Prevalence and molecular characterization of multidrug resistant *M.tuberculosis* in Jiangxi province, China

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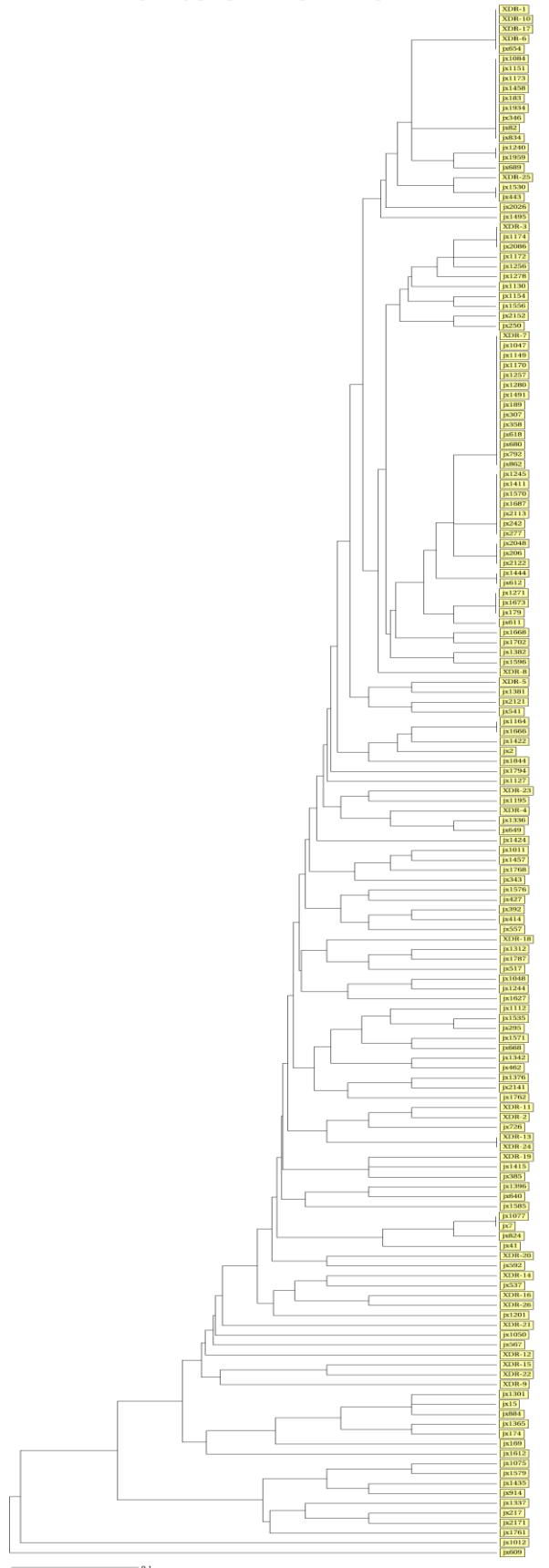
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Additional file 1 UPGMA dendrogram of 157 MDR TB isolates in this study

UPGMA-Tree, MIRU-VNTR (15): Categorical (1), Spoligo: Categorical (1), RD: Categorical (1), SNP: Categorical (1)

Additional table 1 Relation between mutation patterns and clusters or Beijing genotype strains of MDR TB

Mutation	Clustered No. (%)44	Non-clustered No. (%)	OR (95% CI)	P value	Beijing genotypes No. (%)	Non-Beijing genotypes No. (%)	OR (95% CI)	P value
rpoB 531	24	64	1.038 0.579-1.862	0.900	76	14	0.642 (0.324-1.271)	0.201
rpoB 526	6	20	1.298 0.489-3.446	0.600	20	6	1.046 (0.390-2.805)	0.929
rpoB 516	4	7	0.681 0.190-2.443	0.554	11	0	Could not calculate	_
rpoB 533	3	7	0.909 (0.225-3.672)	0.893	9	1	0.387 0.047-3.162	0.359
rpoB513	1	3	1.168 (0.118-11.533)	0.894	4	0	Could not calculate	_
Kat315	33	76	0.897 (0.524-1.534)	0.691	90	18	0.689 (0.367-1.295)	0.246
inhA	12	17	0.552 (0.244-1.249)	0.150	24	5	0.726 (0.258-2.043)	0.543
ahpC	5	14	1.090 (0.371-3.207)	0.875	17	4	0.820 (0.259-2.596)	0.736

Additional table 2 Allelic diversity of different MIRU-VNTR markers for the whole samples and for the Beijing genotype isolates

VNTR Alias	Repeats number	Allelic diversity(h)	Repeat number	Allelic diversity(h)
	All isolates (N=157)		Beijing isolates (N=132)	
Mtub04	1(8); 2(38); 3(89); 4(22)	0.6027	1(5); 2(31); 3(76); 4(20)	0.5935
ETRC	2(2);3(3); 4(152)	0.0626	2(2); 3(2); 4(128)	0.0597
ETRD	1(3); 2(1); 3(150); 4(3)	0.0870	1(3); 2(1); 3(126); 4(2)	0.0888
MIRU40	1(3); 2(20); 3(128); 4(3); 5(3)	0.3496	1(1); 2(10); 3(117); 4(2); 5(2)	0.2097
MIRU10	1(8); 2(26); 3(119); 4(3); 5(1)	0.3976	1(8); 2(13); 3(105); 4(6)	0.3544
MIRU16	1(2); 2(7); 3(126); 4(12)	0.3498	1(1); 2(5); 3(116); 4(11)	0.2210
Mtub21	2(6); 3(21); 4(119); 5(8); 6(3)	0.4058	2(1); 3(11); 4(113); 5(4); 6(3)	0.2607
Qub11b	1(4); 2(2); 3(2); 4(134); 5(13); 7(2)	0.2652	1(2); 2(1); 3(1); 4(115); 5(10); 7(2)	0.2364
ETRA	2(3); 3(27); 4(125); 5(1)	0.3382	2(1); 3(15); 4(115)	0.2297
Mtub30	2(13); 3(1); 4(142)	0.1761	2(5);3(1); 4(125)	0.1025
MIRU26	1(3); 2(1); 3(1); 4(11); 5(19); 6(22); 7(88); 8(9); 9(2)	0.6468	2(1); 4(7); 5(9); 6(17); 7(86); 8(9); 9(2)	0.5507
ETRE	2(5); 3(8); 4(19); 5(108); 6(13); 7(1)	0.5047	2(3); 3(2); 4(18); 5(85); 6(8); 7(1)	0.5657
Mtub39	3(4); 4(131); 5(14); 6(8)	0.2944	3(3); 4(112); 5(12); 6(5)	0.2719
Qub26	2(5); 3(4); 4(5);5(89); 6(3); 7(1); 8(49)	0.5818	2(2); 3(4); 4(4);5(69); 6(3); 7(1); 8(49)	0.5908
Qub4156	0(1); 2(23); 3(128); 5(2); 7(3)	0.3019	2(12); 3(119); 5(2)	0.1802
HGDI		0.9859		0.9803