

Distributional Boundaries of the Geographic Races of
Damaster blaptoides (Coleoptera, Carabidae)
in Northeastern Japan as Deduced from
Mitochondrial ND5 Gene Sequences

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Abstract The phylogenetic relationships of the geographic races of *Damaster blaptoides* inhabiting Hokkaido and the northeastern Tōhoku district, respectively, are analysed using mitochondrial NADH dehydrogenase subunit 5 (ND5) gene sequences. The distributional boundaries of the races do not coincide with those settled for the subspecies. The phylogenetic trees suggest that *D. b. viridipennis* inhabiting north of the Yoneshirogawa–Mabechigawa (Y–M line) is consubspecific with *D. b. rugipennis* in Hokkaido, while that inhabiting south of the line is distinct either from the above race, or from *D. b. babaianus* distributed in the southern Tōhoku district. The trees also suggest that *D. b. rugipennis* in Hokkaido would have been established by invasion of *D. b. viridipennis* of the northern Tōhoku population through the past land-bridges between the Tsugaru Peninsula and Hokkaido.

Introduction

Damaster (s. str.) has been treated as a single species, *blaptoides*, consisting of seven to eight subspecies or geographic races (NAKANE, 1960; ISHIKAWA, 1991). According to these morphological studies, *D. b. rugipennis* and *D. b. viridipennis* are distributed in Hokkaido and in the northern Tōhoku district, respectively, separated by the Tsugaru Straits. The molecular phylogenetic analysis has shown that the distribution of *Damaster blaptoides* is tightly linked to the geohistory of the Japanese Islands. The *Damaster* ancestor first split into two lineages, eastern (E) and western (W), which were further divided into three [HKD (Hokkaido), NTK (northern Tōhoku) and STK (southern Tōhoku)] and five (KTO, CBU, KII, WJN and KYU) geographically linked sublineages (or races), respectively (SU *et al.*, 1998). SU *et al.* (1998) also found that the so-called *D. b. viridipennis* specimens from the northernmost localities in the Tōhoku district form a cluster HKD with *D. b. rugipennis* in Hokkaido, separated from

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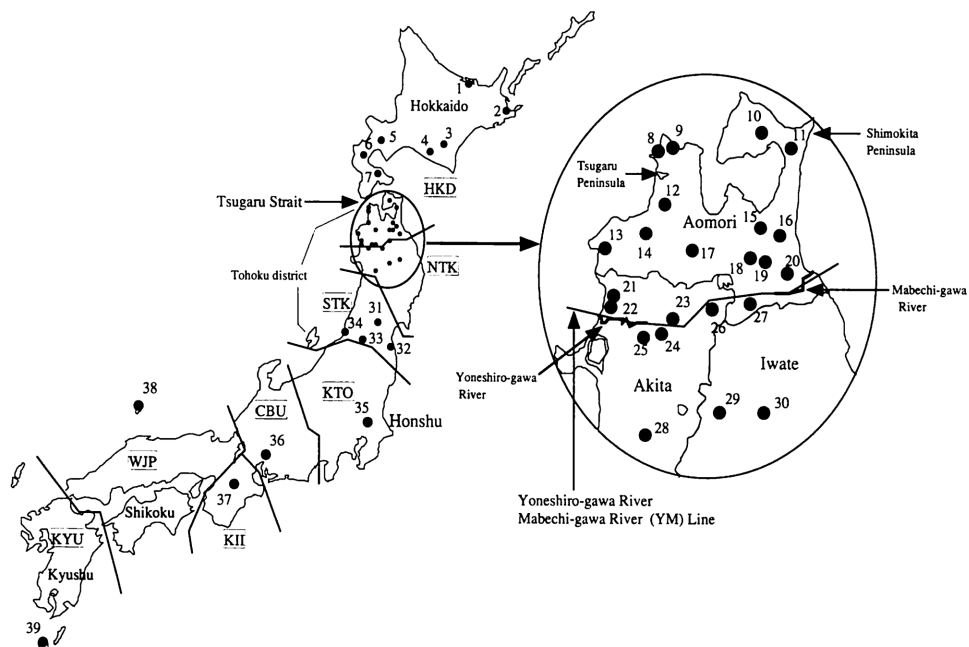


Fig. 1. Locality map of *Damaster* specimens used in this study. Locality numbers correspond to those shown in Table 1 and in Fig. 2. Three-letter codes showing the geographic races (settled by the molecular phylogeny) and the distributional boundaries of the races are according to SU *et al.* (1998).

what has been identified with *D. b. viridipennis* in NTK. Because of the shortage of specimens from the northern Tôhoku region, the distributional boundary between HKD and NTK has remained somewhat ambiguous. In this study, we have analysed the ND5 gene sequences of additional 15 specimens from this region and established a nearly complete distributional boundary between the two races.

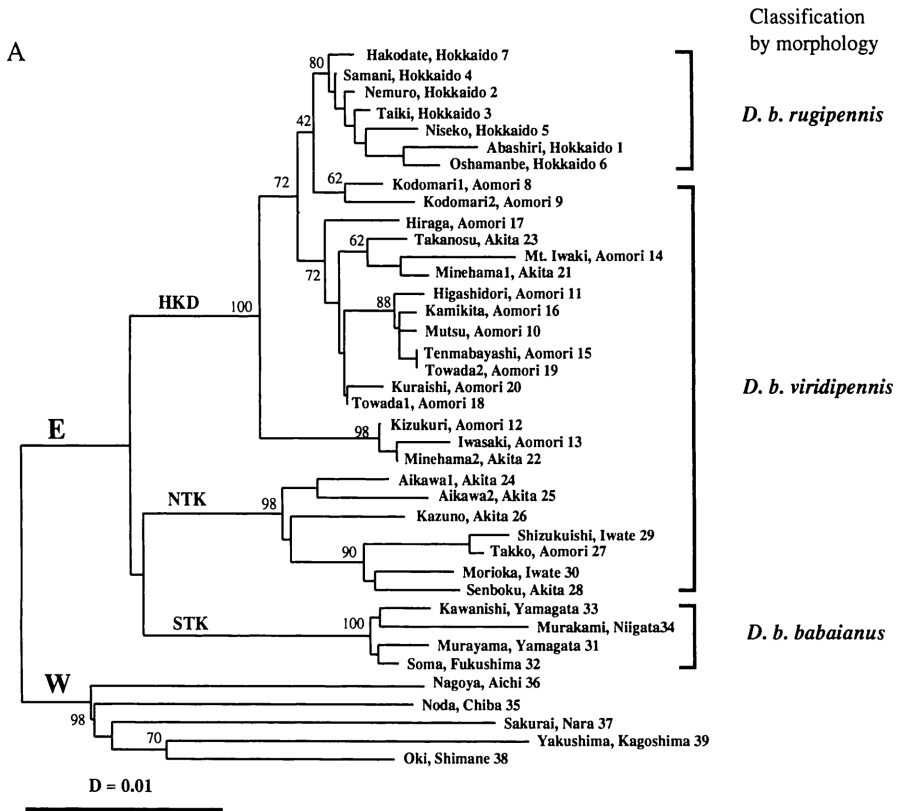
Materials and Methods

Fifteen specimens of *Damaster blaptoides* were collected from various parts of the northern Tôhoku district (Table 1 and Fig. 1), and were used for analyzing the ND5 gene sequences. A single individual from each locality was used for extraction of the total DNA from thorax muscle by proteinase K digestion (KIM *et al.*, 1999). For PCR amplification, sequencing and phylogenetic analyses, see SU *et al.* (1996 a, 1998). Phylogenetic trees were constructed by unweighted pair-group method with arithmetic mean (UPGMA) (KUMAR *et al.*, 1993), and neighbor-joining (NJ) method (SAITOU & NEI, 1987).

Table 1. List of specimens analysed.

Scientific name by morphology	Locality number	Locality	DDBJ/EMBL/GenBank Accession No.	
<i>D. b. rugipennis</i>	1*	Abashiri-Shi, Hokkaido	AB013858	
	2*	Nemuro-Shi, Hokkaido	AB013859	
	3*	Taiki-Cho, Hokkaido	D50351	
	4*	Samani-Cho, Hokkaido	AB013860	
	5*	Niseko-Cho, Hokkaido	AB013861	
	6*	Oshamanbe-Cho, Hokkaido	AB013862	
	7*	Hakodate-Shi, Hokkaido	AB013863	
<i>D. b. viridipennis</i>	8	Kodomari-Mura 1, Aomori Pref.	AB031304	
	9	Kodomari-Mura 2, Aomori Pref.	AB031305	
	10	Mutsu-Shi, Aomori Pref.	AB031306	
	11*	Higashidori-Mura, Aomori Pref.	AB013864	
	12*	Kizukuri-Cho, Aomori Pref.	AB013865	
	13*	Iwasaki-Mura, Aomori Pref.	AB013866	
	14*	Iwaki-Cho, Aomori Pref.	D50428	
	15	Tenmabayashi-Mura, Aomori Pref.	AB031307	
	16	Kamikita-Cho, Aomori Pref.	AB031308	
	17	Hiraga-Cho, Aomori Pref.	AB031309	
	18	Towada-Shi 1, Aomori Pref.	AB031310	
	19	Towada-Shi 2, Aomori Pref.	AB031311	
	20	Kuraishi-Mura, Aomori Pref.	AB031312	
	21	Mizusawa-Gawa 1, Minehama-Mura, Akita Pref.	AB031313	
	22	Mizusawa-Gawa 2, Minehama-Mura, Akita Pref.	AB031314	
	23	Komori, Takanosu-Cho, Akita Pref.	AB031315	
	24	Kamisugi, Aikawa-Cho, Akita Pref.	AB031316	
	25	Konda, Aikawa-Cho, Akita Pref.	AB031317	
	26*	Oyu-Onsen, Kazuno-Shi, Akita Pref.	AB013867	
	27	Hanaki-Dam, Takko-Cho, Aomori Pref.	AB031318	
	28*	Senboku-Cho, Akita Pref.	AB013868	
	29*	Shizukuishi-Cho, Iwate Pref.	AB013869	
	30*	Morioka-Shi, Iwate Pref.	AB013870	
	<i>D. b. babaianus</i>	31*	Murayama-Shi, Yamagata Pref.	AB013931
		32*	Soma-Shi, Fukushima Pref.	AB013932
		33*	Kawanishi-Cho, Yamagata Pref.	AB013933
		34*	Murakami-Shi, Niigata Pref.	AB013934
	<i>D. b. oxuroides</i>	35*	Noda-Shi, Chiba Pref.	AB013945
	<i>D. b. oxuroides</i>	36*	Nagoya-Shi, Aichi Pref.	AB013954
	<i>D. b. blaptoides</i>	37*	Sakurai-Shi, Nara Pref.	AB013962
<i>D. b. brevicaudus</i>	38*	OkI Island, Shimane Pref.	AB013973	
<i>D. b. blaptoides</i>	39*	Yakushima Island, Kagoshima Pref.	AB013981	

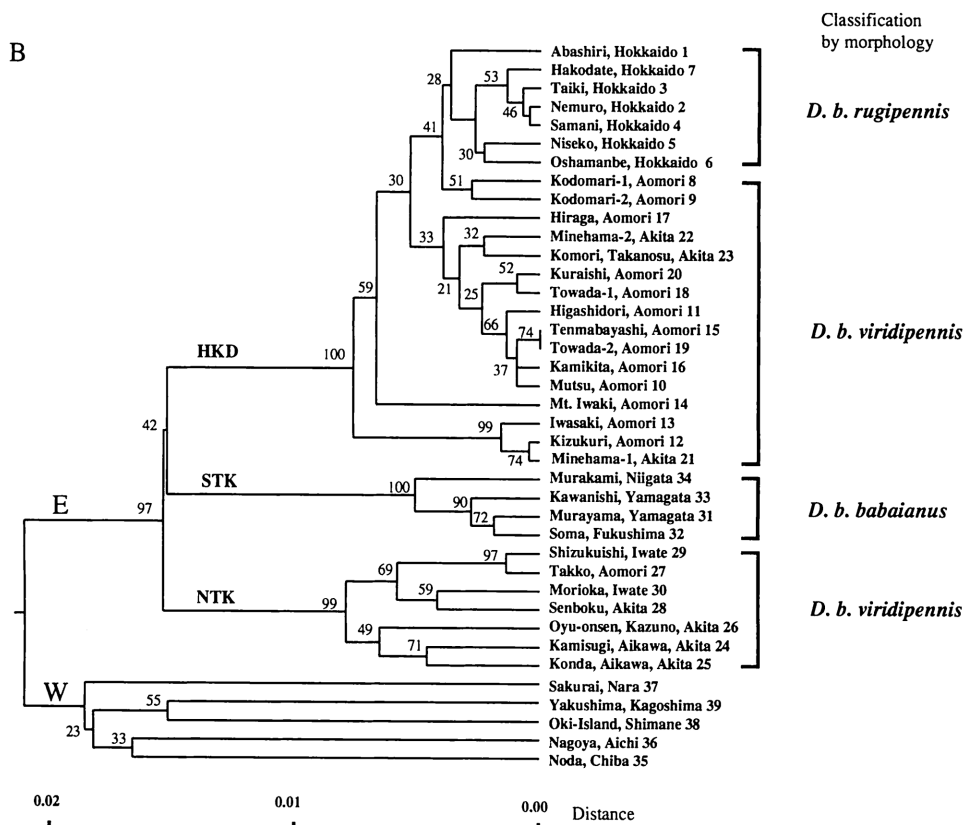
* Taken from SU *et al.*, 1996 b, 1998.



Results and Discussion

Figure 2 shows the ND5 phylogenetic trees for the specimens analyzed, together with those reported by SU *et al.* (1996 b, 1998). As reported in the previous study (SU *et al.*, 1998), two major lineages, the eastern (E) and the western (W), were recognized both in the NJ- and UPGMA-trees. The E lineage was further divided into three (HKD, NTK and STK) and the W lineage into five (Fig. 1) geographically linked sublineages (or races). HKD, NTK and STK in the E lineage were supported by high bootstrap values. They started to diversify almost simultaneously.

The main aim of this study is to settle the distributional boundary between HKD and NTK. As shown in Figs. 1 and 2, HKD consists of specimens from northern Akita Prefecture (loc. nos. 21–23) and those from all over Aomori Prefecture (except No. 27) as well as the *D. b. rugipennis* specimens from Hokkaido. The other three specimens (Nos. 24–26) from northern Akita and one specimen (No. 27) from southern Aomori belong to NTK. These results point to the existence of a boundary between HKD and NTK, running along the Yoneshiro-gawa River in northern Akita and the Mabechi-gawa River in southern Aomori (Y–M line). However, the Y–M line does not necessa-



rely mean that the common ancestor once inhabiting one region was divided into the two races by the river barriers. Perhaps the archipelago formation of the proto-Japanese Islands about 13 million years ago resulted in isolation of proto-HKD and proto-NTK in the separate islands. Following this, the two races expanded their distributions upon an extensive upheaval of the Tōhoku district until they were interrupted by the rivers. The phylogenetic trees show that HKD diversified rather anciently into several clades. The subspecies, *rugipennis* belongs to one of the clades (Fig. 2). It is notable that two specimens of *viridipennis* (loc. nos. 8 and 9) from Kodomari on the Tsugaru Peninsula were closely related to *rugipennis* on the tree (Fig. 2), suggesting that the ancestor inhabiting the northern edge of the Tsugaru Peninsula immigrated to Hokkaido through a land bridge, followed by isolation of the Hokkaido population from the

Fig. 2 (on pp. 638–639). Phylogenetic trees of the mitochondrial ND5 gene (1,069 bp upstream from 3' terminal stop codon) of *Damaster blaptoides*. The NJ tree (A) and the UPGMA tree (B). The bootstrap confidence level (%) (based on 500 resamplings) is shown at each branching point. Distance denotes KIMURA's two-parameter evolutionary distance (KIMURA, 1980). Not all the known sequences for STK and the W lineage are included in the trees. For details, see SU *et al.* (1998).

Tsugaru population upon formation of the Tsugaru Straits. The population of the Shimokita Peninsula would not have directly participated in this immigration because the specimens from there (loc. nos. 10 and 11) are rather remote from *rugipennis* from Hokkaido on the trees (Fig. 2).

Taxonomic notes. The type locality of *rugipennis* is Hakodate (Des environs de Khokodady), Hokkaido (ADAMS, 1861), while that of *viridipennis* is Aomori (Aomori; probably Aoni and the Tsugaru Peninsula) (LEWIS, 1880). Since *rugipennis* and *viridipennis* in HDK are most probably consubspecific, the latter should be treated as *rugipennis*. *Damaster b. viridipennis* in NTK is phylogenetically distinct from *viridipennis* in HKD, and should be named after careful morphological reexamination.

Acknowledgments

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要 約

金 衝坤・斉藤秀生・富永 修・蘇 智慧・大澤省三：ミトコンドリアND5 遺伝子による日本列島東北部におけるマイマイカブリの“亜種”の分布境界線。——これまでの形態の研究では、エゾマイマイカブリは北海道だけに、キタカブリは東北地方の青森県・秋田県・岩手県に分布し、2 亜種の境界線は津軽海峡であるとされてきた。Suら (1998) による分子系統解析の結果では、東北地方の北部に分布しているキタカブリといわれたものはエゾマイマイカブリと同一系統 (HKD) に属し、エゾマイマイと区別できず、またそれより南部のこれまでキタカブリとされていたものは別系統 (NTK) であることが示された。したがって、津軽海峡はマイマイカブリ亜種の分布境界としての意味をもたないことになり、むしろ HKD と NTK の境界が重要となる。しかし、この地域のサンプル数が不足していたため、正確な境界線が確定できなかった。本研究では、Suら (前述) の研究からみて分布境界線であろうと思われる青森県と秋田県／岩手県境を中心に、多数のサンプルのミトコンドリア DNA の分析を行った。その結果、HKD と NTK の分布境界線は、西は秋田県北部の米代川から、東は青森県南部の馬淵川から始まり、ほぼ東西 2 つの川を境界に、北には HKD、南には NTK の分布していることがわかった。本研究で得られた系統樹をみると、より古く青森県の西側に孤立していた集団が、陸地の隆起とともに分布域を広げ、津軽半島を經由して北海道へ進出し、現在のエゾマイマイカブリとなったと考えられる。

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The Intertidal Beetle *Amblopusa magna* ZERCHE (Coleoptera, Staphylinidae, Aleocharinae) New to Hokkaido and the Kuril Archipelago

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The intertidal liparocephaline beetle, *Amblopusa magna*, was described and characterized by ZERCHE (1998) from the Pacific coast of Russia. AHN and ASHE (1996) and ZERCHE (1998)