Lancet flukes of the genus *Dicrocoelium* parasitize in the bile duct and gall bladder of domestic and wild ruminants. Dicrocoeliasis caused by the lancet flukes produces generally mild symptoms and occasional severe economic losses in the domestic industry [6]. Three species, *Dicrocoelium dendriticum*, *D. hospes* and *D. chinensis* are recognized as the causative agents of the diseases. *Dicrocoelium dendriticum* has been reported in Europe, Asia, northern Africa and North America [8], whereas *D. hospes* is distributed in Africa [8] and *D. chinensis* in Eastern Asia and Europe [7, 9].

*Dicrocoelium dendriticum* (synonym for *D. lancelatum*) and *D. chinensis* occur in Japan, and the former species has been reported in the Japanese serow (*Capricornis crispus*) [5, 12], wild rabbits (*Lepus brachyurus*) [12], Japanese deer (*Sika nippon nippon*, syn. *Cervus nippon centralis*) [13] and sika deer (*Cervus nippon yezoensis*) [2], whereas the latter species has been detected in sika deer (*Cervus nippon centralis*) [9].

This study dealt with the morphological and molecular identification of *Dicrocoelium* flukes obtained from the Japanese serow and sika deer in Iwate Prefecture in northern district of Japan, and herein, we report that the two lancet flukes are distributed in the prefecture and that the Japanese serow is a new final host of *D. chinensis*.

We collected 42 lancet flukes from the bile ducts of 4 Japanese serows and 9 sika deer in the twelve districts (Morioka, Shizukuishi, Nishiwaga, Tono, Sumita, Yamada, Otsuchi, Kamaishi, Ofunato, Rikuzentakata and Ichinoseki) of Iwate Prefecture, Japan, during 1993 and 2006, and the flukes were kept in 70% ethanol until analysis (Table 1).

| Code       | Species     | Species   | Location     |
|------------|-------------|-----------|--------------|
| Dd#1–Dd#7 | *D. dendriticum* | Japanese serow | Morioka       |
| Dd#8–Dd#13 | *D. dendriticum* | Japanese serow | Shizukuishi   |
| Dd#14–Dd#15 | *D. dendriticum* | Japanese serow | Nishiwaga     |
| Dc#1–Dc#2 | *D. chinensis* | Japanese serow | Rikuzentakata |
| Dc#3–Dc#5 | *D. chinensis* | Sika deer   | Ofunato       |
| Dc#6–Dc#8 | *D. chinensis* | Sika deer   | Kamaishi      |
| Dc#9–Dc#11 | *D. chinensis* | Sika deer   | Ohtsuchi      |
| Dc#12–Dc#13 | *D. chinensis* | Sika deer   | Tono          |
| Dc#14–Dc#16 | *D. chinensis* | Sika deer   | Sumita        |
| Dc#17–Dc#19 | *D. chinensis* | Sika deer   | Rikuzentakata |
| Dc#20–Dc#22 | *D. chinensis* | Sika deer   | Kawai         |
| Dc#23–Dc#25 | *D. chinensis* | Sika deer   | Yamada        |
| Dc#26–Dc#27 | *D. chinensis* | Sika deer   | Ichinoseki    |

The flukes were morphologically identified based on the descriptions of Yamaguti [14], Tang and Tang [10], Otranto et al. [7] and Taira et al. [9], and discrimination between *D. dendriticum* and *D. chinensis* relied on the testes orientation (tandem in *D. dendriticum* and bilateral in *D. chinensis*).

Molecular identification of the flukes was performed based on the nucleotide sequence of the second internal transcribed spacer (ITS2) of nuclear ribosomal DNA. Total DNA was extracted from individual flukes using E.Z.N.A Mollusc DNA kits (Omega Bio-tek, Doraville, GA, U.S.A.) according to the manufacturer’s instruction. DNA fragments were amplified by the polymerase chain reaction (PCR) using ITS2-F and ITS2-R primers [1]. PCR was performed in a 25-μl reaction volume containing 2 μl of DNA template, 0.2 mM of each dNTP, 0.1 μM of each primer, 1.25 U of Go-Taq DNA polymerase (Promega, Madison, WI, U.S.A.) and the manufacturer-supplied reaction buffer. Reaction cycles consisted of an initial denaturing step at 94°C for 90 sec, followed by 30 cycles at 94°C for 90 sec, 53°C for 90 sec and 72°C for 1 min.

The flukes obtained from the Japanese serow were exclusively detected in the western and coastal and eastern areas of Iwate Prefecture, respectively. This geographically distinct occurrence of the two *Dicrocoelium* species would be associated with the distribution of the final hosts, sika deer for *D. chinensis* and Japanese serow for *D. dendriticum*. This study also reports that *Capricornis crispus* is a new final host of *D. chinensis*.

**KEy wORdS:** *Capricornis crispus*, *Cervus nippon*, *Dicrocoelium chinensis*, *Dicrocoelium dendriticum*, new host record doi: 10.1292/jvms.14-0175; J. Vet. Med. Sci. 76(10): 1415–1417, 2014
72°C for 120 sec, with a final extension at 72°C for 10 min using the GeneAmp PCR Systems 2700 (Applied Biosystems, Tokyo, Japan). PCR amplicons were precipitated with ethanol / sodium acetate and dissolved in untrapure water and directly sequenced in both directions using a bigdye Terminator v3.1 cycle Sequencing Kit (Applied biosystems, Foster city, CA, U.S.A.). The sequencing reactions were run on a 3500 Genetic Analyzer (Applied biosystems). The ITS2 sequences were aligned and compared with those of Dicrocoelium spp. deposited in Genbank using GENETYX ver. 10.0.2 (Genetyx, Tokyo, Japan).

Of the 42 flukes, 15 (Dd#1 – Dd#15) from 3 serows in the three western districts (Morioka, Shizukuishi and Nishiwaga) were morphologically identified as D. dendriticum, and the remaining 27 (Dc#1 – Dc#27) from 9 sika deer and 1 serow in the nine eastern and coastal districts were identified as D. chinensis (Table 1, Fig. 1). ITS2 fragments were amplified in the total DNA of the 42 flukes. The ITS2 sequences (239bp) of D. dendriticum were identical exclusive of those of the 2 flukes (Dd#6 and Dd#10) from deer in the Kamaishi and Otsuchi districts, which showed heterogeneous nucleotides (Y and R) in the 120 and 210 positions, respectively, from the 5’ terminal of the ITS2 (Fig. 2). The 15 sequences of D. dendriticum showed high nucleotide similarities between 99.6% and 100% and similarities between 98.8% and 99.2% with the sequence (DQ379986) of D. dendriticum from cattle in the southern Italy. The ITS2 sequences (238bp) of D. chinensis were also identical exclusive of that of one fluke (Dc#19) from deer in the Rikuzentakata district, which showed heterogeneous nucleotides (M and S) in the 5’ and 190 positions from the 5’ terminal of the ITS2 (Fig. 2). The sequences of D. chinensis showed the similarities within the range of 98.2–99.6% with that (EF547131) of D. chinensis from sika deer in Austria. The nucleotide similarities between D. dendriticum and D. chinensis were within the range of 94.6–96.4%, and those among the two species and D. hospes(EF102026) were 86.2–87.0%. Those molecular findings strongly supported species identification based on morphological characteristics of lancet flukes in this study. The sequences of the ITS2 analyzed in this study were deposited in the DNA data bank of Japan (DDBJ) as accession numbers AB367789, AB367790 and AB369980 to AB369982.

This study reconfirmed that morphological and molecular markers (testis orientation and ITS2 sequence) clearly dif-
differentiate *D. dendriticum* and *D. chinensis* as reported by Otranto *et al.* [7], because the results of morphological and molecular identification of the two lancet flukes were completely identical.

The present study clarified that *D. dendriticum* was detected in the western area and not in the coastal and eastern areas, while *D. chinensis* was detected in the coastal and eastern areas and not in the western area. The previous study also revealed that a single species *D. chinensis* was detected from sika deer in the coastal area of Iwate Prefecture [9].

This study from differentiates the molecular identification of the two lancet flukes were from sika deer in the coastal area of Iwate Prefecture [9]. This study revealed that the testes of the flukes located obliquely or tandemly, suggesting possibility of *D. dendriticum*. These reports indicate no distribution of *D. chinensis* in Hokkaido. Interestingly, sika deer populations derived from Hokkaido and Iwate, and possibly from other regions in Japan, closely relate to each other in molecular phylogeny [4]. These findings indicate that *D. chinensis* has not been introduced into Hokkaido together with geographical isolation of sika deer (*C. n. yezoensis*).

The present study revealed that a Japanese serow from Rikuzentakata of the coastal area was infected with *D. chinensis*. Dicrocoelium chinesis has been detected in sheep in China [10], several cervid species, such as musk deer (*Moschus moschiferus*), in the Soviet Union, moufflon (*Ovis ammon musimon*) and roe deer (*Capreolus capreolus*) in Austria and Italy [7], and sika deer (*Cervus nippon centralis*) in Japan [9]. We herein report that Japanese serow (*Capricornis crispus*) is a new final host of *D. chinensis*.

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