





WHO Policy Update: Interpretation of DST



Dr Christopher Gilpin Senior Scientist

FIND and NDWG Symposium

The 48th Union World Conference on Lung Health Guadalajara, Mexico, 11-14 October 2017

Technical Expert Consultation

FIND conducted systematic review of available minimum inhibitory concentration (MIC) data for phenotypically wild type (pWT) strains, as well as genotypically non-wild type (gNWT) strains, including strains from allelic-exchange experiments for second-line antituberulosis medicines.

The medicines included in the review were the second-line injectable agents (kanamycin, amikacin and capreomycin); clofazimine and bedaquiline; cycloserine and terizidone; linezolid; delamanid; and the fluoroquinolones (ofloxacin, levofloxacin, gatifloxacin and moxifloxacin).

Media reviewed: Löwenstein-Jensen, Middlebrook 7H10/7H11; BACTEC™ Mycobacterial Growth Indicator Tube™ 960 (MGIT).







Meeting Report

Fechnical Expert Group: critical concentrations for drug susceptibility testing for TB medicines

Phenotypic methods for the diagnosis of DR-TB

Phenotypic, culture methods are based on assessment of the ability of *M. tuberculosis* to grow in culture media (solid or liquid) containing a critical concentration of specific anti-TB agents (which indicates resistance) or, conversely, its inability to grow in the same media (which indicates susceptibility).

The indirect proportion method is the most common method Resistance is defined when at least 1% of growth is observed at the critical concentration of drug in the culture medium.

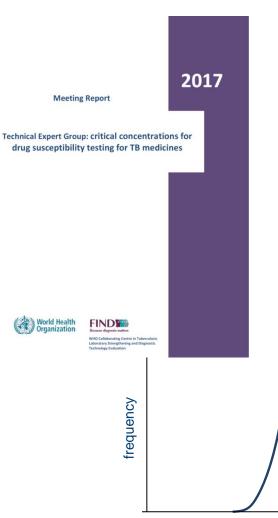
Commercial liquid culture systems for DST reduce the time to result to as little as 10 days, compared with the 28–42 days needed for DST using solid media







Revised definition: critical concentration



Critical concentration (CC) of an anti-tuberculous agent has been adopted and modified from international convention. The critical concentration is defined as the lowest concentration of an anti-TB agent that will inhibit the growth of at least 95% of wild-type strains of *M*. *tuberculosis*.

The critical concentration is typically the same or one dilution higher than the epidemiological cut-off value in order not to misclassify phenotypically wild-type strains as phenotypically non wild-type.





CC

MIC

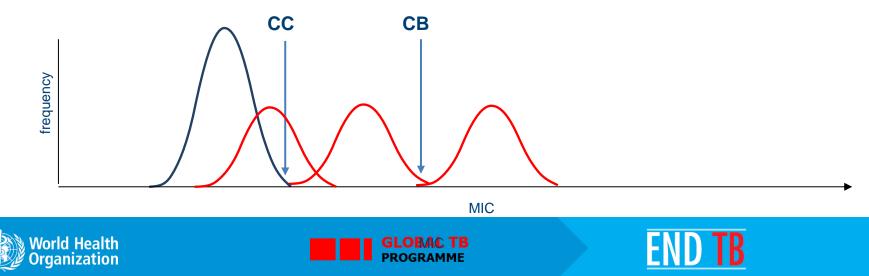


New definition: clinical breakpoint

Clinical breakpoint (CB)- is the concentration or concentrations of an antimicrobial agent which defines an MIC which separates strains which will likely respond to treatment from those which will likely not respond to treatment. This concentration is determined by correlation with available clinical outcome data, MIC distributions, genetic markers, and PK/PD data including drug dose.

A dose increase can be used to overcome resistance observed at lower dosing, up until the maximum tolerated dose, and therefore a higher clinical breakpoint above which the particular drug is not recommended for use.

The clinical breakpoint is commonly different to the critical concentration generally recommended for a given agent.



Phenotypic wild type (pWT) e.g. amikacin MIC distributions on MGIT media

15 studies were identified that reported AMK MIC data for the pWT population with MGIT (Table 23). All studies had MICs for more than 10 pWT isolates. The MIC distributions reaffirmed the CC of 1 mg/L in MGIT.

												AM	K MIC	[mg/l	.]						
Studies	Lab	Isolate origin	Unique isolates Tot	al MICs Type of isolates	Sequencing results 0.06	5 0.12	0.25	0.5 1	L	1.5	2	2.5 4	8	16	5 20	32	64	128	256	512	1024
21) Rüsch-Gerdes	15-17	clinical	10	30 H37Rv ATCC 27294 & pan-S				30				_									
2006	15-17	clinical	21	63 different levels of R				36	9		3	15									
	18		1	1 H37Rv ATCC 27294				1				_									
22) Rodrigues 2008	18	clinical	10	10 pan-S				10													
	18	cinical	20	20 different levels of R				16	2		1	1									
23) Gonzalo 2015	19		1	2 H37Rv			1	1													
23) Gonzalo 2015	19	clinical	20	40	gWT	1	20	19													
24) Sturegård 2015	3		1	4 H37Rv ATCC 27294				4													
24) Sturegalu 2015	3	clinical	28	28			8	12	3										1	1	3
25) Heyckendorf	15		1	1 H37Rv ATCC 27294				1													
25) Heyckendon	15	clinical	9	9 MDR or XDR	gWT		2	7				_									
26) Tessema 2017	15	clinical	40	40	gWT			19	20			_	1								
27) Zimenkov 2013	20		1	1 H37Rv ATCC 25618					1												
27) Zimenkov 2015	20	clinical	33	33	gWT		20	10	3												
28) Kambli 2016a &	18		1	1 H37Rv ATCC 27294			1														
2016b	18	clinical	31	31	gWT		25	5				_	1								
29) Matt 2012	21	clinical	10	10 pan-S			5		5			_									
	22		1	³ H37Rv ATCC 27294				3													
30) Lin 2009	23		1	14				14													
	23	clinical	29	29				_	14		3	12									
31) Zheng 2016	11		1	1 H37Rv ATCC 25618				1													
51) Zheng 2010	11	clinical	207	207 MDR				38	29		6		14	30 4	2	12	25	11			
32) Sharma 2011	24	clinical	36	36 different levels of R				22	4		1	9									
33) Cambau 2015	1, 3, 7, 15, 21, 24-2	7 clinical	113	113 MDR					113												
557 Cambau 2015	1, 3, 7, 15, 21, 24-2	7	3	3	gWT			_	1			_	2								
34) Sirgel 2012	28		1	1 H37Rv ATCC 27294					1												
54) Sirger 2012	28	clinical	15	15 MDR, XDR	gWT			_	15			_									
35) Springer 2009	21	clinical	11	11	gWT				11												

The green line denotes the current WHO and CLSI CC for AMK DST by MGIT (1 mg/L). Notable limitations:

Only studies 23, 30-32 and 34 have data from unique laboratories.

Systematic review performed by Claudio Köser







Phenotypic wild type (pWT) moxifloxacin MIC distributions on MGIT media

														·6/ -1						
Studies	Lab	Isolate origin	Unique isolates Tota	I MICs Type of isolates	Genotypic results	0.06	0.12	0.18	0.25	0.5	0.75	1	1.5	2	2.5	3	4	5	7.5	8
23) Isaeva 2013,	17		1	1 H37Rv ATCC 25618			1													
Nosova 2013 &	17	clinical	11	11 different levels of R		1	9		1											
Zimenkov 2013	17	clinical	23	23	gWT	1	18		4											
	18		20	20 H37Rv ATCC 27294 & pan-5	i	5	11		3	1										
24) Piersimoni 2007	18	clinical	10	10		2	5		2			1								
	18		1	1	gWT									1						
an) Kembli anan	19		1	1 H37Rv ATCC 27294		1														
25) Kambli 2015	19	clinical	30	30	gWT	26	2		2											
36) Houskondorf	20		1	1 H37Rv ATCC 27294					1											
26) Heyckendorf	20	clinical	16	16 MDR or XDR	gWT	9	7													
27) Tessema 2017	20	clinical	41	41	gWT	8	32		1											
20) Discuts	2		1	5 H37Rv ATCC 27294			- 4	1												
28) Rigouts	2	clinical	9	9	gWT		9													
20) Classel 2012	9		1	6 H37Rv ATCC 27294			6													
29) Sirgel 2012	9	clinical	125	125 different levels of R	gWT		119		5					1						
30) van Ingen 2010	8		1	1 H37Rv ATCC 27294			1													
50) van ingen 2010	8	clinical	28	28 MDR			20		1			1	6							
31) Krüüner 2006	21		132	132 MDR			97			5		16	14							
24) Ismail	6	clinical	57	57 different levels of R			26		12	2		2		12			2			1
34) Ismail	6	clinical	3	3	gWT		2					1								
22111	22	clinical	73	73	gWT		- 44		22	1	1	1	3	1			_			
33) Lin	22	clinical	218	218	gWT				215			2		1						
24) Combour 2015	3, 8, 20, 23-28	clinical	114	114 MDR					114											
34) Cambau 2015	3, 8, 20, 23-28	clinical	3	3	gWT				3											
35) Sharma 2011	29-32	clinical	36	144 different levels of R					101	6		12	25							
26) Kam 2006	33	clinical	108	108 mostly MDR						108										
36) Kam 2006	33	clinical	4	4 MOSTLY MDR	gWT							2		2						
	19		1	1 H37Rv ATCC 27294								1								
37) Rodrigues 2008	19	- United	10	10 pan-S								10								
	19	clinical	20	20 different levels of R								19		1						
201 41 201 5	34		1	1 H37Rv					1			16 14 2 12 2 1 1 3 1 1 2 1 1 1 1 3 1 1 1 3 1 1 1 3 1 1 1 3 1 1 1 2 1 1 12 25 1 1 10 1 1 1								
38) Alvarez 2014	34	clinical	5	5 MDR or XDR	gWT				1	1		2		1						
															-			_		

The blue line denotes the current CLSI CC for MFX DST by MGIT (0.25 mg/L). The red lines denote the current

WHO CCs for MFX DST by MGIT (0.5 and 2 mg/L).

Systematic review performed by Claudio Köser









Table 1. Medicines recommended for the treatment of rifam	inicin-resistant and multidrug-resistant TR = 0
Tuble 1. Hearthearteconninendea for the creatment of fillen	pient resistance and material agreesistance in

Table 1. Medicines recommended for the	chearenne of the	ampient-resistance and	Intercences-	Caracteric 10 1		1	
Drug groups				LI preportion		7H11	MGIT 960
				99999 19999 19999	u∰ l		
A. Fluoroquinolones (1)	Levofloxacin (CC	C)	Lfx ,	The state of the state	1.0	-	1.0
	Moxifloxacin (C	c) ^m	Mfx1	1.0 ^m	0.5	0.5	0.25
	Moxifloxacin (Cl	B) ⁽⁰⁾	-4	₩	2.0	-	1.0
	Gatifloxacin ¹⁰		GÁX 🦄	0.5	-	-	0.25
B. Second-line injectable agents	Amikacin		Am	¶– <u>30</u>	2.0		1.0
	Capreomycin	€	Ban Ba	40	4.0	-	2.5
	Kanamycin	74	Km a *	30	4.0		2.5
	(Streptomycin)	£		4.0	2.0	2.0	1.0
C. Other second-line agents	Ethionamide	. #~~~	Eto	40	5	10	5
	Prothionamide	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	Pto	40	-		2.5
	Cycloserine / Te	erizidoneti 🐨 👘	Cs / Trd	-	-	-	-
	Linezolid	10 m v	Lzd	-	1.0	1.0	1.0
	Clofazimine	_ <u>`</u>	Cfz	-	-		0.5
D. Add-on agents		Pyrazinamide	Z	-	-		100
(not part of the core MDR-TB regimen)	. 25	Ethambutol	E	2.0	5.0	7.5	5.0
	4 4 4 F	Bedaquiline ⁽⁶⁾	Bdg	-		0.25	1.0
4	I Also	Delamanid ⁽²⁾	Dim	-	-	0.016	0.06
	And A	p-aminosalicylic acid	PAS		-		-
ل یک میں	r_~ ⊨	Imipenem-cilastatin	Ipm	-	-		-
- 490 Ta		Meropenem	Mpm	-	-	-	-
4. all 40. 40.	1	Amoxicillin-	Amx-Clv				
- 4° 4° 4°		clavulanate	(T)				
199 Mg		Thioacetazone)					
ъ.			-			-	· –

CC Critical concentration; CB Clinical breakpoint

Molecular methods for the diagnosis of DR-TB

Molecular (genotypic) methods detect specific DNA mutations in the genome of the *M. tuberculosis*, which are associated with resistance to specific anti-TB drugs.

Molecular methods have considerable advantages for programmatic management of drug-resistant TB, in particular with regard to their speed, the standardization of testing, their potentially high throughput and the reduced requirements for laboratory biosafety.

Molecular tests for detecting drug resistance to rifampicin alone or in combination with isoniazid have been recommended for use by WHO since 2008







Molecular methods for the diagnosis of DR-TB - limitations

There remains imperfect correlation between phenotypic and genotypic methods.

Molecular methods had high specificity but lower sensitivity which varies for different drugs

- Rifampicin *rpo*B 95% sensitivity, 99% specificity
- Isoniazid *inh*A and *kat*G ~90% sensitivity, 99% specificity
- Fluoroquinolones gyr A and gyrB ~86% sensitivity, 99% specificity
- Secondline injectable agents --rrs and eis ~86% sensitivity, 99% specificity

The predictive values of imperfect tests depend on the pre-test probability of resistance







The ReSeqTB Solution: A Standardized System for Grading Mutations

Observed frequency of a mutation found in phenotypically resistant and susceptible strains

- Literature data were used to calculate the frequency of each mutation
- Likelihood ratio (LR) and odd ratio (OR) were used; p-values and 95% confidence intervals associated with LR and OR have been also considered
- Thresholds used most commonly in evidence-based medicine have been adapted to grade *M. tuberculosis* mutations:

LR	+ V OR	Interpretation	Symbol
<i>p-</i> adj	value	inter pretation	Symbol
		High Confidence for association with resistance - strong association of the mutation with	
<0.05	> 10	phenotypic drug resistanc; sufficient evidence that the mutation confers or is strongly	
		associated with drug resistance	
		Moderate Confidence for association with resistance – moderate association of the mutation	
<0.05	$5 < \le 10$	with phenotypic drug resistanc; additional data desirable for improved evidence that the	
		mutation confers or is strongly associated with drug resistance	
		Low Confidence for association with resistance – weak association of the mutation with	
<0.05	$1 < \le 5$	phenotypic drug resistanc; inconclusive evidence that the mutation confers or is strongly	
		associated with drug resistance. Substantial additional data required	
<0.05	<1	No association with resistance – No evidence of association between the mutation and drug	
<0.05	< 1	resistance	
≥0.05	-	Indeterminate – no statistically significant threshold reache; additional data required	Indeter

Slide courtesy of Paolo Miotto







NWT MFX MIC distributions of gyrA clinical mutants by MGIT

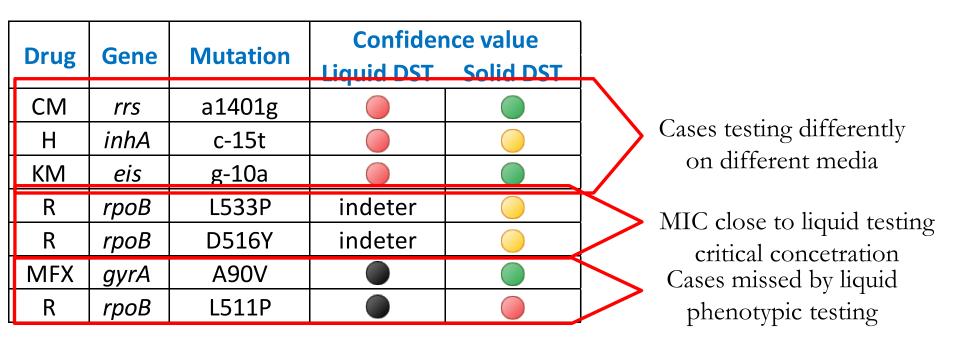
										IVIFX	IVIIC (mg/L)	8					
Studies	Medium	Total MICs	Genotypic results	0.12	0.18	0.25	0.5	0.75	1	1.5	2	2.5	3	4	5	7.5	8	10
23) Isaeva 2013,		F	gyrA D94A				2		3		1							
25) Kambli 2015			gyrA D94A				2		1		-	3						
28) Rigouts			gyrA D94A			3	5		3									
29) Sirgel 2012			gyrA D94A						4		3							
34) Ismail			gyrA D94A				1											
33) Lin			gyrA D94A				1	3	1	1								
33) Lin	MGIT	3	gyrA D94A				1		2									
34) Cambau 2015		2	gyrA D94A									2						
36) Kam 2006		5	gyrA D94A				1		4									
33) Lin		1	gyrA D94F						1									
23) Isae		13	gyrA D94G								13							
24) Pier DC	94G	2	gyrA D94G								2							
25) Kam			gyrA D94G						9			32					1	
28) Rigc muta	ations		gyrA D94G				1		9	10								
JUL CIPAL			murA DO/IC	_	_	_		_	5		1/	-			_		_	
34) Ismail			gyrA D94G								1			1				
33) Lin			gyrA D94G						2	5	4		2	2				
33) Lin			gyrA D94G						1		13		1	1				
34) Cambau 2015			gyrA D94G									6				1		
36) Kam 2006			gyrA D94G						2		11			1				
38) Alvarez 2014			gyrA D94G						2		2					_		
34) Cambau 2015			gyrA <u>G88C</u> , D94G									1						
34) Cambau 2015			gyrA A90V, D94G	-					1		4						1	
29) Sirgel 2012			gyrA A90V, D94G	-	_	_			1	_	1	_		-	-		-	
23) Isaeva 2013,			gyrA S91P , <u>D94N</u> gyrA D94H								1							
23) Isaeva 2013, 25) Kambli 2015			gyrA D94H						1		T	2						
28) Rigouts			gyrA D94H						Т		1	2						
33) Lin			gyrA D94H					-		2	2							
34) Cambau 2015			gyrA D94H							L	2	1						
36) Kam 2006			gyrA D94H								1	+						
23) Isaeva 2013,			gyrA D94N								-			1				
28) Rigouts			gyrA D94N									1		+				
29) Sirgel 2012			gyrA D94N				1				4	-		1				
34) Ismail			gyrA D94N						1		1							
33) Lin			gyrA D94N							-				1				
33) Lin			gyrA D94N								2		2	2				
34) Cambau 2015			gyrA D94N									1						
29) Sirgel 2012			gyrA D94G , D94N								2							
23) Isaeva 2013,			gyrA D94Y			C.	10±-		_ 1			-	f					مانحا
28) Rigouts			gyrA D94Y			2	yste	ema	TIC	rev	iew	pe	ITO	rme	sa r	by C	lau	dio I
34) Ismail			gyrA D94Y								1			1		-		







Addressing current knowledge gaps



Slide courtesy of Paolo Miotto







Addressing current knowledge gaps

- Correlation of phenotypic DST critical concentrations with molecular methods – revised critical concentrations are under review
- Incomplete cross resistance within the classes of key drugs such as the FQs – mechanisms better understood
- 3. Technical guide on the use of DNA sequencing as a surveillance tool and the potential use and limitations as a diagnostic tool under development to determine mutations associated with elevated MICs for certain drugs
- PK/PD data challenging our dogma around suitable dosing for key drugs especially for moxifloxacin, rifampicin and pyrazinamide



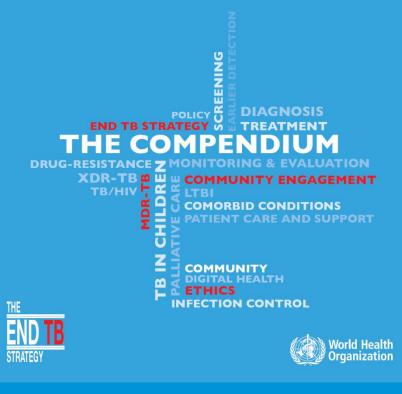






Compendium of WHO guidelines and associated standards:

ensuring optimum delivery of the cascade of care for patients with tuberculosis



THANK YOU

gilpinc@who.int



