Supplemental Material

Supplemental figure

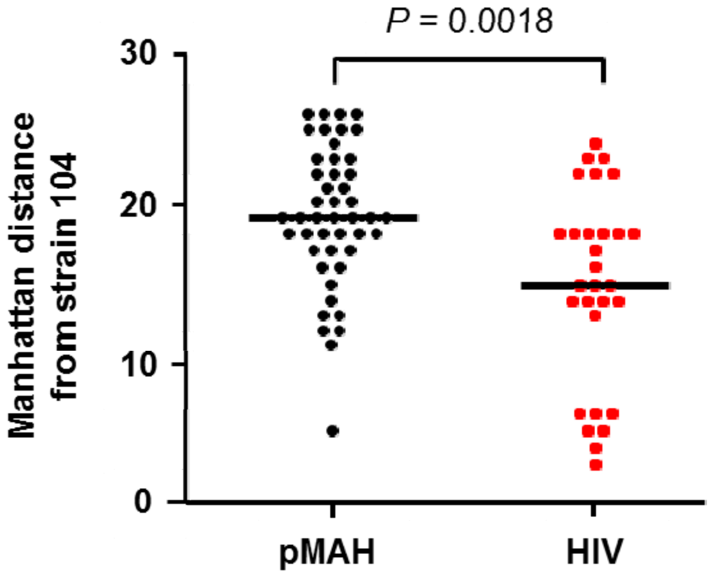

FIG S1 Genetic distances of MAH isolates from different hosts. The genetic distance was calculated as the Manhattan distance of MAH isolates from the reference strain 104. The results are shown for MAH isolates from pulmonary MAH disease patients and HIV-positive patients. Horizontal lines indicate the mean value of genetic distance for the group; *p* values were calculated using a Mann–Whitney U test.

Supplemental Tables

TABLE S1 MIC distributions of test drugs for 46 isolates from pulmonary MAH disease patients

Antimicrobial agent	MIC (µg/mL)												
	< 0.03	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	> 32
Clarithromycin			1		15	13	14	1		1			1
Rifampicin	8		10	6	7	2	6	4	2				1
Ethambutol								1	6	20	17	1	1
Streptomycin							5	11	16	10	4		
Kanamycin							1	4	10	16	12	3	
Amikacin							2	9	14	14	7		
Ethionamide								2	14	23	7		
Levofloxacin					1	6	11	19	9				

TABLE S2 MIC distributions of test drugs for 30 isolates from HIV-positive patients

Antimicrobial agent	MIC (µg/mL)												
	< 0.03	0.03	0.06	0.125	0.25	0.5	1	2	4	8	16	32	> 32
Clarithromycin	3		5	6	4	6	3						3
Rifampicin	5		7	4	6	2	3	3					
Ethambutol						1	2	4	10	7	5		1
Streptomycin			1		3	2	8	8	3	3	2		
Kanamycin				2		2	5	8	5	4	4		
Amikacin						6	3	7	6	5	3		
Ethionamide							2	5	13	8	2		
Levofloxacin			1	5	1	5	7	5	5	1			

TABLE S3 Relationships between VNTR-based genotype and isolates from different hosts

Cluster[a]	pulmonary MAH disease patients (n = 46)	HIV-positive patients (n = 30)	*P* value[b]
I	3 (6.5%)	11 (36.7%)	0.0031
II	19 (41.3%)	11 (36.7%)	
III	24 (52.2%)	8 (26.7%)	

Cluster	pulmonary MAH disease patients (n = 46)	HIV-positive patients (n = 30)	*P* value
I	3 (6.5%)	11 (36.7%)	0.0017
II + III	43 (93.5%)	19 (63.3%)	

[a] Each cluster was classified by the phylogenetic analysis as shown in FIG. 1.

[b] *P* values were calculated using Fisher's exact test.

TABLE S4 Comparison of drug resistance and susceptibility in isolates within the three VNTR clusters

Antimicrobial agent	Cluster[a] I (n = 14)		Cluster II (n = 30)		Cluster III (n = 32)		*P* value[b]			
	R[c] (%)	S[c] (%)	R (%)	S (%)	R (%)	S (%)	Clusters I vs II vs III	Clusters I vs II	Clusters I vs III	Clusters II vs III
Clarithromycin	0 (0)	14 (100)	2 (6.7)	28 (93.3)	2 (6.2)	30 (93.8)	1	1	1	1
Rifampicin	0	14 (100)	0 (0)	30 (100)	1 (3.1)	31 (96.9)	1	1	1	1
Ethambutol	7 (50.0)	7 (50.0)	18 (60.0)	12 (40.0)	27 (84.4)	5 (15.6)	0.030	0.745	0.027	0.046
Streptomycin	0	14 (100)	7 (23.3)	23 (76.7)	12 (37.5)	20 (62.5)	0.019	0.078	0.009	0.277
Kanamycin	0	14 (100)	7 (23.3)	23 (76.7)	12 (37.5)	20 (62.5)	0.019	0.078	0.009	0.277
Amikacin	0	14 (100)	3 (10.0)	27 (90.0)	7 (21.9)	25 (78.1)	0.122	0.540	0.083	0.304
Ethionamide	2 (14.3)	12 (85.7)	23 (76.7)	7 (23.3)	15 (46.9)	17 (53.1)	≤0.001	≤0.001	0.049	0.020
Levofloxacin	0	14 (100)	1 (3.3)	29 (96.7)	0 (0)	32 (100)	0.579	1	1	0.484

[a] Each cluster was classified by the phylogenetic analysis as shown in FIG. 1.

[b] *P* values were calculated using Fisher's exact test.

[c] The breakpoints of the antimicrobial agents were determined according to the criteria described in the BrothMIC NTM manual and the Materials and Methods. R, resistant; S, susceptible.

TABLE S5 Association between presence of IS*Mav6* and drug resistance

Antimicrobial agent	IS*Mav6* positive (n = 31)		IS*Mav6* negative (n = 45)		*P* value[a]
	R[b] (%)	S[b] (%)	R (%)	S (%)	IS*Mav6* positive vs negative
Clarithromycin	4 (12.9)	27 (87.1)	0 (0)	45 (100)	0.025
Rifampicin	1 (3.2)	30 (96.8)	0 (0)	45 (100)	0.408
Ethambutol	24 (77.4)	7 (22.6)	28 (62.2)	17 (37.8)	0.212
Streptomycin	12 (38.7)	19 (61.3)	7 (15.6)	38 (84.4)	0.031
Kanamycin	13 (41.9)	18 (58.1)	6 (13.3)	39 (86.7)	0.007
Amikacin	9 (29.0)	22 (71.0)	1 (2.2)	44 (97.8)	≤0.001
Ethionamide	15 (48.4)	16 (51.6)	25 (55.6)	20 (44.4)	0.642
Levofloxacin	0 (0)	31 (100)	1 (2.2)	44 (97.8)	1

[a] *P* values were calculated using Fisher's exact test.

[b] The breakpoints of the antimicrobial agents were determined according to the criteria described in the BrothMIC NTM manual and the Materials and Methods. R, resistant; S, susceptible.

TABLE S6 Relationships between presence of IS*Mav6* and VNTR-based genotype

Cluster[a]	IS*Mav6* positive (n = 31)	IS*Mav6* negative (n = 45)	*P* value[b]
I	0 (0.0%)	14 (31.1%)	≤0.001
II	9 (29.0%)	21 (46.7%)	
III	22 (71.0%)	10 (22.2%)	

[a] Each cluster was classified by the phylogenetic analysis as shown in FIG. 1.

[b] *P* values were calculated using Fisher's exact test.