Chapter 4

Characterization of the complete internal transcribed spacer region of the nuclear ribosomal DNA of *Typhula incarnata*, the *T. ishikariensis* complex and *T. phacorrhiza*

ABSTRACT

Isolates of the Typhula ishikariensis complex, T. incarnata and T. phacorrhiza from around the world were characterized by sequence analyses of the complete internal transcribed spacer region (CITS) of nuclear ribosomal DNA. The hypotheses tested were that the sequence could be used (i) to identify the Typhula spp. and (ii) to distinguish the two biological species of the T. ishikariensis complex (BSI and BSII). DNA was extracted from the isolates, the CITS region was amplified by PCR and then cloned into a plasmid. Next, the plasmid was transformed into E. coli and allowed to multiply, thus amplifying the plasmid containing the CITS region. The plasmid was isolated from the bacteria and then the CITS region was sequenced. Percentage of sequence identity for the 44 sequences from the 30 Typhula spp. isolates ranged from 59 to 100% with a 0 to 30% divergence. The 26 sequences from the 20 T. ishikariensis isolates were 87 to 100% identical to each other with a 0 to 8% divergence. The 26 sequences from the 20 T. ishikariensis isolates were 59 to 78% identical to 11 sequences of five T. incarnata isolates, three sequences from two T. phacorrhiza isolates and four sequences from three unidentified Typhula-like isolates with a 22 to 30% divergence. These results indicated that the CITS region can be used to differentiate the Typhula spp. "Signature sequences" were identified that differentiate BSI and BSII of the T. ishikariensis complex, however, sequence analyses infer they are the same species undergoing speciation.

INTRODUCTION

Conventional methods for the identification and characterization of fungal plant pathogens sometimes fail when such fungal isolates exhibit atypical phenotypic profiles or morphological characteristics that overlap fungal species concepts. Recent advancements in DNA sequencing technology have greatly enhanced the ability of plant pathologists to identify fungal isolates. DNA sequence information is relatively objective and sequence databases¹ are readily available via the internet (Maidak et al., 1999; Benson et al., 1999). Nucleotide sequences of target DNA genes can be rapidly and accurately obtained from fungal plant pathogens (Hillis, 1996). However, DNA of known genes have not been a primary source of data for *Typhula* species characterization. This study will determine if DNA sequencing of the complete internal transcribed spacer region (CITS) of the nuclear ribosomal DNA (nrDNA) can aid in identifying *Typhula* species.

Rapid and accurate identification of *Typhula* species pathogenic to turfgrasses is an important part of managing the diseases that they cause. The sclerotia of the *Typhula* spp. are the primary diagnostic feature in the taxonomy of the genus (Remsberg, 1940; Corner, 1950; MacDonald, 1961). Unfortunately, at optimal *in vitro* conditions, sclerotia start to form 6 to 16 days for *T. incarnata* and 4 to 20 days for *T. ishikariensis* and both species only grow 2 mm per day (Sweets and Steinstra, 1980). Molecular based identification has the potential to expedite disease diagnosis, improve pathogen characterization and perhaps aid in disease management.

Furthermore, it is not easy to identify the *T. islukariensis* complex, and the taxonomy of these fungi remains unclear (Smith et al., 1989). The dikaryon-monokaryon mating experiments (Chapter 3) revealed that there are at least two genetically different groups of the *T. ishikariensis* complex in Wisconsin golf courses (Wisconsin group 1 and Wisconsin group 2). Unfortunately, the dikaryon-monokaryon mating experiments are tedious and time

consuming. A rapid and accurate fungal identification technique is needed to expedite identification of the *T. ishikariensis* complex isolates.

Studies of the genotypic differences between *Typhula* species have centered on mating experiments involving compatibility groups (Bruehl et al., 1975; Årsvoll and Smith, 1978; Bruehl and Machtmes, 1979; Matsumoto et al., 1996). However, the only investigations utilizing molecular markers to identify snow mold pathogens are the application of random ly amplified polymorphic DNA (RAPDs) markers to detect genets belonging to *T. ishikariensis* biotype A (Matsumoto et al., 1996) and to analyze *Coprinus psychromorbidus* (sclerotial low temperature basidiomycete, SLTB) strains (Larouche et al., 1995).

An appropriate and effective method for analysis and characterization of closely related species and their boundaries is DNA sequencing of a rapidly evolving nuclear gene target (Hillis et al., 1996). As of yet, no one has characterized DNA sequences of known genes of *Typhula* species. One such target is the complete internal transcribed spacer regions (CITS) of the nuclear ribosomal RNA gene array (nrDNA, Fig. 4.1) which has proven useful for fine scale comparisons (Hillis et al., 1996). Sequences of nrDNA have been used to compare various plant taxa (Zhang et al., 1997; Alice and Campbell, 1999; Steane et al., 1999), bacterial taxa (Lee et al., 1998; Kolbert and Persing, 1999), fungal taxa (Olsen et al., 1986; White et al., 1990; Rafin et al., 1995; Chen et al., 1996), nematode taxa (Al-Banna et al., 1997), fish taxa (Sajdak and Phillips, 1997) and insect taxa (Black et al., 1997).

Also, the characterization of the CITS of nrDNA has been a useful molecular tool in plant pathogen detection and identification. Recently, this technique was used to differentiate *Fusarium* spp. (O'Donnell and Cigelinik, 1997), to detect *Phialophoragregata* in soybean tissues (Chen et al., 1996), to detect *Monosporascus* spp. (Lovic et al., 1995), to identify *Magnaporthe poae* (Bunting et al., 1996) and to characterize *Rhizoctonia solani* (Kanematsu and Naito, 1995; Salazar et al., 1999). The PCR-mediated analysis of the CITS region of nrDNA has illustrated, "a convenient approach to developing 'molecular tools' for detection of



Figure 4.1. Schematic representation of the complete internal transcribed spacer (CITS) region of the nuclear ribosomal DNA (nrDNA). The shadowed boxes represent the ribosomal subunits. The arrows denote the position of the PCR sequencing primers. ITS-1 primer: (TCCGTAGGTGAACCTGCGG) and ITS-4 primer: (TCCTCCGCTTATTGATATG, White et al., 1990). plant pathogenic fungi without necessarily having any detailed knowledge of their genome organization" (Lovic et al., 1995). Sequence analyses of the CITS region has been particularly useful in species identification (van Herwerden et al., 1999). This molecular method might offer advances in describing the genotypic differences between *T. ishikariensis*, *T. incarnata* and *T. phacorrhiza* while also clarifying the taxonomic classification of the *T. ishikariensis* complex.

The objective of this research was to genetically characterize the *T. ishikariensis* complex, *T. incarnata* and *T. phacorrhiza* isolates by utilizing sequence analysis of the CITS region of the nrDNA. Specifically, the hypotheses being tested were (i) the nucleotide sequence of the CITS of the nrDNA will vary among isolates of *T. incarnata*, the *T. ishikariensis* complex and *T. phacorrhiza* and can be used to infer phylogenetic relationships and (ii) the *T. ishikariensis* complex isolates can be separated into two groups based on nucleotide sequence of the CITS region of the nrDNA.

First, DNA was extracted from *Typhula* isolates from Wisconsin and tester isolates from around the world. The CITS region of the nrDNA was then amplified by the PCR-reaction with the CITS universal primers (Fig. 4.1, White et al., 1990). The PCR product was then inserted into a plasmid and transformed into *E. coli*. The bacteria were allowed to grow thus amplifying the plasmid DNA containing the PCR product insert. The plasmid DNA was then isolated from the bacteria. Finally, the PCR insert within the plasmid DNA was sequenced. Phylogenetic inferences were made based upon the DNA sequence of the CITS region.

Percentage of sequence identity of the CITS for the 44 sequences from the 30 Typhula spp. or Typhula-like isolates ranged from 59 to 100% with a 0 to 30% divergence. The 26 CITS sequences from the 20 T. ishikariensis isolates were 87 to 100% identical with a 0 to 8% divergence. The 26 sequences from the 20 T. ishikariensis isolates were 59 to 78% identical to 11 sequences of five T. incarnata isolates, three sequences from two T. phacorrhiza isolates

and four sequences from three unidentified Typhula-like isolates with a 22 to 30% divergence.

The results of the molecular identification experiments indicate that the CITS region of the nrDNA can be used to differentiate *T. incarnata*, *T. ishikariensis* and *T. phacorrhiza*. However, analysis of the CITS and the ITS 1 region of the nrDNA infer that isolates of the two *T. ishikariensis* groups (WIG1-BSI and WIG2-BSII) are the same species but perhaps are undergoing speciation or lineage divergence. Signature sequences were found within the ITS 1 region that could possibly be used to differentiate between biological species I and biological species I and biological species II of the *T. ishikariensis* complex.

1. A few DNA sequence internet sites include: the DNA Data Bank of Japan (DDBJ). Mishima, Japan at http://www.ddbj.nig.ac.jp/; European Molecular Biology Laboratory, Nucleotide Sequence Database, Hinxton, UK (EMBL/EBI) at http://www.ebi.ac.uk/; GenBank, National Center for Biotechnology Information, Bethesda, Maryland at http://www.ncbi.nlm.nih.gov; and the Ribosomal Database Project II, National Science Foundation, U. S. Department of Energy and Michigan State University at http://www.cme.msu.edu/RDP/.

MATERIALS AND METHODS

Fungal Isolates

The Typhula isolates used in this work are listed in Table 4.1. All imported isolates were obtained according to the USDA permit PPQ-526 requirements. The isolates T. ishikariensis biotype A (isolates PR9-4-3 and PR7-6-7, Matusmoto and Tajimi, 1993), T. ishikariensis Norway group I (isolate 2-5BS-1, Matsumoto et al., 1996), T. ishikariensis var. ishikariensis (isolate 92-32-MI, Tkachenko et al., 1997) T. ishikariensis biotype B (isolate 35-8, Matsumoto and Tajimi, 1991), T. ishikariensis Norway group II (isolate 4-3S-5. Matsumoto et al., 1996) and T. ishikariensis var. canadensis (isolate Can21m, Arsvoll and Smith, 1978) were obtained from N. Matsumoto, National Institute of Agro-Environmental Sciences, Tsukuba, Japan. The isolate T. ishikariensis var. canadensis (isolate JD13) was obtained from J. D. Smith, Canada, which he collected from North Battleford golf course. Prince Albert, Canada in 1992. The isolates T. ishikariensis biotype A (isolate 56263. Matsumoto et al., 1982), T. ishikariensis var. ishikariensis (isolate 38649, Årsvoll and Smith. 1978), T. ishikariensis biotype B (isolate 56264, Matsumoto et al., 1982) and T. idahoensis (isolate 32642, Bruehl et al., 1975) were obtained from American Type Culture Collection. Manassas, Virginia (http://www.atcc.org/). Two unidentified Typhula isolates, G2 (from Gaillardia sp.) and G4 (from Chenopodium alba), were collected by C. R. Grau, University of Wisconsin, Madison in the spring of 1998. The other isolates were collected from the survey of Wisconsin golf courses (Chapter 2). Also, the isolates T. ishikariensis WIG2-2.136 and WIG2-2.105 were dedikaryotized by growing them on PDA amended with 2% oxgall (Matsumoto and Tronsmo, 1995) to determine if there were differences in DNA sequence of the CITS region between dikaryons and monokaryons of the same isolate.

DNA Extraction

Typhula spp. isolates were grown in 1.5-ml microcentrifuge tubes with 1 ml of potato dextrose broth for one month and the DNA was extracted as described in Protocol #3 (for small

Typhula species	Subspecies appellations	Identification code	Geographical origin
Typhula ishikariensis	WIG1 ^a	1.93	Wisconsin Dells, WI
Typhula ishikariensis	WIGI	2.183	Ogdensburg, WI
Typhula ishikariensis	WIGI	3.120	Woodruff, WI
Typhula ishikariensis	Biotype A	PR9-4-3	Japan
Typhula ishikariensis	Biotype A	PR7-6-7	Japan
Typhula ishikariensis	Biotype A	56263	Japan-ATCC ^b
Typhula ishikariensis	Norway Group I	2-5BS-1	Norway
Typhula ishikariensis	var. ishikariensis	38649	Norway-ATCC
Typhula ishikariensis	var. ishikariensis	92-32-MI	Russia
Typhula ishikariensis	WIG2 ^a	1.31	Jefferson, WI
Typhula ishikariensis	WIG2	2.97	Stevens Point, WI
Typhula ishikariensis	WIG2	2.105	Stevens Point, WI
Typhula ishikariensis	WIG2	3.122	Woodruff, WI
Typhula ishikariensis	Biotype B	35-8	Japan
Typhula ishikariensis	Biotype B	56264	Japan-ATCC
Typhula ishikariensis	Norway Group II	4-38-5	Norway
Typhula ishikariensis	var. canadensis	JD 13	Canada
Typhula ishikariensis	var. <i>canadensis</i>	Can21m	Canada
Typhula ishikariensis	WIG2	2.100A	Stevens Point, WI
Typhula idahoensis	NAª	32642	Washington-ATCC
Typhulaincarnata	NA	1.35	Jefferson, WI
Typhulaincarnata	NA	2.100B	Stevens Point, WI
Typhulaincarnata	NA	2.136	Wautoma, WI
Typlulaincarnata	NA	3.279	Hurley, WI
Typhulaincarnata	NA	3.114	Woodruff, WI
Typhula phacorrhiza	NA	3.120B	Woodruff, WI
Typhula phacorrhiza	NA	2.230A	Marshfield, WI
Unidentified Typhula	NA	G2	Verona, WI
Unidentified Typhula	NA	G4	Arlington, WI
Unidentified Typhula	NA	3.129	Woodruff, WI

Table 4.1. Subspecies appellations, identification codes and geographical origins of thirty *Typhula* species used in the CITS region of nrDNA characterization experiment.

^a WIG1 = Wisconsin group 1, WIG2 = Wisconsin group 2. ^b ATCC = American Type Culture Collection.

 \circ NA = not applicable.

amounts of cells, tissues, or plant leaves) of the Easy-DNATM Kit (Invitrogen®, Carlsbad, CA; Anonymous a, 1998). Briefly, mycelia were crushed in liquid nitrogen, the cells were lysed by the addition of Solution A and subsequent incubation at 65° C. Proteins and lipids were precipitated and extracted by the addition of Solution B and chloroform. The solution was then centrifuged to separate it into two phases with a solid interface separating the two phases. The DNA was in the upper, clear aqueous phase, the proteins and lipids were in the solid interface, and the chloroform formed the lower phase. The DNA was then removed, precipitated with ethanol, and resuspended in TE buffer. In general, the total time for DNA extraction per isolate took approximately 90 minutes. The DNA was then ready for PCR or stored at +4° C for less than 12 hours.

DNA amplification

The polymerase chain reaction was performed with some modifications from a standard protocol (Anonymous, 1996). An automated thermal cycler The Rapid CyclerTM (Idaho Technologies Inc., Idaho Falls, ID) was used for the amplification reaction. Primers used for the amplification of the CITS region were ITS-1 and ITS-4, Fig. 4.1 (White et al., 1990). Amplification reactants from The Rapid Cylcer Optimizer Kit #1761 were used to make 26 μ l mixtures in individual wells of a microtiter plate. The 26 μ l mixtures contained 2.5 μ l of Low Mg buffer [10 mM MgCl₂; 50 mM Tris; and 250 μ g/ml bovine serum albumin (BSA)], 1 μ l Ficoll, 2.5 μ l dNTPs (200 μ M dNTP), 2.5 μ l ITS-1 primer (0.5 μ M), 2.5 μ l ITS-4 primer (0.5 μ M), 2.5 μ l genomic DNA (5 ng/ μ I), 2.5 μ l diluted *Taq* DNA polymerase (0.4 U/10 μ l *Taq* DNA polymerase (Promega, Madison, WI); and 250 μ g/ml BSA) and 10 μ l of distilled sterilized water (Anonymous, 1992). The 26 μ l mixtures were loaded into 30 μ l borosilicate capillary tubes (Idaho Technology Inc., Part #1706) and flame sealed at both ends (Anonymous, 1996). The preprogrammed Rapid CyclerTM protocol C57 was used as the cycling parameters. Protocol C57 includes 30 cycles of denaturation for 10 sec. at 94° C,

annealing for 10 sec. at 55° C and elongation for 35 sec. at 72° C (approximately 28 total min.). Each PCR product was visualized by 1.2% agarose gel electrophoresis. The minigel apparatus voltage was set at 110 mV for 20 to 30 min. Ethidium bromide was used to stain the DNA bands and then the DNA fragments were visualized by UV illumination.

Cloning

The TOPOTM TA Cloning[®] kit (Invitrogen, Carlsbad, CA) was used to directly insert the *Taq* polymerase-amplified PCR products into a plasmid vector. The TOPO TA Cloning Kit uses the pCR[®] 2.1-TOPO vector with covalently bound topoisomerase I enzyme for fast and efficient PCR cloning (total time is approximately 5 min.) (Anonymous, 1998b). Briefly, a 5 μ l cloning reaction was set up containing 1 μ l of fresh PCR product (10 ng/ μ l), 3 μ l of sterile distilled water and 1 μ l of pCR[®]-TOPO vector. The reaction was mixed gently and incubated for 5 min. at room temperature. The tube was then placed on ice while vials of TOPO10F' One ShotTM (Invitrogen, Carlsbad, CA) competent *Escherichia coli* cells were thawed on ice.

Transformation

For the transformation reaction, 2 μ l of 0.5 M ß-mercaptoethanol was added to each vial of TOPO10F' One ShotTM cells of *E. coli* and gently mixed. Then 2 μ l of the TOPOcloning reaction was added to a vial of TOPO10F' One ShotTM cells and gently mixed. The vial was then incubated on ice for 30 min. The TOPO10F' One ShotTM transformation reaction was then heat shocked for 30 sec. at 42° C without shaking, followed by incubation on ice for 2 min. To grow the competent cells, 250 μ l of room temperature SOC medium was placed in the vials and gently mixed. The vials were tightly capped and shaken horizontally at 37° C for 30 min. Then 50, 75 and 100 μ l from each transformation was spread evenly on Luria-Bertani (LB) agar plates containing 50 μ g/ml ampicillin, 40 μ l of 40 mg/ml X-Gal (5-Bromo-4-chloro-3-indolyl-β-D-galactopyranoside) and 40 μ l of 100 mM IPTG (isopropyl-β-Dthiogalactopyranoside) that had been warmed to 37° C for at least 1 hr. (Anonymous, 1998b). The LB agar plates were inverted and incubated overnight at 37° C. The next day, 10 white colonies were selected for analysis. The white colonies were cultured in 2 ml of LB broth (Anonymous, 1998b) containing 50 μ g/ml ampicillin (LBa) and shaken in a 37° C water bath for 2 to 4 hours. For stored samples of the clones, 100 μ l of the culture was placed in 1 ml of LBa and incubated overnight in a 37° C water bath. The next day, 220 μ l of sterile glycerol was added to the tube, briefly vortexed and then stored immediately in a -80° C freezer. To multiply the competent cells containing the PCR inserts, 100 μ l of each culture was placed in 10 tubes containing 1.5 ml of LBa and incubated and shaken overnight in a 37° C water bath.

Plasmid DNA isolation

The plasmid DNA was isolated from the cultures by using the S. N. A. P.™ Miniprep Kit (Invitrogen, Carlsbad, CA). The S. N. A. P. Miniprep Kit is a plasmid DNA purification system designed to yield ultra-pure plasmid DNA for automated sequencing in 25 min. (Anonymous, 1998c). Briefly, the ten overnight cultures of each clone were centrifuged for 5 min. at 4,000 rpm at room temperature (RT) into two 1.5-ml microcentrifuge tubes (5 culture tubes per microcentrifuge tube). The supernatant was removed and the pellet was resuspended in 150 μ l of Resuspension Buffer by briefly vortexing. Then 150 μ l of Lysis Buffer was added and the tube was gently inverted 5 to 6 times and incubated for 3 minutes at RT. Next, 150 μ l of ice-cold Precipitation Salt was added and then the tube was inverted 6 to 8 times to mix components. The tube was then centrifuged at RT at 14,000 rpm for 5 min. The supernatant from the two microcentrifuge tubes were then pipetted into one sterile microcentrifuge tube while the pellets were discarded. To the supernatant, 600 μ l of Binding Buffer was added and the tube inverted 5 to 6 times. The entire solution was then poured onto the S. N. A. P.™ Mini-prep Column/Collection Tube. The S. N. A. P.™ Mini-prep Column/Collection Tube was then centrifuged at RT at 1,000 rpm for 30 sec. The column flow through liquid was discarded. To the column, 500 μ l of Wash Buffer was added and again centrifuged RT at 1,000 rpm for 30 sec. Following this step, 900 μ l of Final Wash Buffer was added and then centrifuged at RT at 1,000 rpm for 30 sec. The resin in the column

was dried by centrifuging at maximum speed for one min. To elute the plasmid DNA, the resin column was transferred to a sterile microcentrifuge tube and 60 μ l of sterile distilled water was added onto the column. The wet resin column was then incubated at RT for at least 3 min. Finally, the plasmid DNA was eluted by centrifugation at maximum speed for 30 sec.

To check the plasmid DNA for the PCR inserts, an *Eco*Rl digestion was performed on the S. N. A. P. minipreped DNA. This reaction mixture contained 6.5 μ l of sterile distilled water, 1 μ l of Dellaporta buffer (Dellaporta et al., 1983), 2 μ l of S. N. A. P. Minipreped DNA, and 0.5 μ l of *Eco*Rl enzyme. The digestion reaction was incubated and shaken at 37° C overnight. Gel electrophoresis (as described previously) was used to visualize the presence of the PCR insert. A TKO 100 Dedicated Mini Fluorometer (Hoefer Scientific Instruments, San Francisco, CA) was used to determine and/or adjust the plasmid DNA concentration to 200 to 250 ng/ml. Automated (fluorescence) DNA sequence analysis was performed on 10 μ l of 200 to 250 ng/ml plasmid DNA at the DNA Sequence Laboratory in the Nucleic Acid and Protein Facility at the University of Wisconsin Biotechnology Center (UWBC), University of Wisconsin-Madison, WI. The M13F and M13R primers were used to sequence the 700 to 800 bp PCR product insert.

Sequence Analysis

Sequence files from the UWBC were viewed, evaluated and corrected within the EditViewTM Version 1.0 (Automated DNA Sequence Viewer) and SeqEdTM Version 1.03 (DNA Sequence Editor) software (Applied Biosystem Inc., Perkin-Elmer Corp.) according to on-line help and the manuals provided by the UWBC (Anonymous, 1995; Anonymous, 1998d). Corrected SeqEdTM sequences were exported as Genetics Computer GroupTM files (GCG, Madison, WI) and the percent identity comparisons were determined by the GAP function within the GCG software. The GCG files were then imported into EditSeqTM files were then imported into the MegalignTM software (DNAStar, Madison, WI). The sequence files were aligned using the Clustal method and the percentages of sequence divergence were calculated (Table 4.9). The alignment was exported as a NEXUS file and phylogenetic trees were constructed with PAUP Version 4.0 software (Center for Biodiversity, Illinois Natural History Survey, Champaign, IL). Two types of tree-making methods were employed: distance matrix methods and maximum parsimony methods (Felsenstein, 1988). In the distance matrix methods, evolutionary distances (the number of nucleotide substitutions separating two taxonomic units) were computed for all pairs of taxa, and a phylogenetic tree was constructed from the total character differences. In maximum parsimony methods, the nucleotides at each site were used, and the shortest pathway leading to these character states was chosen as the phylogenetic tree.

RESULTS

The CITS region of the nrDNA region of the Typhula species ranged in size from 719 to 832 base pairs (bp) in length (Tables 4.2, 4.3 and 4.4). The CITS region length for T. ishikariensis ranged from 772-803 bp (Fig. 4.2), for T. incarnata 814-832 bp (Fig. 4.3), for T. phacorrhiza (Fig. 4.4) and for the unidentified Typhula-like fungi 709-798 bp (Fig. 4.4). There was a small difference (2-3 bp) between the dikaryotic isolate T. ishikariensis 2.105D (sequence 16 = 772 bp) and the monokaryotic isolates 2.105M1 (sequence 17 = 774 bp) and 2.105M2 (sequence 18 = 775 bp), Fig. 4.2. Also, there was a larger difference (4 to 13 bp) between the dikaryotic T. incarnata 2.136D.1 (sequence 33 = 828 bp) and the monokaryotic T. incarnata 2.136.2 (sequence 34 = 832 bp) and 2.136.3 (sequence 35 = 815 bp), Fig. 4.3. Furthermore, there were small differences in CITS region bp length between clones of the same isolate (Tables 4.2 and 4.4): sequence 8 and 9 = 3 bp difference; sequence 10 and 11 = 1bp difference; sequence 12 and 13 = 4 bp difference; and sequence 41 and 42 (3 bp difference). The sequences 39 and 40 were both 721 bp in length (Table 4.4). There were greater differences between different DNA extractions of the same isolate (Tables 4.2 and 4.3): sequences 5 and 6 varied by 13 bp; sequences 16, 17 and 18 varied from 1 to 3 bp; sequences 27, 28 and 29 varied from 1 to 3 bp; and sequences 33, 34 and 35 varied from 4 to 17 bp.

Also, there were bp length differences of the three parts of the CITS region (ITS 1, 5.8 S and ITS 2 regions; Tables 4.5, 4.6 and 4.7). The ITS 1 region bp length ranged from 282 to 307 bp for the *T. ishikariensis* complex sequences, 270 to 286 bp for the *T. incarnata* sequences, 240 to 241 bp for the *T. phacorrhiza* sequences and 246 to 271 bp for the unidentified *Typhula* spp. The 5.8 S region ranged from 147 to 159 bp for the *T. ishikariensis* complex sequences, 149 to 156 bp for the *T. incarnata* sequences, 155 bp for the *T. phacorrhiza* sequences. The ITS 2 region ranged from 239 to 254 bp for the *T. ishikariensis* complex sequences, 302 to

-	Sequence Number	Typhula ishikariensis isolate	Identification Code	Sequence length of CITS (bp)	Genbank accession number a
	01	T. ishikariensis WIG1	1.93**b	785	AF193347
	02	T. ishikariensis WIG1	2.183**	789	AF193348
	03	T. ishikariensis WIG1	3.120**	790	AF193349
	04	T. ishikariensis Biotype A	PR9-4-3*	793	AF193350
	05	T. ishikariensis Biotype A	PR7-6-7.1°*	790	AF193351
	06	T. ishikariensis Biotype A	PR7-6-7.2°*	803	AF193352
	07	T. ishikariensis Biotype A	56263**	803	AF193353
	08	T. ishikariensis Norway group I	2-5BS-1.1d*	785	AF193354
	09	T. ishikariensis Norway group I	2-5BS-1.2d*	785	AF193355
	10	T. ishikariensis var. ishikariensis	38649.1d*	783	AF193356
	11	T. ishikariensis var. ishikariensis	38649.24*	784	AF193357
	12	T. ishikariensis var. ishikariensis	92-32-MI.1d**	789	AF193358
	13	T. ishikariensis var. ishikariensis	92-32-MI.2d**	785	AF193359
	14	T. ishikariensis WIG2	1.31**	769	AF193360
	15	T. ishikariensis W1G2	2.97**	777	AF193361
	16	T. ishikariensis WIG2	2.105Dc**	772	AF193362
	17	T. ishikariensis W1G2	2.105M1c*	774	AF193363
	18	T. ishikariensis WIG2	2.105M2c*	775	AF193364
	19	T. ishikariensis WIG2	3.122**	776	AF193365
	20	T. ishikariensis Biotype B	35-8*	794	AF193366
	21	T. ishikariensis Biotype B	56264**	795	AF193367
	22	T. ishikariensis Norway group II	4-3S-5*	774	AF193368
	23	T. ishikariensis var. canadensis	JD 13**	774	AF193369
	24	T. ishikariensis var. canadensis	Can21m*	775	AF193370
	25	T. ishikariensis WIG2	2.100A**	775	AF193371
	26	T. idahoensis	32642*	784	AF193372

Table 4.2. Sequence number, karyotic state, sequence length and Genbank accession number of the complete internal transcribed spacer regions (CITS) of the nuclear ribosomal DNA of *Typhula ishikariensis* from Wisconsin, Canada, Japan, Norway and Russia.

² Genbank: http://www.ncbi.nlm.nih.gov.
^b *= monokaryotic isolate, ** = dikaryotic isolate.
^c DNA sequence obtained from different DNA extractions of the same isolate.

⁴ DNA sequence obtained from different clones of the same DNA extraction.

Table 4.3. Sequence number, karyotic state, sequence length and Genbank accession number of the complete internal transcribed spacer regions (CITS) of the nuclear ribosomal DNA of *Typhula incarnata* isolates from Wisconsin.

Sequence Number	Typhula incarnata	Identification Code	Sequence length of CITS (bp)	Genbank accession number ^a
27	T. incarnata	1.35.1 ^{b**c}	820	AF193373
28	T. incarnata	1.35.2 ^{b**}	821	AF193374
29	T. incarnata	1.35.3 ^b **	818	AF193375
30	T. incarnata	2.100B.15**	821	AF193376
31	T. incarnata	2.100B.2b**	826	AF193377
32	T. incarnata	2.100B.3 ^{b**}	814	AF193378
33	T. incarnata	2.136D.1 ^b **	828	AF193379
34	T. incarnata	2.136M.2 ^b *	832	AF193380
35	T. incarnata	2.136M.3 ^b *	815	AF193381
36	T. incarnata	3.279**	818	AF193382
37	T. incarnata	3.114**	819	AF193383

a Genbank: http://www.ncbi.nlm.nih.gov.

b DNA sequence obtained from different DNA extractions of the same isolate.
 c * = monokaryotic isolate, ** = dikaryotic isolate.

Table 4.4. Sequence number, karyotic state, sequence length and Genbank accession number of the complete internal transcribed spacer regions (CITS) of the nuclear ribosomal DNA of *Typhula phacorrhiza* and unidentified *Typhula* species from Wisconsin.

Sequence Number	Typhula isolate	Identification Code ^a	Sequence length of CITS (bp)	Genbank accession numbers ^b
38	T. phacorrhiza	3.120B	720	AF1933
39	T. phacorrhiza	2.230A.1°	721	AF1933
40	T. phacorrhiza	2.230A.2°	721	AF1933
41	Unidentified Typhula	G2.1°	798	AF1933
42	Unidentified Typhula	G2.2°	795	AF1933
43	Unidentified Typhula	G4	709	AF1933
44	Unidentified Typhula	3.129	719	AF1933

^a All isolates were dikaryotic.

^b Genbank: http://www.ncbi.nlm.nih.gov.

c DNA sequence obtained from different clones of the same DNA extraction.

Sequence	CITS	Complete	Complete	Complete
	795	709	150	246
1	790	298	150	240
2	789	298	153	247
3	/90	297	155	247
4	793	300	155	247
5	790	298	154	247
6	803	301	159	252
7	803	307	158	247
8	785	297	147	247
9	785	298	154	247
10	783	291	152	249
11	784	294	152	247
12	789	296	155	247
13	785	297	151	246
14	769	283	151	244
15	777	286	157	243
16	772	284	154	243
17	774	282	158	243
18	775	285	156	243
19	776	290	156	239
20	794	294	155	254
21	795	295	155	254
22	774	285	155	243
23	774	285	155	243
24	775	286	155	243
25	775	287	155	242
26	784	296	153	244
range	772-803	282-307	147-159	239-254

Table 4.5. Base pair length of the complete internal transcribed spacer region (CITS), the internal transcribed spacer region 1 (ITS 1), the 5.8 S region and the internal transcribed spacer region 2 (ITS 2) of the *Typhula ishikariensis* complex sequences.

• See Table 4.2 for specific information about each sequence.

Sequence number ^a	CITS length	Complete ITS 1 length	Complete 5.8 S length	Complete ITS 2 length
27	820	271	154	304
28	821	271	155	304
29	818	271	153	303
30	821	271	155	304
31	826	276	156	303
32	814	270	150	303
33	828	277	156	304
34	832	286	152	303
35	815	272	149	303
36	818	271	154	302
37	819	271	154	303
range	814-832	270-286	149-156	302-304

Table 4.6. Base pair length of the complete internal transcribed spacer region (CITS), the internal transcribed spacer region 1 (ITS 1), the 5.8 S region and the internal transcribed spacer region 2 (ITS 2) of the *T. incarnata* isolates (sequences 27 to 37).

* See Table 4.3 for specific information about each sequence.

Table 4.7. Base pair length of the complete internal transcribed spacer region (CITS), the internal transcribed spacer region 1 (ITS 1), the 5.8 S region and the internal transcribed spacer region 2 (ITS 2) of the *T. phacorrhiza* isolates (sequences 38 to 40) and unidentified *Typhula* isolates (sequences 41-44).

Sequence number ^a	CITS length	Complete ITS 1 length	Complete 5.8 S length	Complete ITS 2 length
38	720	240	155	234
39	721	241	155	234
40	721	241	155	234
41	798	271	144	292
42	795	271	142	291
43	709	246	145	229
44	719	246	155	230
range	709-795	240-271	142-155	230-292

^a See Table 4.4 for specific information about each sequence.

304 bp for the *T. incarnata* sequences, 234 bp for the *T. phacorrhiza* sequences and 229 to 292 bp for the unidentified *Typhula* spp. sequences.

The range of percentage of sequence identities of the CITS between the 44 Typhula sequences are presented in Table 4.8 and the matrices are presented in Appendix C (Tables C.1, C.2, C.3 and C.4. The percent identities of the *T. incarnata* sequences for pairwise comparison ranged from 92 to 100% within the species and from 61 to 78% outside the species. Sequences 41 and 42 were 91 to 97% identical to the *T. incarnata* sequences (Table 4.8), this indicates that the unidentified isolate G.2 is (or closely related to) *T. incarnata*. The *T. ishikariensis* sequences were separated into two biological species (TISH I and TISH II) and analyzed. The percent identities of the TISH I and TISH II sequences ranged from 87 to 100% within the species and from 65 to 74% outside the species. The three *T. phacorrhiza* sequences (38, 39 and 40) were 99 to 100% identical for pairwise comparisons within the species and 63 to 72% outside the species. The unidentified *Typhula* sequences (43 and 44) were 59 to 71% percent identical to all the other sequences.

The percent divergence of the sequence pair distances of the *Typhula* spp. using the clustal method with weighted residue weight table is presented in Table 4.9. The percent divergence ranged from 0 to 8% within each species and from 22 to 31% for outside species comparisons. Sequences 41 and 42 were 1 to 2% divergent from the *T. incarnata* sequences (27-37), and thus these unknown *Typhula* spp. are *T. incarnata*.

The sequences of the CITS were aligned by the clustal method within the DNAStar software and are presented in Figs. 4.2 to 4.16. Unique sequence differences between the two biological species of the *T. ishikariensis* complex are apparent within the ITS 1 region and will be discussed later (Figs. 4.4 and 4.5). The partial sequences of the 18 S (Fig. 4.2) and the 28 S region (Figs. 4.15 and 4.16) are identical for all sequences, while the 5.8 S region is highly conserved but not identical (Figs. 4.7 to 4.10). For the species *T. incarnata* and *T. phacorrhiza*, there are some unique sequence areas within the ITS 1 and ITS 2 regions.

Typhula isolates ^a	Sequence numbers	TISHI	TISHII	TIN	TP	T? (41-42)	T? (43-44)
TISH I	1-13, 26	89-100	87-98	61-76	67-72	65-73	60-68
TISH II	14-25	х	95-100	59-78	68-72	68-74	59-67
TIN	27-37	Х	Х	92-100	65-71	91-97	62-71
ТР	38-40	Х	Х	х	99-100	63-68	63-69
T?	41-42	х	х	х	x	99	64-67
T?	43-44	x	х	x	x	х	92

Table 4.8. Percentage of sequence identity in the complete internal transcribed spacer region (CITS) between *Typhula ishikariensis* biological species I, *T. ishikariensis* biological species II, *T. incarnata, T. phacorrhiza* and the unidentified *Typhula* spp.

^a TISH I = *Typhula ishikariensis* biological species I, TISH II = *T. ishikariensis* biological species II, TIN = *T. incarnata*, TP = T. *phacorrhiza* and T? = unidentified *Typhula* species.

Table 4.9. Percentage of divergence in the complete internal transcribed spacer region (CITS) between *Typhula ishikariensis* biological species I, *T. ishikariensis* biological species II, *T. incarnata*, *T. phacorrhiza* and the unidentified *Typhula* spp.

Typhula isolates ^a	Sequence numbers	TISHI	TISHII	TIN	TP	T? (41-42)	T? (43-44)
TISHI	1-13, 26	0-8	3-8	22-28	22-25	23-27	27-30
TISH II	14-25	х	0-5	22-25	22-24	23-25	27-30
TIN	27-37	X	х	0-2	29-32	1-2	28-31
TP	38-40	х	х	x	0-1	30	27-31
Τ?	41-42	х	х	х	x	0-1	28-30
T?	43-44	Х	х	x	x	x	0-4

^a TISH I = Typhula ishikariensis biological species I, TISH II = T. ishikariensis biological species II, TIN = T. incarnata, TP = T. phacorrhiza and T? = unidentified Typhula species.

	Sequence		60
1	01	TOTOTION CONCERNMENT COM	T-TTAA-AGCT-TGOTTGA-GCTGT
	02	TOTOTA CON A CONTRACT AND TOTOTAL	T-TTAA-AGCT-TGOTTGA-GCTGT
	03		T-TTAA-AGCT-TGGTTGA-GCTGT
	04	TOOTAGO CALCONG LOCATON TO TO CAL	T-TTAA-AGCT-TGGTTGA-GCTGT
T	05	TOOTLOTCAL CONTRACTOR DECISION	T-TTAA-AGCT-TGGTTGA-GCTGT
I	06	TOWNARDARCONTRACTOR	T-TTAA-AGCT-TGGTTGA-GCTGT
S	07	TOUTNOT GRACE SCIENCE STATCGAN	T-TTAA-AGCT-TGGTTGA-GCTGT
B	08	TICHAGTALICTICALAGUATCHTATCGAA	T-TTAA-AGCT-TGGTTGA-GCTGT
	09	TOUT MOTOR ACTION ACTINCA TO TOTAL	T-TTAA-AGCT-TGGTTGA-GCTGT
B	10	TOTALANTARA	T-TTAA-AGCT-TGGTTGA-GCTGT
S	11	TOUT MATCHACTAL CALAGERTCHTT TOGAN	T-TTAN-AGCT-TGGTTGA-GCTGT
1	12	TOUR ACTIGACOTOLOGIA ACCATCHT FICGAN	T-TTAA-AGCT-TGGTTGA-GCTGT
	13	TOUT NOT CHARTER COURSES AND TO THE TOGAN	T-TTAA-AGCT-TGGTTGA-GCTGT
1	14	TOUTAGTGANCTOCTALCETCATTICGAN	T-TTAA-AGCT-TGGTTGA-GCTGT
	15	PCSPTAGUEGACCTURE ANGENTERT TCGAN	T-TTAN-AGCT-TGGTTGA-GCTGT
	16	TOOTAGUTGAACCTOCTOCTOCTOCTOCTOCTOCTOCTOCT	T-TTAA-AGCT-TGGTTGA-GCTGT
_	17	TCCTTAGOTGAACCTOCOCAACCATCATTATCGAA	T-TTAA-AGCT-TGGTTGA-GCTGT
1	18	TOUGHAGENELACETOCIZIALGCATCATTUTCGAA	T-TTAA-AGCT-TGGTTGA-GCTGT
1	19	TOOTAGUTGLICETUCCULAGUATCATTATCGAA	T-TTAA-AGCT-TGGTTGA-GCTGT
S	20	TOOT AGOT GAME TO COLANGE ATTATCAT	T-TTAA-AGCT-TGGTTGA-GCTGT
ыļ	21	TOTTAGTOANCETOCORRECTORT	T-TTAA-AGCT-TGGTTGA-GCTGT
_	22	TOTOTAGENERACCTOCIDIALOCATCATTATCGAA	T-TTAN-AGCT-TGGTTGA-GCTGT
B	23	TOUT AGUTCHING TOUCHAGEA TOATTATCGAA	T-TTAN-AGCT-TGGTTGA-GCTGT
S	24	TOUT AGOTGAACETTE COANCEATCATT TOGAA	T-TTAA-AGCT-TGOTTGA-GCTGT
ոյ	25	TOTTINGINGALING CONSTRATES TO AND	T-TTAA-AGCT-TGOTTGA-GCTGT
	26	TOUTTAGETURACTOCOTRACCETCATTECCAN	T-TTAA-AGCT-TGOTTGA-GCTGT
1	27	TOUTLOUTGLECTTE CALLGUETCETTETCGAL	T-TTANG-GCTTTGGTTGA-GCTGG
	28	TOUTACOTGUCTOCCCARACETCETT	T-TTANG-GCTTTGGTTGA-GCTGG
	29	TOTAL CONCRETE CONCRETE AND TOTAL	T-TTANG-GCTTTGGTTGA-GCTGG
	30	TOUTLOGICALCETICOULOGATCATTICCAA	T-TTANG-GCTTTGGTTGA-GCTGG
τ	31	TOUTLOUT ALCONOLOGIA GUARDANT TOCAL	T-TTANG-GCTTTGGTTGANGCTGG
	32	TOUR ACOTOLOU TOUR CATCATO TOCAL	T-TTANG-GCTTTGGTTGA-GCTGG
N	33	TOTAL CONCERNMENT OF COMPACT AND TO COM	T-TTANG-GCTTT-GGTTGAGCTGG
**	34	TOUT AGONGARCING AND ANTATTATCGAA	T-TTAAGAGCTTTAGGTTGAGCTGG
	35	TOTAL TOTAL CONTRACT OF A TATATCAN	T-TTAAG-GCTTT-GGTTGAGCTGG
	36	TOTAL ACTION AND AND AND AND AND AND AND AND AND AN	T-TTANG-GCTTTGGTTGA-GCTGG
- 1	37	North Control Local Control Control Control	T-TTANG-GCTTTGGTTGA-GCTGG
_i	38	TOTAL CONTRACTOR OF THE STATE O	T-GTAG-AGGAGTTGTTTA-GCTGG
T	39	MILTING CONCERNING TO A STATISTICAL	T-GTAG-AGGAGTTGTTTA-GCTGG
۲I	40	TOTAL CONTRACTOR AND THE TOTAL	T-GTAG-AGGAGTTGTTTA-GCTGG
1	41	TOTAL CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR	T-TTANG-GCTTTGGPTGA-GCTGG
τ	42	THE REPORT OF THE REPORT OF THE PROCENT	T-TTAAG-GCTTTGGTTGA-GCTGG
2	43	CONTRACTOR LONGER CONTRACTOR CONTRACTOR	AGCTOTAGGCOTTGOTTGT-GCTGG
	44	TOTAL TARANGE ACONTOCICAL ACTIVITY ATTACAN	AGCTOTAGATOTTGOTTGT-GCTGG
'	- 1		
		ITS-1 primer 18 S	ITS 1

Figure 4.2. Alignment of the complete internal transcribed spacer region (CITS) of the 44 Typhula sequences (base pairs 1 to 60) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. ishikariensis biological species I and II, TIN = T. incarnata, TP = T. phacorrhiza and T? = unknown Typhula spp.

Se	quence	61 120
7	01	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
	01	
	02	
	03	
$_{T}$	04	
11	05	
-	06	
2	07	
•	80	
ь і	09	
р I	10	
2	11	
•	12	
	13	
	14	CGCTTCGGCGFTACGTGCCTTGCCTTGCCGTCCATTCC-TCAACACCTGTGCACACTTCAA
	15	CGCTTCGGCGFTACGTGCTCGCCTTGCCGTCCATTCT-TCAACACCCTGTGCACACTTCAA
	16	CGCTTCGGCGTTACGTGCTCGCCTTGCCGTCCATTCT-TCAALACCTGTGCACACTTCAA
т	17	CGCTTCGGCGTTACGTGCTCGCCTTGCCGTCCATTCT-TCAACACCTGTGCACACTTCAA
ī	18	CGCTTCGGCGPTACGTGCTCGCCTTGCCGTCCATTCT-TCAACACCCTGTGCACACTTCAA
ŝ	19	CGCTTCGGCGTTACGTGCTCGCCTCGCCGTCCATTCT-TCAACACCTGTGCACACITCAA
н	20	CGCTTCGGCGTTACGTGCTCGCCTTGCCGTCCATTCT-TCAACACCTGTGCACACITCAA
-	21	CGCTTCGGCGTTACGTGCTCGCCTTGCCGTCCATTCT-TCAACACCTGTGCACACTTCAA
R	22	CGCTTCGGCGTTACGTGCICGCCTTGCCGTCCATTCT-TCAACACCTGTGCACACTTCAA
s	23	CGCTTCGGCGFTACGTGCTCGCCTTGCCGTCCATTCT-TCAACACCTGTGCACACTTCAA
ii I	24	CGCTTCGGCGTTACGTGCTCGCCTTGCCGTCCATTCT-TCAACACCTGTGCACACTTCAA
-	25	CGCTTCGGCGTTACGTGCTCGCCTTGCCGTCCATTCT-TCAACACCTGTGCACACTTCAA
	26	CGCTTCGGCGT-ACGTGCTCGCCTCGCCGTCCATTCT-TCAACACCTGTGCACACTTCAA
	27	CGCTTCG-GTGCAT-GT-GCTT-GCCTT-GTGCTG-TCCATTCTTCAA
	28	CGCTTCG-GTGCAT-GT-GCTT-GCCTT-GTGCTG-TCCATTCTTCAA
	29	CGCTTCG-GTGCAT-GT-GCTT-GCCTT-GTGCTG-TCCATTCTTCAA
	30	CGCTGCG-GTGCAT-GT-GCTT-GCCTI-GTGCTG-TCCATICITCAA
Т	31	CCGCCTGCG-GTGCAT-GT-GCT-GCCTT-GTGCTG-TCCATTCTTCAA
1	32	CGCTGCG-GTGCAT-GT-GCTT-GCCTT-GTGCTG-TCCATTCTTCAA
N	33	CGCTGCG-GTGCAT-GT-GCTT-GCCTT-GTGCTG-TCCATTCTTCAA
	34	CGCTGCGAGTGCATAGT-GCTTAGCCTTAGTGCTGGTCCATTCTTCAA
	35	CGCTGCG-GTGCAT-GT-GCTT-GCCTT-GTGCTGGTCCATTCTTCAA
	36	CGCTGCG-GTGCAT-GT-GCTT-GCCTT-GTGCTG-TCCATTCTTCAA
	37	CGCTTCG-GTGCAT-GT-GCTT-GCCTT-GTGCTG-TCCATTCTTCAA
T	38	CCTTTCGAGGTATTGTGCTCGCTCCTTTCACTCTCTTACCACCTGTGCACCTCTT
p	39	CCTTTCGAGGTATTGTGCICGCTCCTTTCACTCTCTACCACCTGTGCACCTCTT
E	40	CCTTTCGAGGTATTGTGCTCGCTCCTTTCACTCTCTTACCACCTGTGCACCTCTT
	41	CGCTGCG-GTGCAT-GT-GCTT-GCCTT-GTGCTG-TCCATTCTTCAA
τ	42	CGCTGCG-GTGCAT-GT-GCTT-GCCTT-GTGCTG-TCCATTCTTCAA
?	43	CTCTCCGGAGTAATGTGCACGCCCGTCTCACTCTCACCTTCATTCA
	44	CTCTCCGGAGTAATGTGCACGCCCGTCTCACTCTCACTCA

ITS 1

Figure 4.3. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 61 to 120) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. *ishikariensis* biological species I and II, TIN = T. *incarnata*, TP = T. *phacorrhiza* and T? = unknown Typhula spp.

	Sequence	121 190
1		
	02	ASTALCGTC-TOTCCCATCUGCTTOTACCGGGGGA-GTTOTGAAAAAGGGATCAT-T
	02	ASTANICGITCTOTCCCATCCCGCTTOTACCGGGGGA-GTTOTGAAAAAGGGATCAT-T
	03	AGTAATUGTTCTGTCCCATCCCGCTTGTACGGGGGA-GCTGTGAAAAAGGGATCAT-T
т	04	AGTAATCGTTCTGTCCCATCCCGCTTGTACGGGGGAAGTTGTGAAAAAGGGATCAT-T
i	205	AGTAATCGTTCTGTCCCATCCCGCTTGTACGGGGGA-GTTGTGAAAAAGGGATCAT-T
ŝ	06	AGTAATCGTTCTGTCCCATCCCGCTTGTACGGGGGA-GTTGTGAAAAAGGGATCAT-T
Б	07	AGTAATCGGTCTGT-CCCCATCCCACTTGTATGGGGGA-GTTGTGAAAAAGGGATCATAT
ц	80	AGTAATCGTTCTGTCCCATCCCGCTTGTACGGGGGA-GTTGTGAAAAAGGGATCAT-T
D	09	AGTAATCGTTCTGTCCCATCCCGCTTGTACGGGGGA-GTTGTGAAAAAGGGATCAT-T
с С	10	AGTAATCGTTCTOTCCCATCCCGCTTOTACGGGGGG-GTTOTGAAAAAGGGATCAT-T
5	11	AGTAATCGTTCTGTCCCATCCCGCTTGTACGGGGGA-GTTGTGAAAAAGGGATCAT-T
L.	12	AGTAATCGTTCTOTCCCATCCCGCTTGTACGGGGGA-GTTGTGAAAAAGGGATCAT-T
	13	AGTAATCGTTCTGTCCCATCCCGCTTGTACGGGGGA-GTTGTGAAAAAGGGATCAT-T
	14	AGTAATCGTTCTGTCCCATCCCACTTGTATGGGGGA-GTTGTAAGGATCAT-T
	15	AGTAATCGTIC-TGTCCCATCCCACTTGTATGGGGGA-GTTGTAAGGATCAT-T
	16	AGTAATCGTTCTGTCCCATCCCACTTGTATGGGGGA-GTTGTAAGGATCAT-T
т	17	AGTAATCGTTCTGTCCCATCCCACTTGTATGGGGGGA-GTTGTAAGGATCAT-T
ī	18	AGTAATCGTTC-TGTCCCATCCCACTTGTATGGGGGGA-GTTGTAAGGATCAT-T
ŝ	19	AGTAATCGTTCCTTGTCCCATCCCACTTGTACGGGGGA-GTTGTAAGGATCAT-T
ñ	20	AGTAATCGTTCTGTCCCAATCCCCACTTGTATGGGGGGA-GTTGTAAGGATCAT-T
**	21	AGTAATCGTTCTGTCCCCAATCCCCACTTGTATCGGGGGA-GTTGTAAGGATCAT-T
R	22	AGTAATCGTTCTGTCCCCATCCCCCTTGTATGCGGGGA-GTTGTAAGGATCAT-T
s	23	AGTAATCGTTC TOTCCCATCCCCCTTOTATCCCCCCGA-GTTOT AAGCATCAT-T
п	24	AGTAATCGTTC
	25	AGTAATCGTTCTOTCCCATCCCACTIGIATCCCCCCCAGT_TOTAAGGATCAT_T
	26	AGTAATCETTCAGTAATCETCAAAAAGCAATCETCAAAAAAGC_AATCAT
i	27	
	28	
	29	
	30	
T	21	
-11	22	CAC-CTURG-CACAC-TITOTAGT-TGACTCTTFIGITTA-TCT
	32	CAC-CTUTG-CACAC-TTTGTAGT-TGACTCTTTTGTTTA-TCT
-	24	CAC-CTORG-CACACATTIGIG-AATGIGACACITCITTIGOTTAATCT
1	25	CAC-CTOTG-CACACATTTOTG-AGAATGTGACACTTCTTTTGOTTAATCT
	33	CAC-CTGTG-CACAC-TTTGTAAT-TGA-ACTTTTTGGTTAATCT
	30	CAC-CTOTG-CACAC-TTTOTAGT-TGACTCTTTTGTTTA-TCT
I	3/	ACT-CTOTG-CACAC-TTTGTAGT-TGACTCTTTTGTTTA-TCT
T	38	-GTAGICTITTTGTATTCCTCTTCGGAGGAAGGCGGAGTGTTGCCGTGCGCAA
P	39	-GTAGTCTTTTTGTATTCCTCTTCGGAGGAGGGGGGGGGG
	40	-GTAGICTITTIGTATICCTCTICGGAGGAAGGCGGAGTGTTGCCGTGCGCAA
_	41	CAC-CROTG-CACAC-TTTOTAGT-TGACTCTTTTGTTTA-TCT
	42	CAC-CTOTG-CACAC-TTTOTAGT-TGACTCTTTTGTTTA-TCT
?{	43	TGACGGATGGG-ATATCTTTCCGCTTCTCAGAAGCGGGTTTGGGGGGTCAAGC
1	44	TGACGGATGGGGATATCTTTCCGCTTCTGGCGGGGTTTGGGGGGTCAGGC
		ITS 1

Figure 4.4. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 121 to 180) using the Clustal method with weighted residue weight table. *Typhula ishikariensis* "signature sequence" indicated by box. TISH BSI and BSII = T. ishikariensis biological species I and II, TIN = T. incarnata, TP = T. phacorrhiza and T? = unknown Typhula spp.

Sequence 181					
	umber				
	01	ATTIGATITCICITITATAGCI			
	02	ANTIGOTTICICITITIATAGCI			
	EU	AATTTGGTTTCTCTCTTTTATAGCT	TICCAAAGAGAGGGTAAGACGTTACAAGAAC		
т	04	AATTTGGTTTCPCPTPTTATAGCT	TTCCAAGAGAGAGGG-GTAAGACGTTAAAAGAAC		
Ŷ	05	AATTTGGTTTCPCPTTTTATAGCT	TICCAAAGAGAGGGTAAGACGTTAAAAGAAC		
-	06	AATTTGGTTTCTCTTTTTATAGCT	TTTCCAAGAGAAGGTAAGACGTTACAAGAACC-		
о П	07	CATTTTGGG-CICITCTIATAGCT-	TTCCAAAGAGAGGGGGAAGGACGCTAAAAGAAC		
EI	80	AATITGGITTCICITITATAGCI	TTCCAAAGAGAGGG-TAAGACGTTAAAAGAAC		
n	09	AATTTGGTTTCTCTTTTTATAGCT-	TTCCAAAGAGAGGGTAAGACGTTAAAAGAAC		
B	10	AATITGGITTCICTTITTATAGCT-	TTCCAAAGAGAGGGTAAGACGTTACAAGAAC		
S	11	AATTTGGTTPCTCTTTTTATAGCT	TTCCAAAGAGAGGGTAAGACGTTACAAGAAC		
I	12	AACITGGTTTCTCTTTTATAGCT-	TTCCAAGGAGAGGGTAAGACGTT-CAAGAAC		
	13	AACITGGITTCTCTTTTATAGCT-	TTCCAAGGAGAGGGTAAGACGTTACAAGAAC		
1	14	CATTIGGT-CITCTCI-	CTCCAAAGAGAGGGTAAGACGCTTCAAGAAC		
	15	CATTTGGTTCTTCTCT-	CTCCAAAGAGAGGGTAAGACGCTACAAGAAC		
	16	CATTTGGTTCTTCTCT-	CTCCAAAGAGAGGGTAAGACGCTACAAGAAC		
-	17	CATTTGGTTCTTCTCT	CTCCAAAGAGAGGGTAAGACGCTACAAGAAC		
-	18	CATTEGOTICITCICI	CTCCAAAGAGAGGGTAAGACGCTACAAGAAC		
1	19	AATTTGGTTCTCTC	CTCTCCAAAGAGAGGGTAAGATGTTACAAGAAC		
5	20	CATTERGETECTCTCTCTCCAA			
н	21	CATTERGETCTTCTCTCCCAA-	AGAGAGGGTGTGTAAGACGTTACAAGAGC		
_	22	CATTERGOTICTTCT	CTCCAAAGAGAGGGTA		
B	23		CTCCAAAGAGAGGGTAAGACGCTACAAGAAC		
S	74				
П	24				
	25				
	20	AATTIGOTTICICCTTTATAGCI			
	27 G-TTCA-TCTCTCTCTGACTCCGGTCTCTGTGAAGGGGTGCCTGGCTTTTCGAAAGCA				
	28	G-TFCA-TETETETETETEACTCCGG			
	29	G-TFCA-TCTCTCTCTCTGACTCCGG			
	30	G-TFCA-TCTCTCTCTTGACTCCGG	TCTCTGTGAAGGGGTGCGTGGCTTTTCGAAAGTA-		
T	31	G-TTCA-TCTCTCTCTTGACTCCGG	TCTCTGTAAAGGGGTGCGTGGCTTTTCGAAAGTA-		
1	32	G-TTCA-TCTCTCTCTTGACTCCGG	TCTCTGTAAAGGGGTGCGTGGCTTTTCGAAAGTA-		
N	33	GGTTCAATCTCTCTCTTGACTCCGG	TCTCTGTGAAGGGGIGCGTGGCTTT-CGAAAGTA-		
	34	GGTTCAATCTCTCTCTTGACTCCGG	tetetgtgaaggggggggggggettt-cgaaagta-		
	35	GGTT-AATCTCTCTCTGACTCCGG	TCICTOTGAAGGGGTGCGTGGCTTT-CGAAAGTA-		
	36	G-TTCA-TCTCTCTCTGACTCCGG	TCTCTGTGAAGGGGTGCGTGACTTTTCGAAAGTA-		
	37	G-TTCA-TCTCTCTCTCACTCCGG	TCTCTGTGAAGGGGTGCGTGGCTTTTCGAAAGCAA		
τI	38	GCATTGGCTCTACTCCA-	TCTCAAAAGGA		
p	39	GCATTGGCTCTACTCCA-	ICICAAAAGGA		
1	40	GCATTGGCTCTACTCCA-	TCTCAAAAGGA		
Í	41	G-TTCA-TCTCTCTCTTGACTCCGG	TCTCTGTGAAGGGGTGCGTGGCTTTTCGAAAGTA-		
Т	42	G-TTCA-TCTCTCTCTTGACTCCGG	TCTCTGTGAAGGGGTGCGTGGCTTTTCGAAAGTA-		
?	43	G-TTCACTOGOGTTTTTCCCCCTGCTTT-CCCA			
	44 G-TTCACTOGOGTTTTTCCCCTTCCCA				
•					

ITS 1

Figure 4.5. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 181 to 240) using the Clustal method with weighted residue weight table. *Typhula ishikariensis* "signature sequence" indicated by box. TISH BSI and BSII = T. ishikariensis biological species I and II, TIN = T. incarnata, TP = T. phacorrhiza and T? = unknown Typhula spp.

amber 241 01 GATCTTTG-CCTTATAACA-TACCCTTCTTT-THAMAMATGTTTAT-GAACA 02 GATCTTTG-CCTTATAACA-TACCCTTCTTT-THAMAMATGTTTAT-GAACA 03 GATCTTTG-CCTTATAACA-TACCCTTCTTT-THAMAMATGTTTAT-GAACA 04 GATCTTTG-CCTTATAACA-TACCCTTCTTT-THAMAMATGTTTAT-GAACA	300 ССПСАЛАЛАА ЭТСАЛАЛАЛА ЭТСАЛАЛАЛА ЭТСАЛАЛАЛА ЭТСАЛАЛАЛА СПАЛАЛАЛА СПАЛАЛАЛА
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29 GGTCCTCTATGTTATTATTATACACC-CTTTACAAAAACAAGTCCAT-E	GAACGTCCA
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132 GGTCCTCTATGTCAT-ATTATACACC-CTTTACAAAAAAAAAA	GAACGTCCA
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34 GGTCCTCTATGTTAT-ATTATACACC-CTTTACAAAAAAACAAGTC-AT	AGACGTCCA
35 GGTCCTCTATGTTAT-ATTATACACC-CTTTACAAAAAAAAAA	AGACGTCCA
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41 GGTCCTCTATGTTAT-ATTATACACC-CTTTACAAAAAAACAAGTCCAT-A	GAACGTCCA
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Figure 4.6 Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 241 to 300) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. *ishikariensis* biological species I and II, TIN = T. *incarnata*, TP = T. *phacorrhiza* and T? = unknown *Typhula* spp.

	Sequence	301	
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m	04	ATG-TAG-GCTCGCCTTAAAAA-CGTGTAGCTGAAATT-ATAAAATTATAC	20-777
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L	06	ATGGTAG-CTTCGCCTTAAAAACCGFGFAGCTGAAAATATTAAATTATTC	CHC-2755
S	07	ATG-CAC-GCTCGCCTTAAAAACGGTGTAGCGTGAAATTATAAAATTATAC	CLOCKER I
H	08	ATG-TAG-GCTCGCCTTAAAAA-CGTGTAGCTGAAATT-ATAAAATTATAC	
	09	ATG-TAG-GCTCGCCTTAAAAA-CGTGTAGCTGAAATT-ATAAAA-TTATAC	
B	10	ATG-TAG-GCTCGCCT-AAAAACCGTGTAGCTGAAATATAAATATTC	2
S	11	-TG-TAG-GCTCGCCTTAAAAAACGTGTAGCTGAAATATAAATATAC	C-754
I	12	-TG-TAG-GCTCGCCTTAAAAA-CGTGTAGCTGAAATT-ATAAAATTATAC	
	13	-TG-TAG-GCTCGCCTTAAAAA-CGTGTAGCTGAAATT-ATAAAATTATAC	
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H	20	ATG-TAG-GCTCGCCTTAAAAA-CGTGTAGCTGAAATTTATAAAAA-TTATAC	
	21	ATG-TAG-GCTCGCCTTAAAAA-CUFUTAGCTGAAATTTATAAAAAATTATAC	Statistics States
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	25	-TG-TAG-GCTCGCCTTAAAAA-CGTGTAGCTGAAATT-ATAAAATTATAC	746-717
. !	26	ATG-TAG-GCTCGCCTTAAAAA-CGTGIAGCTGAAATT-ATAAAATTATAC	AC-TT
	27	ATGTAGGCGCA-GCGTAAAACACTGTTTGCT-GAAA-TTAT-AAAACTTATAC	AC-717
	28	ATGTAGGCGCA-GCGTAAAACACTGTTTGCT-GAAA-TTAT-AAAACTTATAC	AC-TTZ
	29	ATGTAGGCGCA-GCGTAAAACACTGTTTGCT-GAAA-TTAT-AAAACTTATAC	AC-TIL
- 1	30	ATGTAGGCGCA-GCGTAAAACACTGTTTGCT-GAAA-TTAT-AAAACTTATAC	AC-157
T	31	ATGTAGGCGCAAGCGTAAAACACTGTTTGCT-GRAA-TTAT-AAAACTTATAC	
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	35	ATGTAGGCGCA-GCGTAAAACACTGTTTGCTTGAAA-TTAT-AAAACTTATAC	x-C-791
	36	ATGTAGGCGCA-GCGTAAAACACTGTTIGCT-GAAA-TTAT-AAAACTTATAC	
	37	ATGTAGGCGCA-GCGTAAAACACTGTTTGCT-GAAA-TTAT-AAAACTTATAC	
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Figure 4.7. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 301 to 360) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. *ishikariensis* biological species I and II, TIN = T. *incarnata*, TP = T. *phacorrhiza* and T? = unknown Typhula spp.

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Figure 4.8. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 361 to 420) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. *ishikariensis* biological species I and II, TIN = T. *incarnata*, TP = T. *phacorrhiza* and T? = unknown Typhula spp.



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Figure 4.9. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 421 to 480) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. ishikariensis biological species I and II, TIN = T. incarnata, TP = T. phacorrhiza and T? = unknown Typhula spp.



Figure 4.10. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 481 to 540) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. *ishikariensis* biological species I and II, TIN = T. *incarnata*, TP = T. *phacorrhiza* and T? = unknown Typhula spp.

Sequence		
	number	541 600
	01	-GGTTTGTTACAGACTTTACGAGGCTT-GGACTTTTGGAGTGTGCCGGTCT-C
	02	-CGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
	03	-CGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
_	04	-CGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCCGTCT-C
T	05	-CGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
1	06	TCGGTTGGTTAC-CAGACTTTACGAAGGCT-GGACTTT-GAAGTGTGCGGGTCTTC
S	07	TCGTTTGTTTACAGACITTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
н	08	-CGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
_	09	-CGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
В	10	TCGTTTGTTACAGACTTTACGAGGCTT-GGACTTT-GAAGTGTGCCGGTCTTC
S	11	-CGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
I	12	-CGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
	13	-CGTTTGTTTACAGACTTTACGAGGCTT-G-ACTTT-GAAGTGTGCCCGGTCT-C
	14	TGGTTTGTTT-ACAGACTTTACGAGGCTT-GACTTTT-GGAGTGTGCCGGTCT-C
	15	TCGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
	16	TCGTTTGTTTACAGACTTTACGACGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
т	17	TCGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
-	18	TCGTTTGTTTACAGACITTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
2	19	CCGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
5	20	TCGTTTGTTTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCTCT
	21	TCGTTTGTTTTTACAGACTTTACGACGCTT-GGACTTT-GGAGTGTGCCCGGTCTCT
	22	TCGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
0	23	TCGTTTGTTTACAGACITTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
а п	24	TCGTTTGTTTACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
u	25	TCGTTTGTTT-ACAGACTTTACGAGGCTT-GGACTTT-GGAGTGTGCCGGTCT-C
	26	-CGTTTGTTTACAGACTTTACGAGCCTTTGGACTTTTGGAGTGTGCCGGTCT-C
1	27	ATGTTTTTATTAACGTAGTTCTTGTGGCTTGGATCTTGGAGTTTGTGCCGG-TAAACCTT
	28	ATGTTTTTATTAACGTAGTTCTTGTGGCTTGGATCTTGGAGTTTGTGCCCGG-TAAACCTT
	29	ATGTTTTTATTAACGTAGTTCTTGIGGCTTGGATCTIGGAGTTTGTGCCGG-TAAACCTT
	30	ATGTTTTTATTAACGTAGTTCTTGTGGCTTGGATCTTGGAGTTTGTGCCGG-TAAACCTT
т	31	ATGTTTTTATTAATGTAGTTCTTGTGGCPTGGATCTTGGAGTTTGTGCCGG-TAAACCTT
-	32	ATGTTTTTATTAATGTAGTTCTTGIGGCTTGGATCTIGGAGTTTGTGCCGG-TAAACCTT
Ň	33	ATGTTTTATTAACGTAGTTCTTGTGGCTTGGATCTTGGAGTTTGTGCCGGGTAAACCTT
*1	34	ATGTTTTATTAACGTAGTTCTTGTGGCTTGGATCTTGGAGTTTGTGCCGG-TAAACCTT
	35	ATGTTTTATTAACGTAGITCTTGTGGCTTGGATCTTGGAGTTTGTGCCCG-TAAACCTT
	36	ATGTTTTATTATTATGTAGTTCTTGTGGCTTGGATCTTGAAGTTTGC-CCGG-TAAACCTT
	37	ATGTTTTATTAACGTAGITCTTGTGGCTTTGGATCTTGGAGTTTTGCCCCG-TAAACTTT
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Figure 4.11. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 541 to 600) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. *ishikariensis* biological species I and II, TIN = T. *incarnata*, TP = T. *phacorrhiza* and T? = unknown Typhula spp.

amber 601 OC 01 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 02 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 03 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 04 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 105 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 106 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 107 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 108 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 11 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 12 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 13 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 14 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 15 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 16 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 17 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 18 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 19 TAACGAGATCGACTCC-TCITTANATGCATTAGCTGGAACCTC-TT-GTGGACC-AG 20		Sequence		~~~
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TAGTTAGGTGGTCCCCCTCTTT-AMATGCATTAGCTGGACCTC-TTGGGGGCCAG TAGTTAGGTGTGGCCCCCCTTT-AMATGCATTAGCTGGACCTC-TTGTGGGGCCAG TAGTTAGGTGGTGGCCCCCTCTT-AMATGCATTAGCTGGACCTC-TTGTGGGGCCAG TAGTTAGGTGGTGGCCCCCTCTT-AMATGCATTAGCTGGACCTC-TTGTGGGGCCAG TAGTTAGGTGTGGCCCCCTCTTT-AMATGCATTAGCTGGACCTC-TTGTGGGGCCAG TAGTTAGGTGTGGCCCCCTCTTT-AMATGCATTAGCTGGACCTC-TTGTGGGGCCAG TAGTTAGGTGTGGCCCCCTCTTT-AMATGCATTAGCTGGACCTC-TTGTGGGGCCAG TAGTTAGGTGTGGCCCCCCTCTT-AMATGCATTAGCTGGACCTC-TTGTGGGGCCAG TAGTTAGGTGGTGCCCCCCTCTTT-AMATGCATTAGCTGGACCTC-TTGTGGGGCCAG TAGTTAGGTGGTGCCCCCCTCTTT-AMATGCATTAGCTGGACCTC-TTGTGGGGCCAG TAGTTAGGTGGTGCC-GCTCAC-TTTAMATGCATTAGCTGGACCTC-TTGTGGGGCCAG TAGTTGAGTCGGCTCAC-TTTAMATGTATTAGC-GGAACCTC-T-GCG-ACCCAT TAGTTGAGTCGGCTCAC-TTTAMATGTATTAGC-GGAACCTC-TGCG-ACCCAT TAGTTGAGTCGGCTCGCCCTTTT-AMATGCATTAGCCGGAACCTC-TGCG-ACCCAT TAGTTGAGTCGGCTCGCCCCTTTT-AMATGCATTAGCCGGAACCTC-TGCG-ACCCAT TAGTTGAGTCGGCTCGCCCCTTTT-AMATGCATTAGCCGGAACCTC-TGCG-ACCCAT TAGT-AGGT-GTTGGCTCCTCTTTTAMATGCATAGCATCGAACCTC-TTGTGGGGCCAG TAGT-AGGT-GTTGGCTCCCCTTTTAMATGCATAGCCACGACCTC-TGCG-ACCCAT TAGT-AGGT-GTTGGCTCCCCTTTTAMATGCATAGCCTC-TTGTGGGCCAG TAGC-AGAGCCGGCTCCCTTTAMATGCATAGCCACGACTCCGTCGCTGACCG UTS 2		20		nG NG
TAGTTAGGTGGTCGGCTCACTTTAAATGCATTAGCTGGAACCTC-TTGGGGCCAG TAGTTAGGTGTGGCCCCCTTT-AAATGCATTAGCTGGAACCTC-TTGGGGCCAG TAGTTAGGTGTGGCCCCCTTT-AAATGCATTAGCTGGAACCTC-TTGGGGCCAG TAGTTAGGTGGTGGCCCCCTTT-AAATGCATTAGCTGGAACCTC-TTGGGGCCAG TAGTTAGGTGTGGCCCCCTTT-AAATGCATTAGCTGGAACCTC-TTGGGGGCCAG TAGTTAGGTGTGGCCCCCTTT-AAATGCATTAGCTGGAACCTC-TTGGGGGCCAG TAGTTAGGTGTGGCCCCCTTT-AAATGCATTAGCTGGAACCTC-TTGGGGGCCAG TAGTTAGGTGTGGCCCCCTTT-AAATGCATTAGCTGGAACCTC-TTGGGGGCCAG TAGTTAGGTGGTGGCCCCCTTT-AAATGCATTAGCTGGAACCTC-TTGGGGGCCAG TAGTTAGGTGGTGCCGCTCAC-TTTAAATGCATTAGCTGGAACCTC-TTGGGGGCCAG TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT TAGTTGAGTCGGCTCCCCTTTT-AAATGTATTAGC-GGAACCTC-TGCG-ACCCAT TAGTTGAGTCGGCTCCCCTTTT-AAATGCATTAGCTGGAACCTC-TTGGGGCCAG TAGT-AGGT-GTTGGCTCCCTTTTAAATGTATTAGCGAGACCTC-TTGGGGCCAG ACCCAGAGCCGGCTCCCTTTAAATGTATTAGCGAGACCTCC-TTGGGGCCAG TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGCCGGCCAG TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGCCGGCCAG LTCS 2		23		
T TAGTTAGTTGGCTCCCTTT-AAATGCATTAGCTGGACCTC-TTTGTGTGCCAG I TAGTTAGTTGTGGCTCCCTTT-AAATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 33 TAGTTAGTTGTGGCTCCCTTT-AAATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 34 TAGTTAGTTGGCTCCCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGTGCCAG 35 TAGTTAGTTGGCTCCCTCTT-AAATGCATTAGCTGGAACCTC-TTTGTGGTGCCAG 36 TAGTTAGGTTGTGGCTCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGTGCCAG 36 TAGTTAGGTTGTGGCTCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGTGCCAG 37 TAGTTAGGTGTGGCCCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGTGCCAG 38 TAGTTGGGTCGGCTCACTTTAAATGCATTAGCTGGAACCTC-TTGGGTGCCAG 39 TAGTTGAGTCGGCTCACTTTAAATGCATTAGCCGGAACCTC-TGCG-ACCCAT 7 39 TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT 40 TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TTGGGGCCAG 41 TAGT-AGGT-GTTGGCTCCTCTTT-AAATGCATATGCAT-AGCTGGACCTC-TTGGGGCCAG 7 42 TAGT-AGGT-GTTGGCTCCTCTTTTAAATGCAT-AGCTGGACCTC-TTGGGGCCAG 7 41 TAGT-AGGT-GTTGGCTCCTCTTTTAAATGCAT-AGCTGGACCTC-TTGGGGCCAG 8 TAGT-AGGT-GTTGGCTCCCTTTTAAATGCAT-AGCTGGACCTC-TTGGGGCCAG 9 TAGT-AGGT-GTTGGCTCCCCTTTTAAATGCAT-AGCTGGACCCCTTGGGGGCCAG 10 TAGT-AGGT-GCTGGCCCCCCCTTTTAAATGATATAGCCGAGGACCTCC-TTGGGGCCAG		30		AG
$\begin{bmatrix} 1 & 32 & TAGTTAGJTGTGCCTCCTCTT-AAATGCATTAGCTGGACCTC-TTTGTGGGGCCAG 34 TAGTTAGJTGTGGCTCCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGGGCCAG 34 TAGTTAGJTGTTGGCTCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGGGCCAG 35 TAGTTAGJTGTGGCTCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGGGCCAG 36 TAGTTAGJTGTGGCTCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGGGCCAG 37 TAGTTAGJTGTGGCTCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGGGCCAG 38 TAGTTGAJTCGGCTCACTTTAAATGCATTAGCTGGAACCTC-TTGTGGGGCCAG 39 TAGTTGAJTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT 40 TAGTTGAJTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT 41 TAGT-AGGT-GTTGGCTCCTCTTT-AAATGCATAAGCTGGAACCTC-TTTGTGGGGCCAG 42 TAGT-AGGT-GTTGGCTCCTCTTT-AAATGCATAAGCTGGAACCTC-TTTGTGGGGCCAG 43 TAGT-AGGT-GTTGGCTCCTCTTTAAATGCATAGCTGGAACCTC-TTTGTGGGGCCAG 44 TAGT-AGGT-GTTGGCTCCC-CTTTAAATGTATTAGCGAGGACTCCGTCGGCTGGCCAG 45 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGGCTGGCCG 46 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGGCCGGCCAG 47 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGGCCGGCCAG 48 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGGCCGGCCAGG 49 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGGCCGGCCAGG 40 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGGCCGGCCAGG 40 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGGCCGCCCG 41 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGGCCGGCCAGGCCAGG$	Т	31	TAGTTAGOTTGTTGGCTCCTCTTT-AAATGCATTAGCTGGGACCTC-TTTGTGGTGCC	AG
N 33 TAGTIAGJITGTTGGCTCCTCTTT-AAATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 34 TAGTIAGJITGTTGGCTCCTCTTT-AAATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 35 TAGTIAGJITGTTGGCTCCTCTTT-AAATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 36 TAGTIAGJITGTTGGCTCCTCTTT-AAATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 37 TAGTIAGJITGTTGGCTCCTCTTT-AAATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 38 TAGTTGAGTCGT-GCTCACTTTAAATGCATTAGC-GGAACCTC-TTGTGGTGCCAG 40 TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT 41 TAGT-AGGI-GTTGGCTCCTCTTT-AAATGCATTAGCTGGACCTC-TGCG-ACCCAT 42 TAGT-AGGI-GTTGGCTCCTCTTT-AAATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 7 43 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGGAGACTCCGTCGCTGGCCC-G 44 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGCTGACCG 45 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGCTGACCG	Ц	32	TAGTTAGOFIGTTGGCCCCCCCTCTT-AAATGCATTAGCTGGGACCTC-TTTGTGGTGCC	AG
34 TAGTTAGJTGTGGCICCICTTT-AMATCATTAGTGGACCTC-TTTGTGGTGCCAG 35 TAGTTAGJTGTGGCICCICTTT-AMATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 36 TAGTTAGJTGTGGCICCTCTTT-AMATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 37 TAGTTGGTGTGGCICCTCTTT-AMATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 38 TAGTTGGGTCGCTCCCTTTT-AMATGCATTAGCTGGAACCTC-TTGTGGGGCCAG 9 TAGTTGGGTCGGCTCACTTTAMATGTATTAGC-GGAACCTC-TGCG-ACCCAT 40 TAGTTGGGTGCCTCCTCTTT-AMATGTATTAGC-GGAACCTC-TGCG-ACCCAT 41 TAGT-AGGT-GCTCGCTCCTCTTT-AMATGCATTAGCTGGAACCTC-TTGTGGTGCCAG 7 42 TAGT-AGGT-GTTGGCTCCTCTTT-AMATGCATAGCTGGAACCTC-TTGTGGTGCCAG 7 43 TAGC-AGAGCCGGCTCCCTTTAMATGTATTAGCGGGGACCTCGTCGCCGCTGACCA-G 14 TAGC-AGAGCCGGCTCCCTTTAMATGTATTAGCGAGGACTCCGTCGCCTGACCA-G 15 TAGC-AGAGCCGGCTCCCTTTAMATGTATTAGCGAGGACTCCGTCGCCGCTGACCA-G 16 TAGC-AGAGCCGGCTCCCTTTAMATGTATTAGCGAGGACTCCGTCCGCTGACCA-G 17 S TAGC-AGAGCCGGCTCCCTTTAMATGTATTAGCGAGGACTCCGTCGCCGCTGACCA-G	N	13	TAGTTAGOTIGTIGGCICCICITT-AAATGCATTAGCIGGACCTC-TTIGTGGFGCC	AG
$\begin{bmatrix} 35 & TAGTTAGJTGTTGGCTCCCTTT-AAATGCATTAGCTGGACCTC-TTTGTGGTGCCAG36 & TAGTTAGJTGTTGGCTCCTCTTT-AAATGCATTAGCTGGACCTC-TTTGTGGTGCCAG37 & TAGTTGGGTCGCTCGCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGTGCCAG38 & TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT40 & TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT41 & TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT42 & TAGTTGAGT-GTTGGCTCCTCTTT-AAATGCATTAGCTGGACCTC-TTGTGGTGCCAG43 & TAGT-AGGT-GTTGGCTCCTCTTTTAAATGTATTAGCGGGACCTCCGTTGGTGGCCAG? 43 & TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGCCTGACCGITS 2$		34	TAGTTAGGTTGTTGGCTCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGTGCC	AG
36 TAGTTAGGTTGTTGGCTCCCTTTT-ANATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 37 TAGTTAGGTTGTGGCTCCTCTTT-ANATGCATTAGCTGGACCTC-TTTGTGGTGCCAG 18 TAGTTGAGTGGGCTCACTTTANATGTATTAGC-GGAACCTC-TGCG-ACCCAT 9 TAGTTGAGTGGGCTCACTTTANATGTATTAGC-GGAACCTC-TGCG-ACCCAT 40 TAGTTGAGTGGGCTCACTTTANATGTATTAGC-GGAACCTC-TGCG-ACCCAT 41 TAGTTGAGTGGCTCGCTCCTCTTT-ANATGTATTAGC-GGAACCTC-TGCG-ACCCAT 42 TAGT-AGGT-GTTGGCTCCTCTTT-ANATGCATAGCTGGGACCTC-TTTGTGGTGGCCAG 7 42 TAGT-AGGT-GTTGGCTCCTCTTTTANATGCAT-ASCTGG-ACCTC-TTTGTGGTGGCCAG 7 43 TAGC-AGAGCCGGCTCCCTTTANATGTATTAGCGAGGACTCCGTCGCCGCTGACCG 44 TAGC-AGAGCCGGCTCCCTTTANATGTATTAGCGAGGACTCCGTCGCCGCTGACCG 45 TAGC-AGAGCCGGCTCCCTTTANATGTATTAGCGAGGACTCCGTCGCCGCTGACCG 47 TAGC-AGAGCCGGCTCCCTTTANATGTATTAGCGAGGACTCCGTCGCCGCTGACCG		35	TAGTTAGGTTGTTGGCFCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGTGCC	AG
$ \begin{bmatrix} 37 & TAGTTAGGTTGTTGGCTCCTCTTT-AAATGCATTAGCTGGAACCTC-TTTGTGGTGCCAGTAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT7 & TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT40 & TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT41 & TAGT-AGGT-GCTGGCTCCTCTTTT-AAATGCATTAGCTGGGACCTC-TTTGTGGTGGCCAG7 & 42 & TAGT-AGGT-GTTGGCTCCTCTTTTAAATGCAT-AGCTGGAACCTC-TTTGTGGTGGCCAG43 & TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGCCGCTGACCG44 & TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCGCCGCTGACCG17 & 20 & 10$		36	TAGTTAGGTTGTTGGCTCCTCTTT-AAATGCATTAGCTGGGACCTC-TTTGTGGTGCC	AG
$ \begin{array}{r} T \\ 38 \\ TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT \\ 9 \\ 40 \\ TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT \\ 41 \\ TAGT-AGGT-GCTGGCTCCTCTTT-AAATGCATTAGCTGGGACCTC-TTTGTGGGGCCAG \\ 42 \\ TAGT-AGGT-GTTGGCTCCTCTTTTAAATGCAT-AGCTGG-ACCTC-TTTGTGGGGCCAG \\ 43 \\ TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGACTCCGTCGCCGACCG \\ 44 \\ TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGACTCCGTCGCCGCTGACCG \\ ITS 2 \\ \end{array}$		37	TAGTTAGGITGITGGCICCICITT-AAATGCATTAGCTGGAACCTC-TTTGTGGIGCC	AG
P 39 TAGTTGAGTCGGCTCACTTTANATOTATTAGC-GGAACCTC-TGCG-ACCCAT 40 TAGTTGAGTCGGCTCACTTTANATOTATTAGC-GGAACCTC-TGCG-ACCCAT 41 TAGT-AGGT-GTTGGCTCCCTTTT-ANATGCATAGCTGGGACCTC-TTTGTGGGTGCCAG 7 42 TAGT-AGGT-GTTGGCTCCCTCTTT-ANATGCAT-AGCTGGACCTC-TTTGTGGGGCCAG 8 TAGC-AGAGCCGGCTCCCTTTANATGTATTAGCGAGGACTCCGTCGGCCGGCTGACCG 44 TAGC-AGAGCCGGCTCCCTTTANATGTATTAGCGAGGACTCCGTCGGCCGGCCCGGC	T	38	TAGTTGAGTCGGCTCBCTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCC	AT
40 TAGTTGAGTCGGCTCACTTTAAATGTATTAGC-GGAACCTC-TGCG-ACCCAT 41 TAGT-AGGT-GTTGGCTCCTCTTT-AAATGCATTAGCTGGGACCTC-TTTGTGGGGCCAG 7 42 TAGT-AGGT-GTTGGCTCCTCTTTTAAATGCAT-AGCTGGGACCTC-TTTGTGGGGCCAG ? 43 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCCGCCGGCCGCGCCAG 44 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCCGCCGCCGACCG IT S. 2 2	P	39	TAGTIGAGICGGCICACTTTANATGIATTAGC-GGAACCTC-TGCG-ACCC	AT
41 TAGT-AGGT-GTTGGCTCCTCTTT-ANATGCATTAGCTGGGACCTC-TTTGTGGGGGCCAG 7 42 TAGT-AGGT-GTTGGCTCCTCTTTTAAATGCAT-AGCTGG-ACCTC-TTTGTGGGGGCCAG ? 43 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCCGCCGGCCGGCC	1	40	TAGTIGAGICGGCTCBCTITAAAIGIATIAGC-GGRACCTC-TGCG-ACCC	AT
T 42 TAGT-AGGT-GTTGGCTCCTCTTTTAAATGCAT-AGCTGG-ACCTC-TTTGTGGGGCCAG ? 43 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCCGCCGGCCGACCG 44 TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCCGCCGGCCGACCG ITS 2	- [41	TAGT-AGGT-GTTGGCTCCTCTTT-AAATGCATTAGCTGGGACCTC-TTTGTGGTGCC	λG
? 43 TAGC-AGAGCCGGCTCCCTTTANATGTATTAGCGAGGACTCCGTCCGCCGACCG 44 TAGC-AGAGCCGGCTCCCTTTANATGTATTAGCGAGGACTCCGTCCGCCGACCG ITTS 2	T	42	TAGT-AGGT-GTTGGCTCCTCTTTTAAATGCAT-AGCTGG-ACCTC-TTTGTGGTGCCC	AG
44 TAGC-AGAGCCGGCTCCCTTTANATGTATTAGCGAGGACTCCGTCCGCTGACCG	?	43	TAGC-AGAGCCGGCTCCCTTTAAATGTATTAGCGAGGACTCCGTCCGCTGACC	-G
ITS 2		44	TAGC-AGAGCCGGCTCCCTTTANATGTATTAGCGAGGACTCCGTCCGCTGACC-	-G
			ITS 2	

Figure 4.12. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 601 to 660) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. *ishikariensis* biological species I and II, TIN = T. *incarnata*, TP = T. *phacorrhiza* and T? = unknown Typhula spp.

	Sequence	
	aumber	661 720
	01	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
	02	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
	03	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
	04	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
Т	05	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
I	06	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-CTGTGAAGCA-CTTTATTGTTACGA
S	07	ACTACGGTGTGATAAT-TATCTACGGTGTTGGTGC_TTGTGABGCA_CTTTATTGTTACGA
Н	08	ACTACCCTVCATAAT_TERCTACCCTCCTCCCTCCTCCALCCA_CTTCACCA
	09	
в	10	
S	11	
ĩ	11	ACTACGGIGIGIGIAAT-TATCTACGCIGITGGIC-TIGIGAGCA-CITITATIGITACGA
•	12	ACTACGGIGIGIGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
	113	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
	14	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
	15	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
	16	ACTACGGTGTGATAAT-TATCTACGCTGPTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
т	17	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
ī	18	ACTACGGTGTGATAAT-TATCTACGCTGITGGTC-TTGTGAAGCA-CTTTATTGTTACGA
•	19	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
а п	20	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
n	21	ACTACGGTGTGATAAT-TATCTACGCTGTTGGTC-TTGTGAAGCA-CTTTATTGTTACGA
-	22	ACTACGGTGTGATAAT-TATCTACGCTCTTGTGCAGCA-TTTTATTGTTACGA
В	23	ACTACCGTGTGATAAT-TATCTACCCTCTTCTCCTC_TTCTCAACCA_CTTTATTCTACGA
S	74	ACTACIGTY STATE THE THE CONCERCIPTION OF THE ACTAL OF THE ACTACITY OF THE ACTA
П	25	
	25	
i	20	ACTACOGIGITAATAAT-TATCTACGCTGTGTC-TTGTGAAGGA-CTTTATTGTACGA
	20	ACTATOGICIGATAAT-TATCTACGCTQTGGTTTGTTGCGCTGCGAATTTAACTATOG
	28	ACTATOGIGIGATAAT-TATCTACGCTGTGGTTTGTTGCGCTGCGAATTTAACTAIGG
	29	ACTATGGTGTGATAAT-TATCTACGCTGTGGTTTGTTGCGCTGCGAATTTAACTATGG
	30	ACTATGGTGTGATAAT-TATCTACGCTGTGGTTTGTTGCGCTGCGAATTTAACTATGG
T	31	ACTATGGTGTGATAAT-TATCTACGCTGTGGTTTGTTGCGCTGCGAATTTAACTATAG
I	32 ·	ACTATGGTGTGATAAT-TATCTACGCTGTGGTTTGTTGCGCTGCGAATTTAACTATAG
N	33	ACTATGGTGTGATAAT-TATCTACGCTGTGGTTTGTTGCGCTGCGAATTTAACTATGG
	34	ACTATGGTGTGATAAT-TATCTACGCTGTGGTTTGTTGTGCTGCGAATTTAACTATGG
	35	ACTATGGTGTGATAAT-TATCTACGCTGTGGTTTGTTGCGCTGCGAATTTAACTATGG
	36	ACTATGGTGTGATAAT-TATCTACGCTGTGGTTTGTTGCGCTGCGAATTTAACTATGG
	37	ACTATGGTGTGATAAT-TATCTACGCTGTGGTTTGTTGCGCTGCGAATTTAACTATGG
\mathbf{T}	38	-CATTGGTGTGATAATCTATCTACCCTATTGGTGCAAGCCTTCTTTATTGAAGTTG
1	39	-CATTGGTGTGATAATCTATCTACCTTATTCT
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i	A 1	ACTATIGNTER AN TRANSFER CONTRACTOR CONTRACTOR ANTINAL ACTATIG
T	42	
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•	44	
1		ICICICUCUCUCUCUCUCUCUCUCUCUCUCUCUCUCUCU
		ITS 2

Figure 4.13. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 661 to 720) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. *ishikariensis* biological species I and II, TIN = T. *incarnata*, TP = T. *phacorrhiza* and T? = unknown Typhula spp.

	Sequence	791
	augnber	/21 /20 /20 /20 /20 /20 /20 /20 /20 /20 /20
	01	GOTICITICITATUSICUTIT
	02	GOTICTGCTTCTAATCGTCCTTTACTGCGACAATG
	0.3	GOTICIGCITUTARICGICCITT
т	02	GOFICTICITATUSTCUTTT
Ť	05	GOFICTGCITCTAATUGTCUTTTACTGTGACAATG
é	06	GOTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
่ง บ	07	GOTTCTGCTTCTAATCGTCCTTTACTGTGACAATG
п	08	GGTTCTGCTTCTAATCGTCCTTTACTGTGACAATG
р	09	GGTTCTGCITCTAATCGTCCTTTACTGTGACAATG
D C	10	GGITCTGCTTCTAATCGTCCTTTACTGTGACAATG
3	11	GGTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
1	12	GGITCTGCTTCTAATCGTCCTTTACTGCGACAATG
	13	GGITCTGCTTCTAATCGTCCTTTACTGCGACAATG
	14	GGTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
i	15	GGITCTGCITCIANTOGTCCTTTACTGCGACAATG
	16	GGITCTGCTTCTAATCGTCCTTTACTGCGACAATG
т	17	GGTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
ī	18	GGTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
s	19	GGTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
Ħ	20	GGTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
••	21	GGTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
	22	GGTTCTGCTTCTAATCGTCCTTTBCTGCGACAATG
ы	23	GGTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
6	24	GGTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
3	25	GGTTCTGCTTCTAATCGTCCTTTACTGCGACAATG
ч	26	GGCTCTGCTTCTAATCGTCCTTTACTGCGACAATG
1	27	GGTTCTGCTTCTAATCGTCCCTTTTCAAAGGACAGTATAGAGTGTGGTGGTGGTGGGGGTTGCT
	28	GGTTCTGCTTCTAATCGTCCCTTTTCAAAGGACAGTATAGAGTGTGGTGGTGGGGGTTGCT
	29	GGTTCTGCTTCTAATCGTCCCTTTTCAAAGGACAGTATAGAGTGTGGTGGTGGGGGTTGCT
	30	GGTTCTGCTTCTAATCGTCCCTTTTCAAAGGACAGTATAGAGTGTGGTGGTGGGGGTTGCT
т	31	GGTTCTGCTTCTAATCGTCCCTTT-CAAAGGACAGTATAGAGTGTCGCCGTCCCCGTTGCT
il	32	GGTTCTGCTTCTAATCGTCCCTTT-CAAAGGACAGTATAGAGHGTCGCCGTCGTCGCCGTCCT
Ň	33	GOTICTGCTTCTAATCGTCCCTTT-CAAAGGACAGTATAGAGTGTCCCGTCCTCCT
	34	GOTYCTGCTYCTAATCGTCCCTTT-CAAAGGACAGTATAGAGTATAGAGTACTCCTCCTCCTCCTCCTCCT
	35	GOTTCTGCTTCTAATCGTCCCTTT-CAAAGGACAGTATAGACHOTCCTCCTCCTCCTCCT
	36	GOTTCTAATCGTCCCTTT-CAAAGGACAGTATAGACTGTCGTCGTCGGCCCCCTTCCT
- 1	37	GGTTCTGCTTCTAATCGTCCCTTTTCAAAGGACAGTATAGACTGTCGTCGTCCCCCCTTCC
	38	GAT-CAGCTTCTAACCGTCTTCG
T	39	GAT-CAGCATCTAACCGTCTTCG
P	40	GAT-CAGCETCTAACCGTCTTCG-
i	41	GOTTCTGCTTCTAATCGTCCCTTT-CAAAGGACACTATAGACTACTACTACTACTACTACTACTACTACTACTACTACTA
\mathbf{T}^{\dagger}	42	GOTTCINCINCIANTOSTCCCTTT-CANACCACACTATACACIONGICGCGCCCCCC
2	43	
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Figure 4.14. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 721 to 780) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. ishikariensis biological species I and II, TIN = T. incarnata, TP = T. phacorrhiza and T? = unknown Typhula spp.

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I	18	A-GUGTITICITITITGGAATTCC-TTTGACAT	
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H	20	AAGGGTITTCTATTTT-ATTTTGGAATTCCC-TTTGACAT	Constant of
	21	AAGGGTTTTCTATTTT-ATTTTGGAATTCCC-TTTGACAT	11.44
	22		100
в	23		TAXCO.
s	24		Trans.
n	25	A-GGGTTTTCTTTTTTGGAATTCC-TTTGACAT	1.2.0
-	26	A-GGGTGTT-CTCTTTTGAATGCC-TTTGACAG	di TChi
	27	TTCAAGGGGTTCGCCTCTTGTGTTACAATCTTGCCCTTTACCTCTTATTGACAT	Thur Case
	28	TTCAAGGGGTTCGCCTCTTGTGTTACAATCTTGCCCTTTACCTCTTATTGACAT	1.1.6.4
	29	TTCAAGGGGTTCGCCTCTTGTGTTACAATCTTGCCCTTTACCTCTTATTGACAT	10110
	30	TTCAAGGGGTTCGCCTCTTGTGTTACAATCTTGCCCTTTACCTCTTATTGACAT	1.1.1
Т	31	TTCAAGGGGTTCGCCTCTTGTGTTACAATCTTGCCCTTTACCTCTTATTGACAT	
I	32	TTCAAGGGGTTCGCCTCTTGTGTTACAATCTTGCCCTTTACCTCTTATTGACAT	100
N	33	TTCAAGGGGTTCGCCTCTTGTGTTACAATCTTGCCCTTTACCTCTTATTGACAT	1111-1-1-1
	34	TYCAAGGGGTTCGCCTCTTGTGTTACAATCTTGCCCTTTACCTCTTATTGACAT	Tavie
	35	TYCANGGGGTTCGCCTCTTGTGTTACAATCITGCCCTTTACCTCTTATTGACAT	12:35
	36	TTCAAGGGGTTCGCCTCTTGTGTTACAATCTTGCCCTTTACCTCTTATTGACAT	1225
	37	TTCANGGGGTTCGCCTCTTGTGTTACAATCTTGACATTTACCTCTTATTGACAT	Land Street
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T	42	TTCANGGGGTTCGCCTCTTGTGTTACMATCTTGCCCTTTACCTCTTATTGACAT	1.1.
?	43	TTGCTTCATCTTCAC	1
	44	TTGCTTCATCTTGAC	
		ITS 2	200
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Figure 4.15. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 781 to 840) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. *ishikariensis* biological species I and II, TIN = T. *incarnata*, TP = T. *phacorrhiza* and T? = unknown Typhula spp.

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	E		
		28 S	TTS-4 primer

Figure 4.16. Alignment of the complete internal transcribed spacer region (CITS) of the 44 *Typhula* sequences (base pairs 841 to 893) using the Clustal method with weighted residue weight table. TISH BSI and BSII = T. *ishikariensis* biological species I and II, TIN = T. *incarnata*, TP = T. *phacorrhiza* and T? = unknown Typhula spp.

Two phylogenetic trees were constructed from the CITS of forty-four aligned sequences of the *Typhula* species. First, a slanted cladogram of the distance measure analysis showing the relationships of the *Typhula* sequences is presented in Fig. 4.17. The data were resampled with 5,000 bootstrap replicates (Felenstein, 1985) by using the heuristic search option of PAUP. The percentage of bootstrap replicates that yielded each grouping (group frequencies) was used as a measure of statistical confidence and are indicated above the cladogram branches (see Fig. 4.17). Three *T. phacorrhiza* sequences (38, 39 and 40) were set as the outgroup. The slanted cladogram clustered the sequences into three groups: the unidentified *Typhula* sequences (43, 44), *T. incarnata*, and the *T. ishikariensis* complex. The *T. ishikariensis* complex formed a topology that displayed a tendency to form two groups (BSI = sequences 1 to 13 and 26, and BSII = sequences 14 to 25) but the group frequencies ranged from 70 to 100%, which indicated variability between the two groups (BSI and BSII) but not enough to infer that they are different species.

The second tree constructed from the CITS of the *Typhula* species was based on parsimony analysis. A strict consensus phylogram of the CITS parsimony analysis showing the relationships among the *Typhula* species is presented in Fig. 4.18. The data were resampled with 10,000 jackknife replicates (Felenstein, 1985) by using the heuristic search option of PAUP. The percentage of jackknife replicates that yielded each grouping (jackknife percentages) are indicated above the phylogram branches (see Fig. 4.18). The three *T. phacorrhiza* sequences (38, 39 and 40) were again used as an outgroup. The branch lengths of the phylogram represent genetic distances between groups. The *T. incarnata*, *T. ishikariensis* and the unidentified *Typhula* sequences were separated into three groups with no clear separation within the *T. ishikariensis* complex.

The alignment of the forty-four *Typhula* CITS sequences indicated the presence of unique sequence differences between the two biological species of the *T. ishikariensis* complex within the ITS 1 region (Figs. 4.4 and 4.5). The sequences of the ITS 1 region of the *T*.



Figure 4.17. Slanted cladogram of distance measure analysis showing relationships of twenty-six *Typhula ishikariensis*, thirteen *T. incarnata*, two unidentified *Typhula* spp. and three *T. phacorrhiza* sequences. The cladogram was derived from the nucleotide sequences of the complete internal transcribed (CITS) region of the nuclear ribosomal DNA (nrDNA). The sequences were aligned by DNAStar Clustal alignment and the cladogram was generated by PAUP 4.0. Three *T. phacorrhiza* sequences (38, 39 and 40) were set as the outgroup. The numbers above branches indicate group frequencies from 5,000 bootstrap replicates. Sequences are identified by numbers as described in Tables 4.2, 4.3 and 4.4. The species are marked on the right. * = T. ishikariensis WIG1; ** = T. ishikariensis WIG2.



Figure 4.18. Strict consensus phylogram of parsimony analysis showing relationships among twenty-six Typhula ishikariensis, thirteen T. incarnata, two unidentified Typhula spp. and three T. phacorrhiza sequences. The nucleotide sequences of the complete internal transcribed spacer (CITS) regions of the nuclear ribosomal DNA (nrDNA) were aligned by DNAStar Clustal alignment and the phylogram was generated by PAUP 4.0. Three T. phacorrhiza sequences (38, 39 and 40) were set as the outgroup. The numbers above branches indicate the percentages from 10,000 jackknife replicates. Horizontal lengths represent genetic distances and the scale for branch lengths is indicated. Sequences are identified by numbers as described in Tables 4.2, 4.3 and 4.4. The species are marked on the right. * = T. ishikariensis WIG1; ** = T. ishikariensis WIG2. *ishikariensis* complex were aligned by the Clustal method within the DNAStar software program and the "signature sequence" where the biological species can be differentiated is presented in Fig. 4.19. This signature sequence is approximately forty-four bp long and ranges from approximately 145 bp to 189 bp within the ITS 1 region.

Also, from the *T. ishikariensis* complex ITS 1 region alignment, two phylogenetic trees were constructed. First, a slanted cladogram of the distance measure analysis showing the relationships of the *T. ishikariensis* complex ITS 1 sequences is presented in Fig. 4.20. The data were resampled with 5,000 bootstrap replicates (Felenstein, 1985) by using the heuristic search option of PAUP. The percentage of bootstrap replicates that yielded each grouping (group frequencies) was used as a measure of statistical confidence and are indicated above the cladogram branches (see Fig. 4.20). The *T. incarnata* sequence 27 was set as the outgroup. The slanted cladogram clustered the *T. ishikariensis* complex sequences into two groups: biological species I (1 to 13 and 26 and biological species II (14 to 25). However, the *T. ishikariensis* complex formed a topology that displayed a tendency to form two groups (BSI = sequences 1 to 13 and 26, and BSII = sequences 14 to 25) but the group frequencies were 58 and 67%, which indicated variability between the two groups (BSI and BSII) but not enough to infer that they are different species.

The second tree constructed from the ITS 1 region of the *T. ishikariensis* complex was based on parsimony analysis. A strict consensus phylogram showing the relationships among the *T. ishikariensis* complex is presented in Fig. 4.21. The data were resampled with 10,000 jackknife replicates (Felenstein, 1985) using the heuristic search of PAUP. The percentage of jackknife replicates that yielded each grouping are indicated above the phylogram branches (see Fig. 4.21). The *T. incarnata* sequence 27 was set as the outgroup. The branch lengths represent genetic distances between groups. The *T. ishikariensis* sequences were separated into three groups with only 78, 67 and 76% jackknife percentages, which indicates variation between the two biological species but not enough to infer that they are different species.



Figure 4.19. Signature sequence within the ITS 1 region of the nrDNA that differentiates the biological species of the *Typhula ishikariensis* complex. The sequence is highlighted and the approximate range and distance within the ITS 1 region are shown.



Figure 4.20. Slanted cladogram of distance measure analysis showing relationships of twenty-six *Typhula ishikariensis* and one *T. incarnata* sequences. The cladogram was derived from the nucleotide sequences of the internal transcribed region 1 (ITS1) of the nuclear ribosomal DNA (nrDNA). The sequences were aligned by DNAStar Clustal alignment and the cladogram was generated by PAUP 4.0. One *T. incarnata* sequence (27) was set as the outgroup. The numbers above branches indicate group frequencies from 5,000 bootstrap replicates. Sequences are identified by numbers as described in Tables 4.2 and 4.3. The species are marked on the right. * = T. ishikariensis WIG1; ** = T. ishikariensis WIG2.



Figure 4.21. Strict consensus phylogram of parsimony analysis showing relationships among twenty-six *Typhula ishikariensis* and one *T. incarnata* sequences. The nucleotide sequences of the internal transcribed spacer region 1 (ITS1) of the nuclear ribosomal DNA (nrDNA) were aligned by DNAStar Clustal alignment and the phylogram was generated by PAUP 4.0. One *T. incarnata* sequence (27) was set as the outgroup. The numbers above branches indicate the percentages from 10,000 jackknife replicates. Horizontal lengths represent genetic distances and the scale for branch lengths is indicated. Sequences are identified by numbers as described in Tables 4.2 and 4.3. The species are marked on the right. * = *T. ishikariensis* WIG1; ** = *T. ishikariensis* WIG2.

DISCUSSION

Sequence analyses of the CITS region of the nrDNA is a consistent and accurate method for fungal plant pathogen identification. The technique consistency can be roughly estimated by calculating the percent identities of sequences that were derived from different DNA extractions of the same isolate and from different clones of the same DNA extraction of the same isolate (Table 4.10). The percent identities of different DNA extractions of the same isolate ranged from 94 to 100% identical, while sequences derived from different clones of the same DNA extraction of the same isolate ranged from 94 to 100% identical, while sequences derived from different clones of the same DNA extraction of the same isolate ranged from 96 to 100% identical. This level of technique consistency supports further use of this technique as a rapid and accurate identification tool.

Sequences derived from different DNA extractions and different clones are consistent (94 to 100% identical, Table 4.8), but are there sequence differences between monokaryons and dikaryons of the same isolate? Sequence 16 (dikaryotic *T. ishikariensis* isolate 2.105) versus sequences 17 and 18 (monokaryotic *T. ishikariensis* isolate 2.105) were 99 to 100 % identical (Appendix C, Table C.1). Also, sequence 33 (dikaryotic *T. incarnata* isolate 2.136) versus sequences 34 and 35 (monokaryotic *T. incarnata* isolate 2.136) were 96 to 98% identical (Appendix C, Table C.3). The percent identities for dikaryons versus monokaryons of the same isolate ranged from 96 to 100%. However, this is not enough evidence to reject the theory that there are differences between monokaryons and dikaryons of the same isolate. Future experiments could be designed to determine sequence differences between monokaryotic and dikaryotic states of the same isolate by increasing the number of sequence comparisons. Also, it would be interesting to determine if dikaryotic hybrids from a monokaryotic BSI (or WIG1) isolate with a monokaryotic BSII (or WIG2) isolate mating would produce a "new hybrid" CITS nrDNA sequence.

The results of the molecular identification experiments indicate that the CITS region of the nrDNA can be used to differentiate *T.incarnata*, *T. ishikariensis* and *T.phacorrhiza*. The

Table 4.10. Percent identities of different DNA extractions of the same isolate and of different clones of the same DNA extraction of the same isolate.

Sequences of Different DNA extractions ^a	Typhula spp.	Percent identity	Sequences of Different clones ^b	Typhula spp.	Percent identity
5,6	T. ishikariensis	94	8, 9	T. ishikariensis	100
16, 17, 18	T_ ishikariensis	99-100	10, 11	T. ishikari en sis	96
27, 28, 29	T. incarnata	99-100	12, 13	T. ishikariensis	99
30, 31, 32	T.incarnata	97-100	39, 40	T.phacorrhiza	100
33, 34, 35	T.incarnata	96-98	41, 42	T. phacorrhiza	99

* Different DNA extractions of the same isolate.

^b Different clones of the same isolate.

percent identities, cladogram and phylograms of the CITS region of the nrDNA clearly differentiate the three *Typhula* species.

Also, analyses of the CITS and the ITS1 regions of the nrDNA infer that isolates of the two *T. ishikariensis* groups (WIG1-BSI and WIG2-BSII) are the same species but perhaps are undergoing speciation or lineage divergence. The 26 CITS sequences from the 20 *T. ishikariensis* isolates were 87 to 100% identical with a 0 to 8% divergence. Percentage of sequence identity of the CITS for the 44 sequences from the 30 *Typhula* spp. or *Typhula*-like isolates ranged from 59 to 100% with a 0 to 30% divergence. The 26 sequences from the 20 *T. ishikariensis* isolates were 59 to 78% identical to the eleven sequences of five *T. incarnata* isolates, three sequences from two *T. phacorrhiza* isolates and four sequences from 3 unidentified *Typhula*-like isolates and had a 22 to 30% divergence.

More work on the ITS 1 region "signature sequence" is needed as conflicting sequence data has been reported (Hsiang and Wu, 1999). The percentage of sequence identities of Hsiang and Wu's sequences as compared to the 26 *T. ishikariensis* sequences reported here are presented in Table 4.11. The percentage of sequence identities among the three sequences ranged from 93 to 95%. These three sequences along with the 26 *T. ishikariensis* sequences from this study were aligned using the Clustal method option of DNAStar and the signature sequence area within the ITS 1 region is presented in Fig. 4.22. Both *Typhula ishikariensis* varieties *canadensis* and *ishikariensis* sequences from (Hsiang and Wu, 1999) have the BSII signature sequence (Fig. 4.22). This conflicts with sequences 10, 11, 12 and 13 (*T. ishikariensis* var. *ishikariensis*) that have the signature sequence of BSI not BSII. The *T. ishikariensis* var. *idahoensis* sequence (Hsiang and Wu, 1999) does have the *T. idahoensis* signature as in this study.

The *T. ishikariensis* phylogenetic trees constructed from the ITS1 region of the CITS of nrDNA (Figs. 4.20 and 4.21) support the grouping of the *T. ishikariensis* complex into two diverging groups (biological species I and biological species II). The only exception is the

Table 4.11. Percentage of sequence identity in the complete internal transcribed spacer region between the University of Wisconsin study *Typhula ishikariensis* sequences (1 to 26), one *T. incarnata* sequence (27) and three sequences downloaded from GenBank, *T. ishikariensis* var. canadensis (AF134711), *T. ishikariensis* var. idahoensis (AF134712) and *T. ishikariensis* var. ishikariensis (AF134713) (Hsiang and Wu, 1999).

Sequence number	T. ishikariensis var. ishikariensis	T. ishikariensis var. idahoensis	T. ishikariensis var. canadensis
1	95	93	92
2	95	93	92
3	96	95	93
4	95	95	93
5	96	95	93
6	90	90	86
7	89	87	86
8	95	94	92
9	94	93	92
10	92	89	88
11	95	94	92
12	96	94	93
13	94	93	91
14	96	92	93
15	97	93	94
16	98	95	95
17	98	94	95
18	9 8	95	95
19	96	94	93
20	96	92	93
21	97	92	93
22	98	95	95
23	98	95	96
24	98	95	95
25	98	95	96
26	95	97	92
27	72	72	67

Sequence		5' BGT TWG) primer 3'
ID		
BSI	01	TACGGGGGA-GTTGTGAAAAAGGGATCAT-TAATTTGGTTTCTCTTTTTATAGCTTTCCAAAGAGGGG-TAAGACGTTACAAGAAG
	02	TACGGGGGA-GTTGTGAAAAAGGGATCAT-TAATTTGGTTTCTCTTTTTATAGCTTTCCAAGAGAGGG-TABGACGTTACABGAC
	03	TACGGGGGA-GCTGTGAAAAAGGGATCAT-TAATTTGGTTTCTCTTTTTATAGCTTTCCAAGAGAGGG-TAAGAGGTTACAAGAA
	04	TACGGGGGGAAGTTGTGAAAAAGGGATCAT-TAATTTGGTTTCTCTTTTTATAGCTTTCCAAAGAGAGGG-GTAAGACGTTABABGABC
	05	TACGGGGGA-GTTGTGAAAAAGGGATCAT-TAATTTGGTTTCTCTTTTTATAGCTTTCCAAAGAGAGGGTAAGACGTTAAAAGAAC
	06	TACGGGGGA-GTTGTGAAAAAGGGATCAT-TAATTTGGTTTCTCTTTTTATAGCTTTTCCAAGAGAAGGT-AAGACGTTACAAGAAC
	07	TATGGGGGA-GTTGTGAAAAAGGGATCATATCATTTTGGGC-TCTTCTTATAGCTTTCCAAAGAGAGGGGGGAAGGACGCTAAAAGAAC
	08	TACGGGGGA-GTTGTGAAAAAGGGATCAT-TAATTTGGTTTCTCTTTTTATAGCTTTCCAAAGAGAGGGGTAAGACGTTAAAAGAAC
	09	TACGGGGGA-GTTGTGAAAAAGGGATCAT-TAATTTGGTTTCTCTTTTTATAGCTTTCCAAAGAGAGGGGTAAGACGTTAAAAGAAC
	10	TACGGGGGA-GTTGTGAAAAAGGGATCAT-TAATTTGGTTTCTCTTTTTATAGCTTTCCAAAGAGGGGTAAGACGTTACAAGAAC
	11	TACGGGGGA-GTTGTGAAAAAGGGATCAT-TAATTTGGTTTCTCTTTTTATAGCTTTCCAAAGAGGGGTAAGACGTTACAAGAAC
	12	TACGGGGGA-GTTGTGAAAAAGGGATCAT-TAACTTGGTTTCTCTTTTTATAGCTTTCCAAGGAGGGGTAAGACGTT-CAAGAAC
	13	TACGGGGGA-GTTGTGAAAAAGGGATCAT-TAACTTGGTTTCTCTTTTTATAGCTTTCCAAGGAGAGGGGTAAGACGTTACAAGAAC
	26	TACGGGGGAGTTTGTGAAAAAGG-ATCAT-TAATTTGGTTTCTCCTTTATAAGCTTCCCAAAGAGAGGGGTAAGACGTTACAAGAAAC
	14	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGT-CTTCTCTCTCCAAAGAGAGGGGTAAGACGCTTCAAGAAC
	15	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGTTCTTCTCTCTCCAAAGAGGGGGTA-AGACGCTACAAGAAC
	16	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGTTCTTCTCTCTCCAAAGAGAGGGTAAGACGCTACAAGAAC
	17	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGTTCTTCTCTCTCCAAAGAGAGGGTAAGACGCTACAAGAAC
	18	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGTTCTTCTCTCTCCAAAGAGAGGGTAAGACGCTACAAGAAC
	19	TACGGGGGA-GTTGTAAGGATCAT-TAATTTGGTTCTCTCCTCTCTCCAAAGAGAGGGGTAAGATGTTACAAGAAC
BSII	20	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGTTCTTCTCTCTCCCAAAGAGAGGGTGTGTAAGAGCGTTACAAGAGC
	21	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGTTCTTCTCTCCAAAGAGAGGGTGTGTAAGACGTTACAAGAGC
	22	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGTTCTTCTCTCTCCAAAGAGAGGGTA-AGACGCTACAAGAAC
	25	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGTTCTTCTCTCTCCAAAGAGAGGGTATAAGACGCTACAAGAAC
	23	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGTTCTTCTCTCTCCAAAGAGAGGGGTA-AGACGCTACAAGAAC
	24	TATGGGGGA-GTTGTAAGGATCAT-TCATTTGGTTCTTCTCTCTCCCAAAGAAGGGGTA-AGATGCTACAAGAAC
	130	5' BSII ITS 1 primer 3' ITS 1 217

Figure 4.22. Signature sequence alignment within the ITS 1 region of the nrDNA that differentiates the biological species of the *Typhula ishikariensis* complex. Hsiang and Wu's (1999) sequences* are highlighted. Potential primer sites are indicated by arrows. Sequences 10, 11, 12 and 13 are from *T. ishikariensis* var. *ishikariensis* which is the same as Hsiang and Wu's "ish*".

placement of sequence 19 (T. ishikariensis WIG2 isolate 3.122). Sequence 19 contains the "signature sequence" that distinguishes it as biological species II, Fig. 4.19. However, sequence 19 is placed within the biological species I clade of the phylogenetic trees, Figs. 4.20 and 4.21. One possible explanation for the placement of sequence 19 in the biological species I clade is that it is a hybrid of the two biological species. Christen and Bruehl (1978) reported that hybrids of T. ishikariensis X T. idahoensis can exist in nature and maybe T. ishikariensis WIG2 isolate 3.122 is a hybrid of T. ishikariensis biological species I X T. ishikariensis biological species II. It is possible that a T. ishikariensis biological species I X T. ishikariensis biological species II hybrid could possibly give conflicting CITS sequence data, intermediate dikaryon-monokaryon mating reactions and atypical morphological characteristics. Isolate 3.122 was also one of the six isolates (out of 46 total) that had a positive or intermediate mating reaction with T. ishikariensis Norway group III isolate 6-IBS-4 (Tables 3.3 and 3.4). Four of these six isolates were collected from the same golf course: Trout Lake Golf and Country Club, Woodruff, WI. It was estimated that 45% of the sampled fairways of this golf course were damaged by Typhula blight and that T. incarnata, T. ishikariensis, T. phacorrhiza and an unidenitified Typhula species were collected (Table 2.22).

Minor support of the grouping of the *T. ishikariensis* isolates into two diverging groups was demonstrated by comparison of the results of the dikaryon-monokaryon pairings with the CITS results (Tables 4.12 and 4.13). The average percent identities between 3 WIG1 sequences X 7 BSI sequences and 6 WIG2 sequences X 3 BSII sequences were both 98% (Tables 4.12 and 4.13). On the other hand, the average percent identities for the WIG1XBSII comparison was 96% and for the WIG2XBSI comparison it was 95%. These differences may or may not be significant, but when these average % identities are connected with the percent dikaryotization (WIG1XBSI = 98%, WIG1XBSII = 0%, WIG2XBSI = 0% and WIG2XBSII = 56%; Table 4.15), two separate groups are apparent.

The potential use of this technique as a rapid and accurate diagnostic tool is

Table 4.12. Dikaryon-monokaryon mating reactions and percentage sequence identities between Wisconsin group 1 and Wisconsin group 2 isolates versus biological species I, biological species II and Norway group III isolates.

[Isolate number	Dikaryon-monokaryon reaction / % sequence identity										
Wisconsin		Biological species I sequence number						Biological species II sequence number			Norway group III	
grouping / sequence number		Japan Biotype A PR9-4-3	Japan Biotype A PR7-6-7		Russia var. ishikariensis 92-32-M1		Norway Group 1 2-5BS-1		Japan Biotype B 35-8	Norway Group 11 4-3,S-5	Canada var. <i>canadensis</i> Can21m	Norway Group III 6-IBS-4
		4	5	6	12	13	8	9	20	22	24	NA*
WIG1/1	1.93	+ / 97	±/+ / 97	±/+ / 96	+ / 98	+ / 96	+ / 98	+ / 98	-194	- / 97	- / 96	-
WIG1/2	2.183	+ / 98	+ / 99	+ / 93	+ / 99	+ / 97	+ / 98	+ / 97	- 195	- / 97	- / 97	•
WIG1/3	3,120	+ / 99	+ / 99	+ / 94	+ / 99	+ / 98	+ / 99	+ / 98	- / 95	- / 98	±1-198	±
WIG2/14	1.31	- / 95	- / 95	- / 89	- / 95	- / 93	- / 94	- / 94	- / 96	- / 96	+ / 97	
WIG2/15	2.97	- / 95	- 1 96	- / 93	- / 96	- / 95	- / 94	- 1 94	±/+ / 96	- / 98	+ / 98	-
W102/16	2.105	- 197	- / 98	- / 92	- 1 97	- / 96	- 1 96	- / 96	- / 98	+ / 100	+ / 100	-
WIG2/17	2.105	-197	- 1 98	- / 92	- 1 97	- / 96	- 1 97	- / 97	- / 98	+ / 99	+ / 100	-
WIG2/18	2.105	- 197	- / 98	- / 92	- / 97	- 1 96	- / 96	- / 95	- / 98	+ / 99	+ / 100	-
WIG2/19	3,122	- 1 96	- 1 92	- / 92	- / 97	- / 96	• / 96	- / 94	+ / 94	-/+ / 98	+ / 97	+/ ±

• NA = Norway group III isolate was not sequenced.

Table 4.13. Percent dikaryotization and average percent identity between Wisconsin group 1 and 2 versus biological species I and II.

Wisconsin grouping	BSI % dikaryotization*	BSI average Hidentity	BSII & dikaryoùzationª	BSII average Hidentity
WIGI	98%	98%	0%	96%
WIG2	0%	95%	5 6%	98%

• WIG1 vs. BSI: dikaryon-monokaryon pairings 19 (+), 2 (\pm /+) = 98% dikaryotization; WIG1 vs. BSII: dikaryon-monokaryon pairings 8 (-), 1 (\pm /-) = 0% dikaryotization; WIG2 vs. BSII: dikaryon-monokaryon pairings 42 (-) = 0% dikaryotization; and WIG2 vs. BSII: dikaryon-monokaryon pairings 10 (+), 6 (-), 1 (\pm /+), 1 (-/+) = 56% dikaryotization.

demonstrated by the molecular identification of the unidentified *Typhula* species isolate G2 (collected from *Gaillardia* spp. by C. R. Grau). In vitro the G2 isolate had morphological characteristics that resembled both *T. phacorrhiza* and *T. incarnata*. The sclerotia were large and appeared to have a small stipe attaching it to the plant debris. However, the color and rind cell patterns were intermediate between the two species. The sequences (41 and 42) of this isolate were 91 to 97% identical to the *T. incarnata* isolates, Table B.4. This high level of % identity indicates that the G2 isolate is *T. incarnata*.

However, a disadvantage of this technique is that tester isolates or reported sequence data is needed before unknown isolates are positively identified. The failure to identify the isolates G4 (sequence 43) and T? 3.129 (sequence 44) illustrates this disadvantage. These two isolates were 92% identical to each other but their morphological characteristics were vastly different. Isolate T? 3.129 had large dark brown to almost black sclerotia with light cream colored outer edges on culture media. The T? 3.129 sclerotia coalesced into linear bands on the surface of the PDA. On the other hand, isolate G4 had large brown stipullate sclerotia that were singular on the surface of PDA. It may be that isolate G4 and T? 3.129 are closely related. However, further characterization of these isolates is needed before their identity is revealed.

Future studies centered on the CITS region should include more *T. idahoensis* and *T. ishikariensis* var. *idahoensis* isolates from around the world. In this study only one *T. idahoensis* isolate was sequenced (sequence 26). The *T. idahoensis* sequence was grouped within the biological I species, Figs. 4.17 and 4.18. However, the biological I species concept considers *T. idahoensis* to be within the biological II species concept, Fig. 3.1. This conflict could be clarified if more *T. idahoensis* and *T. ishikariensis* var. *idahoensis* isolates are sequenced.

Further sequencing of the ITS 1 region of T. ishikariensis complex isolates should be conducted to investigate the potential use of the "signature sequence" as an identification tool.

After more sequences are compared and if the "signature sequences" are consistently found, then primers can be designed to readily identify an unknown isolate as being either similar to biological species I or biological species II. Fig. 4.22 illustrates the 5' to 3' primers (BSI primer and BSII primer) that could be created and paired with the ITS-2 primer (White et al., 1990; which is a 3' to 5' primer located within the 5.8 S region). The design of these primers would then eliminate the need to sequence the whole CITS region in order to make a molecular identification. If the implementation of these primers is successful, molecular identification of the biological species could then be completed within one day, or even hours.

- Al-Banna, L., Williamson, V., and Gardner, S. L. 1997. Phylogenetic analysis of nematodes of the genus *Pratylenchus* using nuclear 26S rDNA. Mole. Phylogen. Evol. 7:94-102.
- Alice, L. A., and Campbell, C. S. 1999. Phylogeny of *Rubus* (Rosaceae) based on nuclear ribosomal DNA internal transcribed spacer region sequences. Am. J. Bot. 86:81-97.
- Anonymous. 1992. Optimizing rapid cycle DNA amplification reactions. The Rapid Cyclist 1:1-8.
- Anonymous. 1995. Peak height patterns observed in dye terminator sequencing with AmpliTaq DNA polymerase, FS. Applied Biosystems, Inc. Foster City, CA.
- Anonymous. 1996. The Rapid Cyler ™ User's Guide. Idaho Technology Inc., Idaho Falls, ID.
- Anonymous. 1998a. Easy-DNA ™ Kit Genomic DNA Isolation. Version C. Instruction Manual. Invitrogen® Corporation, Carlsbad, CA.
- Anonymous. 1998b. TOPO [™] TA Cloning[®]. Version E. TOPO[™] TA Cloning[®] five minute cloning of Taq polymerase-amplified PCR products. Invitrogen, Carlsbad, CA.
- Anonymous. 1998c. S. N. A. P.[™] Miniprep Kit. Simple Nucleic Acid Preparation Instruction Manual. Invitrogen® Corporation, Carlsbad, CA.

- Anonymous. 1998d. Data evaluation and troubleshooting. Applied Biosystems, Inc. Foster City, CA.
- Årsvoll, K., and Smith, J. D. 1978. Typhula ishikariensis and its varieties, var. idahoensis comb. nov. and var. canadensis var. nov. Can. J. Bot. 56:348-364.
- Benson, D. A., Boguski, M. S., Lipman, D. J., Ostell, J., Ouellette, B. F., Rapp, B. A., and Wheeler, D. L. 1999. GenBank. Nucleic Acids Res. 27:12-17.
- Black, W. C., IV, Klompen, J. S., and Keirans, J. E. 1997. Phylogenetic relationships among tick subfamilies (Ixodida:Ixodidae:Argasidae) based on the 18S nuclear rDNA gene. Mole. Phylogen. Evol. 7:129-144.
- Bruehl, G. W., Machtmes, R., and Kiyomoto, R. 1975. Taxonomic relationships among *Typhula* species as revealed by mating experiments. Phytopathology 65:1108-1114.
- Bruehl, G. W., and Machtmes, R. 1979. Alleles of the incompatibility factors of Typhula ishikariensis. Can. J. Bot. 57:1252-1254.
- Chen, W., Gray, L. E., and Grau, C. R. 1996. Molecular differentiation of fungi associated with brown stem rot and detection of *Phialophoragregata* in resistant and susceptible soybean cultivars. Phytopathology 86:1140-1148.
- Dellaporta, S. L., Wood, J., and Hickes, J. B. 1983. A plant DNA minipreparation: version II. Plant Mol. Rep. 1:19-21.

- Felsenstein, J. 1988. Phylogenies from molecular sequences Inference and reliability. Annu. Rev. Genet. 22:521-565.
- Hillis, D. M., Moritz, C., and Mable, B. K. 1996. Molecular Systematics. 2nd Ed. Sinauer, Assoc., Inc. Sunderland, MA.
- Hsiang, T., and Wu, C. 1999. Genetic relationships of pathogenic *Typhula* species assessed by RAPD, ITS-RFLP and ITS sequencing. Mycol. Res. In press.
- Kolbert, C. P., and Persing, D. H. 1999. Ribosomal DNA sequencing as a tool for identification of bacterial pathogens. Curr. Opin. Microbio. 2:299-305.
- Larouche, A., Gaudet, D. A., Schaalje, G. B., Erickson, R. S., and Ginns, J. 1995. Grouping and identification of low temperature basidiomycetes using mating, RAPD and RFLP analyses. Mycol. Res. 99:297-310.
- Lee, C., Helweg-Larsen, J., Tang, X., Jin, S., Li, B., Bartlett, M. S., Lu, J., Lundgren, B., Lundgren, J. D., Olsson, M., Lucas, S. B., Roux, P., Cargnel, A., Atzori, C., Matos, O., and Smith, J. W. 1998. Update on *Pneumocystis carinii* f. sp. *hominis* typing based on nucleotide sequence variations in internal transcribed spacer regions of rRNA genes. J. Clin. Microbiol. 36:734-741.
- McDonald, W. C. 1961. A review of the taxonomy and nomenclature of some lowtemperature forage pathogens. Can. Plant Dis. Survey 41:256-260.

Maidak, B. L., Cole, R. R., Parker, Jr., C. T., Garrity, G. M., Larsen, N., Li, B., Lilburn,

T. G., McCaughey, M. J., Olsen, G. J., Overbeek, R., Pramanik, S., Schmidt, T.
M., Tiedje, J. M., and Woese, C. R. 1999. A new version of the RDP (Ribosomal Database Project). Nucleic Acids Res. 27:171-173.

- Matsumoto, N., and Tajimi, A. 1991. Typhula ishikariensis biotypes B and C, a single biological species. Trans. Mycol. Soc. Jpn. 32:273-281.
- Matsumoto, N., and Tajimi, A. 1993. Interfertility in *Typhula ishikariensis* biotype A. Trans. Mycol. Soc. Jpn. 34:209-213.
- Matsumoto, N., Sato, T., and Araki, T. 1982. Biotype differentiation in the Typhula ishikariensis complex and their allopatry in Hokkaido. Ann. Phytopath. Soc. Jpn. 48:275-280.
- Matsumoto, N., Tronsmo, A. M., and Shimanuki, T. 1996. Genetic and biological characteristics of *Typhula ishikariensis* isolates from Norway. Europ. J. Plant Path., 102:431-439.
- Olsen, G. J., Lane, D. J., Giovannoni, S. J., and Pace, N. R. 1986. Microbial ecology and evolution: a ribosomal RNA approach. Ann. Rev. Microbiol. 40:337-365.
- Rafin, C., Brygoo, Y., and Tirilly, Y. 1995. Restriction analysis of amplified ribosomal DNA of Pythium spp. isolated from soilless culture systems. Mycol. Res. 99:277-281.

Remsberg, R. E. 1940. Studies in the genus Typhula. Mycologia 32:52-96.

- Sajdak, S. L., and Phillips, R. B. 1997. Phylogenetic relationships among Coregonus species infered from the DNA sequence of the first internal transcribed spacer (ITS1) of ribosomal DNA. Can. J. Fish. Aquat. Sci. 54:1494-1503.
- Smith, J. D. #309-318 108th St., Saskatoon, SK, Canada 57N1P8.
- Steane, D. A., Scotaland, R. W., Mabberley, D. J., and Olmstead, R. G. 1999. Molecular systematics of *Clerodendrum* (Lamiaceae): ITS sequences and total evidence. Am. J. Bot. 86:98-107.
- Sweets, L. E., and Stienstra, W. C. 1980. Factors affecting growth of *Typhula incarnata* and *T. ishikariensis* in culture. pp. 449-458. In R.W. Shead (Ed.), Proc. 4Th Int. Turfgrass Res. Conf. Guelph, Ontario, Canada, July, 1981. The Ontario Agric. Col., Univ. of Guelph, Ontario.
- Tkachenko, O. B., Matsumoto, N., and Shimanuki, T. 1997. Mating patterns of east-European isolates of *Typhula ishikariensis* S. Imai with isolates from distant regions. Mikologiya I Fitopatologiya 31:68-72.
- van Herwerden, L., Blair, D., and Agatsuma, T. 1999. Intra- and interindividual variation i n ITS1 of Paragoniums westermani (Trematoda: Digenea) and related species: implications for phylogenetic studies. Mol. Phylogen. Evol. 12:66-73.
- White, T. J., Bruns, T., Lee, S., and Taylor, J. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. pp. 315-322. In: Innis, M. A., Gelfand, D. H., Sninsky, J. J., and White, T. J. (Eds) PCR protocols. A guide to

methods and applications. Academic Press, San Diego, CA.

Zhang, W., Wendel, J. F., and Clark, L. G. 1997. Bamboozled Again! Inadvertent isolation of fungal rDNA sequences from bamboos (*Poaceae:Bambusoideae*) Mol. Phylogen. Evol. 8:205-217.