

Supplementary materials

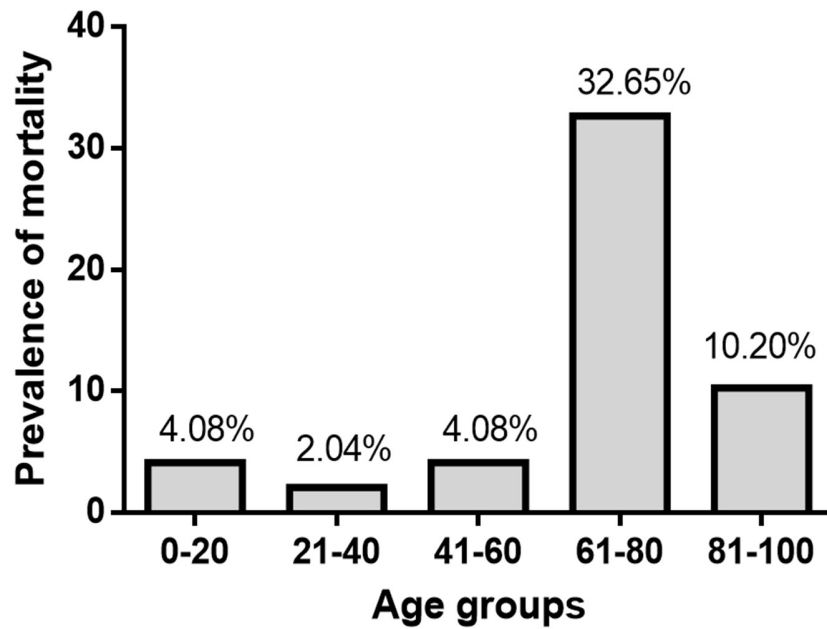


Figure S1. Mortality rate by age group among patients with candidemia.

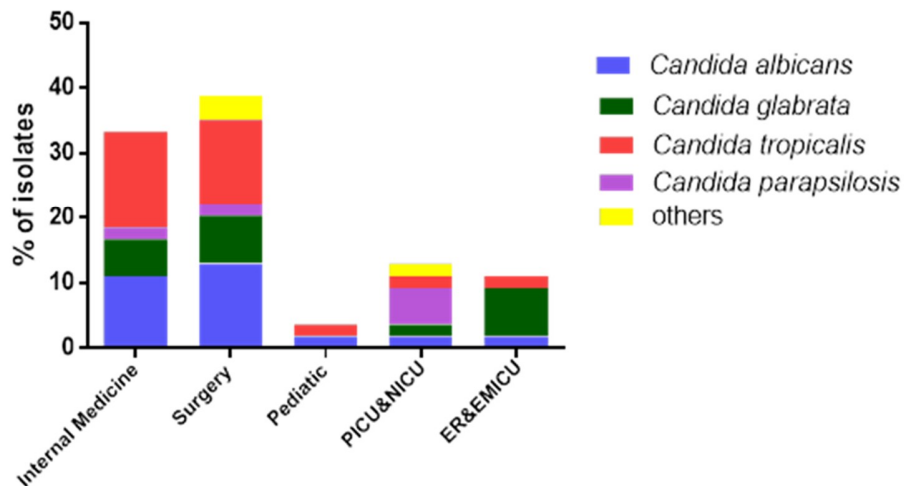


Figure S2. The composition of *Candida* species isolated from blood culture in different hospital units.

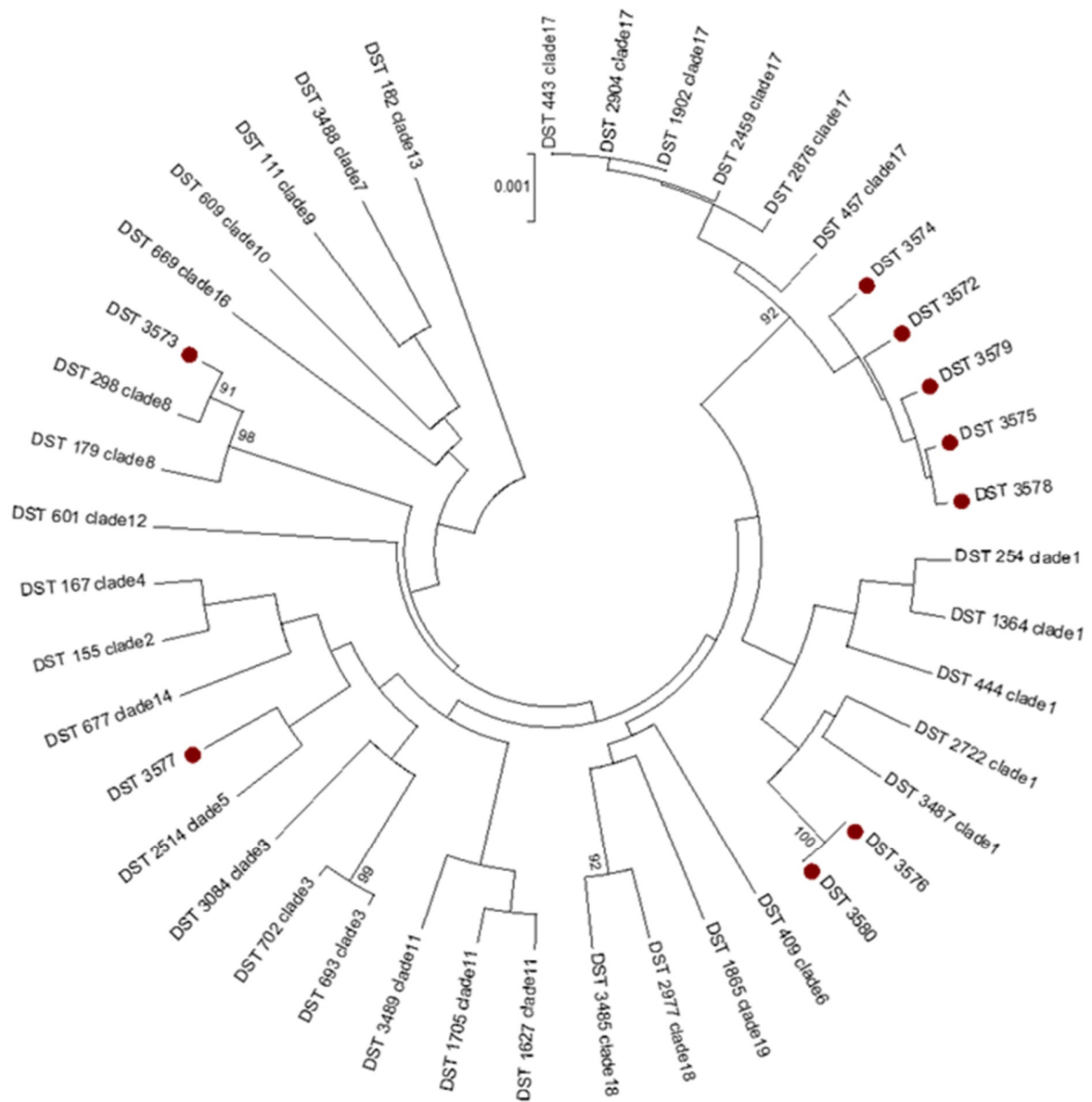


Figure S3. A phylogram was constructed via the unweighted pair group method with arithmetic mean based on the concatenated sequence of seven loci of *Candida albicans*. Clades were assigned by comparing the sequences obtained in this study to the reference sequences. Each sequence type in this study is represented as a brown dot.

Table S1. Primer sequence and PCR condition

Primer name	Primer Sequence (5' – 3')	Product size (bp)	Annealing temperature (°C)	Ref
ITS-4	5'-TCCTCCGCTTATTGATATGC-3'	520-871	55	(8)
ITS-5	5'-GGAAGTAAAAGTCGTAACAAGG-3'			
<i>Candida albicans</i> MLST loci.				
AAT1a-F	5'-ACTCAAGCTAGATTTTTTGGC-3'	478	55	(9)
AAT1a-R	5'-CAGCAACATGATTAGCCC-3'			
ACC1-F	5'-GCAAGAGAAATTTTAATTCAATG-3'	519	55	(9)
ACC1-R	5'-TTCATCAACATCATCCAAGTG-3'			
ADP1-F	5'-GAGCCAAGTATGAATGATTTG-3'	537	55	(9)
ADP1-R	5'-TTGATCAACAAACCCGATAAT-3'			
MPI b-F	5'-ACCAGAAATGGCCATTGC-3'	486	55	(9)
MPI b-R	5'-GCAGCCATGCATTCAATTAT-3'			
SYA1-F	5'-AGAAGAATTGTTGCTGTTACTG-3'	543	55	(9)
SYA1-R	5'-GTTACCTTTACCACCAGCTTT-3'			
VPS13-F	5'-TCGTTGAGAGATATTCGACTT-3'	741	55	(9)
VPS13-R	5'-ACGGATGGATCTCCAGTCC-3'			
ZWF1b-F	5'-GTTTCATTTGATCCTGAAGC-3'	702	55	(9)
ZWF1b-R	5'-GCCATTGATAAGTACCTGGAT-3'			
<i>Candida glabrata</i> MLST loci.				
FKS-F	5'-GTCAAATGCCACAACAACAACCT-3'	589	55	(11)
FKS-R	5'-AGCACTTCAGCAGCGTCTTCAG-3'			
LEU2-F	5'-TTTCTTGTATCCTCCCATTTGTTCA-3'	512	54	(11)
LEU2-R	5'-ATAGGTAAAGGTGGGTTGTGTTGC-3'			
NMT1-F	5'-GCCGGTGTGGTGTTCCTGCTC-3'	607	59	(11)
NMT1-R	5'-CGTTACTGCGGTGCTCGGTGTCG-3'			
TRP1-F	5'-AATTGTTCCAGCGTTTTTGT-3'	419	50	(11)
TRP1-R	5'-GACCAGTCCAGCTCTTTCAC-3'			
UGP1-F	5'-TTTCAACACCGACAAGGACACAGA-3'	616	57	(11)

UGP1-R	5'-TCGGACTTCACTAGCAGCAAATCA-3'			
URA3-F	5'-AGCGAATTGTTGAAGTTGGTTGA-3'	602	53	(11)
URA3-R	5'-AATTCGGTTGTAAGATGATGTTGC-3'			
<i>Candida tropicalis</i> MLST loci.				
ICL1-F	5'-CAACAGATTGGTTGCCATCAGAGC-3'	737	52	(10)
ICL1-R	5'-CGAAGTCATCAACAGCCAAAGCAG-3'			
MDR1-F	5'-TGTTGGCATTACCCCTTCCT-3'	663	52	(10)
MDR1-R	5'-TGGAGCACCAAACAATGGGA-3'			
SAPT2-F	5'-CAACGATCGTGGTGCTG-3'	658	52	(10)
SAPT2-R	5'-CACTGGTAGCTGAAGGAG-3'			
SAPT4-F	5'-TGCTTCTCCTACAACCTTCACCTCC-3'	483	52	(10)
SAPT4-R	5'-ATTCCCATGACTCCCTGAGCAACA-3'			
XYR1-F	5'-AGTTGGTTTCGGATGTTG-3'	479	52	(10)
XYR1-R	5'-TCGTAAATCAAAGCACCAGT-3'			
ZWF1a-F	5'-GGTGCTTCAGGAGATTAGC-3'	647	52	(10)
ZWF1a-R	5'-ACCTTCAGTACCAAAAGCTTC-3'			