**Phylogenetic Relationship among the Bumblebees (Hymenoptera: Apidae)
Common in Korea Inferred from Mitochondrial 16S rRNA Sequences**

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Obiectives

We provide a molecular study intending to derive an estimate of the relationships within the genus *Bombus*, 10 species which span 6 subgenera common collected from several regions of Korea and *B. terrestris* imported from several foreign countries for pollination using a portion of mitochondrial 16S ribosomal RNA.

Materials and Methods

Materials - insect: bumblebee, 10 species collected from several regions of Korea and *B. terrestris* imported from three countries

Methods - Bee samples and DNA extraction, PCR amplification and sequencing of nucleotides, Analysis of DNA sequences and phylogenetic analysis by PAUP and PHYLIP

Results and Discussion

The genetic divergence and phylogenetic relationships were analyzed from ten species of bumblebees (Bombini, Apidae), collected from several regions of Korea and *B. terrestris* imported from several foreign countries for pollination using a portion of mitochondrial 16S ribosomal RNA. The length of the gene ranged from 496bp to 508bp and sequence divergence ranged from 1.7% to 16.4% among 11 species. There was no intraspecific variation except for *B. terrestris* (two haplotypes among three individuals). According to the phylogenetic tree derived from parsimony and maximum-likelihood analysis, *B. terrestris* was clustered with *B. hypocrita sapproensis* with 47% and 53% bootstrap values. These two species made a subgroup with *B. ignitus* showing 100% and 97% bootstrap values. *B. consobrinus wittenburgi* and *B. koreanus* clustered in a subgroup with strong value of confidence (100% and 99% bootstrap values). *B. ardens ardens* and *B. modeatus* also clustered together with 99% and 95% of bootstrap values. With the increasing number of bumblebee, more robust bumblebee phylogeny will be obtained.

Table 3. Pairwise comparisons of 16S rRNA gene sequences among 11 bumble bees

	1	2	3	4	5	6	7	8	9	10	11
1. <i>B. a. ardens</i> (146)	-	0.106	0.114	0.118	0.106	0.100	0.131	0.133	0.135	0.114	0.197
2. <i>B. c. wittenburgi</i> (B9)	55	-	0.110	0.124	0.017	0.151	0.104	0.081	0.127	0.122	0.181
3. <i>B. h. sapporoensis</i> (B1)	59	57	-	0.062	0.118	0.153	0.131	0.129	0.143	0.058	0.191
4. <i>B. ignitus</i> (B66)	61	64	32	-	0.124	0.151	0.116	0.124	0.137	0.056	0.187
5. <i>B. koreanus</i> (B23)	55	9	61	64	-	0.149	0.102	0.077	0.127	0.124	0.178
6. <i>B. modeatus</i> (B30)	52	78	79	78	77	-	0.172	0.166	0.160	0.160	0.226
7. <i>B. s. albidopleuralis</i> (B32)	68	54	68	60	53	89	-	0.106	0.137	0.131	0.195
8. <i>B. ussurensis</i> (B12)	69	42	67	64	40	86	55	-	0.131	0.120	0.189
9. <i>P. coreanus</i> (B20)	70	66	74	71	66	83	71	68	-	0.143	0.203
10. <i>B. terrestris</i> (B39, B51)	59	63	30	29	64	83	68	62	74	-	0.199
11. <i>X. a. circumvolans</i> (B33)	102	94	99	97	92	117	101	98	105	103	-

Numbers above the diagonal are mean distance values; numbers below the diagonal are absolute distance values.

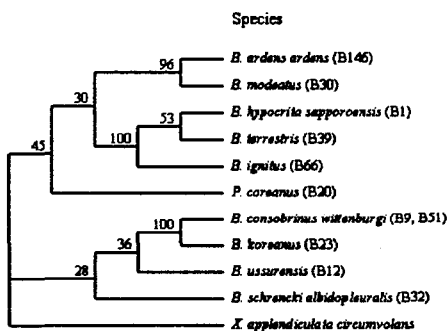


Fig. 1. PAUP analysis of mitochondrial 16S rRNA sequences using mtDNA sequence of 12 bees obtained from this study.

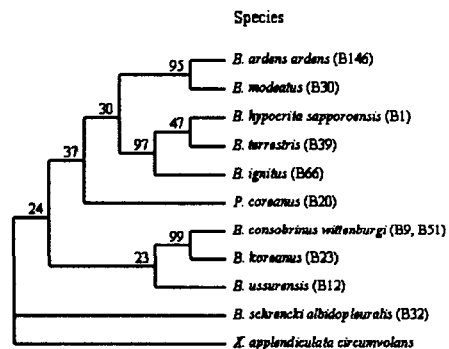


Fig. 2. PHYLIP analysis of mitochondrial 16S rRNA sequences using mtDNA sequence of 12 bees obtained from this study.

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