

SUPPLEMENTARY DATA FILE

A cohort study of the airway mycobiome in adult cystic fibrosis patients: differences in community structure of fungi compared to bacteria reveal predominance of transient fungal elements

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Rolf Kramer^{1#}, Annette Sauer-Heilborn², Tobias Welte^{2,3}, Carlos A. Guzman¹, Wolf-Rainer Abraham¹ and Manfred G. Höfle¹

¹Department Vaccinology and Applied Microbiology, Helmholtz Centre for Infection Research, Braunschweig, Germany; ²Department of Pneumology, Hanover Medical School, Hannover, Germany; ³Member of the German Centre for Infection Research and German Centre for Lung Research, Hannover, Germany

Running title: Transient elements in the mycobiome of CF patients

#Address correspondence to Rolf Kramer, Rolf.Kramer@up.ac.za

Supplemental Tables

S1: Bacteria

OTU designation	Taxonomic class	Sputa no. pos. (%)	Patients no. pos. (%)	RDP score	Closest described bacterial species (% similarity, accession no.)
<i>Pseudomonas aeruginosa</i>	<i>Gammaproteo bacteria</i>	50 (69.4 %)	38 (67.8 %)	1.000	100%_CP003149.1_Pseudomonas aeruginosa DK2
<i>Streptococcus parasanguis</i>	<i>Bacilli</i>	41 (56.9 %)	36 (64.2 %)	0.990	99%_AY281078_Streptococcus mitis ATCC 903**
<i>Streptococcus salivarius</i>	<i>Bacilli</i>	41 (56.9 %)	35 (62.5 %)	1.000	100%_FR873482.1_Streptococcus salivarius JIM8777
<i>Streptococcus mitis</i>	<i>Bacilli</i>	31 (43.0 %)	29 (51.7 %)	0.988	99%_FN568063.1_Streptococcus mitis B6
<i>Rothia mucilaginosa</i>	<i>Actinobacteria</i>	31 (43.0 %)	28 (50.0 %)	0.969	99%_DQ409140.1_Rothia mucilaginosa strain C90
<i>Staphylococcus aureus</i>	<i>Bacilli</i>	18 (25.0 %)	15 (26.7 %)	1.000	99%_AB680391.1_Staphylococcus aureus subsp. aureus strain NBRC 13276
<i>Gemella sanguinis</i>	<i>Bacilli</i>	16 (22.2 %)	14 (25.0 %)	1.000	100%_NR_026419.1_Gemella sanguinis strain 2045-94
<i>Granulicatella -2</i>	<i>Bacilli</i>	14 (19.4 %)	13 (23.2 %)	1.000	100%_FR822389.1_Granulicatella adiacens strain CCUG 60768
<i>Actinomyces graevenitzii</i>	<i>Actinobacteria</i>	12 (16.6 %)	11 (19.6 %)	0.964	99%_NR_042167.1_Actinomyces graevenitzii strain CCUG 27294
<i>Gemella haemolysans</i>	<i>Bacilli</i>	7 (9.7 %)	7 (12.5 %)	1.000	100%_NR_025903.1_Gemella haemolysans strain ATCC 10379
<i>Streptococcus anginosus</i>	<i>Bacilli</i>	6 (8.3 %)	5 (8.9 %)	0.986	99%_AF306838.1_Streptococcus anginosus genotype VA8466
<i>Achromobacter xylosoxidans</i>	<i>Betaproteo bacteria</i>	6 (8.3 %)	5 (8.9 %)	1.000	99%_EU266588.1_Achromobacter xylosoxidans strain CS5
<i>Prevotella histicola</i>	<i>Bacteroidia</i>	5 (6.9 %)	5 (8.9 %)	1.000	100%_AB547685.1_Prevotella histicola strain JCM 15637
<i>Prevotella melaninogenica</i>	<i>Bacteroidia</i>	5 (6.9 %)	5 (8.9 %)	0.985	99%_JN867309.1_Prevotella melaninogenica strain SEQ236
<i>Fusobacterium nucleatum</i>	<i>Fusobacteria</i>	5 (6.9 %)	4 (7.1 %)	0.951	98%_AB588016.1_Fusobacterium nucleatum subsp. nucleatum JCM 6328
<i>Streptococcus intermedius</i>	<i>Bacilli</i>	5 (6.9 %)	4 (7.1 %)	1.000	100%_AF104671.1_Streptococcus intermedius strain ATCC 27335
<i>Veillonella -1</i>	<i>Negativicutes</i>	4 (5.5 %)	4 (7.1 %)	0.985	99%_HM596287.1_Veillonella sp. oral taxon 158 strain F0412
<i>Rothia -2</i>	<i>Actinobacteria</i>	4 (5.5 %)	4 (7.1 %)	1.000	100%_AY594189.1_Rothia dentocariosa strain Inje LI
<i>Stenotrophomonas maltophilia</i>	<i>Gammaproteo bacteria</i>	3 (4.1 %)	3 (5.3 %)	1.000	99%_JX848739.1_Stenotrophomonas maltophilia strain Sal10
<i>Prevotella pallens</i>	<i>Bacteroidia</i>	3 (4.1 %)	3 (5.3 %)	0.945	99%_AB547703.1_Prevotella pallens strain JCM 11140
<i>Streptococcus gordonii</i>	<i>Bacilli</i>	2 (2.7 %)	2 (3.5 %)	0.973	99%_AY281088.1_Streptococcus gordonii ATCC 12396
<i>Prevotella nanceiensis</i>	<i>Bacteroidia</i>	2 (2.7 %)	2 (3.5 %)	0.976	99%_JN867319.1_Prevotella nanceiensis strain SEQ246
<i>Prevotella oris</i>	<i>Bacteroidia</i>	2 (2.7 %)	1 (1.7 %)	0.924	99%_AB547700.1_Prevotella oris strain JCM 12252

S1: *Bacteria* (continued)

OTU designation	Taxonomic class	Sputa no. pos. (%)	Patients no. pos. (%)	RDP score	Closest described bacterial species (% similarity, accession no.)
<i>Bordetella petrii</i>	<i>Betaproteo bacteria</i>	1	1	1.000	100%_AJ870969.1_ <i>Bordetella petrii</i> strain GDH030510
<i>Streptococcus sanguinis</i>	<i>Bacilli</i>	1	1	1.000	100%_AB596946.1_ <i>Streptococcus sanguinis</i> JCM 5708
<i>Granulicatella elegans</i>	<i>Bacilli</i>	1	1	1.000	100%_Y15413.1_ <i>Granulicatella elegans</i> strain 4067-96
<i>Capnocytophaga gingivalis</i>	<i>Flavobacteria</i>	1	1	0.942	99%_AB638448.1_ <i>Capnocytophaga gingivalis</i> strain JCM 12953
<i>Streptococcus australis</i>	<i>Bacilli</i>	1	1	0.929	98%_NR_036936.1_ <i>Streptococcus australis</i> strain ATCC 700641
<i>Actinomyces odontolyticus</i>	<i>Actinobacteria</i>	1	1	1.000	100%_GQ131411.1_ <i>Actinomyces odontolyticus</i> strain F0309
<i>Burkholderia cepacia</i>	<i>Betaproteo bacteria</i>	1	1	1.000	100%_AB680641.1_ <i>Burkholderia cepacia</i> NBRC 14595
<i>Prevotella pleuritidis</i>	<i>Bacteroidia</i>	1	1	0.937	99%_AB278593.1_ <i>Prevotella pleuritidis</i> strain JCM 14110
<i>Prevotella</i> -8	<i>Bacteroidia</i>	1	1	0.741	90%_GU409582.1_ <i>Prevotella</i> sp. oral taxon 306 clone DO004
<i>Prevotella tanneriae</i>	<i>Bacteroidia</i>	1	1	0.973	99%_AF183406.1_ <i>Prevotella tanneriae</i> strain 93-1-2
<i>Nocardia</i> sp.	<i>Actinobacteria</i>	1	1	1.000	100%_GU992878.1_ <i>Nocardia</i> sp. W9912
<i>Atopobium parvulum</i>	<i>Actinobacteria</i>	1	1	0.985	99%_CP001721.1_ <i>Atopobium parvulum</i> DSM 20469
<i>Streptococcus peroris</i>	<i>Bacilli</i>	1	1	0.943	99%_GU425263.1_ <i>Streptococcus peroris</i> clone GD031
TM7	TM7 candidate class	1	1	0.766	99%_GU410609.1_ TM7 phylum sp. oral taxon 352 clone DR034
<i>Prevotella</i> -9	<i>Bacteroidia</i>	1	1	0.670	99%_GU409603.1_ <i>Prevotella</i> sp. oral taxon 308 clone GD054

Table S1. OTU designation for bacterial sequences that were found in sputa. For each OTU, accession number of closest described bacterial sequence is given, matching representative sequences of ssDNA bands from SSCP electrophoresis. Total number of positive (no. pos.) sputum samples and patients are shown. The respective occurrence frequencies (%) for repeatedly detected OTUs are given in brackets. OTUs with ambiguous results in databases were defined according to the closest shared taxonomic level. Highest RDP scores for described species are shown.

**Strain reclassified into *Streptococcus parasanguinis*

S2.a. Ascomycota, Saccharomycetes

OTU designation	Taxonomic class	Sputa no. pos. (%)	Patients no. pos. (%)	Closest described fungal species (% similarity, accession no., name)	Accession no(s) Eur. Nucleotide Archive (ENA)
<i>Candida albicans</i>	<i>Saccharo mycetes</i>	32 (44.4 %)	27 (48.2 %)	100%_JX094781_Candida albicans strain ATCC 96901 *JX094781	LN835855 - LN835885
<i>Candida dubliniensis</i>	<i>Saccharo mycetes</i>	17 (23.6 %)	14 (25.0 %)	100%_DQ105856_Candida dubliniensis strain DSM 13628 *DQ105856	LN835886 - LN835901
<i>Saccharomyces cerevisiae</i>	<i>Saccharo mycetes</i>	14 (19.4 %)	13 (23.2 %)	100%_AM900403_Saccharomyces cerevisiae strain MUCL28071 *FN393997	LN835902 - LN835908
<i>Candida parapsilosis</i>	<i>Saccharo mycetes</i>	10 (13.8 %)	7 (12.5 %)	100%_FJ872015_Candida parapsilosis strain ATCC 22019 *FJ872015	LN835909 - LN835918
<i>Candida glabrata</i>	<i>Saccharo mycetes</i>	9 (12.5 %)	6 (10.7 %)	100%_AF336836_Candida glabrata strain ATCC 2001 *AF336836	LN835919 - LN835926
<i>Candida tropicalis</i>	<i>Saccharo mycetes</i>	3 (4.1 %)	3 (5.3 %)	100%_AY939810_Candida tropicalis strain ATCC 750 *AY939810	LN835927 - LN835929
<i>Cyberlindnera jadinii</i> (synonyms: <i>Candida utilis</i> , <i>Pichia jadinii</i>)	<i>Saccharo mycetes</i>	3 (4.1 %)	3 (5.3 %)	100%_FJ865435_Pichia jadinii isolate M9 *DQ249199	LN835930 - LN835932
<i>Candida sake</i>	<i>Saccharo mycetes</i>	2 (2.7 %)	2 (3.5 %)	98%_AJ549822_Candida sake strain CBS 159 *AJ549822	LN835933 - LN835934
<i>Galactomyces geotrichum</i>	<i>Saccharo mycetes</i>	1	1	100%_EU789402_Galactomyces geotrichum strain M0163 *EU789402	LN835935
<i>Meyerozyma guilliermondii</i> (synonym: <i>Pichia guilliermondii</i>)	<i>Saccharo mycetes</i>	1	1	100%_JQ425356_Meyerozyma guilliermondii strain AUMC 7771 *JQ425356	LN835936
<i>Kazachstania unispora</i> (synonym: <i>Saccharomyces unisporus</i>)	<i>Saccharo mycetes</i>	1	1	100%_EU789404_Kazachstania unispora strain M01621 *EU789404	LN835937
<i>Candida humilis</i>	<i>Saccharo mycetes</i>	1	1	100%_AY188851_Candida humilis strain CBS 6897 *AY188851	LN835938
<i>Debaryomyces hansenii</i>	<i>Saccharo mycetes</i>	1	1	100%_HE967326_Debaryomyces hansenii strain MRL2 *HE967326	LN835939
<i>Clavispora lusitaniae</i>	<i>Saccharo mycetes</i>	1	1	100%_JN391310_Clavispora lusitaniae isolate PUMY044 *EF568023	LN835940
<i>Yarrowia lipolytica</i>	<i>Saccharo mycetes</i>	1	1	100%_EU252546_Yarrowia lipolytica ATCC 9773 *EU252546	LN835941
<i>Kluyveromyces marxianus</i>	<i>Saccharo mycetes</i>	1	1	100%_HQ014731_Kluyveromyces marxianus strain WM10.112 *HQ014731	LN835942
<i>Candida deformans</i>	<i>Saccharo mycetes</i>	1	1	100%_FJ515168_Candida deformans strain SM21 *FJ515168	LN835943
<i>Candida cellae</i>	<i>Saccharo mycetes</i>	1	1	100%_GQ149495_Candida cellae strain UAF-93 *GQ149495	LN835944
<i>Hanseniaspora uvarum</i>	<i>Saccharo mycetes</i>	1	1	100%_AJ512432_Hanseniaspora uvarum strain CBS 314 *AJ512432	LN835945

S2.b. Ascomycota, non-Saccharomycetes

OTU designation	Taxonomic class	Sputa no. pos. (%)	Patients no. pos. (%)	Closest described fungal species (% similarity, accession no., name)	Accession no(s) Eur. Nucleotide Archive (ENA)
<i>Cladosporium cladosporioides</i> (teleomorph: <i>Davidiella</i> sp.)	<i>Dothideo mycetes</i>	8 (11.1 %)	7 (12.5 %)	100%_JQ768323_Cladospo- ridium cladosporioides strain CFP14 *JQ768323	LN835946 - LN835952
<i>Cladosporium herbarum</i> (teleomorph: <i>Davidiella tassiana</i>)	<i>Dothideo mycetes</i>	7 (9.7 %)	6 (10.7 %)	100%_HQ263359_Davidiel- la tassiana strain ATCC MYA-4682 *HQ263359	LN835953 - LN835958
<i>Scedosporium apiospermum</i> complex	<i>Sordario mycetes</i>	3 (4.1 %)	2 (3.5 %)	100%_AY213682_Pseudalles- cheria boydii strain UWFP 806 *AY213682	LN835959 - LN835961
<i>Exophiala dermatitidis</i>	<i>Eurotio mycetes</i>	3 (4.1 %)	2 (3.5 %)	100%_JX473286_Exophiala der- matitidis strain PW2643 *JX473286	LN835962 - LN835964
<i>Aspergillus fumigatus</i>	<i>Eurotio mycetes</i>	2 (2.7 %)	2 (3.5 %)	99%_HQ026746_Aspergillus fu- migatus strain ATCC 1022 *HQ026746	LN835965 - LN835966
<i>Blumeria graminis</i>	<i>Leotio mycetes</i>	2 (2.7 %)	2 (3.5 %)	100%_AB273556_Blumeria gra- minis isolate MUMH2335 *AB273556	LN835967 - LN835968
<i>Lewia infectoria</i> (anamorph: <i>Alternaria infectoria</i>)	<i>Dothideo mycetes</i>	2 (2.7 %)	2 (3.5 %)	100%_FJ214897_Lewia infec- toria strain CBS 112250 *FJ214897	LN835969 - LN835970
<i>Coniothyrium fuckelii</i> (teleomorph: <i>Leptosphaeria coniothyrium</i>)	<i>Dothideo mycetes</i>	1	1	98%_FJ228185_Coniothyrium fu- ckelii isolate 7a-1 *FJ861383	LN835971
<i>Aureobasidium pullulans</i>	<i>Dothideo mycetes</i>	1	1	100%_AF121281_Aureobasidium pu- llulans strain ATCC11942 *AF121281	LN835972
<i>Phaeosphaeria</i> sp.	<i>Dothideo mycetes</i>	1	1	98%_AF439488_Phaeosphaeria ju- ncophila isolate CBS 575.86 *HM172819	LN835973
<i>Leotiomycetes</i> -2	<i>Leotio mycetes</i>	1	1	97%_JN995647_Phialocephala sp. AU_BD20 *JX317257	LN835974
<i>Ascomycota</i> -22	unknown	1	1	89%_FJ487945_Pichia norvegensis strain ZH2Aea *EU343827	LN835975
<i>Aspergillus conicus</i>	<i>Eurotio mycetes</i>	1	1	99%_EF652039_Aspergillus con- icus isolate NRRL 149 *EF652039	LN835976
<i>Neosartorya pseudofischeri</i> (anamorph: <i>Aspergillus thermomutatus</i>)	<i>Eurotio mycetes</i>	1	1	100%_AF459729_Neosartorya pseu- dofischeri NRRL 180 *AF459729	LN835977
<i>Leptosphaeria</i> sp.	<i>Dothideo mycetes</i>	1	1	99%_EU852362_Uncultured Lepto- sphaeria clone 21a *EU852362	LN835978
<i>Didymella exitialis</i>	<i>Dothideo mycetes</i>	1	1	100%_EU167564_Didymella exiti- alis strain CBS 446.82 *EU167564	LN835979
<i>Phoma exigua</i>	<i>Dothideo mycetes</i>	1	1	100%_EU770244_Phoma exigua strain ICMP 16989 *EU770244	LN835980
<i>Aspergillus versicolor</i>	<i>Eurotio mycetes</i>	1	1	100%_EF652449_Aspergillus ver- sicolor isolate NRRL 239 *EF652449	LN835981
<i>Septoria</i> sp.	<i>Dothideo mycetes</i>	1	1	100%_JX480493_Septoria erigeron- tis voucher KUS-F25759 *JX480493	LN835982
<i>Penicillium</i> sp.	<i>Eurotio mycetes</i>	1	1	100%_JN983439_Penicillium sp. mcp2728 *JN983439	LN835983
<i>Fusarium oxysporum</i>	<i>Sordario mycetes</i>	1	1	100%_HQ829111_Fusarium oxyspor- um strain CID 207 *HQ829111	LN835984
<i>Colletotrichum circinans</i>	<i>Sordario mycetes</i>	1	1	99%_EU400140_Colletotrichum cir- cinans strain DAOM151616 *EU400140	LN835985

S2.c. Basidiomycota

OTU designation	Taxonomic class	Sputa no. pos. (%)	Patients no. pos. (%)	Closest described fungal species (% similarity, accession no., name)	Accession no(s) Eur. Nucleotide Archive (ENA)
<i>Sporobolomyces roseus</i>	<i>Puccinio mycetes</i>	8 (11.1 %)	7 (12.5 %)	100%_AY069997_Sporobolomyces roseus strain CBS 993 *AY069997	LN835986 - LN835993
<i>Sporobolomyces ruberrimus</i>	<i>Puccinio mycetes</i>	4 (5.5 %)	3 (5.3 %)	100%_JN246564_Sporobolomyces ruberrimus strain CRUB 1041 *JN246564	LN835994 - LN835997
<i>Rhodotorula glutinis</i>	<i>Microbotryo mycetes</i>	2 (2.7 %)	2 (3.5 %)	100%_AF335948_Rhodotorula glutinis strain ATCC 32765 *AF335948	LN835998 - LN835999
<i>Udeniomyces pannonicus</i>	<i>Tremello mycetes</i>	1	1	100%_AB072231_Udeniomyces pannonicus strain JCM 11148 *AB072231	LN836000
<i>Plicaturopsis crispa</i>	<i>Agarico mycetes</i>	1	1	100%_DQ534576_Plicaturopsis crispa strain FP-101310-SP *HQ871872	LN836001
<i>Rhodotorula -2</i>	<i>Microbotryo mycetes</i>	1	1	100%_AM160641_Rhodotorula sp. HB 1211 *AB026015	LN836002
<i>Basidiomycota -18</i>	<i>unknown</i>	1	1	77%_DQ411529_Trechispora alnicola isolate AFTOL-ID 665 *FR682413	LN836003
<i>Megacollybia platyphylla</i>	<i>Agarico mycetes</i>	1	1	100%_EU623713_Megacollybia platyphylla voucher LE 256-2004 *EU623713	LN836004
<i>Cryptococcus -3</i>	<i>Tremello mycetes</i>	1	1	96%_JN400817_Cryptococcus tephrensensis *AM160648	LN836005
<i>Cryptococcus victoriae</i>	<i>Tremello mycetes</i>	1	1	100%_AM160647_Cryptococcus victoriae strain HB 1221 *AM160647	LN836006
<i>Agaricomycetes -8</i>	<i>Agarico mycetes</i>	1	1	99%_GQ221186_Undifferentiated Agaricomycetes strain FSU6258 *GQ221186	LN836007
<i>Malassezia restricta</i>	<i>Exobasidio mycetes</i>	1	1	100%_JQ088240_Malassezia restricta isolate HIV+92 *JQ088240	LN836008
<i>Piptoporus betulinus</i>	<i>Agarico mycetes</i>	1	1	100%_DQ491423_Piptoporus betulinus strain CBS 378.51 *JQ700297	LN836009
<i>Polyporus gayanus</i>	<i>Agarico mycetes</i>	1	1	100%_AF518757_Polyporus gayanus strain CIEFAP136 *AF518757	LN836010
<i>Strobilurus sp.</i>	<i>Agarico mycetes</i>	1	1	100%_GQ892818_Strobilurus albipilatus voucher TFB11910 *GQ892818	LN836011
<i>Baeospora sp. #</i>	<i>Agarico mycetes</i>	1	1	95%_EU770252_Baeospora sp. ICMP 16979 *EU770252	LN836012
<i>Hyphodontia sp.</i>	<i>Agarico mycetes</i>	1	1	100%_FJ197950_Uncultured Hyphodontia clone Bo2gLR21_A21 *FJ197950	LN836013
<i>Cryptococcus curvatus</i>	<i>Tremello mycetes</i>	1	1	100%_EU266558_Cryptococcus curvatus strain ATCC 10567 *EU266558	LN836014

Table S2. OTU designation for fungal sequences that were found in sputa, grouped by **a. Saccharomycetes**; **b. Ascomycota (non-Saccharomycetes)**; **c. Basidiomycota**. Names of teleomorphs have priority. Names of anamorphs are only given if asexual state is reported more frequently from clinical samples. Total number of positive (no. pos.) sputum samples and patients are shown. Occurrence frequencies (%) for repeatedly detected OTUs are given in brackets. For each OTU, the accession number of the closest described fungus matching sequence is given and accession numbers of submitted sequences (to ENA) are listed. *Accession numbers of representative sequences used for phylogenetic trees in **Figures S5, S6** #100% sequence similarity with *Mucronella* sp. PDD 95742

Patient	Age	Gender	Additional diagnose	FEV1	PaO2	Culture	SSCP
A1	30	female	none	34	55	yeast species	none
A2			infection	37	60	yeast species	<i>C. dubliniensis</i> , <i>C. glabrata</i> , <i>Coniothyrium fuckelii</i>
B1	31	male	none	56	75	<i>C. dubliniensis</i>	<i>C. dubliniensis</i>
B2			weak infection	58	79	yeast species	<i>C. dubliniensis</i>
C1	26	male	none	28	68	<i>C. parapsilosis</i> , <i>C. albicans</i> , <i>C. glabrata</i>	<i>C. albicans</i> , <i>C. parapsilosis</i> , <i>Exophiala dermatitidis</i>
C2			infection	25	66	none	<i>C. parapsilosis</i> , <i>Exophiala dermatitidis</i>
D1	35	female	none	21	61	none	<i>C. albicans</i> , <i>C. glabrata</i>
D2			n/a	n/a	n/a	n/a	<i>C. albicans</i> , <i>C. glabrata</i>
E1	22	male	ABPA	45	86	<i>Aspergillus fumigatus</i>	<i>C. dubliniensis</i> , <i>Cladosporium herbarum</i> , <i>Sporobolomyces roseus</i> , <i>Sporobolomyces ruberrimus</i> , <i>Scedosporium apiospermum</i> , <i>Aspergillus fumigatus</i>
E2			ABPA	60	90	<i>Scedosporium apiospermum</i> , <i>Penicillium</i> sp.	<i>C. dubliniensis</i> , <i>Cladosporium cladosporioides</i> , <i>Cladosporium herbarum</i> , <i>Sporobolomyces roseus</i> , <i>Sporobolomyces ruberrimus</i> , <i>Scedosporium apiospermum</i> , <i>Penicillium</i> sp., <i>Fusarium oxysporum</i> , <i>Baeospora</i> sp.
F1	41	female	none	26	<60	none	<i>C. albicans</i> , <i>Sporobolomyces roseus</i>
F2			none	19	<60	none	none
G1	42	male	none	17	51	filamentous fungus	<i>C. parapsilosis</i>
G2			none	18	52	none	<i>C. parapsilosis</i> , <i>Cladosporium herbarum</i> , <i>Aureobasidium pullulans</i>
H1	30	male	infection	22	64	yeast species	<i>C. albicans</i> , <i>C. parapsilosis</i>
H2			infection	29	64	<i>C. albicans</i>	<i>C. albicans</i> , <i>C. parapsilosis</i> , <i>Clavispora lusitaniae</i>
I1	27	female	none	32	62	yeast species	<i>C. albicans</i> , <i>C. tropicalis</i> , <i>S. cerevisiae</i> , <i>Cyberlindnera jadinii</i> , <i>Cladosporium herbarum</i> , <i>Sporobolomyces roseus</i>
I2			none	36	67	none	<i>C. dubliniensis</i>
J1	40	male	none	38	68	<i>Aspergillus fumigatus</i>	<i>C. albicans</i>
J2			infection	46	87	<i>Aspergillus fumigatus</i>	<i>C. parapsilosis</i> , <i>Kluyveromyces marxianus</i>
K1	32	male	none	25	59	none	<i>C. dubliniensis</i> , <i>C. parapsilosis</i> , <i>C. glabrata</i>
K2			none	28	68	<i>C. dubliniensis</i> <i>C. glabrata</i> , <i>C. parapsilosis</i>	<i>C. dubliniensis</i> , <i>C. glabrata</i> , <i>S. cerevisiae</i>
L1	38	male	none	48	66	none	<i>C. albicans</i>
L2			none	38	66	none	<i>C. albicans</i> , <i>Cladosporium cladosporioides</i>
M1	47	male	none	30	71	<i>Scedosporium apiospermum</i>	<i>C. albicans</i> , <i>Aspergillus versicolor</i> , <i>Plicaturopsis crista</i> , unknown fungus, <i>Rhodotorula glutinis</i> , <i>Rhodotorula</i> -2,
M2			none	23	66	none	<i>C. albicans</i> , <i>C. parapsilosis</i> , <i>S. cerevisiae</i> , <i>Cladosporium cladosporioides</i> , <i>Sporobolomyces roseus</i> , <i>Malassezia restricta</i>

Table S3. Subcohort of 13 CF patients with repeatedly collected sputum samples. Host factors, clinical data and microbial diagnoses for each time point (1, 2) are given. FEV1 indicates the forced expiratory volume in 1 second and PaO2 indicates the partial pressure of oxygen in arterial blood. Microbial diagnosis by routine clinical microbiology (culture) was performed by the clinic and results are presented as communicated. Microbial diagnosis by SSCP was performed as previously described.

Phylum	Class (total no. of incidences)	Major species	% pos. samples
<i>Firmicutes</i>	<i>Bacilli</i> (185)	<i>Streptococcus salivarius</i>	56.9
		<i>Streptococcus parasanguis</i>	56.9
		<i>Streptococcus mitis</i>	43.0
		<i>Staphylococcus aureus</i>	25.0
		<i>Gemella sanguinis</i>	20.8
		<i>Granulicatella</i> -2	19.4
		<i>Gemella haemolysans</i>	11.1
		<i>Streptococcus anginosus</i>	8.3
		<i>Streptococcus intermedius</i>	6.9
	<i>Negativicutes</i> (4)	<i>Veillonella</i> -1	5.5
<i>Proteobacteria</i>	<i>Gammaproteobacteria</i> (53)	<i>Pseudomonas aeruginosa</i>	69.4
		<i>Stenotrophomonas maltophilia</i>	4.1
	<i>Betaproteobacteria</i> (8)	<i>Achromobacter xylosoxidans</i>	8.3
		<i>Bordetella petrii</i>	1.3
<i>Actinobacteria</i>	<i>Actinobacteria</i> (50)	<i>Rothia mucilaginosa</i>	43.0
		<i>Actinomyces graevenitzi</i>	13.8
<i>Bacteroidetes</i>	<i>Bacteroidia</i> (21)	<i>Prevotella histicola</i>	6.9
		<i>Prevotella melaninogenica</i>	6.9
	<i>Flavobacteria</i> (1)	<i>Capnocytophaga gingivalis</i>	1.3
<i>Fusobacteria</i>	<i>Fusobacteria</i> (5)	<i>Fusobacterium nucleatum</i>	6.9
<i>TM7</i> candidate phylum	<i>TM7</i> candidate class (1)	<i>TM7</i>	1.3

Table S4. Prevalence of major OTUs defined by partial 16S rRNA sequence comparison. Table comprises bacterial OTUs mentioned in the text or observed in >4 sputum samples. Bacterial OTUs are grouped according to taxonomic classification and ranked according to number of positive samples (in %). Additionally, the absolute number of detected incidences for each class is given in brackets (considering all detected OTUs including unique species).

Supplemental Figures

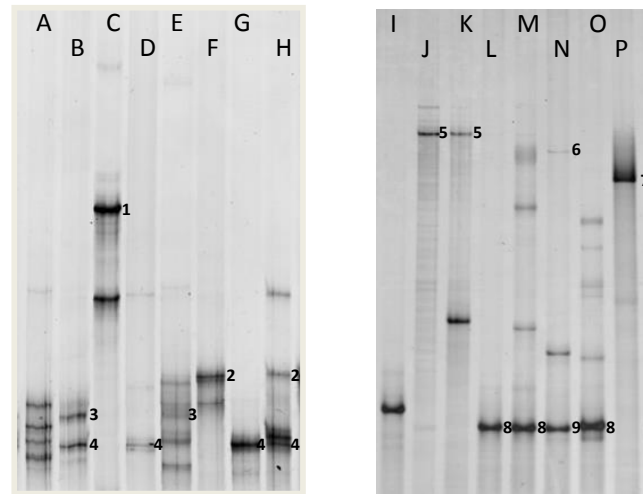


Figure S1. Molecular fingerprints by SSCP electrophoresis from bacteria (left panel) and fungi (right panel). Each lane (A-H; I-P) represents one sputum sample. Each band represents ssDNA from one microbial species. Species were identified by differences in mobility through the gel and by sequence analyses. Bands at the same height were the same species. Exemplarily, some species (but not all) identified by sequencing of the respective bands were indicated by numbers: bacterial SSCP fingerprints based on 16S rRNA gene amplicons: 1= *Bordetella petrii*, 2= *Staphylococcus aureus*, 3= *Streptococcus salivarius*, 4= *Pseudomonas aeruginosa*; fungal SSCP fingerprints based on 18S rRNA ITS gene amplicons 5= *Saccharomyces cerevisiae*, 6= *Candida glabrata*, 7= *Exophiala dermatitidis*, 8= *Candida albicans* and 9= *Candida dubliniensis*. Discrimination between *C. albicans* and *C. dubliniensis* can only be achieved by sequencing.

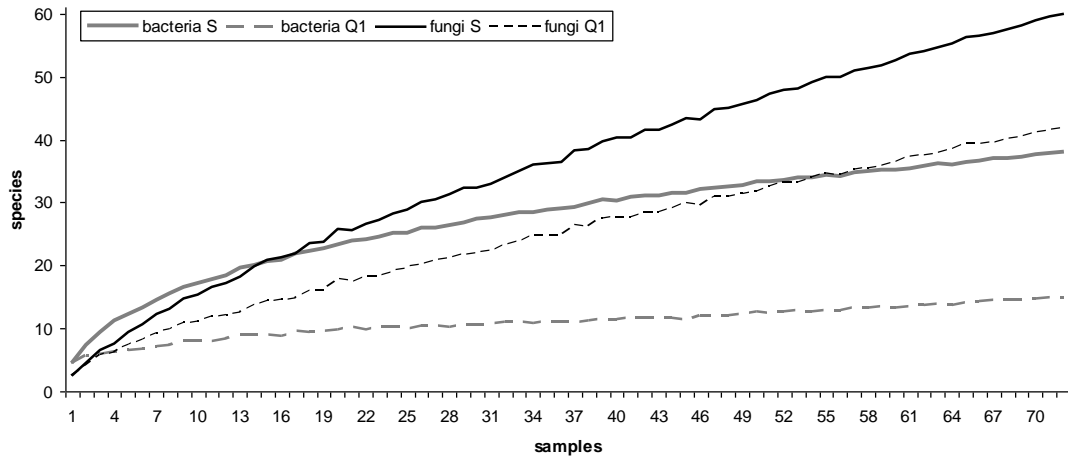


Figure S2. Species accumulation curves for bacterial and fungal OTUs detected in 72 sputum samples from 56 patients. Averaged curves show the number of detected species versus number of samples. Curves for bacteria are shown in grey and curves for fungi are shown in black. Full lines show observed species counts (richness S; Mao Tao) and dashed lines show unique species counts (Q1; species which occur in only one sample).

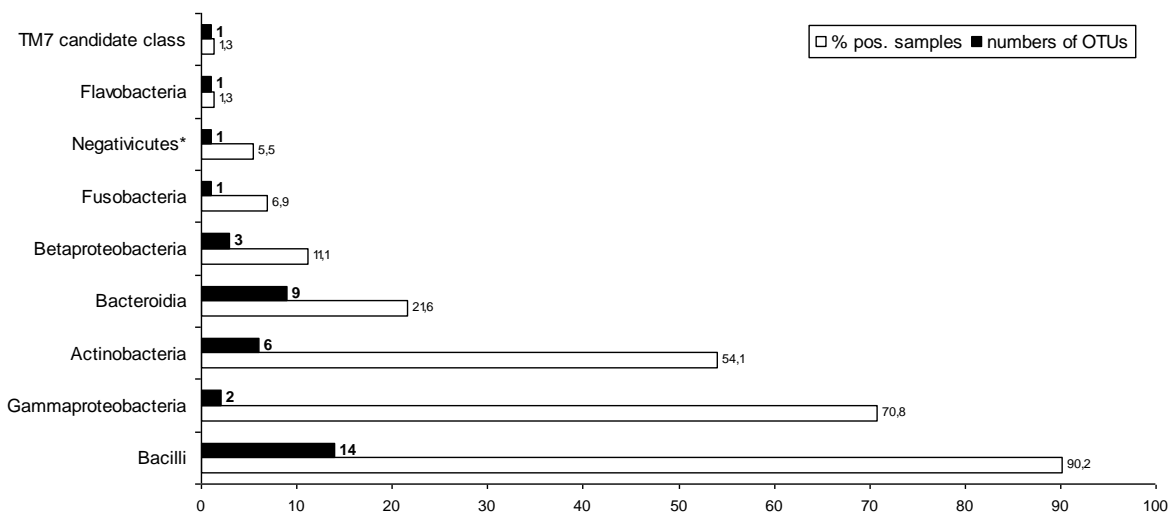


Figure S3. Frequency of taxonomic classes of bacteria detected in 72 CF sputum samples. Black bars give number of OTUs observed for each class. White bars indicate percentage of positive samples of respective OTUs. Precise values for each bar are given in the figure.

*Formerly member of the class *Clostridia*

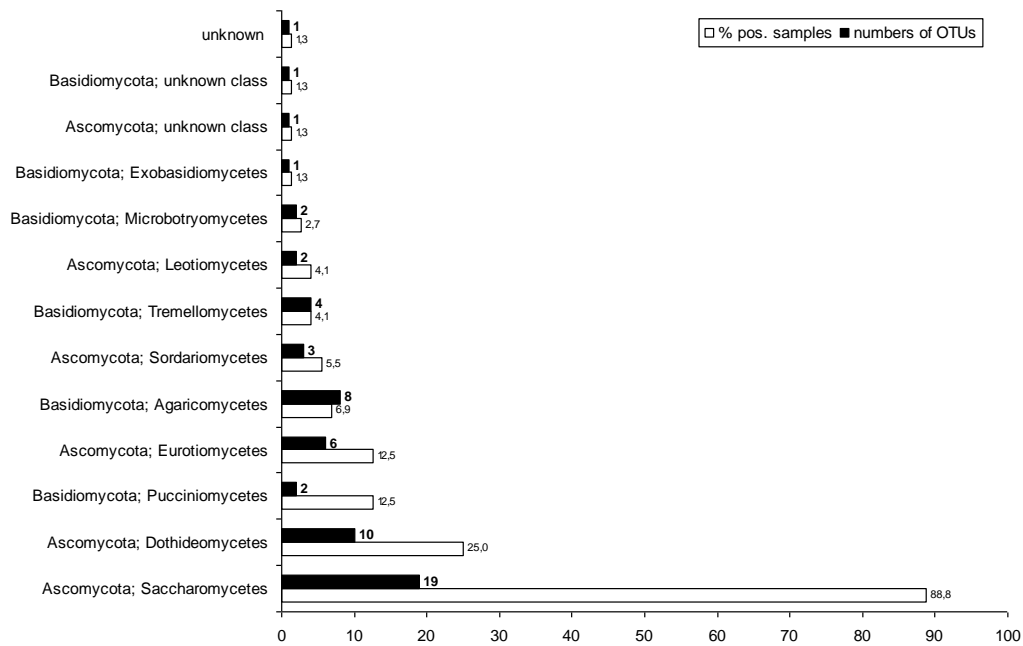


Figure S4. Frequency of taxonomic classes of fungi detected in 72 CF sputum samples. Black bars give number of OTUs considered for each class. White bars indicate incidence of associated OTUs. Specific values for each bar are given in the graphic.

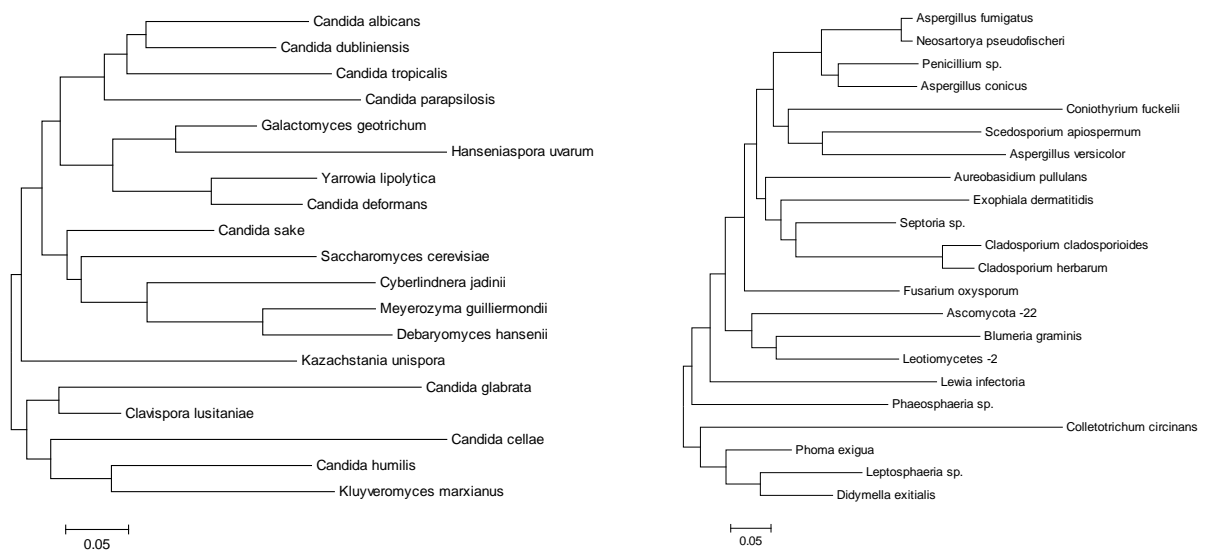


Figure S5. Phylogenetic trees for fungal OTUs observed from the division *Ascomycota* based on ITS region sequence comparisons. On the left: *Saccharomycetes* species found in the CF cohort. *C. albicans* and *C. dubliniensis* were the most frequently found fungi in the CF cohort. On the right: non-*Saccharomycetes* OTUs including filamentous fungi considered to be major CF pathogens like *Aspergillus* species, *Exophiala dermatitidis* and the *Scedosporium apiospermum* complex. Scale bar represents base substitution per site.

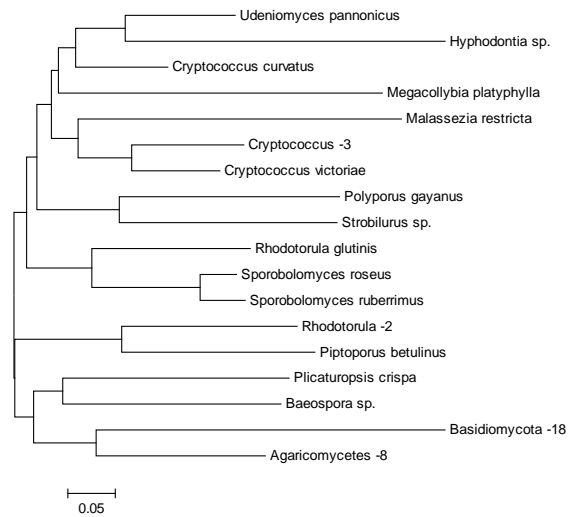


Figure S6. Phylogenetic tree for fungal OTUs observed from the division *Basidiomycota* based on ITS region sequence comparisons. Species from several *Basidiomycetes* classes were detected. Scale bar represents base substitution per site.