

# *Setaria tundra* in a roe deer (*Capreolus capreolus*) in the Donau-Ries district of Bavaria, Germany<sup>#</sup>

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## *Setaria tundra* bei einem Reh (*Capreolus capreolus*) im Landkreis Donau-Ries in Bayern, Deutschland

In den nördlichen Breiten ist *Setaria tundra* als häufiger Parasit von silvatischen Huftieren bekannt. Obwohl meist von geringer Pathogenität, wurde jedoch bei Rentieren (*Rangifer tarandus tarandus*) schwere Krankheitsausbrüche und bedeutende wirtschaftliche Verluste beobachtet. Die Ausbreitung und Entwicklung von *Setaria* spp. sind entscheidend abhängig von Wirtsdichte und klimatische Faktoren. Fünf adulte *S. tundra* wurden einem Rehbock in Bayern, Deutschland, diagnostiziert. Das Desoxyribonukleinsäure (DNA)-Barcoding bestätigte die morphologische Identifizierung. Die Cyclooxygenase-1-Gensequenzen zeigten 98,73–99,68% Ähnlichkeit mit Sequenzen anderer *S. tundra*-Exemplare, welche bei Hirschen (*Cervidae*) und Stechmücken (*Culicidae*) gefunden wurden. Die Ergebnisse bestätigen das Vorkommen von *S. tundra* in einem bisher unbekanntem Endemiegebiet und sind die Grundlage für umfassendere Untersuchungen, um die Biologie und Verbreitung dieses Parasiten im Rehwild sowie in anderen potentiellen Endwirten zu untersuchen.

**Schlüsselwörter:** Fallbericht, Hirsch, DNA-Barcoding, Filarioide Nematoden, Jagd

## Summary

*Setaria tundra* is known as a common parasite of sylvatic ungulates in Northern latitudes. Although mostly considered of low pathogenicity, severe disease outbreaks and remarkable economic losses have been observed in reindeer (*Rangifer tarandus tarandus*). Host density and climatic factors are major drivers of the expansion of *Setaria* spp. facilitating their development and spread. Five adult specimens of *S. tundra* were retrieved from a male roe deer in Bavaria, Germany. Deoxyribonucleic acid (DNA) barcoding confirmed morphological identification. Cyclooxygenase 1 gene sequences showed 98,73–99,68% similarity to sequences of other *S. tundra* specimens found in deer (*Cervidae*) and mosquitoes (*Culicidae*). The results raise awareness for the presence of *S. tundra* in a hitherto unknown endemic region and represent a starting point for broader investigations to understand the biology and distribution of this parasite in roe deer as well as other potential definitive hosts.

**Keywords:** Case report, deer, DNA barcoding, Filarioid nematodes, hunting

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## Introduction

Filarioid nematodes cause infections in humans and animals all over the world.<sup>15</sup> Haematophagous arthropods serve as intermediate hosts and vectors.<sup>15</sup> Since the first description of *Setaria tundra* in reindeer in the Archangelsk region (Northern Russia),<sup>13</sup> this nematode has been detected in Germany,<sup>3</sup> Switzerland,<sup>1</sup> and other European countries.<sup>4</sup> Although *Setaria* spp. usually are of low pathogenicity, *S. tundra* has been associated with severe peritonitis in semi – domesticated, herded reindeer (*Rangifer tarandus tarandus*) in Finland.<sup>9</sup> The knowl-

edge of their occurrence is limited; therefore, discovery of nematodes on the serosa of game may be a concern for local hunters in areas where observations of the parasite are accidental. This publication should raise awareness for this pathogen. We discuss this finding by comparing the Deoxyribonucleic acid (DNA) of one of these specimens to sequences presented in former studies, since various *S. tundra* haplotypes have been suspected to be linked to different degrees of pathogenicity.<sup>10</sup>

Short communication:  
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## Case Report

Five adult female filarioid specimens were retrieved and identified as *S. tundra* from the peritoneal cavity of a male roe deer (*Capreolus capreolus*). The finding was considered incidental due to the lack of pathologic lesions. The male roe deer was hunted in an arable and forestry habitat in Oberndorf am Lech, in the district of Donau-Ries, Bavaria, Germany. The deer was approximately eight months old and weighed 12 kg after evisceration. No evidence of disease or abnormal odor was found on gross examination, serosal membranes appeared to be smooth and clear. The five nematodes were found in the abdominal cavity (Figure 1) during the field dressing of the roe deer. The nematodes were initially left in place within the carcass until manual collection and conservation in 70% ethanol within an hour. Specimens were incubated in 50% lactic acid to brighten the morphological structures. Species diagnosis was based on morphological characteristics (Figure 2).<sup>11</sup>

One specimen was analysed by DNA barcoding,<sup>14</sup> using PCR and sequencing methods according to Folmer et al. (1994),<sup>6</sup> and Hebert et al. (2003)<sup>7</sup> at a specialized DNA

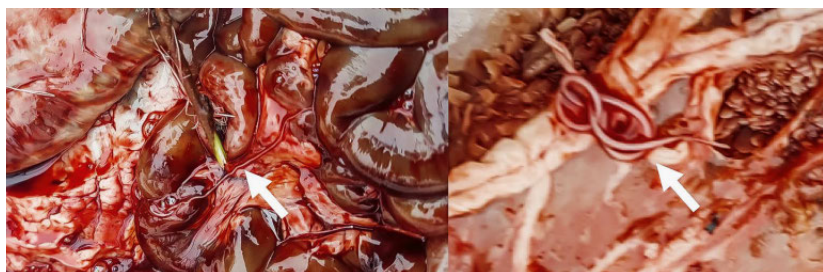
barcoding laboratory (Advanced Identification Methods AIM GmbH, Munich, Germany). Primers LCO1490 (59-GGTCAACAAATCATAAAGATATTGG-39) and HCO2198 (59-TAAACTTCAGGGTGACCAAAAAA-TCA-39) were used to amplify a 658 base pair fragment of the Cyclooxygenase 1 (COX-1) gene.<sup>6,7</sup> The generated sequence was aligned using Barcode of Life Data (BOLD) systems (<http://www.boldsystems.org>)<sup>14</sup> and GeneBank™ (<https://www.ncbi.nlm.nih.gov/genbank/>). Sequence analysis confirmed the result of the morphological differentiation. The sequence of the COX-1 gene presented in this study was deposited on GenBank™ under the accession number [MN103544](https://www.ncbi.nlm.nih.gov/nuccore/MN103544). The COX-1 gene sequence showed 98,73 – 99,68% similarity to sequences of other *S. tundra* specimens found in roe deer, reindeer, and mosquitos in Europe (Table 1).

## Discussion

Keeping in mind the potential haplotypic variability of *S. tundra* as reported by previous work,<sup>10</sup> it is important to emphasize that solely one of the discovered specimens was analysed and other haplotypes may have been present in this individual as well. With the publication of this case, we recall the presence of this parasite as a common incidental finding and point out that only few extensive studies on the distribution of *S. tundra* in some European countries as well as on the prevalence and severity of infection in potential definitive hosts have been published so far. Future work is needed to classify this finding in a broader context, e.g. by initiating a study on the prevalence and severity.

Büttner (1978),<sup>3</sup> was the first to morphologically prove the occurrence of *S. tundra* in roe deer in Bavaria, Germany. Later, *S. tundra* DNA was detected in mosquitoes in Baden – Württemberg, Bavaria, Lower – Saxony, and Rhineland – Palatinate.<sup>5,8</sup> These have been the only reports on this parasite in Germany; therefore, the present work provides the first identification of *S. tundra* within the definitive host in Germany confirmed by molecular analyses. This nematode might have been widespread in Europe for a long time and the increasing number of recent studies may reflect growing interest or geographic expansion, or expansion of the host range or just little attention in the past due to low pathogenicity.

The comparison of the COX-1 genes of the different isolates of *S. tundra* throughout Europe showed a high level of similarity (98,73–99,68%). The highest similarity of our isolate (99,68%) was found with isolates from Denmark and Spain. Interestingly, isolates from Finland found to be pathogenic in reindeer differed in four base pairs and hereby showed the least similarity. Whether this variation reflects different degrees of pathogenicity



**Figure 1:** In-situ localisation of *S. tundra* within the abdominal cavity of the roe deer. Adult *Setaria* specimens are indicated by a white arrow.



**Figure 1:** Microscopic presentation of *S. tundra*. Morphology of cephalic (left) and caudal (right) end of an adult nematode recovered from a roe deer in Bavaria. The cephalic region shows the peribuccal crown with the typical bifid projections. In *S. tundra*, the crown is oval and the projections are bifurcated without lateral lips. The caudal end is characterised by a long, slender, slightly bent tail with many superficial bosses forming a collar at the tip of the tail which terminates in a bud – like knob typical for females of *S. tundra*. In males, a longer spicule and a shorter spicule are present. Males have 3 precloacal and 1 postcloacal papillae.<sup>11</sup>

\*pc peribuccal crown

\*bp bifid projections

**Table 1.** Overview of findings of *S. tundra* in Europe.

Accession Number (GenBank)	Origin of isolate	Similarity to present isolate (in %)
KU508982,1	Roe deer, Denmark	99,37
KF692103,1	Mosquito, Germany	99,37
AM749298,1	Roe deer, France	99,37
KM370867,1	Mosquito, Poland	99,34
KP760209,1	Not specified	98,73
DQ097309,1	Reindeer, Finland	98,73
KU508983,1	Roe deer, Denmark	99,37
KF692104,1	Mosquito, Germany	99,05
AJ544874,1	Not specified	99,05
KU508985,1	Roe deer, Denmark	99,68
KU508984,1	Roe deer, Denmark	99,68
KX599455,1	Roe deer, Spain	99,68
KX599456,1	Roe deer, Spain	99,68

The origin and the similarity of the isolates identified throughout Europe to the isolate of the present report (in %) indicate a strong similarity (98,73–99,68%) between different isolates of *S. tundra*.

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remains unclear and requires further analyses of a larger sample of *S. tundra* specimens from across Europe. Furthermore, the current phylogenetic analysis could not include very recent findings from Croatia,<sup>4</sup> and Poland,<sup>12</sup> because these parasites were not analysed genetically.

If the parasites infect organs of the definite host determined for human consumption, the question arises if meat is suitable for human consumption. This is of particular interest to local hunters who have a key role in meat hygiene of game and may not be familiar with finding nematodes in the abdominal cavities. In the present report, the discovery of *S. tundra* was an incidental finding which was associated with a considerable level of uncertainty of the involved hunters, as they had

not been confronted with this parasite earlier and no report of *S. tundra* in this area had been present. If carcasses are heavily infested or show signs of organoleptic alterations of tissues, we recommend discarding at least these parts of the carcass. If only mild changes are visible or none at all except for the nematodes in the abdominal cavity, these parts may be discarded and the carcass itself may well be fit for consumption.

### Acknowledgements

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### Brève communication: *Setaria tundra* chez un chevreuil (*Capreolus capreolus*) dans le district de Donau-Ries en Bavière, Allemagne

*Setaria tundra* est connu comme un parasite commun des ongulés sylvatiques aux latitudes septentrionales. Bien que généralement considéré comme faiblement pathogène, de graves épidémies et des pertes économiques significatives ont été observées chez le renne (*Rangifer tarandus tarandus*). La densité d'hôtes et les facteurs climatiques sont les principaux moteurs de l'expansion de *Setaria spp.*, facilitant leur développement et leur diffusion. Cinq spécimens adultes de *S. tundra* ont été récupérés sur un chevreuil mâle en Bavière, en Alle-

### *Setaria tundra* in un capriolo (*Capreolus capreolus*) nel distretto di Donau-Ries nella Baviera, Germania

La *Setaria tundra* è nota come un comune parassita degli ungulati selvatici nelle latitudini settentrionali. Anche se viene considerata a bassa patogenicità, si sono osservati gravi epidemie e quindi notevoli perdite economiche per le renne (*Rangifer tarandus tarandus*). La densità della popolazione e i fattori climatici sono i principali artefici dell'espansione della *Setaria spp.* che ne hanno facilitato lo sviluppo e la diffusione. Cinque esemplari di *S. tundra* adulti sono stati ritrovati in un capriolo maschio in Baviera, Germania. L'identificazione morfologica è stata confermata dalla codifica dell'acido de-

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magne. Le séquençage de l'acide désoxyribonucléique (ADN) a confirmé l'identification morphologique. Les séquences du gène de la cyclooxygénase 1 ont montré une similarité de 98,73 à 99,68% avec les séquences d'autres spécimens de *S. tundra* trouvés chez les cerfs (*Cervidae*) et les moustiques (*Culicidae*). Les résultats sensibilisent à la présence de *S. tundra* dans une région endémique jusqu'alors inconnue et représentent un point de départ pour des investigations plus larges pour comprendre la biologie et la distribution de ce parasite chez le chevreuil ainsi que d'autres hôtes définitifs potentiels.

**Mots clés:** Rapport de cas, cerf, séquençage ADN, nématodes filarioïdes, chasse

### *Setaria tundra* tier in cavriël (*capreolus capreolus*) el district Donau-Ries ella Baviera, Tiaratutestga

*Setaria tundra* ei enconuschenta ella ladezia geografica dil nord sco frequent parasit d'animals d'ual cun greflas. Schebein ch'ella caschuna il bia mo pintga patogenitad, han ins observau renns (*Rangifer tarandus tarandus*) pertuccai grevamein dalla malsogna cun sperditas economicas considerablas. La derasaziun ed il svilup da *Setaria* spp. ein dezisivamein dependents dalla spessaglia dil hospitont e da facturs climatics. Tschun *S. tundra* adultas ein vegnidias diagnosticadas tier in buc cavriël ella Bavaria, Tiaratudestga. Il barcoding digl acid

desoxiribonucleico (DNA). Le sequenze del gene della cicloossigenasi 1 hanno rilevato il 98,73–99,68% di somiglianza con le sequenze di altri esemplari di *S. tundra* trovati in cervi (*Cervidae*) e zanzare (*Culicidae*). I risultati confermano la presenza di *S. tundra* in una regione endemica finora sconosciuta e rappresentano un punto di avvio per delle indagini più vaste per capire la biologia e la distribuzione di questo parassita nei caprioli e in altri ospiti potenziali.

**Parole chiave:** Rapporto caso, cervo, DNA, ADN, barcoding, nematodi filariosi, caccia

desoxiribonuclein (DNA) ha confirmau l'identificaziun morfologica. Las sequenzas geneticas cyclooxygenasa-1 han mussau in'analogia da 98.73–99.68% cun sequenzas dad auters exemplars da *S. tundra*, chein vegni anflai in tscharvas (*Cervicidae*) e muschins (*Culicidae*). Ils resultats confirmeschan l'existenza da *S. tundra* en in intschess endemic buca enconuschents tochen ussa ed ein la basa per retschercas extendidas per intercurir la biologia e la derasaziun da quei parasit tier cavreuls ed auters hospitonts finals potenzials.

**Plaid-clav:** Rapport din cass, cavriël, DNA-barcoding, nematods filaroids, catscha

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