SUPPLEMENTARY INFORMATION

TITLE: Altered community compositions of *Proteobacteria* in adults with bronchiectasis

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	Parameters	All bronchiectasis (n=106)	Exacerbation (n=22)	Healthy subjects (n=17)
	Age (yrs)	44.4±13.8	39.7±13.9	50.7±16.4
Anthropometry	BMI (cm/kg ²)	20.6±3.3	19.6±2.5	24.0 ± 3.0
	Female (No., %)	58 (54.7%)	12 (54.5%)	12 (70.6%)
Smoking status	Never smokers (No., %)	97 (91.5%)	21 (95.5%)	16 (94.1%)
	Duration of bronchiectasis (yrs)	15.0 (10.8)	13.0 (9.8)	-
	Exacerbations within previous 2 yrs	2.0 (4.0)	5.0 (2.2)	-
Disease-related	No. of bronchiectatic lobes	5.0 (3.0)	4.5±1.4	-
parameters	HRCT score	8.7±4.2	9.5±4.5	-
	Bronchiectasis Severity Index	6.0 (6.0)	7.1±4.2	-
	24-hour sputum (ml)	30.0 (11.1)	32.5 (53.8)	-
	FVC predicted%	73.0±19.9	81.1 (43.0)	93.9±10.7
Spirometry	FEV ₁ predicted%	59.7±23.5	57.6±23.8	91.6±12.1
	FEV ₁ /FVC (%)	69.3±14.0	66.7±11.0	81.5±6.3
Madiantians used	Inhaled corticosteroids (No., %)	27 (25.5%)	4 (18.2%)	-
within 6 months	Macrolides (No., %)	50 (47.2%)	10 (45.5%)	-
	Mucolytics (No., %)	80 (75.5%)	18 (81.8%)	-
	Post-infectious (No., %)	35 (33.0%)	8 (36.4%)	-
Frielow	Immunodeficiency (No., %)	19 (17.9%)	2 (9.1%)	-
Eulology	Miscellaneous (No., %) *	17 (16.0%)	4 (18.2%)	-
	Idiopathic (No., %)	39 (36.8%)	9 (40.9%)	-
Snutum	Pseudomonas aeruginosa (No., %)	45 (42.5%)	10 (45.5%)	-
sputum	Other PPMs (No., %) **	41 (38.7%)	7 (31.8%)	-
Dacteriology	Commensals (No., %)	20 (18.9%)	5 (22.7%)	-

Table S1Demographic and baseline levels of all bronchiectasis included in baseline analysis,
exacerbation cohort and healthy subjects

BMI: body-mass index; PPMs: potentially pathogenic microorganisms; FVC: forced vital capacity; FEV₁: forced expiratory volume in one second; HRCT: high-resolution computed tomography * Other known etiologies consisted of gastroesophageal reflux (n=4, 3.8%), asthma (n=3, 2.8%), Kartagener's syndrome (n=2, 1.9%), diffuse panbronchiolitis (n=2, 1.9%), lung maldevelopment (n=2, 1.9%), aspergillosis (n=1, 0.9%), rheumatoid arthritis (n=1, 0.9%), and cystic fibrosis transmembrane regulator-related disorder (n=1, 0.9%).

** Among all bronchiectasis patients when clinically stable, other potentially pathogenic bacteria comprised *Haemophilus influenzae* (n=14, 13.2%), *Haemophilus parainfluenzae* (n=8, 7.5%), *Escherichia coli* (n=5, 4.7%), *Klebsiella pneumonae* (n=4, 3.8%), *Rothia mucilaginosa* (n=2, 1.8%), *Streptococcus pneumoneae* (n=1, 0.9%), *Moraxella catarrhalis* (n=1, 0.9%), *Proteus mirabilis* (n=1, 0.9%), *Acinectobacter haemolyticus* (n=1, 0.9%), *Achromobacter xylosoxidans* (n=1, 0.9%), *Haemophilus haemolyticus* (n=1, 0.9%), *Stenotrophomonas maltophilus* (n=1, 0.9%), and *Bordetella bronchiseptica* (n=1, 0.9%). Sputum bacteriology was analyzed for results when clinically stable in all bronchiectasis patients and the exacerbation groups.

All bronchiectasis patients could spontaneously produce sputum for high-throughput sequencing because this was deemed to be one of the inclusion criteria, whereas all healthy subjects underwent hypertonic saline for induction.

None of the samples simultaneously grew *Pseudomonas aeruginosa* and *Haemophilus influenzae*. The total proportion of individual etiology was greater than 1 because a minority of patients had dual etiologies.

Numerical data were presented as mean \pm standard deviation for normal distribution or otherwise median (interquartile range). Categorical data were expressed as number (percentage) and compared with chi-square test.

No patient was receiving oral or inhaled antibiotics during the study.

	Parameters	Patients included (n=106)	Patients excluded (n=103)
	Age (yrs)	44.4±13.8	45.4±14.4
Anthronometry	BMI (cm/kg ²)	20.6±3.3	20.3 (3.5)
Antin opometry	Female (No., %)	58 (54.7%)	65 (63.1%)
	Never smokers (No., %)	97 (91.5%)	90 (87.4%)
	Duration of bronchiectasis (yrs)	15.0 (10.8)	10.0 (17.0)
	Exacerbations within previous 2 yrs	2.0 (4.0)	3.0 (4.0)
Disease-related	No. of bronchiectatic lobes	5.0 (3.0)	3.0 (3.0)
parameters	HRCT score	8.7±4.2	5.0 (4.0)
	Bronchiectasis Severity Index	6.0 (6.0)	5.0 (6.0)
	24-hour sputum (ml)	30.0 (11.1)	5.0 (15.0)
	FVC predicted%	73.0±19.9	83.6 (23.2)
Spirometry	FEV ₁ predicted%	59.7±23.5	74.8±22.5
	FEV ₁ / FVC (%)	69.3±14.0	75.3±13.2
Madications used	Inhaled corticosteroids (No., %)	27 (25.5%)	18 (17.5%)
within 6 months	Macrolides (No., %)	50 (47.2%)	39 (37.9%)
	Mucolytics (No., %)	80 (75.5%)	70 (68.0%)
	Post-infectious (No., %)	35 (33.0%)	22 (21.4%)
Ftiology	Immunodeficiency (No., %)	19 (17.9%)	10 (9.7%)
Luuugy	Miscellaneous (No., %) *	17 (16.0%)	19 (18.4%)
	Idiopathic (No., %)	39 (36.8%)	53 (51.5%)
Snutum	Pseudomonas aeruginosa (No., %)	45 (42.5%)	21 (20.4%)
bactarialogy	Other PPMs (No., %) **	41 (38.7%)	28 (27.2%)
Jacteriology	Commensals (No., %)	20 (18.9%)	54 (52.4%)

 Table S2. Comparison of demographic and clinical characteristics of bronchiectasis patients

 included and excluded for analysis

BMI: body-mass index; PPMs: potentially pathogenic microorganisms; FVC: forced vital capacity; FEV_1 : forced expiratory volume in one second; HRCT: high-resolution computed tomography Numerical data were presented as mean \pm standard deviation for normal distribution or otherwise median (interquartile range). Categorical data were expressed as number (percentage) and compared with chi-square test.

No patient was receiving oral or inhaled antibiotics during the study.

Sample	Sex	Total tags	Filtered tags	Total OTUs	Unique OTUs	Group
002V	F	105,418	103,959	747	9	Comm
004V	F	101,845	99,909	1,612	39	PA
006V	F	83,815	82,715	1,838	53	Comm
012V	М	87,096	85,113	1,265	45	PPM
015V	F	69,446	68,713	1,590	25	Comm
019V	F	63,653	61,455	2,093	44	PA
021V	F	44,043	43,304	1,090	46	PA
025V	F	83,430	81,118	1,908	35	PA
027V	М	112,394	110,762	1,084	19	PPM
028V	М	106,785	105,581	1,589	41	PPM
032V	F	107,574	105,217	1,723	22	Comm
036V	M	81,623	80,138	1,675	42	Comm
038V	F	95,173	93,163	1,849	57	PPM
040V	F	97,175	96,202	1,149	66	PPM
043V	F	93,816	92,496	1,875	35	PA
047V	М	96,244	93,015	1,874	33	PA
058V	F	95,174	94,100	1,746	70	PPM
063V	М	87,821	86,628	1,536	27	PPM
065V	М	52,386	51,014	1,727	35	PA
070V	F	79,726	78,398	1,738	41	PA
075V	F	112,895	110,727	1,782	53	Comm
078V	F	94,597	93,207	1,706	43	PA
079V	F	100,211	98,206	2,434	53	PA
083V	М	88,268	86,223	1,984	24	PPM
085V	М	105,317	103,595	2,026	43	PPM
088V	М	113,923	112,198	2,039	46	PA
089V	М	70,956	69,987	1,378	44	PA
090V	F	110,440	107,692	1,715	35	PPM
093V	F	81,422	80,143	1,390	44	PA
095V	F	91,537	90,335	1,172	40	PPM
102V	F	90,351	89,065	1,823	45	PA
103V	М	91,756	89,153	1,431	35	PPM
107V	F	45,682	44,823	1,033	30	PA
110V	F	112,058	110,896	959	14	PPM
114V	M	116,167	114,660	1,218	19	PPM
115V	F	99,258	96,691	2,537	41	PA
116V	M	84,575	82,940	1,781	31	PA
119V	M	128,734	126,522	2,114	33	PPM
120V	F	108,083	106,272	1,899	49	PA
126V	F	113,939	112,152	1,790	48	Comm
130V	F	122,506	120,017	1,814	45	PA
132V	F	102,638	98,519	2,499	20	Comm
134V	M	113,454	110,981	2,109	43	PPM

 Table S3. Sequence characteristics of samples from bronchiectasis patients and healthy subjects

136V	F	76,871	75,191	2,068	38	PA
139V	М	86,490	84,147	1,695	35	PPM
142V	F	92,706	91,394	1,539	30	PPM
143V	М	80,920	79,639	1,705	44	PA
145V	F	103,259	101,948	1,437	35	Comm
149V	М	103,851	102,426	1,333	21	Comm
151V	F	94,397	92,910	1,421	30	PPM
152V	F	40,066	39,322	859	30	PA
153V	М	107,346	106,071	1,186	9	PPM
154V	М	99,441	98,386	1,094	38	PPM
155V	F	95,435	92,783	2,017	41	PA
160V	F	136,059	133,690	1,613	33	PPM
161V	F	91,507	90.162	1,566	56	PPM
163V	F	82,941	81,799	1,344	28	PPM
164V	М	90,611	89,365	1,826	49	PA
166V	F	82,275	80,923	1,671	30	PA
167V	М	108,391	106,909	1,591	24	PPM
170V	М	81,209	80,252	1,264	18	PPM
171V	М	104,915	103,411	1,861	53	PA
173V	F	116,824	114,275	1,798	54	PA
174V	F	119,069	118,114	1,540	56	PPM
175V	М	115,795	113,392	2,067	41	PA
176V	M	116,046	113,793	1,975	35	PA
178V	F	106,260	104,222	861	32	PPM
179V	М	117,050	114,625	2,473	48	PA
180V	F	110,619	107,959	1,928	41	Comm
181V	М	101,623	99,235	2,197	55	PA
182V	М	90,504	89,231	1,462	26	PA
184V	М	85,512	83,345	1,863	38	PA
185V	F	88,514	87,513	1,618	41	PA
186V	М	110,281	109,345	1,122	53	PPM
188V	М	106,751	104,608	1,508	30	PA
189V	М	82,541	81,430	1,270	41	PPM
190V	М	44,394	43,624	1,129	43	Comm
191V	М	43,951	43,356	1,105	22	Comm
192V	М	108,449	107,199	1,038	26	PPM
193V	М	98,829	96,832	1,575	37	Comm
194V	F	45,144	44,432	602	13	PPM
195V	М	43,846	43,322	810	13	PPM
196V	М	42,217	41,478	1,092	35	PA
197V	М	46,262	45,551	1,086	39	PA
198V	F	75,227	72,134	2,088	54	PPM
199V	F	41,981	41,175	1,219	45	PA
200V	F	65,313	63,357	1,240	13	PPM
201V	F	79,402	77,148	1,997	37	Comm
202V	F	41,333	40,598	970	29	PA
204V	F	66,616	63,413	2,028	17	Comm
205V	M	47,105	45,893	474	9	PPM

206V	М	62,554	60,389	1,748	39	PA
207V	F	41,114	39,344	589	40	PPM
208V	F	69,558	67,596	936	17	Comm
209V	М	82,374	79,729	1,519	22	PPM
210V	М	66,118	64,409	1,349	23	Comm
211V	F	73,619	71,105	2,231	43	PPM
212V	F	56,189	54,363	1,618	40	PA
213V	F	41,213	40,546	941	14	Comm
214V	М	76,812	74,056	1,602	23	PPM
215V	F	65,430	63,061	1,889	36	PA
217V	М	73,846	71,638	2,086	45	PA
219V	М	79,929	77,867	1,854	39	PA
220V	М	39,799	39,040	593	12	Comm
221V	М	49,854	48,693	1,043	16	PPM
222V	М	57,881	55,963	1,333	63	PA
H01	F	61,075	59,647	1,323		-
H02	F	47,178	46,274	1,220		-
H04	М	51,269	49,891	1,086		-
H05	М	39,978	39,231	917		-
H07	M	57,369	54,943	953		-
H08	M	49,741	48,570	1,264		-
H09	М	85,499	82,249	2,254		-
H10	F	56,609	55,348	1,315		-
H11	F	47,044	45,696	1,060		-
H12	F	44,990	43,562	1,013		-
H14	F	47,310	46,300	901		-
H15	F	46,269	45,141	914		-
H16	M	48,081	46,754	854		-
H17	F	48,289	46,784	1,120		-
H18	F	45,292	43,900	863		-
H20	F	53,384	51,938	1,261		-
H21	F	49,191	47,691	926		-

OTUs: Operational taxonomic units; F: female; M: male; PA: Pseudomonas aeruginosa; PPM: potentially pathogenic microorganism; Comm: Commensals; V: clinically stable; H: Healthy subjects

	PA	PPM	Comm	Healthy	P value				
	group	group	group	subjects	а	b	c	d	e
Dominant phyla	-	-	-	-	-	-	-	-	-
No.	45	41	20	17	-	-	-	-	-
Proteobacteria	92.07	82.83	67.13	75.33	<0.001	0.001	0.056	0.353	<0.001
Firmicutes	4.30	8.59	11.49	10.49	<0.001	0.001	0.124	0.532	<0.001
Bacteroidetes	1.57	5.25	13.30	8.97	<0.001	<0.001	0.017	0.615	<0.001
Dominant genera of									
Proteobacteria	-	-	-	=	-	-	-	-	-
Pseudomonas	60.46	14.17	19.67	17.73	<0.001	<0.001	0.387	0.843	<0.001
Haemophilus	2.71	25.53	4.05	6.30	<0.001	<0.001	0.161	0.749	<0.001
Neisseria	2.06	3.02	3.36	2.93	0.133	0.085	0.453	0.593	0.115
Serratia	18.48	19.70	26.39	33.79	<0.001	<0.001	<0.001	0.070	0.038
Dominant genera of	-	-	-	-	-	-	-	-	-
Firmicules	1.(1	2.50	4.61	2.17	-0.001	0.003	0.572	0.166	-0.001
Streptococcus	1.61	3.50	4.61	3.17	<0.001	0.003	0.573	0.166	<0.001
Dominant genera of	-	-	-	-	_	-	-	-	_
Bacteroidetes									
Prevotella	0.94	2.52	3.39	5.50	<0.001	<0.001	0.034	0.170	<0.001
Other bacterial genera	-	-	-	-	-	-	-	-	-
Others	11.55	26.86	24.76	25.86	<0.001	<0.001	0.330	0.385	<0.001

Table S4. Mean relative abundance (%) of bacterial phyla and genera among clinically stable bronchiectasis patients and healthy subjects

^a P values were derived from the comparisons among the four groups.

^b P values were derived from the comparisons between PA group and healthy subjects.

^c P values were derived from the comparisons between PPM group and healthy subjects.

^d P values were derived from the comparisons between Comm group and healthy subjects.

^e P values were derived from the comparisons among PA, PPM and Comm group.

Others denoted all bacteria genus detected with high-throughput sequencing apart from *Pseudomonas, Serratia, Haemophilus, Neisseria, Porphyromonas, Streptococcus,* and *Prevotella.*

Data in bold indicated the statistical analysis with significance.

PA: P. aeruginosa; PPM: other potentially pathogenic microorganism; Comm: commensals

	PA group	PPM group	Comm group	Healthy subjects	P value	P value	P value	P value	P value e
Phyla levels	-	-	-	-	-	-	-	-	-
No.	45	41	20	17	-	-	-	-	-
Shannon-Wiener diversity index	0.33	0.55	0.87	0.77	<0.001	<0.001	0.044	0.637	<0.001
Simpson diversity index	0.14	0.25	0.43	0.36	<0.001	0.001	0.052	0.437	<0.001
Richness	9.3	10.1	11.0	11.5	<0.001	<0.001	0.004	0.244	0.004
Genera levels	-	-	-	-	-	-	-	-	-
Shannon-Wiener diversity index	1.24	1.71	2.13	2.13	<0.001	<0.001	0.020	0.939	<0.001
Simpson diversity index	0.52	0.67	0.79	0.78	<0.001	<0.001	0.068	0.532	<0.001
Richness	70.5	78.0	84.9	94.5	<0.001	<0.001	<0.001	0.025	<0.001

Table S5. Mean Shannon-Wiener diversity index, Simpson diversity index, and richness of bacterial phyla and genera among clinically stable bronchiectasis patients and healthy subjects

^a P values were derived from the comparisons among the four groups.

^b P values were derived from the comparisons between PA group and healthy subjects.

^c P values were derived from the comparisons between PPM group and healthy subjects.

^d P values were derived from the comparisons between Comm group and healthy subjects.

^e P values were derived from the comparisons among PA, PPM and Comm group.

Data in bold indicated the statistical analysis with significance.

PA: P. aeruginosa; PPM: other potentially pathogenic microorganism; Comm: commensals

	-	J		
Phyla	Mean abundance	Mean	%	Cumulative %
		contribution	contribution	
Proteobacteria	0.84	74.97	92.07	92.07
Genus	Mean abundance	Mean	%	Cumulative %
		contribution	contribution	
Pseudomonas	0.35	19.64	38.33	38.33
Serratia	0.20	13.17	25.71	64.04
Other bacteria	0.20	12.20	23.80	87.84
Haemophilus	0.12	2.19	4.27	92.11

 Table S6. The percentage similarity of microbial community in bronchiectasis patients when clinically stable

Shown in the table are the major categories of phyla or genera which contributed most to the similarity in community structure when clinically stable.

Table S7. Mean relative abundance of Proteobacteria, and Shannon-Wiener diversity index, Simpson diversity index, and richness at phyla levels among clinically stable bronchiectasis patients when stratified by *Pseudomonas aeruginosa* colonization status and macrolide use upon enrollment

Mean levels	PA colonized	Non-PA colonized*	P value	Macrolide use	No macrolide use	P value
No.	35	10	-	50	56	-
Relative abundance of <i>Proteobacteria</i>	0.923	0.911	0.461	0.850	0.827	0.606
Shannon-Wiener diversity index	0.320	0.368	0.420	0.482	0.545	0.533
Simpson diversity index	0.138	0.159	0.453	0.221	0.254	0.584
Richness	9.0	10.2	0.032	9.8	10.1	0.360

* We only focused on the issue whether PA colonization differed in terms of the four parameters listed above compared with PA isolation, therefore the data from bronchiectasis patients who had PPM or commensals isolated at baseline were not included for analysis in this table.

Non-PA colonized denoted patients who had PA isolated at baseline but not thereafter during the study.

PA: P. aeruginosa

Data in bold indicated the statistical analysis with significance.

Parameters	Relative abundance		Shannon-Wiener diversity index *		Simpson divers	sity index	Richness	
	Standardize d estimate	P value	Standardize d estimate	P value	Standardized estimate	P value	Standardized estimate	P value
No. of exacerbations in previous 2 years	-0.082	0.426	0.091	0.365	0.085	0.402	-0.077	0.447
The No. of bronchiectatic lobes	-0.321	0.069	0.333	0.053	0.326	0.060	0.238	0.166
HRCT total score	0.226	0.260	-0.235	0.229	-0.231	0.241	-0.262	0.182
FEV ₁ % predicted	-0.197	0.174	0.258	0.069	0.248	0.082	-0.061	0.663
Bronchiectasis Severity Index	0.119	0.339	-0.149	0.218	-0.139	0.254	-0.313	0.011

Table S8. Correlation coefficient (β) between key clinical parameters and the relative abundance of airway *Proteobacteria*, Shannon-Wiener diversity index, Simpson diversity index and richness of different bacterial phyla in clinically stable bronchiectasis

All estimates of correlation were calculated based on multiple linear regression model, with the use of coercive entering algorithm.

* Denoted the diversity of all different bacterial phyla (including *Proteobacteria*).

Data in bold indicated the statistical analysis with significance.

Supplementary Information template:

		P	roteobacter	ia	Pseudomonas			
Subject ID	Group	Visit 1	Visit 2	SD	Visit 1	Visit 2	SD	
089V	PA	98.21	90.22	5.65	61.17	22.96	27.02	
110V	PPM	94.70	96.66	1.38	4.01	8.46	3.14	
164V	PA	80.05	88.87	6.24	34.27	23.15	7.86	
178V	PPM	99.41	98.53	0.62	3.26	80.74	54.78	
199V	PA	88.16	96.42	5.84	70.59	46.47	17.06	

 Table S9. Comparison of the variation in the relative abundance of *Proteobacteria* and *Pseudomonas* sampled at two separate time points when clinically stable

Visit 1 was the visit in which the data were included for analysis in the main manuscript. Visit 2 was the repeat clinically stable visit in which sputa were sampled at approximately three months apart.

SD: standard deviation; ID identification

PA: P. aeruginosa; PPM: other potentially pathogenic microorganism; Comm: commensals

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Figure S2. Bacterial compositions at phyla levels corresponding to sputa samples derived from bronchiectasis patients and healthy subjects



The bright red, purple, black and brown boxes denote samples derived from culture-negative (Comm), other PPM-positive (PPM), and *P. aeruginosa*-positive (PA) bronchiectasis patients, and healthy subjects (Healthy control).

The figure demonstrated the percentage of relative abundance of individual bacterial phylum. Demonstrated in the right panel are the bacterial phyla detected with the highest relative abundance in this study, including *Proteobacteria*, *Spirochaetes*, *Bacteroidetes*, *Firmicutes*, *Fusobacteria*, *Actinobacteria*, *Synergistetes* and others (all other phyla with relatively low abundance were combined).

The bright red, orange, green and dark bands represented the Comm, PPM, PA group and healthy subjects, respectively.

Comm: commensals; PPM: potentially pathogenic microorganism; PA: *P. aeruginosa;* H: Healthy subjects



Figure S3. The difference in the relative abundance of airway microbial compositions at phyla levels

Figure S3-A. The difference in the relative abundance of airway microbial compositions at phyla levels among all bronchiectasis patients (n=106) and healthy subjects (n=17)

Figure S3-B. The difference in the relative abundance of airway microbial compositions at phyla levels in PA group (n=45) and healthy subjects (n=17)

Figure S3-C. The difference in the relative abundance of airway microbial compositions at phyla levels in PPM group (n=41) and healthy subjects (n=17)

Figure S3-D. The difference in the relative abundance of airway microbial compositions at phyla levels in Comm group (n=20) and healthy subjects (n=17)

Shown in the longitudinal axis of individual panels are the % difference in the relative abundance of bacterial phyla, with the vertical axis denoting no difference (0%) between the two groups. A difference of greater than 0% in the right direction indicated greater relative abundance of the corresponding phylum in patients with bronchiectasis, whereas a difference of below 0% in the left direction indicated greater relative abundance of the corresponding phylum in healthy subjects. Comm: commensals; PPM: potentially pathogenic microorganism; PA: *P. aeruginosa*



Figure S4. The difference in the relative abundance of airway microbial compositions at genera levels

Figure S4-A. The difference in the relative abundance of airway microbial compositions at genera levels among all bronchiectasis patients (n=106) and healthy subjects (n=17)

Figure S4-B. The difference in the relative abundance of airway microbial compositions at genera levels in PA group (n=45) and healthy subjects (n=17)

Figure S4-C. The difference in the relative abundance of airway microbial compositions at genera levels in PPM group (n=41) and healthy subjects (n=17)

Figure S4-D. The difference in the relative abundance of airway microbial compositions at genera levels in Comm group (n=20) and healthy subjects (n=17)

Shown in the longitudinal axis of individual panels are the % difference in the relative abundance of bacterial genus, with the vertical axis denoting no difference (0%) between the two groups. A difference of greater than 0% in the right direction indicated greater relative abundance of the corresponding genus in patients with bronchiectasis, whereas a difference of below 0% in the left direction indicated greater relative abundance of the corresponding genera in healthy subjects. Comm: commensals; PPM: potentially pathogenic microorganism; PA: *P. aeruginosa*



Figure S5. Comparison of bacterial richness and Simpson diversity index in bronchiectasis patients and healthy subjects

Figure S5-A. The difference in bacterial richness at phyla levels among all bronchiectasis patients (n=106) and healthy subjects (n=17)

Figure S5-B. The difference in Simpson diversity index at phyla levels among all bronchiectasis patients (n=106) and healthy subjects (n=17)

Figure S5-C. The difference in bacterial richness at genera levels among all bronchiectasis patients (n=106) and healthy subjects (n=17)

Figure S5-D. The difference in Simpson diversity index at genera levels among all bronchiectasis patients (n=106) and healthy subjects (n=17)

Comm: commensals; PPM: potentially pathogenic microorganism; PA: P. aeruginosa





Figure S6-A, Changes in the relative abundance of *Proteobacteria* in PA group (n=10) Figure S6-B, Changes in the relative abundance of *Proteobacteria* in PPM group (n=7) Figure S6-C, Changes in the relative abundance of *Proteobacteria* in Comm group (n=5) Figure S6-D, Changes in the Shannon-Wiener diversity index of *Proteobacteria* in PA group (n=10) Two patients did not undergo convalescence visit and therefore their data were analyzed only for baseline and exacerbation visits.

Figure E6-E, Changes in the Shannon-Wiener diversity index of *Proteobacteria* in PPM group (n=7) One patient did not undergo convalescence visit and therefore the data were analyzed only for baseline and exacerbation visits.

Figure E6-F, Changes in the Shannon-Wiener diversity index of *Proteobacteria* in Comm group (n=5)

One patient did not undergo convalescence visit and therefore the data were analyzed only for baseline and exacerbation visits.

Grouping was purely based on the sputum culture findings at baseline visits (when clinically stable). Therefore, sputum bacteriology was not applied for grouping during exacerbation or convalescence. The black lines indicated the trend of changes in 16s copies of *Proteobacteria* and Shannon-Wiener diversity index from baseline to exacerbations, whereas the gray lines indicated the trend of changes in 16s total copies of *Proteobacteria* and Shannon-Wiener diversity index from exacerbations to convalescence.

Comm: commensals; PPM: potentially pathogenic microorganism; PA: P. aeruginosa

Figure S7. Comparison of the Simpson diversity index at phyla levels when clinically stable and during exacerbations and convalescence



Figure S7-A. Simpson diversity index at phyla levels in PA group (n=10) when clinically stable and during exacerbations and convalescence

Figure S7-B. Simpson diversity index at phyla levels in PPM group (n=7) when clinically stable and during exacerbations and convalescence

Figure S7-C. Simpson diversity index at phyla levels in Comm group (n=5) when clinically stable and during exacerbations and convalescence

Comm: commensals; PPM: potentially pathogenic microorganism; PA: *P. aeruginosa* V: clinically stable; AE: exacerbation; R: convalescence

Figure S8. Comparison of bacterial richness at phyla levels when clinically stable and during exacerbations and convalescence



Figure S8-A. Bacterial richness at phyla levels in PA group (n=10) when clinically stable and during exacerbations and convalescence

Figure S8-B. Bacterial richness at phyla levels in PPM group (n=7) when clinically stable and during exacerbations and convalescence

Figure S8-C. Bacterial richness at phyla levels in Comm group (n=5) when clinically stable and during exacerbations and convalescence

Comm: commensals; PPM: potentially pathogenic microorganism; PA: P. aeruginosa

V: clinically stable; AE: exacerbation; R: convalescence