

genomic subtypes (patient 7) were detected. Results from 3 genetic methods revealed that *L. pneumophila* serogroup 1 and 13 strains are closely related, although the serogroups differ. Results of this study were consistent with the hypothesis that multiple infections are more likely with less virulent strains and more likely in persons with medical conditions predisposing them to Legionnaires' disease (10).

Our study of this outbreak suggests that the spa house was colonized by several *L. pneumophila* strains that were genetically related despite belonging to different serogroups and that 2 strains caused infection. Further analysis of the divergence of outbreak strains in genomes related to *Legionella* serogroup and sequence types is ongoing. This analysis clarifies the in-depth genetic relations among *L. pneumophila* strains, such as recombination sites and periods required for divergence. We recommend that the spa house provide high quality management and effective infection control practices according to an infection control manual (e.g., completion of documentation relating to infection control practices and training of employees) and that customers be aware of the sanitary status of spa houses.

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Dr. Kuroki is a director of the Department of Microbiology at Kanagawa Prefectural Institute of Public Health, Kanagawa, Japan. His research interests include epidemiology of protozoan and bacterial infectious diseases.

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Address for correspondence: Toshiro Kuroki, Department of Microbiology, Kanagawa Prefectural Institute of Public Health, 1-3-1 Shimomachiya, Chigasaki, Kanagawa, 253-0087, Japan; email: kuroki.gcg3@pref.kanagawa.jp

Diphyllobothrium nihonkaiense Tapeworm Larvae in Salmon from North America

Roman Kuchta, Mikuláš Oros, Jayde Ferguson, Tomáš Scholz

Author affiliations: Biology Centre of the Academy of Sciences of the Czech Republic, České Budějovice, Czech Republic (R. Kuchta, T. Scholz); Slovak Academy of Sciences, Košice, Slovak Republic (M. Oros); State of Alaska Department of Fish and Game, Anchorage, Alaska, USA (J. Ferguson)

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Diphyllobothriosis is reemerging because of global importation and increased popularity of eating raw fish. We detected *Diphyllobothrium nihonkaiense* plerocercoids in the musculature of wild pink salmon (*Oncorhynchus gorbuscha*) from Alaska, USA. Therefore, salmon from the American and Asian Pacific coasts and elsewhere pose potential dangers for persons who eat these fish raw.

The Japanese broad tapeworm, *Diphyllobothrium nihonkaiense* (Yamane, Kamo, Bylund et Wikgren, 1986) (Cestoda: Diphyllbothriidea), is the second most common causative agent of diphyllbothriosis in humans; $\approx 2,000$ cases have been reported, mainly from northeastern Asia (1). However, recent studies that used molecular methods indicate that the number of human cases caused by this tapeworm may have been highly underestimated (1). In addition, increasing popularity of eating raw fish is probably responsible for the increased number of imported cases in regions where this infection is not endemic (1).

In 1986, the Japanese broad tapeworm was recognized as a human parasite separate from the most common broad fish tapeworm, *Diphyllobothrium latum* (L.), in Japan (2). The validity of the Japanese broad tapeworm was later confirmed by molecular data, especially the *cox1* gene sequences (1). Evidence indicates that virtually all previous cases of diphyllbothriosis in humans in Japan, South Korea, and the Pacific coast of Russia that were attributed to *D. latum* tapeworms were caused by *D. nihonkaiense* tapeworms (1,3). Moreover, *D. klebanovskii* (Muratov et Posokhov, 1988) described from the Pacific coast of Russia was recently synonymized with the Japanese broad tapeworm (1,4).

Studies on the transmission of the Japanese broad tapeworm in Japan and eastern Russia (Primorsky Region) have identified 4 species of Pacific salmon as the principal sources of human infection: chum salmon (*Oncorhynchus keta*), masu salmon (*O. masou*), pink salmon (*O. gorbuscha*), and sockeye salmon (*O. nerka*). These anadromous fish become infected in brackish water along the coast of the North Pacific Ocean (1,5). Tapeworm larvae infective for humans (plerocercoids) have been described in only a few studies performed in eastern Russia and Japan, (e.g., as plerocercoids type F from the musculature of chum salmon in Kamchatka, Russia) (2,6,7).

For decades, the possible occurrence of the Japanese broad tapeworm on the Pacific coast of North America was ignored; but since 2008, human infection with adult tapeworms and natural infection of carnivores (wolves and bears) with adult tapeworms have been confirmed by use of molecular markers (1,8–10). We report finding Japanese broad tapeworm plerocercoids in North America. Our main intent is to alert parasitologists and medical doctors about the potential danger of human infection with this long tapeworm resulting from consumption of infected salmon imported (on ice) from the Pacific coast of North America and elsewhere.

In July 2013, we examined 64 wild Pacific salmon of 5 species: 1 chinook salmon (*O. tshawytscha*), 1 coho salmon (*O. kisutch*), 23 pink salmon, 8 rainbow trout (*O. mykiss*), and 31 sockeye salmon in south-central Alaska, USA. The salmon were collected by angling (under permit no. SF2013–218) or obtained from local fishermen.

The musculature was filleted to narrow slices, and internal organs were observed under a magnifying glass. Several morphotypes of diphyllbothriid plerocercoids were found, including a single larva in the musculature of pink salmon collected in Resurrection Creek (near Hope, Alaska). This plerocercoid, which was later identified as that of the *D. nihonkaiense* tapeworm, was found unencysted, deep in the musculature of the anterior part of the fish, near the spinal cord (Figure). It was highly motile, had a retracting scolex, and measured 8–15 mm long, depending on the state of elongation or contraction (Figure; Video, <https://wwwnc.cdc.gov/EID/article/23/2/16-1026-V1.htm>). After fixation with hot water, the plerocercoid was 10 mm long, had an elongate scolex 1.05 mm long and 0.60 mm wide, and possessed 2 narrow bothria opened on the apical end (Figure). The sequences of the *cox1* and 28S rRNA genes (*lsrDNA*)

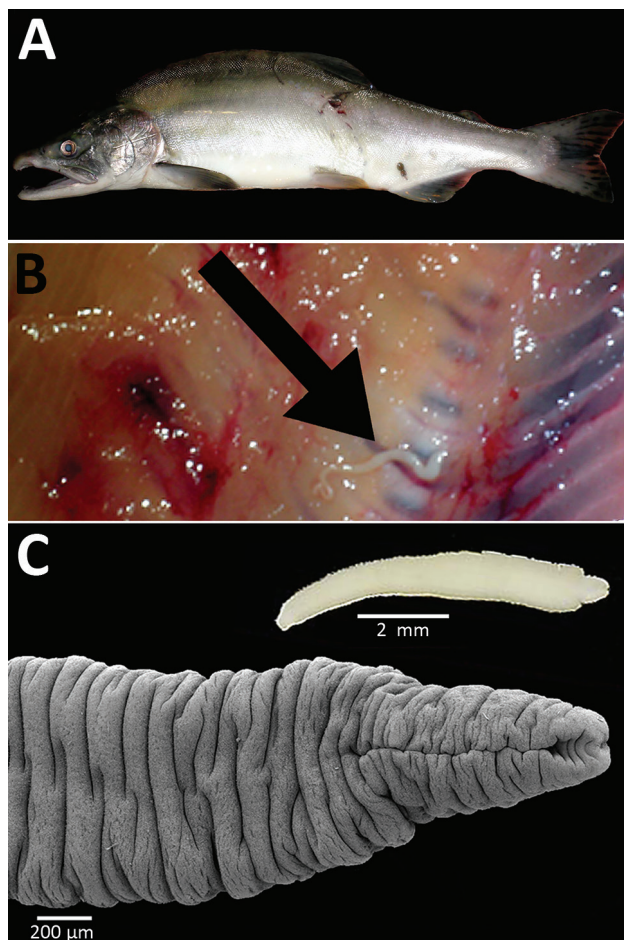


Figure. A) Pink salmon (*Oncorhynchus gorbuscha*) from Alaska, USA. B) Plerocercoid of Japanese broad tapeworm (*Diphyllobothrium nihonkaiense*) (arrow) deep in the muscles of the salmon. C) Live *D. nihonka* plerocercoid in saline (left) and scanning electron micrograph after fixation with hot water; note the scolex with a long, slit-like bothrium opened anteriorly.

were almost identical to those of the Japanese broad tapeworm available in the GenBank database (sequence similarities of 99% [GenBank accession no. KY000483] and 100% [KY000484], respectively), thus providing unequivocal support that this plerocercoid was a larva of the *D. nihonkaiense* tapeworm reported from North America.

This report provides additional evidence that salmon from the Pacific coast of North America may represent a source of human infection. Because Pacific salmon are frequently exported unfrozen, on ice, plerocercoids may survive transport and cause human infections in areas where they are not endemic, such as China, Europe, New Zealand, and middle and eastern United States (1). It is probable that most diphyllbothriosis cases originally attributed to *D. latum* may have been caused by *D. nihonkaiense* tapeworms. For more effective control of this human foodborne parasite, detection of the sources of human infection (i.e., host associations), and critical revision of the current knowledge of the distribution and transmission patterns of individual human-infecting tapeworms are needed.

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Dr. Kuchta is a researcher at the Institute of Parasitology, Czech Academy of Sciences. His research interests include biology, phylogeny, and molecular diagnosis of parasitic helminths, mainly those that cause diphyllbothriosis and sparganosis.

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Address for correspondence: Roman Kuchta, Biology Centre of the Academy of Sciences, Institute of Parasitology, Branišovská 31 České Budějovice 370 05, Czech Republic; email: krtek@paru.cas.cz

Hepatitis E Virus Infection in Solid Organ Transplant Recipients, France

Sebastien Lhomme, Laurent Bardiaux, Florence Abravanel, Pierre Gallian, Nassim Kamar, Jacques Izopet

Author affiliations: Institut National de la Santé et de la Recherche Médicale, Toulouse, France (S. Lhomme, F. Abravanel, N. Kamar, J. Izopet); Centre Hospitalier Universitaire de Purpan, Toulouse (S. Lhomme, F. Abravanel, J. Izopet); Université Paul Sabatier, Toulouse (S. Lhomme, F. Abravanel, N. Kamar, J. Izopet); Etablissement Français du Sang Pyrénées Méditerranée, Toulouse (L. Bardiaux); Etablissement Français du Sang Alpes Méditerranée, Marseille, France (P. Gallian); Ecole des Hautes Études en Santé Publique, Marseille (P. Gallian); Centre Hospitalier Universitaire de Rangueil, Toulouse (N. Kamar)

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The rate of transfusion-transmitted hepatitis E virus (HEV) in transplant recipients is unknown. We identified 60 HEV-positive solid organ transplant patients and retrospectively assessed their blood transfusions for HEV. Seven of 60 patients received transfusions; 3 received HEV-positive blood products. Transfusion is not the major route of infection in this population.