

Multilocus Sequence Typing Reveals that the Population Structure of *Candida dubliniensis* Is Significantly Less Divergent than That of *Candida albicans*^{∇†}

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Received 8 August 2007/Returned for modification 4 November 2007/Accepted 20 November 2007

The pathogenic yeast *Candida dubliniensis* is phylogenetically very closely related to *Candida albicans*, and both species share many phenotypic and genetic characteristics. DNA fingerprinting using the species-specific probe Cd25 and sequence analysis of the internal transcribed spacer (ITS) region of the ribosomal gene cluster previously showed that *C. dubliniensis* is comprised of three major clades comprising four distinct ITS genotypes. Multilocus sequence typing (MLST) has been shown to be very useful for investigating the epidemiology and population biology of *C. albicans* and has identified many distinct major and minor clades. In the present study, we used MLST to investigate the population structure of *C. dubliniensis* for the first time. Combinations of 10 loci previously tested for MLST analysis of *C. albicans* were assessed for their discriminatory ability with 50 epidemiologically unrelated *C. dubliniensis* isolates from diverse geographic locations, including representative isolates from the previously identified three Cd25-defined major clades and the four ITS genotypes. Dendrograms created by using the unweighted pair group method with arithmetic averages that were generated using the data from all 10 loci revealed a population structure which supports that previously suggested by DNA fingerprinting and ITS genotyping. The MLST data revealed significantly less divergence within the *C. dubliniensis* population examined than within the *C. albicans* population. These findings show that MLST can be used as an informative alternative strategy for investigating the population structure of *C. dubliniensis*. On the basis of the highest number of genotypes per variable base, we recommend the following eight loci for MLST analysis of *C. dubliniensis*: CdAAT1b, CdACC1, CdADP1, CdMPIb, CdRPN2, CdSYA1, exCdVPS13, and exCdZWF1b, where “Cd” indicates *C. dubliniensis* and “ex” indicates extended sequence.

Candida dubliniensis is a pathogenic yeast species that is phenotypically, genetically, and phylogenetically very closely related to *Candida albicans*, the yeast species most commonly associated with infection in humans (49, 51). Despite their close relationship, *C. albicans* is significantly more pathogenic (49, 50). *C. dubliniensis* is most commonly associated with oral carriage and infection in human immunodeficiency virus (HIV)-infected and diabetic patients, although it has been identified as a minor constituent of the commensal floras in the oral cavities of healthy individuals (40, 49, 50). Although *C. dubliniensis* has also been recovered from patients with systemic infections, its incidence is far lower than that of *C. albicans*. While the latter is responsible for 40 to 60% of cases of candidemia, *C. dubliniensis* has been identified in only 1 to

2% of blood culture yeast samples (11, 15, 27, 29–31). These epidemiological data are reflected in the results of animal infection model studies that demonstrated that *C. albicans* is significantly more pathogenic than *C. dubliniensis* (22, 47, 56). The reasons for the lower virulence of *C. dubliniensis* relative to that of *C. albicans* have not been investigated in detail; however, recently published data showed that *C. dubliniensis* has a reduced capacity to produce hyphae that results in lower levels of colonization and tissue invasion (47).

In order to be able to perform meaningful and informative epidemiological studies of *Candida* isolates, it is essential to be able to discriminate between unrelated strains of the species of interest. Ideally, strain differentiation methods should be highly discriminatory, reproducible, and suitable for the analysis of large numbers of isolates. To date, DNA fingerprinting using the species-specific, semirepetitive-sequence-containing DNA probe Cd25 has been the most widely applied and informative tool used for *C. dubliniensis* epidemiology and population analysis. When first developed, data generated using this probe showed that *C. dubliniensis* is comprised of two distinctive major clades, termed Cd25 fingerprint groups I and II (21,

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† Supplemental material for this article may be found at <http://jcm.asm.org/>.

[∇] Published ahead of print on 5 December 2007.

26). Cd25 group I isolates are all closely related, with an average similarity coefficient (S_{AB}) value of approximately 0.8 (range, 0.8 to 0.86), where A and B represent two different strains. These isolates comprise the majority of isolates investigated to date recovered in many countries around the world, mainly from HIV-infected individuals (4, 21, 26). Furthermore, sequence analysis of the internally transcribed spacer (ITS) region of the rRNA gene cluster revealed that Cd25 group I isolates consist of a single ITS genotype: ITS genotype 1 (21). In contrast, Cd25 group II isolates are more diverse, with an average S_{AB} value of 0.52 (range, 0.07 to 0.67) (4), and consist of three separate ITS genotypes (ITS genotypes 2 to 4), which correspond to distinct subclades within the Cd25 group II fingerprinting clade (21). More recently, a third major clade, termed Cd25 group III, was identified among isolates from Egypt and Saudi Arabia and displayed an average S_{AB} value of 0.35 (range, 0.16 to 0.54) (4). The DNA fingerprints of Cd25 group III isolates are very distinctive relative to those of isolates from Cd25 groups I and II, and ITS sequence analysis revealed that they belong to ITS genotypes 3 and 4 (4). All Cd25 group III isolates examined to date exhibit resistance to 5-flucytosine (4).

DNA fingerprinting analysis of large numbers of *C. albicans* isolates using the species-specific, repetitive-sequence-containing Ca3 probe has demonstrated that the population structure of the species is complex, with five major clades, some of which appear to be associated with specific geographic locations (6, 42, 46). In comparison, the population structure of *C. dubliniensis* determined with the Cd25 probe is significantly less complex (4, 21, 26). Although DNA fingerprinting has been shown to be a very useful tool in the molecular epidemiological analysis of *C. albicans* and *C. dubliniensis* populations, it is time-consuming, expensive, and not conducive to interlaboratory comparisons. There are many other molecular strain-typing techniques that have been applied to the analysis of *Candida* species (e.g., karyotyping and randomly amplified polymorphic DNA fingerprinting, etc. [45]). However, all of these methodologies also suffer from drawbacks, particularly in relation to reproducibility. In the late 1990s, multilocus sequence typing (MLST), a technique based on the nucleotide sequence analysis of a set of housekeeping genes, was developed for the population analysis of several bacterial species (28). This technique has also been applied to the analysis of the diploid yeast *C. albicans* (9, 10, 54) and to other *Candida* species (17, 25, 53). In 2002, Bounoux et al. identified six housekeeping gene loci that allowed accurate and reproducible discrimination between unrelated *C. albicans* isolates (9). A study by Tavanti et al. used four of these loci and a further four loci and also showed high levels of discrimination (54). These two groups of researchers subsequently revised the combination of loci used in the MLST analysis of *C. albicans*, aiming to identify the minimum number of loci required to maintain the high discriminatory standard of the scheme (10). An agreed consensus scheme between the different laboratories examined seven loci, *AAT1a*, *ACCI*, *ADP1*, *MPIb*, *SYA1*, *VPS13*, and *ZWF1b*, and allowed the application of MLST to the analysis of *C. albicans* epidemiology and population structure (7–9, 16, 36, 52). MLST analysis has since been demonstrated to be as sensitive as DNA fingerprinting (43), and due to the nature of the data (i.e., DNA sequences of specific loci), these can be used to create a large

database generated by multiple laboratories (7). In the case of *C. albicans*, it has also been shown that the strain groupings identified by MLST correlate with clades of *C. albicans* organisms identified using the species-specific DNA fingerprinting probe Ca3 (52). When applied to specific epidemiological studies, the use of MLST has identified intrafamilial transmission of *C. albicans* from the human digestive tract, strain maintenance, replacement, and microevolution (8).

The purpose of the present study was to determine the usefulness of MLST for investigating the epidemiology and population structure of *C. dubliniensis*. In addition, we hypothesized that if the same set of MLST loci currently used for *C. albicans* could be applied to the analysis of *C. dubliniensis*, then comparative sequence data could be used to provide valuable information concerning the evolutionary relatedness of the two species.

MATERIALS AND METHODS

***C. dubliniensis* isolates.** The 50 epidemiologically unrelated *C. dubliniensis* isolates used in this study are shown in Table 1. Isolates were selected from diverse geographical locations and included representatives of the three Cd25 major fingerprinting clades and all four ITS genotypes. The majority of the isolates studied have been described previously; however, a number of new clinical isolates were also included (Table 1). These new isolates were initially presumptively identified on the basis of dark-green colony coloration on *Candida*-selective chromogenic agar (Oxoid Ltd., Hampshire, United Kingdom) and on the basis of hyphal fringe production on Pal's agar after 48 h of growth at 30°C as described by Al Mosaïd et al. (3). The identities of presumptive *C. dubliniensis* isolates were further confirmed using the API ID 32C yeast identification system (bioMérieux, Paris, France) (37). Definitive identification of *C. dubliniensis* was confirmed by PCR using primers specific for the Cd*ACT1*-associated intron as described previously (18).

Isolates were routinely cultured on potato dextrose agar (Oxoid) medium, pH 5.6, at 37°C. Liquid cultures were grown overnight in yeast extract-peptone-dextrose broth at 37°C in an orbital incubator (Gallenkamp, Leicester, United Kingdom) at 200 rpm.

***C. albicans* isolates.** A selection of 50 *C. albicans* isolates (Table 2) was chosen to represent a range of the 17 MLST clades recently described by Odds et al. (35). Sequence data for each of the 50 *C. albicans* isolates were available at <http://test1.mlst.net/> for the seven collaborative consensus MLST loci, *AAT1a*, *ACCI*, *ADP1*, *MPIb*, *SYA1*, *VPS13*, and *ZWF1b* (35), and at <http://calbicans.mlst.net/> for the *RPN2* locus (9). All locus sequences were treated in a manner identical to that used for the *C. dubliniensis* sequence data, as described below.

Chemicals, enzymes, and oligonucleotides. Analytical-grade or molecular biology-grade chemicals were purchased from Sigma-Aldrich Ireland Ltd. (Tallaght, Dublin, Ireland) or Fisher Scientific Ltd. (Loughborough, United Kingdom). Enzymes were purchased from the Promega Corporation (Madison, WI) or New England Biolabs Inc. (Beverly MA) and used according to the manufacturers' instructions. Custom-synthesized oligonucleotides were purchased from Sigma Genosys Biotechnologies Europe Ltd. (Pampisford, Cambridgeshire, United Kingdom).

***C. dubliniensis* DNA isolation.** Isolates were grown overnight in 5 ml of yeast extract-peptone-dextrose broth, and cells from 1.5 ml of culture were harvested by centrifugation. DNA was extracted from the cells as described by Gallagher et al. (20).

Genotyping of *C. dubliniensis*. Template DNA was tested in separate PCR amplification experiments with each of the primer pairs G1F/G1R, G2F/G2R, G3F/G3R, and G4F/G4R to identify the ITS genotype of the isolate (21). Genotypes are ascribed based on the nucleotide sequences of the ITS1 and ITS2 regions and of the intervening 5.8S rRNA gene (57). Template DNAs from the four reference *C. dubliniensis* isolates (CD36, genotype 1; Can4, genotype 2; CD519, genotype 3, and p7718, genotype 4) previously described by Gee et al. (21) were used in control amplification reactions. Each PCR was carried out with one pair of ITS genotype-specific primers and the universal fungal primers RNAF/RNAR (19), which amplify approximately 610 bp from all fungal large-subunit rRNA genes and were used as an internal positive control. Genotyping experiments were performed on a minimum of two

TABLE 1. *C. dubliniensis* isolates investigated by MLST analysis^c

Isolate	Country of origin	Yr of isolation	Underlying patient condition	Sample	MLST clade ^a	ITS genotype	Cd25 fingerprint group	Reference(s) or source
CD36 ^b	Ireland	1988	HIV pos	Oral	1	1	I	21, 51
CD06033 ^b	Ireland	2006	CF	Sputum	1	1	ND	This study
CD06031	Ireland	2006	CF	Sputum	1	1	ND	This study
CD060213	Ireland	2006	CF	Sputum	1	1	ND	This study
CD06041	Ireland	2006	CF	Sputum	1	1	ND	This study
CD06038 ^b	Ireland	2006	CF	Sputum	1	1	ND	This study
CD06045	Ireland	2006	CF	Sputum	1	1	ND	This study
CD06037 ^b	Ireland	2006	CF	Sputum	2	2	ND	This study
CD06036 ^b	Ireland	2006	CF	Sputum	2	2	ND	This study
CD060215 ^b	Ireland	2006	CF	Sputum	3	3	ND	This study
CD604 ^b	France	2000	HIV asymptomatic	Throat	1	1	ND	This study
CD603 ^b	France	2000	HIV asymptomatic	Throat	1	1	ND	This study
CM1 ^b	Australia	1991	HIV pos	Oral	1	1	I	21, 51
SA105	Saudi Arabia	2002	Diabetes	Oral	1	1	I	4
SA115	Saudi Arabia	2002	Diabetes	Oral	1	1	I	4
SA116	Saudi Arabia	2002	Diabetes	Oral	1	1	I	4
SA108 ^b	Saudi Arabia	2002	Diabetes	Oral	3	3	III	4
SA100 ^b	Saudi Arabia	2002	Leukemia	Oral	3	3	III	4
SA121 ^b	Saudi Arabia	2002	S/P renal tx	Oral	3	4	III	4
Eg202	Egypt	2002	Cancer	Oral	3	4	III	4
Eg203	Egypt	2002	Cancer	Oral	1	1	I	4
Eg204	Egypt	2002	Cancer	Oral	1	1	I	4
Eg207	Egypt	2002	Diabetes	Oral	3	4	III	4
p6785 ^b	Israel	1999	HIV neg	Urine	3	3	II	4, 39
p7276 ^b	Israel	1999	HIV neg	Respiratory tract	3	3	II	4
p7718	Israel	1999	HIV neg	Wound	3	4	III	4, 21
CD71	Argentina	1994	HIV pos	Oral	1	1	I	21, 48
CD98923	India	1998	HIV pos	Oral	1	1	I	2
B1324	United States	1998	NA	Tongue	1	1	ND	This study
B341	United States	1998	NA	Throat	1	1	ND	This study
PM6-2	Chile	2006	NA	NA	1	1	ND	This study
P2	Switzerland	1993	HIV pos	Oral	1	1	I	4, 21
1504	Slovakia	2005	NA	Tonsular swab	1	1	ND	32
8882	Slovakia	2005	Congenital hydrocephalus	Tonsular swab	1	1	ND	32
9097	Slovakia	2005	Leukemia	Tonsular swab	1	1	ND	32
966/3(1) ^b	Slovakia	2005	NA	Sputum	1	1	ND	32
966/3(2)	Slovakia	2005	NA	Sputum	1	1	ND	32
CCY29-177-1	Slovakia	2005	Pelvic organ inflammation	Cervical swab	1	1	ND	32
MLNIH0479	Thailand	2005	Leukemia	Blood	1	1	ND	13
MLNIH0720	Thailand	2005	TB, anemia, diabetes	Oral	1	1	ND	13
49831	Japan	2005	Anemia	Sputum	2	2	ND	13
IFM49883	Japan	2005	NA	NA	2	2	ND	13
IFM0492	Thailand	2005	Cancer	Blood	1	1	ND	13
IFM49832	Japan	2005	Diabetes	Sputum	1	1	ND	13
Can4	Canada	1996	HIV pos	Oral	2	2	II	21, 38
CD539	United Kingdom	1994	AIDS	Oral	2	2	II	21, 38
CBS2747	The Netherlands	1952	HIV neg	Sputum	2	2	II	21, 31
CD514	Ireland	1995	HIV neg	Oral	3	3	II	21
CD519	Ireland	1997	AIDS	Oral	3	3	II	21
CD75004	United Kingdom	1975	Diabetes	Oral	2	2	II	21, 38

^a MLST clades assigned in the present study.

^b Isolate included in assessment of sequence stability and MLST reproducibility.

^c HIV pos, HIV infected; HIV neg, HIV negative; CF, cystic fibrosis; S/P renal tx, stage post-renal transplantation; NA, not available; TB, tuberculosis; ND, not determined.

occasions, with each isolate being tested with separately prepared *C. dubliniensis* template DNA.

Selection of loci for MLST analysis. Due to the high level of sequence homology between the majority of *C. albicans* and *C. dubliniensis* open reading frames (33), all loci previously examined for the purpose of MLST analysis in *C. albicans* were also investigated for their potential use with *C. dubliniensis*. The usefulness of the six genes in *C. albicans* examined as described by Bougnoux et al. (9) (i.e., *ACC1*, *VPS13*, *GLN4*, *ADP1*, *RPN2* and *SYA1*) and the additional

four loci described by Tavanti et al. (54) (i.e., *AAT1a*, *AAT1b*, *MPIb*, and *ZWF1b*) was assessed. The *C. albicans* MLST locus sequences were used in separate BLAST searches against the *C. dubliniensis* genome sequence database (the Wellcome Trust Sanger Institute *C. dubliniensis* genome sequence project, <http://www.sanger.ac.uk/sequencing/Candida/dubliniensis/>). For each MLST locus, sequences were aligned using the CLUSTAL W sequence alignment computer program (55), and the *C. albicans* primer binding regions were identified in the alignment. Any nucleotide differences in the primer binding regions between the

TABLE 2. *Candida albicans* isolates used in the MLST study

Isolate	MLST clade ^a	Reference
APRHRC1	4	35
APRURC3	6	35
APRURM3	1	35
APRURM6	9	35
APRURM7	10	35
BCHURC10	10	35
BCHURC15	11	35
BCHURS24	S	35
BCHURS9	4	35
CCHHCRM11	4	35
CCHHCRM4	14	35
CCHHCRM7	9	35
CCHURM1	15	35
CCHURM12	9	35
CCHURM4	11	35
CCHURM9	16	35
CCHURS10	9	35
CP04	1	35
CP05	S	35
CP06	1	35
CP08	1	35
CP12	4	35
CP15	3	35
CP54	2	35
CP58	4	35
CP85	4	35
DPC111	9	8
DPC118	1	8
DPC168	11	8
DPC18	12	8
DPC2	11	8
DPC206	1	8
DPC208	5	8
DPC22	12	8
DPC25	3	8
DPC28	11	8
DPC35	17	8
DPC37	1	8
DPC44	11	8
DPC47	3	8
DPC5	11	8
DPC55	1	8
DPC6	11	8
DPC65	11	8
DPC66	9	8
DPC70	11	8
DPC81	2	8
DPC90	4	8

^a MLST clades correspond to those recently identified by Odds et al. (35). S stands for singletons, i.e., isolates that were not assigned to any of the 17 clades.

species were adjusted in the corresponding *C. dubliniensis* oligonucleotides to facilitate optimum amplification. All of the *C. dubliniensis*-optimized primer pairs yielded a single PCR product of the expected size (ranging in size from 400 bp to 700 bp) (Table 3).

PCR amplification and sequence determination. PCR assays were carried out in 50- μ l reaction volumes containing a 200 μ M concentration of each deoxynucleoside triphosphate, 1.25 U of GoTaq polymerase (Promega), 10 μ l (1 \times) of GoTaq FlexiBuffer (Promega), 3 μ M MgCl₂, 100 pmol of each primer, and 1 ng of the DNA template. PCR products were purified using a QIAquick 96-well PCR purification kit (Qiagen Science, MD) and were sequenced on both strands using the same primers that had been used previously for amplification. DNA sequencing reactions were performed commercially by Cogenics (Essex, United Kingdom) using an ABI 3730xl DNA analyzer.

Sequence analysis and sequence type determination. Sequence analysis was performed by examination of chromatogram files using the ABI prism Seqscape software, version 2.0 (Applied Biosystems, Foster City, CA). The sequences of all

of the loci examined are provided in the supplemental material. Numbers were assigned to unique genotypes for each locus, and genotype numbers were then combined to yield a diploid sequence type (DST) number. All genotype numbers and DST numbers are also available in the supplemental material. Maximum-parsimony trees and dendrograms based on analysis by the unweighted pair group method with arithmetic averages (UPGMA) were constructed using the Bionumerics software package, version 4.6 (Applied Maths NV, Sint-Martens-Latem, Belgium), based on concatenated *C. albicans* and *C. dubliniensis* MLST sequences. The discriminatory power of each MLST scheme was determined using Hunter's formula (24).

Linkage disequilibrium and clonality. Linkage disequilibrium was assessed using the index of association, as described by Smith et al. (44) and as calculated with the Multilocus 1.3 software package, available at <http://www.agapow.net/software/multilocus/> (1), using genotype numbers for all loci (scheme C) from all 50 *C. dubliniensis* isolates. The levels of significance for nonrandom association between loci were computed under the null hypothesis of a freely recombining population (panmixia).

Stability and reproducibility of the MLST method. The stability and reproducibility of the sequence data at each MLST locus were assessed by carrying out the sequence analysis in duplicate on two randomly selected isolates. For each locus and isolate, the duplicate DNA extractions, PCRs, and sequencing reactions were carried out independently. Resulting sequence duplicates for each isolate were compared to each other.

RESULTS

Development of an MLST scheme for *C. dubliniensis*. All loci previously examined for the purpose of analyzing MLSTs in *C. albicans* were also investigated for their potential use with *C. dubliniensis*. Homologous genes were found in each case, and comparison of the sequences of the complete open reading frames of the orthologous pairs revealed homologies ranging from 89% to 94%, while the parts of the genes that were analyzed for MLST purposes displayed 88% to 100% sequence identity (Table 3).

The current consensus MLST scheme for *C. albicans* examines 2,883 nucleotides from seven loci: *AAT1a*, *ACC1*, *ADP1*, *MPIb*, *SYA1*, *VPS13*, and *ZWF1b*. For the purposes of this study, this scheme is referred to as scheme A (Table 4). The corresponding scheme A loci were examined in the 50 *C. dubliniensis* isolates included in this study. The scheme A loci resulted in 23 single nucleotide polymorphisms (SNPs) from the equivalent 2,883 nucleotides (0.8%) and identified 33 genotypes. In scheme A, only one site (i.e., position 186 in *SYA1*) showed a polymorphism at the same position in both *C. albicans* and *C. dubliniensis*, whereas all other variable sites were at different locations in the two species. Tavanti et al. analyzed eight loci (54) (*AAT1a*, *AAT1b*, *ACC1*, *ADP1*, *MPIb*, *SYA1*, *VPS13*, and *ZWF1b*) for sites of heterozygosity among 50 isolates of *C. albicans*. The group identified 87 sites that displayed polymorphisms, 71 of which (81.6%) also displayed heterozygosity. The same loci were studied for sites of heterozygosity in the 50 isolates of *C. dubliniensis* (Table 1), and of the 30 sites displaying variability, 9 (30%) displayed heterozygosity.

Due to the low levels of polymorphism observed in the *C. dubliniensis* loci examined, we investigated whether increasing the length of the sequences examined had the potential to increase the discriminatory power of the method. To achieve this, additional nucleotide sequence data (range, 100 bp to 280 bp) at each of the loci in both the 5' and 3' directions of the original sequence fragment were also analyzed for the potential presence of polymorphic sites. Sequence analysis of the extended fragments in Cd*VPS13* and Cd*ZWF1b* (exCd*VPS13*

TABLE 3. Oligonucleotide primers and sequences used for *C. dubliniensis* MLST analysis

Locus	Amplicon size (bp) in <i>C. dubliniensis</i>	No. of bases analyzed in <i>C. dubliniensis</i> (bp) ^e	Coordinates of ^f :		Analyzed segment sequence homology (%) ^e	Primer ^d	Analyzed segment start (5') and end (3') points in <i>C. dubliniensis</i> ^e
			<i>C. albicans</i> amplicon	<i>C. dubliniensis</i> amplicon			
<i>CdAAT1a</i>	480	373	+31–+508	+35–+497	91	5'-ATCAAACTACTAAATT TTTGAC-3' (forward) 5'-CGGCAACATGATTA GCC-3' (reverse)	5'-ATTGAAA 3'-CGATT
<i>CdAAT1b</i>	491	341	+736–+1,226	+742–+1,233	95	5'-ATGGCTTATCAAGGT TTTGC-3' (forward) 5'-GTAGCATAAACTGA ATAATCA-3' (reverse)	5'-TTAACTAA 3'-TTGGGATCA
<i>CdACC1</i>	519	407	+3,184–+3,702	+3,190–+3,708	93	5'-GCCAGAGAAAATTTT GATCCAATGT-3' (for- ward) 5'-TTCATCAACATCATC CAAGTG-3' (reverse)	5'-TTTTTGAGAT 3'-TACAAGA
<i>CdADP1</i>	537	443	+868–+1,404	+868–+1,404	90	5'-GAGCCAAAGTATGAA TGACTTG-3' (forward) 5'-TTGATCAACAACCC GATAAT-3' (reverse)	5'-TACGTTGCAA 3'-GGAAATCCAA
<i>CdGLN4</i>	483	404	+82–+564	+82–+564	100	5'-GAGATAGTTAAGAA TAAAAAAGTTG-3' (forward) 5'-GTCCTTTGCTCTTA GGACCCAATC-3' (re- verse)	5'-TCIGCTTTA 3'-TTCAAACC
<i>CdMPlb</i>	486	375	+406–+891	+406–+892	90	5'-ACCAGAAAATGGCC-3' (forward) 5'-GCAGCCATACATTCA ATTAT-3' (reverse)	5'-TTTAAGC 3'-GGGAAAGCA
<i>CdRPN2</i>	447	306	+1,012–+1,458	+1,015–+1,461	90	5'-TTTATGCAATGCTGGT ACTACTIGATG-3' (for- ward) 5'-TAACCCCATACTCAA AGCAGCAGCCT-3' (reverse)	5'-TTGGTCCAAG 3'-GTCITTACGA
<i>CdSYA1</i>	543	391	+2,284–+2,826	+2,284–+2,826	90	5'-AGAAGAATAATGTTG TCITACTG-3' (for- ward) 5'-GTTGCCCTTACCACC AGCTTT-3' (reverse) 5'-CGTTGAGAGATATTC GACTT-3' (forward) 5'-ACGGATCGATCGCC AATCC-3'1 (reverse)	5'-TAAATCCAAG 3'-AGTCTGTATCT 5'-CCTTGTATG 3'-AAAATCTTGG (5'-AGAGCAAAG) (3'-AAAACCTTGG)
<i>Cd/PS13 (exCd/PS13)</i>	741	403 (675)	+4,854–+5,594	+4,858–+5,598	88		

CdZWF1b (exCdZWF1b)	702	491 (621)	+ 787--+ 1,469	+ 766--+ 1,468	93	5'-GTTTCATTGATCCT GAAGC-3' (forward) 5'-GCCATTGATAAGTAC CTGGAT-3' (reverse)	5'-CAAACCAGG 3'-TAGAATTAC (5'-AAAAGTTTTA AAA) (3'-GAAAAATATTT GAAA)
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^a Numbers in parentheses are for extended sequence fragments analyzed for polymorphisms.

^b Nucleotide coordinates for MLST amplicons are numbered based on the adenine residue of the ATG start codon at the 5' end of the gene designated +1.

^c Sequence homology between *C. dubliniensis* and *C. albicans* at the sequenced fragments.

^d Nucleotide bases shown in bold typeface and underlined denote nucleotide bases that vary between *C. albicans* and *C. dubliniensis*.

^e Loci for which additional sequence data were analyzed in both the 5' and 3' directions of the original sequence fragment (range, 100 bp to 280 bp) due to the presence of additional polymorphic sites (underlined and bold). Sequences in parentheses are those used with the extended sequence fragments.

and exCdZWF1b, respectively) revealed the presence of additional SNPs (Table 3). The inclusion of these two extended sequences together with the sequences of the other five loci generated a second MLST scheme, termed scheme B (Table 4), which was made up of the sequences of the CdAAT1a, CdACCI, CdADP1, CdMPIb, CdSYA1, exCdVPS13, and exCdZWF1b loci. Examination of exCdVPS13 revealed one extra SNP, which gave rise to two extra genotypes (Table 5), and exCdZWF1b yielded two further SNPs, which in turn gave rise to one extra genotype. Scheme B resulted in a new total of 3,285 nucleotides, 26 (0.8%) of which displayed SNPs, resulting in four additional genotypes (Table 5).

In a further attempt to improve the discriminatory power of this method for *C. dubliniensis*, three other sequence segments in *C. dubliniensis* that were previously investigated for possible use in the MLST analysis of *C. albicans* were also analyzed, although these were not included in the final consensus *C. albicans* MLST scheme. Sequences from these additional loci, CdAAT1b, CdGLN4, and CdRPN2 (Table 3), comprised an additional 1,051 nucleotides, 11 of which displayed SNPs (1.05%). The 10 sequence fragments (the scheme B loci and the three additional loci) were all analyzed together in a third scheme, termed scheme C (Table 4), which was based on the sequences of the CdAAT1a, CdAAT1b, CdACCI, CdADP1, CdGLN4, CdMPIb, CdRPN2, CdSYA1, exCdVPS13, and exCdZWF1b loci. CdGLN4 displayed four of the further 11 SNPs; however, it gave rise to only two genotypes among the 50 isolates investigated. Similarly, CdAAT1b displayed four SNPs, giving rise to five genotypes, and the CdRPN2 locus contained three polymorphic sites, which gave rise to three genotypes. Scheme C analyzed a total of 4,336 nucleotides, 37 of which (0.85%) displayed SNPs, resulting in a total of 48 genotypes from 50 *C. dubliniensis* isolates. The minimum number of MLST loci for maximum discrimination among isolates of *C. dubliniensis* was determined according to the highest number of genotypes per variable base in each locus (Table 4 and Table 5) and is referred to as scheme D, consisting of the eight loci CdAAT1b, CdACCI, CdADP1, CdMPIb, CdRPN2, CdSYA1, exCdVPS13, and exCdZWF1b. Scheme D displayed a total of 32 SNPs, resulting in 40 genotypes from the 50 isolates of *C. dubliniensis* investigated. Polymorphic sites and resulting genotypes are summarized in Tables 4 and 5.

Nucleotide polymorphisms and amino acid changes. The effect of nucleotide polymorphism on the resulting amino acid sequence was investigated by mapping the triplet codons for each gene fragment and examining the effect that the SNP had on each codon in question. Nucleotide polymorphisms and amino acid substitutions are summarized in Table 6. Of the 37 SNPs identified in the 10 *C. dubliniensis* loci examined (with substitution of CdVPS13 for exCdVPS13 and CdZWF1b for exCdZWF1b), 13 (35%) resulted in nonsynonymous amino acid changes, while all of the remaining nucleotide changes resulted in synonymous polymorphisms. Seven of the 13 nonsynonymous polymorphisms affected the resulting amino acid substantially, i.e., affecting the pH (4 of 7) or polarity (3 of 7) of the amino acid.

Stability and reproducibility of *C. dubliniensis* MLST. Sequence analysis was performed in duplicate for each of two randomly selected isolates (Table 1) per MLST locus, using independently prepared DNA, PCR, and sequencing reac-

TABLE 4. Summary of loci used in individual MLST schemes

MLST scheme	Locus ^a												No. of polymorphic sites	No. of DSTs	Discriminatory power ^b
	<i>AAT1a</i>	<i>AAT1b</i>	<i>ACCI</i>	<i>ADP1</i>	<i>GLN4</i>	<i>MPIb</i>	<i>RPN2</i>	<i>SYA1</i>	<i>VPS13</i>	(ex) <i>VPS13</i>	<i>ZWF1b</i>	(ex) <i>ZWF1b</i>			
A	+	-	+	+	-	+	-	+	+	-	+	-	23	20	0.899
B	+	-	+	+	-	+	-	+	-	+	-	+	26	22	0.901
C	+	+	+	+	+	+	+	+	-	+	-	+	37	26	0.910
D	-	+	+	+	-	+	+	+	-	+	-	+	32	25	0.909
E	+	-	+	+	-	+	+	+	+	-	+	-	26	22	0.906

^a + and - denote the presence and absence, respectively, of individual loci in each MLST scheme.

^b Determined using Hunter's formula (24).

tions. For each MLST locus, duplicate sequences for each isolate showed 100% sequence identity, displaying full conservation of both SNPs and sites of heterozygosity at each locus.

***C. dubliniensis* strain differentiation by MLST.** Examination of the *C. albicans* MLST locus set (scheme A) in the 50 *C. dubliniensis* isolates investigated identified 20 unique DSTs based on the unique combinations of the genotype numbers for the seven loci examined. Application of Hunter's formula (24) to this data set infers that MLST using scheme A has a discriminatory power of 0.899 when applied to *C. dubliniensis*, compared with a value of 0.996 when applied to *C. albicans* (35). Extension of the Cd*VPS13* and Cd*ZWF1b* loci (scheme B) resulted in a further 2 DSTs, and adding the Cd*AAT1b*, Cd*GLN4*, and Cd*RPN2* loci (scheme C in Table 4) resulted in a further 4 DSTs, giving a total of 26 DSTs from the 10 loci. Extending the Cd*ZWF1b* and Cd*VPS13* gene fragments and including the three other loci in scheme C increased the discriminatory power to 0.9102 (Table 4). DST 4 was the most common DST identified using the scheme A set of loci in *C. dubliniensis*, corresponding to 14 of the 50 isolates examined. The set of seven loci identified 11 DSTs that were unique to single *C. dubliniensis* isolates. When the larger set of loci was used in scheme C, the same 14 isolates from DST 4 in scheme A referred to above also gave an identical sequence type, this time termed DST 7, which correlated with the previously identified DST 4, making this the most common DST in the scheme examined for *C. dubliniensis*. Using this larger set of loci, 19 of the 26 DSTs were unique to single isolates.

Population analysis of *C. dubliniensis* using MLST. A UPGMA dendrogram was constructed based on the sequence data from all 10 loci (scheme C) examined in *C. dubliniensis* by using the Bionumerics version 4.6 software program (Fig. 1). At a cutoff node of 99.7% sequence homology, the dendrogram revealed the presence of three major clades of isolates termed C1 to C3, which showed a significant degree of correlation with the major clades previously identified by fingerprinting using the Cd25 fingerprint probe (Fig. 1 and Table 1). Clades C1 and C2 corresponded to the previously identified Cd25 fingerprint groups I and II, respectively, whereas clade C3 included strains previously identified as belonging to Cd25 fingerprint groups II and III, respectively (Fig. 1 and Table 1). Furthermore, clade C1 consisted solely of ITS genotype 1 isolates, clade C2 consisted solely of ITS genotype 2 isolates, whereas clade C3 consisted of ITS genotype 3 and 4 isolates.

Linkage disequilibrium and clonality. Genetic diversity and linkage disequilibria were assessed by using statistics implemented in the Multilocus 1.3 software (1) and genotypes obtained for all loci investigated in this study (scheme C). Each of these statistics tested the null hypothesis of a freely recombining population. Highly significant linkage disequilibria (P was $<10^{-5}$ with 100,000 randomizations) were found for both the total collection of 50 *C. dubliniensis* isolates and a reduced collection of 26 isolates that represented each of the 26 DSTs defined by scheme C (i.e., that did not contain repeated genotypes) (data not shown). These results provide evidence that the sample of *C. dubliniensis* isolates analyzed in this study represents a clonal population.

Comparative population analysis of *C. albicans* and *C. dubliniensis* using MLST. *C. albicans* MLST sequences were available for the seven consensus MLST loci (i.e., *AAT1a*, *ACCI*, *ADP1*, *MPIb*, *SYA1*, *VPS13*, and *ZWF1b*) and an extra locus, *RPN2*. The resulting 3,189 nucleotides from the eight loci resulted in a fifth scheme, termed scheme E (Table 4). All locus sequences were concatenated and treated as one sequence for each of 50 *C. albicans* isolates and the corresponding sequences in 50 *C. dubliniensis* isolates in order to allow comparison between the two species using MLST. These concatenated sequences were used to construct a maximum-parsimony tree in order to assess comparative phylogenies between the species (Fig. 2). The maximum-parsimony tree displays the comparative divergence within the two species, as well as the level of relatedness between the two species. The maximum-parsimony tree demonstrated that *C. albicans* isolates belonging to different MLST clades can differ at as many as 90

TABLE 5. Summary of characteristics of loci used in the MLST analysis

Locus	Length of analyzed sequence	No. (%) of polymorphic nucleotide sites	No. of polymorphic amino acid sites	No. of resulting genotypes
<i>AAT1a</i>	373	1 (0.27)	0	2
<i>AAT1b</i>	341	4 (1.17)	2	5
<i>ACCI</i>	407	3 (0.74)	2	4
<i>ADP1</i>	443	5 (1.13)	1	6
<i>GLN4</i>	404	4 (0.99)	2	2
<i>MPIb</i>	375	2 (0.5)	1	7
<i>RPN2</i>	306	3 (0.98)	0	3
<i>SYA1</i>	391	5 (1.28)	2	5
<i>VPS13</i>	403	2 (0.5)	1	2
(ex) <i>VPS13</i>	675	3 (0.44)	2	4
<i>ZWF1b</i>	491	5 (1.02)	1	4
(ex) <i>ZWF1b</i>	621	7 (1.13)	1	6

TABLE 6. Nucleotide polymorphisms and amino acid substitutions in *C. dubliniensis* loci^d

Gene fragment	Nucleotide position showing polymorphism ^a	Triplet polymorphism ^b	Amino acids ^c	Corresponding codon in <i>C. albicans</i>	Corresponding amino acid residue in <i>C. albicans</i>
CdAAT1a	2	(T/C)TG	L/L	TTG	L
CdAAT1b	105	A(T/A)T	I/N	ATC	I
	114	TC(A/T)	S/S	TCA	S
	121	(G/A)AA	E/K	GAA	E
	129	TC(T/G)	S/S	TCT	S
CdACC1	128	TT(T/C)	F/F	TTC	F
	313	T(T/C)G	L/S	CTG	L
	390	AA(A/T)	K/N	AAA	K
CdADP1	31	AT(C/T)	I/I	ATT	I
	214	AG(C/T)	S/S	AGT	S
	234	G(A/G)G	E/G	GAG	E
	331	TG(T/C)	C/C	TGT	C
	421	TC(G/T)	S/S	TCA	S
CdGLN4	104	GA(A/T)	E/D	GTA	V
	141	AA(T/C)	N/N	AAA	K
	147	GA(T/C)	D/D	GAC	D
	244	(A/G)TT	I/V	ATT	I
CdMP1b	101	A(G/A)A	R/K	AGA	R
	375	GC(A/G)	A/A	GCA	A
CdRPN2	127	TC(C/A)	S/S	TCC	S
	136	GC(C/T)	A/A	GCC	A
	298	GC(T/C)	A/A	GCA	A
CdSYA1	82	AA(C/T)	N/N	AAT	N
	148	TT(A/G)	L/L	TTA	L
	186	AA(T/C)	N/N	AA<u>T</u>	N
	203	G(T/C)T	V/A	GTT	V
	383	(T/G)CT	S/A	GCT	A
	397*	AA(A/G)	K/K	AAG	K
CdVPS13	402†	T(G/C)G	W/S	TGG	W
	45	GA(G/C)	E/D	GAC	D
exCdVPS13	654*	AA(A/G)	K/K	AAG	K
	659†	T(G/C)G	W/S	TGG	W
CdZWF1b	1‡	AC(C/T)	T/T	AAA	K
	28§	AC(G/A)	T/T	ACC	T
	265¶	AA(G/A)	K/K	AAA	K
	299	(G/T)AT	D/Y	GAT	D
	334#	AA(A/G)	K/K	AAA	K
exCdZWF1b	78‡	AC(C/T)	T/T	AAA	K
	105§	AC(G/A)	T/T	ACC	T
	342¶	AA(G/A)	K/K	AAA	K
	376	(G/T)AT	D/Y	GAT	D
	411#	AA(A/G)	K/K	AAA	K
	573	TA(T/C)	Y/Y	TAT	Y
	588	TC(A/T)	S/S	TCA	S

^a Nucleotide positions refer to the positions in the analyzed fragment only.

^b Position of the polymorphism relative to its codon.

^c Amino acid resulting from the codon both before and after polymorphism.

^d The nucleotide sites shown in bold typeface and underlined denote the only common nucleotide sites that display polymorphism in both *C. albicans* and *C. dubliniensis*. Identical polymorphic sites in both of the extended gene segments analyzed and in the shorter sequences that were based on the *C. albicans* scheme lengths are marked with the same symbols.

nucleotide sites but that isolates belonging to the same MLST clade can differ at as many as 31 nucleotide sites (data not shown). In contrast, our data showed that *C. dubliniensis* consisted of three closely related clades, termed clades C1, C2, and C3 (Fig. 2), that show complete agreement with the clades described by the UPGMA dendrogram (Fig. 1). *C. dubliniensis* isolates from the three MLST clades differ from each other at a minimum of 10 nucleotide sites (range, 10 to 23 nucleotides). Isolates belonging to clade C1 differ at a maximum of 10 nucleotide sites, isolates belonging to clade C2 differ at a maximum of 6 nucleotide sites, and isolates belonging to clade C3 differ at a maximum of 8 nucleotide sites (data not shown).

DISCUSSION

MLST has previously been shown to be a useful tool in the analysis of the epidemiology and population structure of *C. albicans* (8–10, 35, 52, 54). The purpose of the present study was to determine the usefulness of MLST in the analysis of *C. dubliniensis*. In addition, we investigated whether the same set of MLST loci currently used for *C. albicans* could be applied to the analysis of *C. dubliniensis* due to the high levels of nucleotide sequence homology (~90%) shared by the two species, thus allowing comparative sequence data to be used to provide valuable information concerning the evolutionary relatedness of the two species.

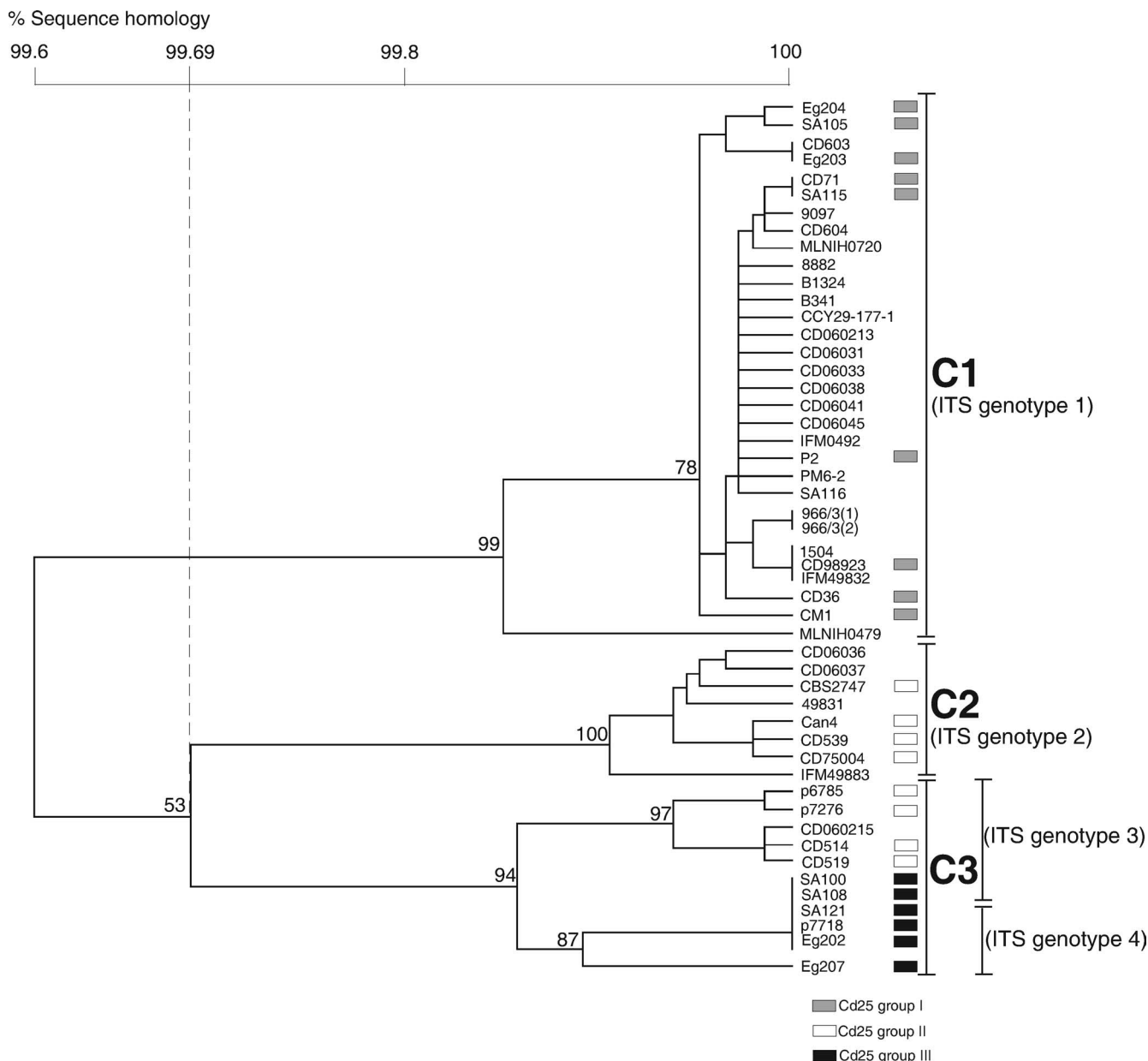


FIG. 1. UPGMA dendrogram based on concatenated sequences from the MLST scheme C loci *CdAAT1a*, *CdACCI*, *CdADP1*, *CdMPIb*, *CdSYA1*, *exCdVPS13*, *exCdZWF1b*, *CdRPN2*, *CdGLN4*, and *CdAAT1b* (Table 3), showing percentages of sequence homology for 50 *C. dubliniensis* isolates from a broad range of geographical locations, including isolates from all known ITS genotypes (Table 1). Three distinct major clades termed clades C1 to C3 are evident at 99.69% sequence homology. C1 consists of ITS genotype 1 isolates exclusively, C2 consists of ITS genotype 2 isolates exclusively, and C3 consists of ITS genotype 3 and 4 isolates. Twenty-three of the 50 isolates included in the study were previously fingerprinted with the *C. dubliniensis*-specific probe Cd25 (4, 21), and the Cd25 fingerprint groups of these isolates are indicated by shaded rectangular boxes.

The current MLST scheme in use for isolates for *C. albicans* examines seven loci: *AAT1a*, *ACCI*, *ADP1*, *MPIb*, *SYA1*, *VPS13*, and *ZWF1b* (scheme A in Table 4) and was also applied in the analysis of *C. dubliniensis* isolates. It demonstrated poor levels of discrimination among *C. dubliniensis* isolates, identifying only 20 DSTs from 50 isolates. SNPs have been detected in 172 of these 2,883 nucleotides (6%) in *C. albicans* (5). To date, 1,391 isolates of *C. albicans* have been examined, identifying 1,005 DSTs (35). An identical scheme demon-

strated poor levels of discrimination among *C. dubliniensis* isolates, identifying only 20 DSTs from 50 isolates. Discriminatory powers were improved by extension of the *CdVPS13* and *CdZWF1b* loci and by incorporation of an additional three loci, *AAT1b*, *GLN4*, and *RPN2*, which had also previously been examined for use in the MLST analysis of *C. albicans*. The scheme (i.e., scheme C) which examined the largest number of loci (Table 4) identified 26 DSTs from the 50 *C. dubliniensis* isolates. The 10 loci included in scheme C were concatenated

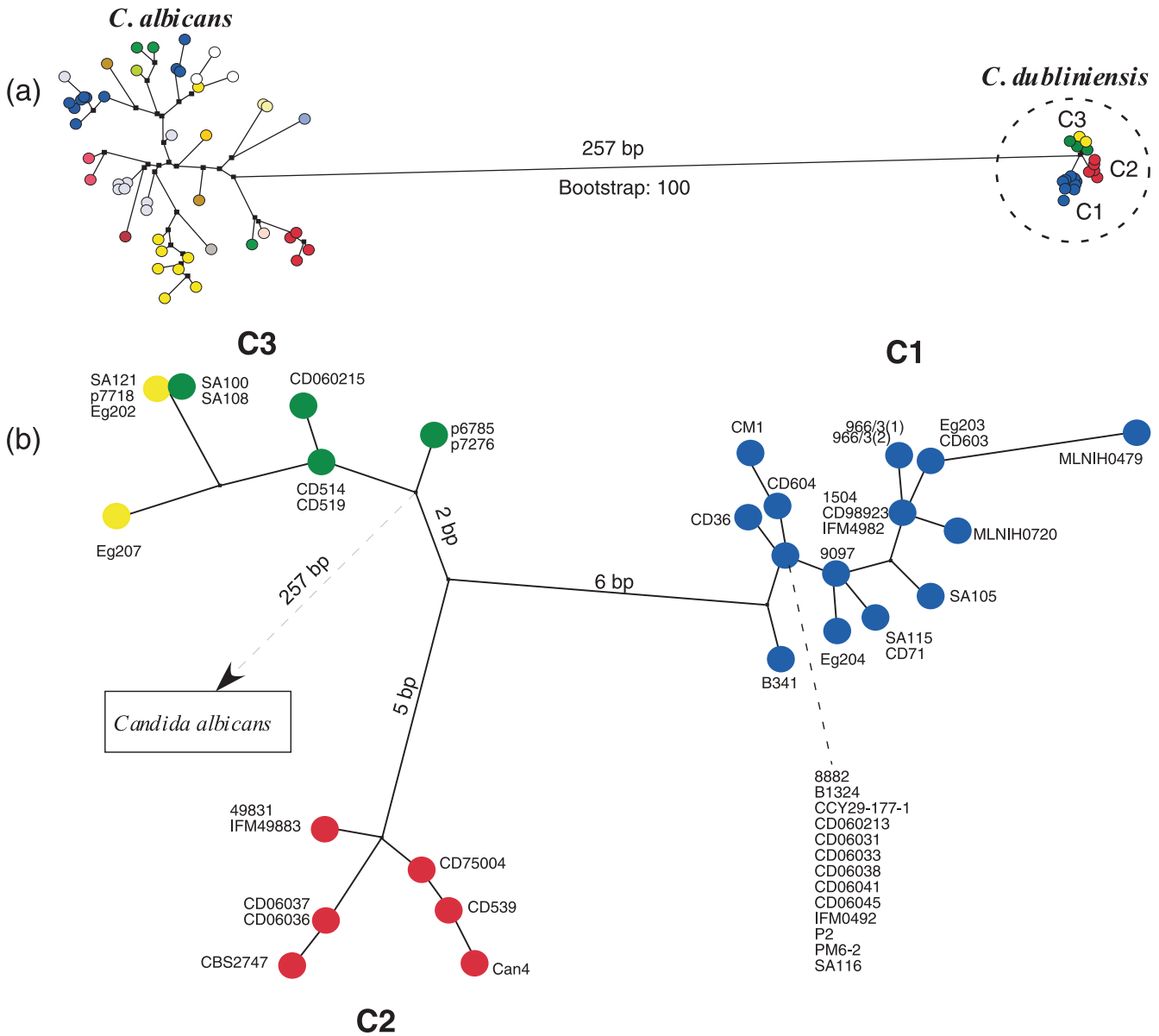


FIG. 2. Maximum-parsimony tree showing the comparative divergences between 50 isolates each of *C. albicans* and *C. dubliniensis* based on concatenated sequences from the MLST loci *AAT1a*, *ACC1*, *ADP1*, *MPIb*, *SYA1*, *VPS13*, *ZWF1b*, and *RPN2* in MLST scheme E. *C. dubliniensis* isolates were selected from a diverse range of geographic locations and from all four ITS genotypes (Table 1). *C. albicans* isolates were selected as representatives of the MLST clades recently described by Odds et al. (35) (Table 2). (a) Comparative divergence between the *C. albicans* and *C. dubliniensis* isolates tested showing that the two species are separated by 257-bp differences. The *C. dubliniensis* isolates formed three closely related groups of isolates (C1 to C3), which correspond to those identified in the UPGMA dendrogram shown in Fig. 1. Isolates from distinct clades are highlighted by specific colors for each species. (b) Enlarged view of the three *C. dubliniensis* major clades encircled in panel a. Clade C1 consists exclusively of ITS genotype 1 isolates (blue), clade C2 consists exclusively of ITS genotype 2 isolates (red), and clade C3 consists of ITS genotype 3 isolates (green) and ITS genotype 4 isolates (yellow).

and used in the construction of a UPGMA dendrogram (Fig. 1), which clustered the isolates into three distinct major clades at a cutoff sequence homology of 99.7%. A maximum-parsimony tree (Fig. 2) was also constructed using concatenated sequence data, this time with a further scheme, scheme E (Table 4), which was based on the seven loci from scheme A and an extra locus, *RPN2* (Table 4). Sequence data for these eight loci were available for both *C. albicans* and *C. dubliniensis*, thus enabling the comparative study of the population

structures for both species. Our study shows that the *C. albicans* clades are more divergent than those observed in *C. dubliniensis* (Fig. 2). The maximum-parsimony tree identified three distinct major clades (C1 to C3) in the population of *C. dubliniensis*, which were identical to those of the UPGMA dendrogram (Fig. 1). Overall, 257 nucleotides of the 3,189 nucleotides analyzed (8%) were identified as being different between the two species, correlating with the level of sequence homology typically exhibited between the two species (33).

The population structure of *C. dubliniensis* as determined by MLST correlated with the population structure previously determined using the complex fingerprinting probe Cd25 and on the basis of ITS genotypes (4, 21, 26). In previous studies, isolates assigned to ITS genotype 1 belonged exclusively to Cd25 group I (4, 21, 26). Similarly, by the MLST method, all of the ITS genotype 1 isolates tested belonged to MLST clade C1 (Fig. 1 and Table 1). Cd25 group II was previously shown to consist of isolates belonging to ITS genotypes 2, 3, and 4 (21). The MLST method breaks Cd25 group II into two groups, assigning all of the ITS genotype 2 isolates to MLST clade C2 exclusively and assigning the ITS genotype 3 and 4 isolates to MLST clade C3 (Fig. 1 and Table 1). Interestingly, a number of ITS genotype 3 and 4 isolates in MLST clade C3 displayed the same DST and localized to the same area on both the UPGMA and maximum-parsimony trees (Fig. 1 and 2). These isolates were all previously associated with Cd25 fingerprint group III (Table 1) and displayed high levels of resistance to the antifungal drug 5-flucytosine (4). The agreement between these three methods suggests that MLST may be applied as a reliable alternative method for studying the population structure of *C. dubliniensis*. MLST is less time-consuming, more reproducible, and more conducive to comparison between laboratories than other methods previously used for this purpose.

The best set of eight loci (*CdAAT1b*, *CdACC1*, *CdADP1*, *CdMPIb*, *CdRPN2*, *CdSYA1*, *exCdVPS13*, and *exCdZWF1b*) proposed for maximum discrimination among isolates of *C. dubliniensis* using the minimum number of MLST loci possible was determined according to the highest number of genotypes per variable base in each locus and is referred to as scheme D (Table 4). The *AAT1b* locus is no longer included among the more discriminatory seven loci currently recommended for use in *C. albicans* MLST studies (10), and therefore the corresponding *CdAAT1b* locus should be replaced with the *CdAAT1a* locus for the purpose of comparative population analysis between the two species. The eight loci recommended for the purposes of comparative population analysis between *C. albicans* and *C. dubliniensis* using MLST are therefore from scheme E: *CdAAT1a*, *CdACC1*, *CdADP1*, *CdMPIb*, *CdRPN2*, *CdSYA1*, *CdVPS13*, and *CdZWF1b* (Table 4).

The MLST data suggest a relatively low level of divergence in the population structure of *C. dubliniensis* relative to that of *C. albicans*. Interestingly, this is in contrast to the findings of electrophoretic karyotypic analysis showing that isolates of *C. dubliniensis* have significantly different major karyotypic patterns due to the processes of microevolution and chromosomal rearrangement (21). The low level of sequence variation throughout the population of *C. dubliniensis* suggests that MLST may not be ideal for local epidemiological studies (e.g., an outbreak in a hospital); in this instance, karyotypic analysis may be more appropriate. Karyotype analysis was able to distinguish the Cd25 group I and II isolates to a large extent but was unable to distinguish among the ITS genotypes. In comparison, the MLST method is able to distinguish readily among certain ITS genotypes, most notably the ITS genotype 1 and 2 isolates. ITS genotype 3 and 4 isolates could not be distinguished reliably by MLST, due to the lack of sequence variation among these isolates, the majority of which to date have been recovered from the Middle East. However, results may possibly be improved with the inclusion of a larger number of

ITS genotype 3 and 4 isolates from geographical locations outside of the Middle East. A possible reason for the low level of discrimination is the relatively small collection of isolates studied. However, isolates were recovered from a broad range of geographical locations and included isolates recovered from both carriage and systemic infection. Another possible reason for the low level of sequence variation and heterozygosity is the lack of divergence within the population of *C. dubliniensis* strains. Results of genotypic diversity and linkage diversity analyses suggested that the sample of 50 *C. dubliniensis* isolates investigated in this study represent a clonal population. However, it is important to emphasize that the sample number was relatively small, even though many of the isolates were recovered from disparate geographic locations around the world. Furthermore, it is possible that a more diverse population of *C. dubliniensis* strains exists in nonhuman hosts and that this is not reflected in the present study (see below). Finally, the recent divergence of *C. dubliniensis* from its ancestor *C. albicans* suggests a *C. dubliniensis* population that is less divergent than that of *C. albicans*, as the latter has had more time to diverge into major and minor clades. *C. dubliniensis* is a poor pathogen in comparison to *C. albicans*, since it rarely causes infections in healthy individuals and therefore may be under less pressure to adapt to different host environments. However, it is also possible that the natural host/reservoir for *C. dubliniensis* is not humans. *Candida* species have also been recovered from nonhuman hosts, such as dogs, cats, birds, and chameleons (12, 14, 41, 52). Recent environmental studies have reported the recovery of ITS genotype 1 *C. dubliniensis* isolates from *Ixodes uriae* ticks on the Great Saltee Island off southeastern Ireland (34), the supposed source being bird excrement. *Candida* species such as *C. albicans*, *C. guilliermondii*, and *C. tropicalis* have been recovered previously from the gastrointestinal tracts and cloacae of birds (12, 14, 23). It is conceivable that humans represent only a minority host for *C. dubliniensis* and that the isolates studied to date represent a relatively small subpopulation of the species. In order to investigate this possibility further, it will be necessary to increase the number of isolates analyzed by MLST, including isolates from avian and possibly other nonhuman hosts. We anticipate that such additional studies will identify additional MLST clades. These studies are currently in progress. Further studies will also include investigating the levels of recombination events in *C. dubliniensis*, as Odds et al. have recently shown that a high frequency of recombination is apparent in *C. albicans* (35).

ACKNOWLEDGMENTS

This study was supported by the Microbiology Research Unit, Dublin Dental School & Hospital. D.D. is the recipient of a Ph.D. fellowship from the Institut National de la Recherche Agronomique.

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