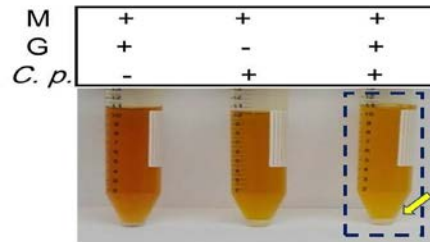
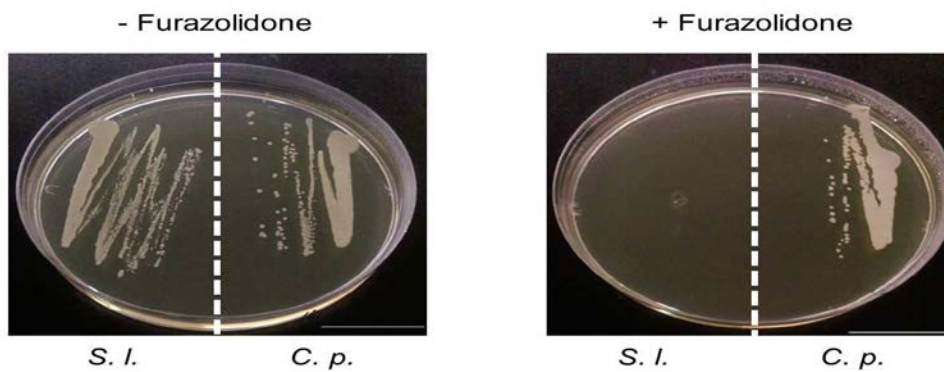


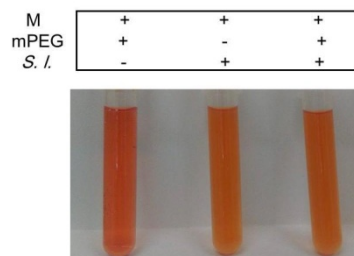
## SUPPLEMENTARY MATERIALS



**Supplementary Figure 1:** The glycerol fermentation of *C. parapsilosis*. (a) *C. parapsilosis* (*C. p.*) ( $10^5$  CFU/ml) was incubated in rich media (M) with or without glycerol (G). Rich media with glycerol alone serve as a control. The yellow media (a blue frame and yellow arrow) were observed four days after glycerol fermentation. Results are representative of three independent experiments.



**Supplementary Figure 2:** Furazolidone inhibits the growth of *S. lugdunensis*, but not *C. parapsilosis*. *S. lugdunensis* (*S. l.*) or *C. parapsilosis* (*C. p.*) ( $10^7$  CFU in 100  $\mu$ l) was spread on MEA plates supplemented with (+) or without (-) 10  $\mu$ g/ml furazolidone for three days. Bars=2.5 cm.



**Supplementary Figure 3:** No mPEG fermentation in *S. lugdunensis*. The *S. lugdunensis* (*S. l.*) bacteria ( $10^5$  CFU/ml) were incubated in rich media (M) with or without 0.0005% mPEG (mPEG). Rich media with mPEG alone serve as a control. The OD560/pH values of media with mPEG alone, *S. lugdunensis* alone or mPEG plus *S. lugdunensis* for 36 h are  $0.51 \pm 0.01/7.32 \pm 0.02$ ;  $0.41 \pm 0.02/7.03 \pm 0.01$ ; and  $0.43 \pm 0.02/7.06 \pm 0.02$ . No significant decrease in OD560 and pH values in the media with mPEG plus *S. lugdunensis* indicated that no mPEG fermentation occurred in the culture of *S. lugdunensis*. Results are representative of three separate experiments.

**Supplementary Table 1:** The sequences and percent identity of both 16S rRNA and D1/D2 5.8S rRNA genes of bacteria and fungi isolated from human dandruff.

**Bacteria:**

100% Identity with *Staphylococcus lugdunensis* HKU09-01, complete genome; NC\_013893.1

```
CACGTAGTTAGCCGTGGCTTTCTGATTAGGTACCGTCAAGACGTGCACAG
TTACTTACACGTTTGTCTTCCCTAATAACAGAGTTTTACGATCCTAAGAC
C TTCATCACTCACGCGGCGTTGCTCCGTCAGGCTTTCGCCCATTGCGGAA
GATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAGTTCC
AGTGTGGCCGATCACCTCTCAGGTCGGCTACGTATCGTTGCCTTGGTG
AGCCGTTACCTACCAACTAGCTAATACGGCGCGGGTCCATCTATAAGTG
ATAGCAAACCATCTTTCACTATTGAACCATGCGGTTCAACATATTATCCG
G
TATTAGCTCCGTTTCCCGAAGTTGTCCCAGTCTTATAGGTAGGTTACCCA
CGTGTTACTACCCGTCGCGCTAACGTCAAAGGAGCAAGCTCCTTATC
TGTTGCTCGACTTGCATGTATTAGGCACGCCGCCAGCGTTCAT
```

100% Identity with *Staphylococcus epidermidis* ATCC 12228 chromosome, complete genome; NC\_004461.1

```
CTGGCACGTAGTTAGCCGTGGCTTTCTGATTAGGTACCGTCAAGACGTGC
ATAGTTACTTACACATTTGTTCTTCCCTAATAACAGAGTTTTACGATCCGA
A GACCTTCATCACTCACGCGGCGTTGCTCCGTCAGGCTTTCGCCCATTGC
GGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCTCAG
TTCCAGTGTGGCCGATCACCTCTCAGGTCGGCTACGCATCGTTGCCTT
GGTAAGCCGTTACCTTACCAACTAGCTAATGCGGCGCGGATCCATCTATA
A
GTGACAGCAAACCGTCTTTCACTATTGAACCATGCGGTTCAATATATTAT
```

C

CGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGTAGGTTAT  
CCACGTGTTACTCACCCGTCCGCCGCTAACGTCAGAGGAGCAAGCTCCT  
CGTCTGTTTCGCTCGACTTGCATGTATTAGGCACGCCGCCAGCGTTCATCC  
TGAG

100% Identity with *Staphylococcus warneri* SG1, complete genome; NC\_020164.1

CTGCTGGCACGTAGTTAGCCGTGGCTTTCTGATCAGGTACCGTCAAGATG  
TGCACAGTTACTTACACATTTGTTCTTCCCTGATAACAGAGTTTTACGATC  
C GAAGACCTTCATCACTCACGCGGCGTTGCTCCGTCAGGCTTTCGCCCAT  
TGCGGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGGACCGTGTCT  
CAGTTCCAGTGTGGCCGATCACCCCTCTCAGGTCGGCTACGTATCGTTGC  
CTTGGTAAGCCGTTACCTTACCAACTAGCTAATACGGCGCGGATCCATCT  
A  
TAAGTGACAGCAAAGCCGCCTTTCCTACTATTGAACCATGCGGTTCAATATG  
T  
TATCCGGTATTAGCTCCGGTTTCCCGAAGTTATCCCAGTCTTATAGGTAGG  
TTATCCACGTGTTACTCACCCGTCCGCCGCTAACGTCAAAGGAGCAAGCT  
CCTTATCTGTTTCGCTCGACTTGCATGTATTAGGCACGCCGCCAGCGTTCA  
TCCTGA

100% Identity with *Staphylococcus capitis* CR01 genomic scaffold,  
ScapHOJ\_3778\_scaffold7, whole genome shotgun sequence;  
NZ\_HG737339.1

TCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACA  
GACGAGGAGCTTGCTCCTCTGACGTTAGCGGCGGACGGGTGAGTAACA  
CGTGGATAACCTACCTATAAGACTGGGATAACTTCGGGAAACCGGAGCT  
A  
ATACCGGATAACATGTTGAACCGCATGGTTCAACAGTGAAAGACGGTCT  
T  
GCTGTCACTTATAGATGGATCCGCGCCGCATTAGCTAGTTGGTAAGGTAA  
CGGCTTACCAAGGCAACGATGCGTAGCCGACCTGAGAGGGTGATCGGC  
CACACTGGAAGTGGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTA  
GGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTGA  
GTGAAGAAGGTCTTCGGATCGTAAACTCTGTTATTAGGGAAGAACA  
T  
GTGTAAGTAACTATGCACGTCTTGACGGTACCTAATCAGAAAGCCACGG  
C TAACTACGTG

**Fungi:**

100% Identity with *Candida parapsilosis* strain YF005 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal; KR089865.1

ATGCTTAAGTTCAGCGGGTAGTCCTACCTGATTTGAGGTCGAATTTGGAA  
GAAGTTTTGGAGTTTGTACCAATGAGTGGAAAAACCTATCCATTAGTTT  
A  
TACTCCGCCTTTCTTTCAAGCAAACCCAGCGTATCGCTCAACACCAAACC  
CGAGGGTTTGAGGGAGAAATGACGCTCAAACAGGCATGCCCTTTGGAAT  
ACCAAAGGGCGCAATGTGCGTTCAAAGATTGATGATTACGAATATCTG  
CAATTCATATTACTTATCGCATTTCGCTGCGTTCTTCATCGATGCGAGAAC  
C  
AAGAGATCCGTTGTTGAAAGTTTTGACTATTAATAATCGGTTGACATTAA  
A  
TAAAATTTGGTTGAGTTTAATCTCTGGCAGGCCCATATAGAAGGCCTACC  
AAAGCAAAGTTTTCAAAAAAAGAAAAACACATGTGTAAGAAAAAATGCA  
GT TAAGCACTTTTCATTCTGTAATGATCCTTCC

100% Identity with *Penicillium citrinum* isolate Bankole Paul 14-PC 28S ribosomal RNA gene, partial sequence; KJ880094.1

AGACGGGTCGCTTACGACCATTATGCCAGCGTCCGAGCCGAAGCGCGTT  
CCTCGGTCCGGGCAGGCCGCATGGCACCCCTGGCTATAAGACGCCCCG  
AGAGGCGTTACCTTCCAGAGGCCTTTGACCGGCCGCCAAACCGACGCT  
GGCCCCGCCGCGGGGAAGTACACCGGCACGAGTGCCGGCTGAACCCC  
GCGGGCGAGTCTGGTCGCAAGCGCTTCCCTTTCAACAATTTACGTGCT  
GTTTAACTCTCTTTTCAAAGTGCTTTTCATCTTTTCGATCACTCTACTTGTGC  
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T AGAGCTGCATTCCCAAACAACCTCGACTCGTCGAAGGAGCTTCACACGGG  
CGCGGCCACCCCATCCCAGACGGGATTCTCACCCCTCTATGACGGCCCGT  
TCCAGGGCACTTAGATGGGGGCGGTTCCCGAAGCATCCTCTGCAAATTA  
CAATGCGGACCCCGAGGGGGCCAGCTTTCAAATTTGAGCTCTTGCCGCT  
TCACTCGCCGTTACTAGGGCAATCCCGGTTGGTTTCTTTTCC