Table 1. Cohort characteristics by mould colonisation status expressed as numbers (sex, genotype, CF related diabetes, LTX, ABPA, chronic bacterial infection) or medians with range (age, respiratory samples, FEV1 % predicted and BMI z-score)

	A No moulds	B Aspergillus, new cases		C Aspergillus persistent*		D Aspergillus, Cleared colonisation		E Other moulds		
	(n=130)	(n=44)	P (A vs. B)	(n=63)	P (A vs. C)	(n=38)	P (A vs. D)	(n=12)	P (A vs. E)	P
Age, median (range)	17.5 (0-51)	18.5 (0-49)	1.0	23.0 (5-57)	0.0149	25.0 (2-47)	0.0173	25.0 (8-36)	0.44	0.0345
Sex F/M (F%)	66/64 (51%)	22/22 (50%)	1.0	38/25 (60%)	0.22	20/18 (53%)	0.86	7/5 (58%)	0.77	0.75
CF genotype										
$\Delta F508/\Delta F508$	80° (62%)	31 (70%)	0.36	45 (71%)	0.20	30 ^b (79%)	0.0536	9 (75%)	0.54	0.26
Δ F508/other	41 (32%)	11 (25%)	0.45	18 (29%)	0.74	5 (13%)	0.0372	3 (25%)	0.75	0.27
other/other	5 (4%)	2 (5%)	1.00	-	0.18	-	0.59	-	1.00	na
CF related diabetes	37 (28%)	13 (30%)	1.00	9 (14%)	0.0318	10 (26%)	0.84	4 (33%)	0.74	0.23
LTX	10 (8%)	5 (11%)	0.53	4 (6%)	1.00	11 (29%)	0.0014	-	1.00	0.0015
ABPA	6 (5%)	1 (2%)	0.68	9 (14%)	0.0405	5 (13%)	0.13	3 (25%)	0.0293	0.0119
Respiratory samples										
No. of samples	1317	490		874		458		197		
Median (range)	10 (1-29)	12 (2-22)	0.16	12 (4-28)	< 0.0001	12 (3-20)	0.0231	17 (8-28)	0.0085	< 0.0001
Proportion positive samples, median (range)	-	0.14 (0.05-1.00)		0.42 (0.09-1.00)		0.15 (0.00-0.67)		0.08 (0.04-0.22)		< 0.0001
FEV1 % predicted, median (range)										
2007°	80.9 (20.0-118.2)	79.3 (36.8-129.7)	0.63	75.4 (29.8-122.5)	0.65	74.6 (22.0-112.9)	0.29	70.9 (40.1-116.1)	0.76	0.77
2009^{d}	81.0 (17.0-115.8)	85.4 (33.1-135.8)	0.25	75.1 (28.8-115.0)	0.46	78.1 (26.8-125.5)	0.90	72.1 (37.5-116.5)	0.37	0.43
mean 2007+2009	81.4 (20.0-117.0)	85.2 (35.0-135.8)		74.8 (29.3-118.7)		74.8 (22.0-119.2)		71.5 (40.2-115.9)		0.32
change 2007 – 2009	0.0 (-16.8-38.7)	0.0 (-19.6-9.2)		-1.0 (-19.8-23.3)		0.0 (-20.0-55.86)		-4.1 (-19.0-8.6)		0.60
BMI z-score, median (range)										
2007 ^e	-0.2 (-3.5-2.2)	-0.3 (-3.8-1.7)	0.90	-0.4 (-2.5-2.7)	0.73	-0.4 (-5.9-0.7)	0.23	0.3 (-1.3-1.2)	0.0945	0.28

2009^{f}	-0.4 (-4.0-2.4)	-0.3 (-2.7-0.9)	0.91	-0.4 (-2.7-2.6)	0.89	-0.3 (-3.1-1.1)	0.77	0.3 (-1.7-1.6)	0.0329	0.27
Chronic bacterial infection, total	63 (48%)	23 (52%)	0.73	41 (65%)	0.0323	28 (74%)	0.0090	8 (67%)	0.37	0.0301
Pseudomonas aeruginosa	37 (28%)	14 (32%)	0.70	25 (40%)	0.14	16 (42%)	0.12	6 (50%)	0.19	0.26
Burkholderia spp.	11 (8%)	2 (5%)	0.52	3 (5%)	0.55	2 (5%)	0.73	-	0.60	na
Achromobacter spp.	10 (8%)	4 (9%)	0.75	6 (10%)	0.78	6 (16%)	0.20	-	1.00	0.46
Stenotrophomonas maltophilia	3 (2%)	-	0.57	3 (5%)	0.39	3 (8%)	0.13	1 (8%)	0.30	na
Other Gram-negative	2 (2%)	2 (5%)	0.22	1 (2%)	1.00	1 (3%)	0.54	1 (8%)	0.23	na
Mycobacteria	-	1 (2%)	0.25	1 (2%)	0.33	-	na	-	na	na
Nocardia spp.	-	-	na	2 (3%)	na	-	na	-	na	na

LTX = lung transplant recipients; ABPA = allergic bronchopulmonary aspergillosis; - = 0, na = criteria for test not fulfilled.

Non-normally distributed continuous data were compared using Kruskal-Wallis test. When Kruskal-Wallis test gave a significant result, the groups were compared to each other, two at a time, using Mann-Whitney test. Categorical data were compared using Chi-square test and Fisher's exact test when comparing two groups.

^{* 57/63} were persistently colonised with *A. fumigatus*; 4/63 were colonised with *A. fumigatus* in 2007 and *A. niger* 2009; 1/63 were persistently colonised with *A. terreus*; 1/63 were colonised with *A. fumigatus* in 2007 and other *Aspergillus* species in 2009.

^a Insufficient data on four patients. ^b Insufficient data on three patients. ^c No. of patients with data in column A, B, C, D and E were 101, 30, 60, 32 and 12, respectively. ^d No. of patients with data in column A, B, C, D and E were 108, 36, 60, 27 and 12, respectively. ^e No. of patients with data in column A, B, C, D and E were 113, 38, 60, 33 and 12, respectively. ^f No. of patients with data in column A, B, C, D and E were 120, 40, 60, 27 and 12, respectively.