

Phylogenetic Relationships of *Dorcus koreanus* Jang and Kawai, 2008 (Coleoptera, Lucanidae): Species or Subspecies?

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Dorcus koreanus Jang and Kawai, 2008 was recently described as a valid species in Haenam, South Korea, based on morphology. However, the taxonomic position and relationships of this new species with the related species *Dorcus japonicus* and *Dorcus carinulatus* were not examined in detail. To address this issue, we evaluated the phylogenetic relationships of *D. koreanus* to its related species based on molecular analyses of mitochondrial 16S rRNA gene sequences. The molecular evidence suggested that *D. koreanus* and *D. carinulatus* are more closely related to each other than either is to *D. japonicus*. The genetic divergence between *D. koreanus* and *D. carinulatus* ranged from 1.2 to 1.6%, whereas that between *D. koreanus* and *D. japonicus* ranged from 9.0 to 9.2%. By comparing the range of nucleotide substitutions within Lucanidae, we determined that the sequence distance between *D. koreanus* and *D. carinulatus* is smaller than that for required for species-level distinction. Therefore, we reduce *D. koreanus* to subspecies rank, as *Dorcus carinulatus koreanus* stat. nov.

Key words: taxonomy, Lucanidae, *Dorcus*, *Dorcus carinulatus koreanus* stat. nov., phylogenetic relationship, 16S rRNA, Korea

INTRODUCTION

The *Dorcus velutinus* species group is a small group in the genus *Dorcus* of the family Lucanidae. The congeners of this group are easily distinguished from other species of *Dorcus* by the following characteristics: generally small mandibles in males, covering of brownish earthy matter on the dorsal surface, and short and erect tufted setae in the dorsal area (Nakane and Makino, 1985). The congeners include six species: *D. velutinus* Thomson, 1862 and *D. ursulus* Arrow, 1938 are known in northeastern India, Myanmar, Thailand, and Bhutan; *D. carinulatus* Nagel, 1941 was described from Taiwan; *D. taiwanicus* and *D. japonicus* were recognized by Nakane and Makino (1985) from Taiwan and Amami Island, Japan, respectively; and most recently, *D. koreanus* Jang and Kawai, 2008 was described from South Korea.

These were several problems with this species group in previous taxonomic studies, including taxonomic changes in generic and specific status, and several misidentifications caused by species similarity (Miwa, 1927; Nagel, 1941; Benesh, 1960; Takai, 1981; Nakane and Makino, 1985; Maes, 1992; Mizunuma and Nagai, 1994; Yang and Chang,

1997; Kim and Kim, 1998; Li, 2004). However, Nagai and Fujii (2005) addressed these issues, using morphological characters and considering the history, geographical distribution, and specific status of each species. They concluded that five species, except for *D. koreanus*, within the *D. velutinus* species group should be regarded as valid species. Moreover, Araya and Hosoya (2005) reconfirmed four species of the *D. velutinus* species group (they did not analyze *D. ursulus*) as valid species based on the results of a molecular phylogenetic study using the mt16S rRNA gene sequence, supporting the findings of Nagai and Fujii (2005).

Regarding the *Dorcus velutinus* species group in Korea, Masui (1942) first reported *D. velutinus* from Mt. Bogaesan in the middle of the Korean Peninsula, but Kim and Kim (1998) regarded this record as a misidentification of *D. taiwanicus*, and also identified 10 individuals collected from three localities in central and southern Korea as *D. taiwanicus*. Kim (2000) regarded *D. taiwanicus* as the only member of the *Dorcus velutinus* species group on the Korean fauna; however, Jang and Kawai (2008) recently described *D. koreanus* based on a collection from a population at Haenam, southern Korea. Therefore, two species have been recorded in Korea: *D. taiwanicus* and *D. koreanus*.

In 2005, before Jang and Kawai (2008) described *D. koreanus*, we had already obtained seven interesting specimens from Haenam. In our initial morphological comparison with members of the *D. velutinus* species group, we temporarily classified these specimens as belonging to an unde-

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terminated species. They had several ambiguous or overlapping features shared by *D. japonicus* and *D. carinulatus*, although our Korean specimens were more similar in appearance to *D. japonicus*. In 2006, to confirm the Korean voucher specimens, we examined the six specimens of *D. taiwanicus* studied by Kim and Kim (1998) and Kim (2000); of these, three specimens collected from Haenam were the same as our undetermined species, and were not *D. taiwanicus*. We also examined the male holotype and a female paratype of *D. koreanus* in October 2008 and confirmed that our seven specimens were identical to the type specimens.

As mentioned above, in our preliminary examination of *D. koreanus*, we had entertained doubts over the taxonomic status of *D. koreanus* and wondered about the evolutionary relationship of this species within its congeners. Other taxonomic tools, such as molecular analysis, were required to prevent erroneous results due to confusion over morphological similarities among apparently related species. Fortunately, two previous phylogenetic studies (Hosoya et al., 2001; Hosoya and Araya, 2005) based on inferences from mitochondrial (mt) 16S rRNA gene sequences had elucidated the inter- and intraspecific relationships within Lucanidae. However, it was necessary to determine a more precise systematic placement for the Korean lucanid species. In this study, we analyzed 16S mtrRNA gene sequence to determine the taxonomic position and species status of *D. koreanus* through comparisons with two related species, *D. japonicus* and *D. carinulatus*.

The molecular evidence suggested that *D. koreanus* has diverged from the *D. carinulatus* lineage, but does not merit species status. Therefore, *D. koreanus* should be replaced as a subspecies, *Dorcus carinulatus koreanus* stat. nov., based on the interpretation of our partial molecular analyses. Here we also discuss a hypothetical speciation pathway for this subspecies.

MATERIAL AND METHODS

Morphology

We obtained seven adult specimens of *D. koreanus* from a decayed *Celtis sinensis* Persson from Mt. Duryunsan, Haenam, JN, South Korea. These specimens were topotypes for *D. koreanus*. All specimens were placed in individual bottles containing 80% ethanol and stored in a freezer at -10°C before morphological examination. The external and internal morphological characteristics were examined under a stereoscopic microscope (Leica MZ16A or MZ 6). Photographs were taken with a Nikon D70S and 14.2 color mosaic digital camera system. Abbreviations for the Korean provinces used in this study are GG (Gyeonggi-do) and JN (Jeonlanam-do). Specimens were deposited in the Seodaemun Museum of Natural History, Seoul, and in the insect collection of the Applied Entomology Division, Department of Agricultural Biology, National Academy of Agricultural Science (NAAS), Suwon, Korea.

DNA extraction, amplification, and sequencing

Genomic DNA was extracted from thoracic tissues, which were obtained in the process of removing the male and female genitalia, by using a QIAamp DNA Mini Kit in accordance with the manufacturer's instructions (Qiagen, Germany). Polymerase chain reaction (PCR) amplification (20 μl) of the 16S rRNA gene was performed by using AccuPower PCR PreMix (Bioneer, Korea) with three previously described primers, 16SB, 16SD, and 16SC (Hosoya et al., 2001). Product yield was monitored by 0.7% agarose gel electrophoresis, and successful amplicons were purified by using a

QIAquick PCR Purification Kit (Qiagen, Germany). DNA sequencing was performed with an ABI 3730xl 96-capillary automated DNA analyzer (Applied Biosystems, USA) and the PCR primers. The initial data set included nine 16S sequences from Hosoya et al. (2001) and Hosoya and Araya (2005), plus five sequences we obtained (GenBank accession nos. GQ380445–GQ380449) (Table 1).

Sequences were aligned in MEGA 4.0 using ClustalW (Tamura et al., 2007). Gaps and regions of uncertain alignment were eliminated from the data matrix, and aligned sequences 652 bp long were analyzed. The partial 16S region analyzed corresponded to positions 13185–13864 (including gaps) in the *Drosophila yakuba* (Drosophilidae, Diptera) mitochondrial genome (Clary and Wolstenholme, 1985).

Table 1. List of species for which 16S sequences were determined in this study or obtained from Genbank (*, Araya and Hosoya 2005).

Species	Locality	GenBank
		Accession no.
<i>D. velutinus</i> DV2m	Chiang Mai, Thailand	GQ380445
<i>D. velutinus</i> DV1f	Chiang Mai, Thailand	GQ380446
<i>D. velutinus</i>	Chiang Mai, Thailand	AB236866*
<i>D. taiwanicus</i>	Nantou, Taiwan	AB236865*
<i>D. taiwanicus</i> DT4f	Nantou, Taiwan	GQ380447
<i>D. japonicus</i>	Kagoshima, Japan	AB236863*
<i>D. carinulatus</i>	Taichung, Taiwan	AB236864*
<i>D. carinulatus koreanus</i> DC1	Haenam, Korea	GQ380448
<i>D. carinulatus koreanus</i> DC2	Haenam, Korea	GQ380449
<i>D. rectus rectus</i>	Aomori, Japan	AB178295*
<i>D. curvidens binodulosus</i>	Yamanashi, Japan	AB178292*
<i>D. titanus pilifer</i>	Kyoto, Japan	AB178293*
<i>D. titanus okinawanus</i>	Okinawa, Japan	AB178294*
<i>Nigidius lewisi</i>	Wakayama, Japan	AB178310*

Phylogenetic analyses

We used the 16S sequence from *Nigidius lewisi* Boileau, 1905 (accession no. AB178310) as the outgroup and analyzed seven species in genus *Dorcus*, including the *D. velutinus* species group, in the ingroup (Table 1).

To examine phylogenetic relationships, neighbor joining (NJ) analyses (Saitou and Nei, 1987) were carried out with MEGA 4.0 (Tamura et al., 2007). Distances were calculated by using Kimura's two-parameter model (Kimura, 1980), selected according to the empirical guidelines of Nei (1991, 1996). Branch support values for clades were estimated by bootstrapping (Bt; 1000 replicates; Felsenstein, 1985) and the interior branch test (Ibt; 1000 replicates; Rzhetsky and Nei, 1992).

A maximum parsimony (MP) analysis was performed with NONA version 2.0 (Goloboff, 1993) in conjunction with WinClada version 1.00.08 (Nixon, 2002), using a heuristic search (search options: hold = 10000; mult*N = 1000; hold/ = 100). Bremer support (Bs; Bremer, 1994) values were calculated in NONA with the following commands: hold 32760; sub 16; find*.

For maximum likelihood (ML), the best-fit model (TrN + I + G; Lset Base = [0.3428 0.0468 0.1742], Nst = 6, Rmat = [1.0000 7.2921 1.0000 1.0000 7.5817], Rates = gamma, Shape = 0.5226, Pinvar = 0.3529) was selected by hierarchical likelihood ratio tests (hLRTs) in Modeltest 3.7 (Posada and Crandall, 1998). The ML analysis was conducted by using heuristic searches in PAUP* 4.0b10. Nodal support for clades was assessed by analysis of 1000 bootstrap replicates.

RESULTS

Morphological comparison within the *D. velutinus* species group

This species group can easily be separated into two subgroups based on mandibular characters. The *D. carinulatus* subgroup, consisting of *D. carinulatus*, *D. koreanus*, and *D. japonicus*, can be identified by the unidentate apex of the

mandible. The *D. velutinus* subgroup, composed of *D. ursulus*, *D. velutinus*, and *D. taiwanicus*, is characterized by the bidentate apex of the mandible (Nakane and Makino, 1985; Nagai and Fujii, 2005). Each species in the *D. carinulatus* subgroup can be distinguished by the following diagnostic characters: the shape of the mandibles, clypeus, nodules in front of the eyes, pronotum, and aedeagus. *Dorcus koreanus* and *D. japonicus* appear to be more similar to each other

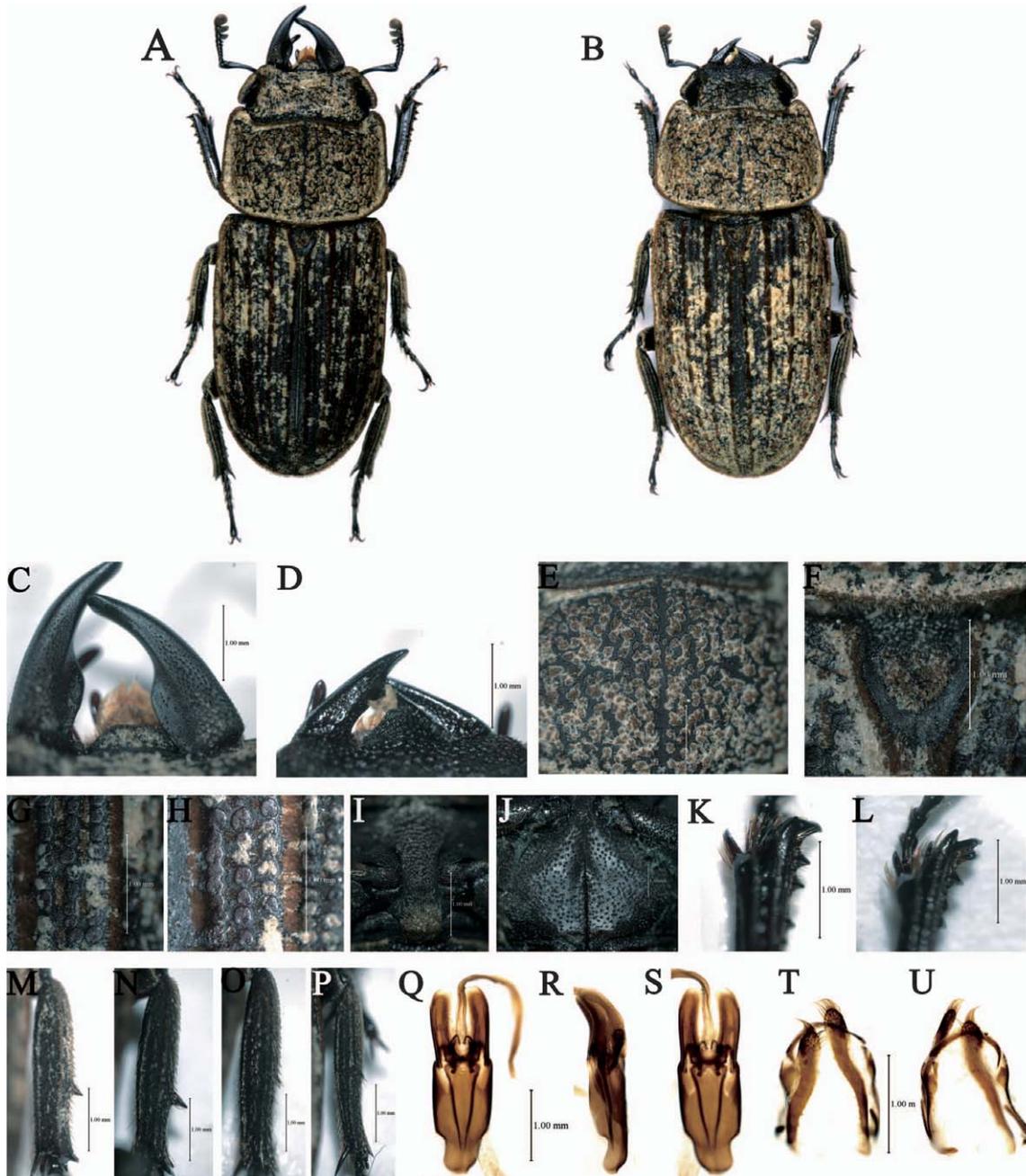


Fig. 1. *Dorcus carinulatus koreanus*. (A, B) Habitus of adults (A, male; B, female). (C, D) Clypeus and mandibles in dorsal view (C, male; D, female). (E) Median longitudinal line and distribution of punctures with tufted setae on the pronotum, in dorsal view. (F) Scutellum. (G, H) Interval punctuation on the elytra (G, anterior part; H, posterior part). (I) Prosternal process in ventral view. (J) Median part of the metasternum in ventral view. (K, L) Anterior apex of the right fore tibia in dorsal view (K, male; L, female). (M, N) Right middle tibia in dorsal view (M, male; N, female). (O, P) Right hind tibia (O, male; P, female). (Q–S) (same scale) Male genitalia (Q, ventral view; R, lateral view; S, dorsal view). (T, U) (same scale) Female genitalia (T, ventral view; U, dorsal view).

than to *D. carinulatus*, based on a number of characters, such as the mandibular apex and inner expansion (lobed broadly to one-third the distance from the base, inner margin slightly arched, pronotal disk with smooth median longitudinal line). However, *D. koreanus* is more similar to *D. carinulatus* rather than to *D. japonicus* in the indistinctly sinuate anterior margin of the clypeus. *Dorcus koreanus* (Fig. 1) is slightly different in several features from the two species above: the lobed inner expansion of the mandible, a small upper tooth present at the base of the mandibles in males, development of nodules in front of the eyes, and the distinct shape of the aedeagus (Nagai and Fujii, 2005; Jang and Kawai, 2008).

Molecular phylogenetic analysis

The final data set, including 652 selected sites, for the 14 sequences for stag beetles analyzed in the ingroup in this study were conserved at 457 sites, variable at 195 sites, and parsimony-informative at 163 sites. The average nucleotide composition of these 16S rRNA fragments was T, 40.2%; C, 7.6%; A, 35.0%; and G, 17.2%. The A + T content showed a maximum value of 75.7%. The transition/transversion (TR/TV) rate ratios were $k_1 = 5.625$ (purines) and $k_2 = 10.421$ (pyrimidines), and the overall TR/TV bias was $R = 1.854$, as determined with MEGA 4.0.

Phylogenetic analyses were performed using the NJ, MP, and ML methods (Figs. 2–4). All methods yielded mostly similar phylograms, and the only difference was observed in the position of the *D. titanus* and *D. curvidens* clade in the ML tree (Fig. 4). Notably, all trees strongly supported the *D. velutinus* species group as monophyletic. These results were consistent with those of previous studies (Araya and Hosoya, 2005).

Additional sequence data (DV1, DV2m, DT4f, DC1, and DC2) (Table 1) for three species in this study enabled comparison of the genetic divergence at the intra- and interspecific levels (Table 2). The intraspecific divergence between sequences for *D. velutinus*, *D. taiwanicus*, and *D. koreanus* was 0.6, 0.2, and 0.5%, respectively. The degree of divergence at the interspecific level was markedly higher, ranging from 5.1 to 22.6%. However, the divergence between *D. koreanus* and *D. carinulatus* ranged from 1.2 to 1.6%. By comparison, divergence between the two subspecies of *D. titanus* defined by traditional taxonomy ranged up to 1.6%.

All phylograms inferred from the NJ, MP, and ML analyses strongly supported the *D. carinulatus* subclade (*D. carinulatus* + *D. koreanus*) as a monophyletic group with high branch support values (Bt/lbt/Bs = 100/99/14) (Figs. 2–4). Consequently, *D. koreanus* and *D. carinulatus* are more closely related to each other than either is to *D. japonicus*.

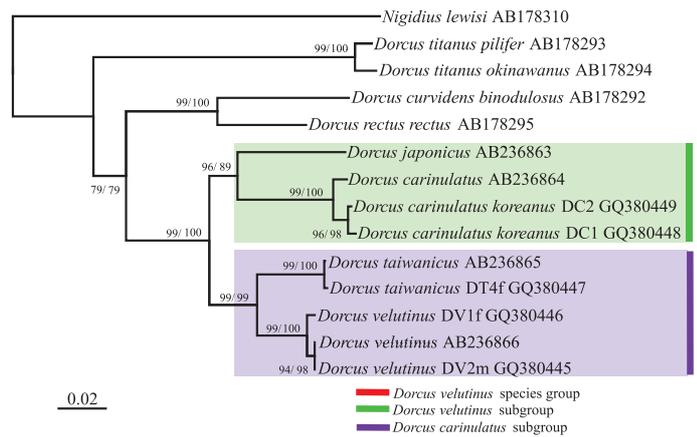


Fig. 2. Neighbor joining (NJ) tree based on Kimura two-parameter distances among partial sequences (652 bp long) of the 16S mtrRNA gene from *Dorcus* species. The first and second numbers for each node indicate values from the interior branch test (lbt) and the bootstrap (Bt) analysis (1000 replicates), respectively. The scale bar at the bottom indicates branch length in substitutions per site.

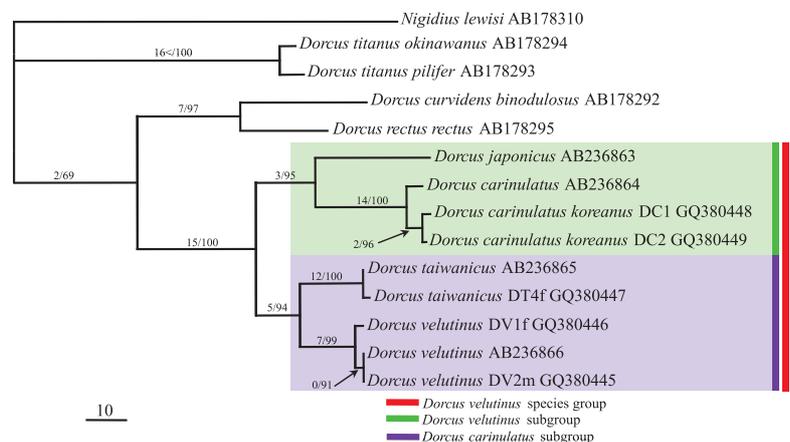


Fig. 3. Maximum parsimony (MP) tree based on an analysis of partial sequences (652 bp long) of the 16S mtrRNA gene performed with NONA in WinClada (CI = 0.76, RI = 0.78, RC = 0.59). The numbers for each node indicate the Bremer support and bootstrap values (1000 replicates), respectively. The scale bar at the bottom indicates branch length in number of mutational steps.

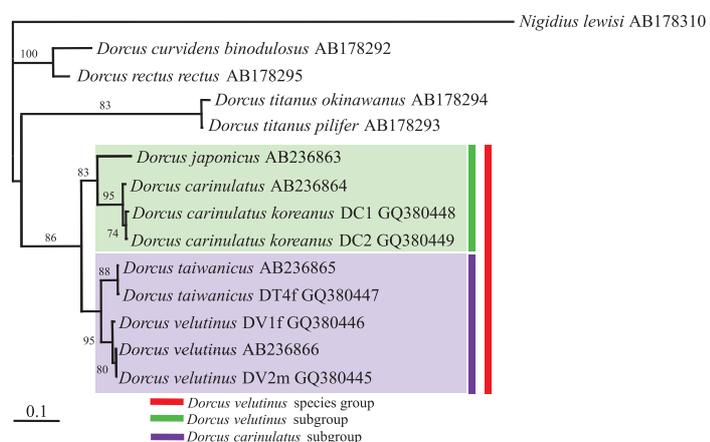


Fig. 4. Maximum likelihood (ML) tree based on an analysis of partial sequences (652 bp long) of the 16S mtrRNA gene implemented with the TrN + I + G model in PAUP*, using heuristic searches and bootstrapping (1000 replicates). The numbers for internal nodes are bootstrap percentages. The scale bar at the bottom indicates branch length in substitutions per site.

Table 2. Evolutionary sequence divergence expressed as the number of nucleotide substitutions per site (Kimura two-parameter model) in the 16S mt rRNA gene sequences (652 bp) analyzed.

	1	2	3	4	5	6	7	8	9	10	11	12	13
1. <i>Dorcus velutinus</i> AB236866													
2. <i>Dorcus velutinus</i> DV1f GQ380446	0.006												
3. <i>Dorcus velutinus</i> DV2m GQ380445	0.000	0.006											
4. <i>Dorcus taiwanicus</i> AB236865	0.051	0.051	0.051										
5. <i>Dorcus taiwanicus</i> DT4f GQ380447	0.053	0.053	0.053	0.002									
6. <i>Dorcus carinulatus</i> AB236864	0.104	0.102	0.104	0.104	0.102								
7. <i>Dorcus carinulatus koreanus</i> DC1GQ380448	0.106	0.104	0.106	0.104	0.106	0.016							
8. <i>Dorcus carinulatus koreanus</i> DC2GQ380449	0.104	0.102	0.104	0.102	0.104	0.012	0.005						
9. <i>Dorcus japonicus</i> AB236863	0.097	0.095	0.097	0.104	0.106	0.090	0.092	0.090					
10. <i>Dorcus curvidens binodulosus</i> AB178292	0.170	0.174	0.170	0.176	0.174	0.173	0.180	0.179	0.180				
11. <i>Dorcus rectus rectus</i> AB178295	0.147	0.151	0.147	0.161	0.159	0.153	0.163	0.161	0.170	0.090			
12. <i>Dorcus titanus okinawanus</i> AB178292	0.205	0.206	0.205	0.214	0.212	0.218	0.222	0.222	0.229	0.212	0.201		
13. <i>Dorcus titanus pilifer</i> AB178293	0.207	0.207	0.207	0.208	0.206	0.216	0.220	0.220	0.226	0.207	0.195	0.016	
14. <i>Nigidius lewisi</i> AB178310	0.273	0.273	0.273	0.275	0.277	0.275	0.284	0.282	0.300	0.294	0.280	0.297	0.300

DISCUSSION

An interesting lucanid population belonging to the *D. velutinus* species group was collected from Haenam in southern Korea and has been treated as *D. japonicus* or *D. taiwanicus* through the websites offered by the Korean insect manias during the past few years (<http://cafe.daum.net/Callipogon/EfNY/665>). We attempted to correctly identify seven specimens first obtained in 2005. However, identification was difficult due to a number of ambiguous or overlapping features between *D. japonicus* and *D. carinulatus*. Jang and Kawai (2008) recently described this Korean population as a new species, *D. koreanus*, based on morphological comparisons. However, this characterization did not include evaluation of the hierarchical relationship between *D. koreanus* and related species. The authors suggested that *D. koreanus* is distinct from the above two related species based on three morphological features: 1) the presence of a small upper tooth at the base of the mandibles in males, 2) the thicker, continuous longitudinal rows with short tufts distributed to two-thirds the length of the elytra, and 3) the slightly emarginate apical margin of the clypeus in males. Their results did not clearly reveal the taxonomic relationship between *D. koreanus* and related species. In addition, their analysis caused confusion regarding the relationships between species. These problems prompted us to question whether the above three species could be classified by homologous characters.

In this study, we attempted to reconstruct the relationships among species by using a 16S mtrRNA gene data set constructed for a previous phylogenetic study of Lucanidae (Araya and Hosoya, 2005). Our results suggest that *D. japonicus* and *D. carinulatus* diverged earlier than *D. carinulatus* and *D. koreanus*. Furthermore, our molecular analysis suggests that the morphological similarities between *D. koreanus* and *D. japonicus* should be considered homoplastic characters.

Our results also raise questions as to how the evolutionary divergences occurred. We can only make inferences based on paleogeography involving eustatic sea level changes in the East China Sea and the Yellow Korean Sea

during glacial and postglacial periods (Park, 1992a, b; Park et al., 1989; Uehara and Saito, 2003). *Dorcus japonicus* is thought to have diverged from a common ancestor as the result of geographic isolation when the Japanese archipelago separated from the Eurasian continent. This common ancestral species of *D. carinulatus* and *D. koreanus* may have been widely distributed from Taiwan to Korea through exposure of the continental shelf of the Yellow Sea during the Ice Age, but not in Japan. Subsequent isolation due to rising sea levels during interglacial periods may have divided ancestral population into two distinct populations adapted to their respective environmental conditions.

Hosoya et al. (2001) and Hosoya and Araya (2005) inferred phylogenetic relationships in Lucanidae using 16S sequence data and based their taxonomic system on the scheme of Mizunuma and Nagai (1994). According to Hosoya and Araya (2005), the degree of genetic divergence at the subspecific level, with subspecies status based on morphology, ranged from 0.6 (*Neolucanus protogenetivus* subsp.) to 2.7% (*Ceruchus lignarius* subsp.). In this study, the degree of genetic divergence shown by *D. koreanus* relative to known sequence divergences in Lucanidae justifies reducing this species to subspecific rank, as *D. carinulatus koreanus* stat. nov.

REDESCRIPTION AND REPLACEMENT OF *DORCUS KOREANUS* JANG AND KAWAI 2008

Family Lucanidae MacLeay, 1819
Subfamily Lucaninae MacLeay, 1819
Genus *Dorcus* MacLeay, 1819

Dorcus carinulatus koreanus (Jang and Kawai, 2008) stat. nov.

(Figs. 1A–U)

Dorcus koreanus Jang and Kawai, 2008, 103–105. (By the original designation.)

Specimens examined. Topotypes: 3 ♂♂, 4 ♀♀, Mt. Duryunsan, Haenam, JN, Korea, 20 Aug. 2005, K. T. Park. Host plant: *Celtis sinensis* Persson.

Male body. 18.9 mm long, including mandibles, 16.5 mm long without mandibles, 7.5 mm wide, elongate oblong, with parallel sides, moderately convex above and beneath,

with comparatively short antennae and legs (Fig. 1A). Surface wholly black, opaque with pale brownish earthy matter generally covering the dorsal surface, giving the body a rusty color. Dorsal surface with large, distinct punctures ocellated with short, erect, brownish tufted setae, generally confluent or irregular in shape; ventral surface with large and small punctures, rather sparse, with short, yellowish, scale-like hairs. Head weakly convex at base, anterior median part suddenly depressed and sloping to apex; median surface with two small, indistinct tubercles; eyes distinctly large, lustrous, almost surrounded by elongate, weakly curved ocular canthus; mandible slightly arched inward near the middle, anterior part simple, broad internally at base, with a small upper tooth at base; clypeus trapezoidal, 3.77 times as wide as long, weakly narrowing toward apex, anterior margin weakly sinuate. (Fig. 1C). Antennae short; 1st antennomere as long as other antennomeres; 2nd 1.25 times as long as wide; 3rd to 7th transverse, a little wider than long; 7th and 8th with weakly elongate inner margins anterolaterally; 8th to 10th transversely broadened, clubbed, lateral inner margins distinctly stout, densely covered with very short sensory hairs; length/width (mm) of each antennomere from 2nd to 10th as follows: 0.25/0.2: 0.15/0.2: 0.125/0.225: 0.1125/0.25: 0.125/0.325: 0.2/0.375: 0.25/0.575: 0.2775/0.6: 0.475/0.6. Pronotum trapezoid, 1.52 times as wide as long, widest near the posterior; edges of pronotal margin entirely surrounded by distinct, dense tufts and clearly depressed, emarginate; pronotal disc moderately convex above, with smooth, longitudinal median line (Fig. 1E); anterior margin clearly arched outward; lateral margins parallel and gradually narrowing toward anterior; posterior margin slightly rounded. Scutellum triangular, 1.14 times as wide as long, gradually arching and narrowing toward apex; punctures small, with simple, rather recumbent setae, without ocellate, confluent punctuation (Fig. 1F). Elytra stout, convex above, 1.50 times as long as wide, anterior margin roundly curving inward; lateral margins parallel from base to two thirds the length and gradually rounded toward posterior; five longitudinal rows of distinct, short, reddish-brown tufts; each interval irregularly and closely punctured, punctures of anterior part rounded (Fig. 1G) but punctures from median to posterior smaller shaped like a horse's hoof (Fig. 1H). Prosternum minutely punctured in medial part, with short, scale-like setae; puncture size gradually increases toward sides; prosternal process slightly convex above but ventral disc flattened, apex truncate and covered with sparse tufts of setae (Fig. 1I). Metasternum flattened in middle, with sparse, minute punctures; sides covered with larger, rougher punctures with long hairs (Fig. 1J). Front tibia with a short terminal fork expanding outward (Fig. 1K); middle tibia with a large, distinct spine in middle laterally (Fig. 1M); hind tibia with a small, short spine in middle laterally (Fig. 1O).

Genitalia rather cylindrical and stout; basal pieces parallel; paramere shorter than basal piece, weakly bent inward and gradually rounding to apex in dorsal and ventral views, clearly bent ventrally from middle and gradually narrowing in lateral view; everted internal sac 1.8 times as long as genitalia, slender; two accessory glands branch from basal half, apex of median everted internal sac weakly expanded and divided.

Female. Sexually dimorphic; differs from male as follows: mandible distinctly shorter than in male, grooved in dorsal view (Fig. 1D), with a small triangular internal tooth growing from inner edge of ventral apical part; clypeus smaller and narrower than in male; pronotum more distinctly arched and narrower (Fig. 1B) than in male; fore tibia with three short, separate teeth extending outward in dorsal view (Fig. 1L); middle tibia with a larger spine (Fig. 1N) than in male; hind tibia very slightly bent outward. Female genitalia as in Fig. 1T–U; tergite IX separated from genital plate, posterior part elongate elliptical, with long hairs at apex and gradually becoming slender toward anterior apex.

Distribution. Korea (Haenam).

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