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1 Effect of study design and setting on tuberculosis clustering estimates using
2 Mycobacterial Interspersed Repetitive Units-Variable Number Tandem
3 Repeats (MIRU-VNTR)

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Abstract

Objectives: To systematically review the evidence for the impact of study design and setting on the interpretation of TB transmission using clustering derived from Mycobacterial Interspersed Repetitive Units – Variable Number Tandem Repeats (MIRU-VNTR) strain typing.

Data sources: Medline, Embase, CINHAL, Web of Science and Scopus were searched for articles published before November 2012

Review methods: Studies in humans that reported the proportion of clustering of TB isolates by MIRU-VNTR were included in the analysis. Univariable meta-regression analyses were conducted to assess the influence of study design and setting on the proportion of clustering.

Results: The search identified 14 eligible articles reporting clustering between 22.1% and 61.2%. The proportion of culture positive isolates and the number of MIRU-VNTR loci typed explained 49% and 34% of the between study variation, respectively, and had a significant association with the proportion of clustering.

Conclusions: Although MIRU-VNTR typing is being adopted worldwide there is a paucity of data on how study design and setting may influence estimates of clustering. We have highlighted study design variables for consideration in the design and interpretation of future studies.

Strengths and Limitations of Study

- This is a timely evaluation of the impact of study design on estimates of TB clustering using MIRU-VNTR strain typing because it has been incorporated into national typing services globally.
- There were insufficient data available to fully explore the impact of study design and setting on estimates of clustering.

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43 **Introduction**

44 The introduction of molecular typing methods has improved our understanding of *Mycobacterium*
45 *tuberculosis* (TB) transmission and has changed local and national control policies [1–5]. The
46 proportion of cases that are clustered is often used to estimate the amount of ongoing transmission
47 within the population, based on the assumption that cases with indistinguishable strain types are
48 part of a chain of transmission. TB molecular typing methodology is changing rapidly and it is
49 important that we better understand how to interpret the outputs and thus act.

50 TB molecular typing methods include Spoligotyping [6], insertion sequence 6110 (IS6110) restriction
51 fragment length polymorphism (RFLP) analysis (the recent gold standard) [7], mycobacterial
52 interspersed repetitive units-variable number tandem repeats (MIRU-VNTR) typing [8], and whole
53 genome sequencing [9–11]. Published reviews have identified factors that might influence or bias
54 clustering by IS6110 RFLP [12,13]. No study has repeated this analysis using more up-to-date typing
55 methods, which is important for understanding of the epidemiology of TB and to shape the
56 application of molecular typing to improve TB control.

57 Published meta-analyses and modelling studies using IS6110 RFLP data show that the proportion of
58 clustering observed can be affected by 1) study design (affecting the proportion of eligible cases that
59 are included in the study); 2) features of the typing method (such as the ability to type isolates with
60 low copy numbers); and 3) study setting (such as characteristics of the study population). For
61 example, the proportion of clustering increases when the fraction of the total data sampled
62 increases [13–15] and when study duration increases [16].

63 MIRU-VNTR is currently the preferred method of molecular typing [17–21], and can be used
64 together with Spoligotyping [8]. Relative to IS6110 RFLP, MIRU-VNTR does not have to exclude
65 isolates with a low IS6110 copy number, has a faster turnaround time, is high throughput and the
66 numeric strain types are more easily compared. MIRU-VNTR strain typing is increasingly being
67 adopted worldwide [1,22–27], yet unlike IS6110 RFLP, the evidence for the interpretation of the
68 findings such as the impact of study design and setting on clustering have not been reviewed.

69 Although the two typing methods have been shown to have a similar discriminatory value, the
70 markers evolve independently and at different rates, resulting in a difference in clustering between
71 the two methods [28]. This suggests that there could be differences in the way study design, typing
72 method and setting affects clustering by the two methods. We conducted a systematic review to
73 assess the evidence for the impact of study design and setting on the interpretation of TB

transmission using clustering derived from MIRU-VNTR strain typing – as has been shown using IS6110 RFLP typing.

Methods

Five electronic databases were searched (EMBASE, ISI Web of Science, CINHALL, Scopus and Medline (Ovid)) up to 1 November 2012. The search strategy combined the following terms with Boolean operators: Tuberculosis, strain typing, and transmission. The search was limited to studies using the standard MIRU-VNTR method [8], in humans only, and in English.

All titles and abstracts from each of the searches were examined. The full text of each paper was obtained and reviewed if the study reported MIRU-VNTR strain typing of *M.tuberculosis* complex isolates with at least 15 of the standardised 24 loci [8,29,30].

Studies using fewer than 15 loci were not included because the level of discrimination is inadequate for epidemiological use (n=97) [8]. Studies that used loci different to the standardised 15 and 24 set were not included in the analysis in order to reduce the heterogeneity between studies (n=11). All publication types were included in this first screen to ensure that no relevant data were missed.

Reviews, letters, editorials, outbreaks or case reports (n=99) were excluded in the second screen. Studies that used incomplete sampling (e.g. random samples, studies using subsets of populations such as MDR patients) (n=30) and studies that had a sample size of less than 50 (n=2) were also excluded.

A reviewer extracted the following data items from all included studies using a form developed in Excel (Microsoft 2010): publication details (year, authors, study country), study details (study duration, loci typed, secondary typing method, study population), the proportion of total TB isolates clustered by MIRU-VNTR strain typing, and the covariates of interest: the number of clustered and unique isolates; the maximum size of clusters; the proportion of clusters containing two cases; the prevalence of culture-positivity among TB patients included in the study; the proportion of culture positive isolates typed; risk factors for clustering; and the Hunter Gaston Discriminatory Index (HGDI) [31]).

Authors were contacted if TB incidence rate was not reported. Where no response was received WHO country estimates of TB incidence for the study year were used [32].

Data were analysed in Stata 12. Where studies reported data from more than one set of loci, the method with the highest discriminatory value was included (i.e. MIRU-VNTR 24 would be chosen

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104 over MIRU-VNTR 15, and MIRU-VNTR 15 plus Spoligotyping would be chosen over MIRU-VNTR 15
105 alone) (n=5). This review was not concerned with summary measures of clustering, but factors that
106 influenced clustering; therefore articles must have included at least one of the covariates.
107 Continuous variables were transformed where the distribution was skewed. The proportion
108 clustered was transformed using the Freeman Tukey transformation [33]. Univariable meta-
109 regression analyses were carried out to determine the effect of the study design covariates on the
110 proportion of clustered isolates. All covariates in the analysis were hypothesised to influence the
111 proportion clustered *a priori*.

112 **Results**

113 The search identified 5607 references resulting in 12 journal articles and 2 conference abstracts
114 included after deduplication and title/abstract/full text screening (Figure 1). The main characteristics
115 of the included studies are shown in Table 1. Studies were published between 2007 and 2011 and
116 the clustering reported varied from 22.1% [34] to 61.2% [35].

117 The univariable meta-regression shows evidence for the proportion of clustering to decrease as the
118 prevalence of culture-positivity among TB patients included in the study increases (p=0.03; Table 2),
119 accounting for 49% of the between study variation. There was also evidence for the proportion of
120 clustering to decrease as the number of MIRU-VNTR loci typed increased from 15 to 24 (p=0.02),
121 explaining 34% of the between study variation. There was no evidence of the other study design or
122 study setting variables significantly influencing the proportion clustered. Though non-significant
123 (p>0.05), the size of the study and the maximum cluster size explained 15% and 27% of the between
124 study variation, respectively.

125 **Discussion**

126 This review identified 14 studies that met the inclusion criteria. We illustrate that the interpretation
127 of studies using MIRU-VNTR to estimate clustering is subject to bias relating to study design;
128 however, there were insufficient data available to fully explore the impact of study design and
129 setting on estimates of clustering.

130 As expected, we found that the proportion of clustering decreased with a greater number of MIRU-
131 VNTR loci typed. Our finding that the prevalence of culture-positivity among TB patients included in
132 the study influences the estimates of transmission within a population is counterintuitive and not
133 consistent with estimates of the influence of sampling on the proportion of clustering using IS6110
134 RFLP typing [36]. This may reflect the relationship between TB burden and resource poor/rich

135 settings and the consequent availability of culture diagnostic laboratory services; i.e. in resource
136 poor settings where there is a high burden of TB (and, therefore, high rates of clustering) the
137 prevalence of culture positive TB cases is low. The finding may also be due to chance, with only 8
138 studies included in the analysis of this variable.

139 The other study design variables included in this analysis, such as study duration, did not significantly
140 influence the proportion of isolates that were clustered, contrary to previous findings [12]. This is
141 likely to be because of a lack of good quality evidence: only 14 studies met the inclusion criteria for
142 the review and of those only three reported all the variables of interest, reducing the power of the
143 analysis and precluding multivariable meta-regression. In addition, the range of the variables may
144 have been too limited to show any impact on clustering estimates. For example, the proportion of
145 culture positive isolates typed had a narrow range from 81.9% to 100%. Furthermore, most of the
146 studies were from low TB burden settings and therefore may be reflecting the rate at which
147 imported cases have matching strain types by chance, rather than rates of recent transmission.

148 This study is a timely evaluation of the impact of study design on estimates of TB clustering using
149 MIRU-VNTR strain typing because it has been incorporated into national typing services globally
150 [23,37]. The findings are relevant where strain typing is used to evaluate TB control systems across
151 different settings because the proportion of clustering is influenced by the prevalence of culture
152 positive TB cases in the study setting. Given that strain typing methods are advancing beyond MIRU-
153 VNTR typing and that the application of whole genome sequencing to TB control and public health
154 strategies has been demonstrated [9–11,38], it is important that the biases in the analysis of such
155 methods are explored and compared. Understanding how to design and compare research studies
156 for public health will greatly improve the benefit gained from newer technologies.

157 This review has highlighted the need for better quality reporting in primary studies to enable future
158 reviews to be more robust. A lack of standards for the molecular epidemiology of infectious diseases
159 may explain the poor quality of reporting; this field would benefit from the introduction of such
160 standards (STROBE-ID, submitted).

161 The use of TB strain typing as a public health tool in TB control programmes is increasing globally.
162 We have identified a lack of good quality studies that can contribute to our understanding in
163 interpreting the molecular typing of TB. We have also shown that the proportion of clustering
164 derived from MIRU-VNTR typing is influenced by the number of loci typed and the prevalence of
165 culture-positivity among TB patients included in the study, highlighting these as important
166 considerations in the design and interpretation of future studies.

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167 **Conflict of interest**

168 Nothing to declare.

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172 **Author contributions**

173 All authors made substantial contributions to the conception and design of the review, and the
174 analysis and interpretation of data. JM drafted the article and PS, IA, TM and TC revised it critically
175 for important intellectual content. All authors approved the final version for publication.

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179 **Ethics**

180 Ethical approval was not required as this review analyses data that is in the public domain.

181 **Data sharing**

182 No additional data are available

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Tables

Table 1: Studies included in the analysis

Reference	Author	Country	Study site ^a	Method ^b	Loci ^c	Study duration (months)	Clustered + unique isolates	TB incidence (per 100,000)	TB/HIV co-infection ^d	Prevalence of culture positivity	% culture positive typed	No. clusters	Max cluster size	HGDI	Proportion clustering	Recent transmission (%)
[39]	Asgharzadeh, M	Azerbaijan	r	15	o	12	156	26.0		94.6	98.7	22	5	0.9966	32.7	18.6
[40]	Allix-Beguec, C	Belgium	r	24	n	24	530	35.2	5.1	86.1	87.9	53	23		29.6	19.6
[41]	Allix-Beguec, C	Belgium	r	24,S	n	39	802	35.2	5.1	81.8	84.7	82			28.8	19.6
[34]	Oelemann, M	Germany	ci	24,S	n	12	154	12.7			100	11			22.1	14.9
[42]	Roetzer, A	Germany	r	24,S	n	48	277	3.2	0.09		100	18	22		27.1	20.6
[43]	Ojo, OO	Ireland	r	24,S	n	36	171	15.3	3.3	79.5	96.1	15	12	0.9996	27.5	18.7
[44]	Dymova, MA	Russia	r	15	o	3	98	94.0	3.8		100	8		0.9900	31.6	23.5
[45]	Bidovec-Stojkovic, U	Slovenia	co	24,S	n	12	196	10.6	0.04		100	29	6	0.9965	36.2	21.4
[46]	Alonso-Rodriguez, N	Spain	r	15	n	27	281	26.0	6		81.9		8		43.1	24.4
[35]	Evans, J	UK	r	15	o	48	4207	15.0	8.2	58.3	100	439			61.2	50.8
[47]	Hamblion, E	UK	r	24	n	9	964	44.9	8.2		100				37.0	
[48]	Mandal, S	UK	co	15	o	48	102		8.2	90.7	87.2	8	12		30.4	22.6
[49]	Sails, A	UK	r	15	o	102	332	18.3	8.2	33.9	100	42	13		42.8	30.1
[50]	Nikolayevsky, V	Ukraine	r	15	o	4	225	80.4	3.9	39.2	97.4	31		0.9700	60.4	46.7

^a ci=city, r=region, co=country^b 15=15 MIRU-VNTR loci, 24=24 MIRU-VNTR loci, S=with Spoligotyping

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^co= old 12 MIRU loci (MIRU 2, 4, 10, 16, 20, 23, 24, 26, 27,30, 31, 39, 40), n=new 12 MIRU loci (MIRU 10, 16, 26, 31, 40 + Mtub 04, 21, 39 + ETR A C + QUB 11b, 26)

^d estimates from the literature of the prevalence of TB/HIV co-infection reported in the study area

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Table 2: Univariable meta-regression showing the coefficients for change in the proportion of clustering and the percentage of between-study variation explained by variables describing the study design and setting.

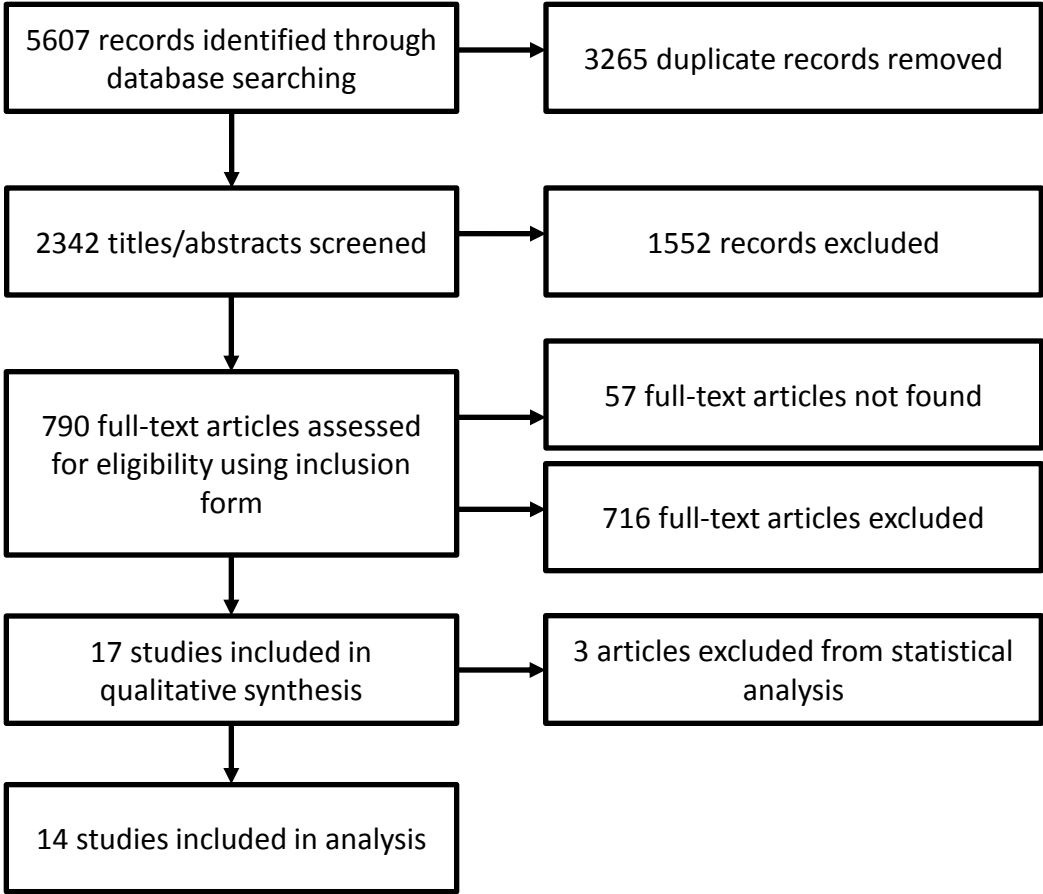
	n	Coefficient ^π	CI	p	Adj R ² [‡]
<u>Study design</u>					
Study duration (months)	14	0.003	-0.063, 0.069	0.919	-8.47
Prevalence of culture positivity	8	-0.913	-1.732, -0.094	0.034	49.36
% culture positive typed	14	0.161	-0.731, 1.053	0.701	-6.99
Study size	14	-4.462	-10.000, 1.076	0.105	14.89
Number of loci (ref 15 loci)					
24 loci	14	-0.282	-0.519, -0.045	0.023	34.1
<u>Study setting</u>					
TB incidence	13	0.082	-0.097, 0.22	0.334	0.04
TB/HIV co-infection	12	0.088	-0.087, 0.263	0.288	3.28
Maximum cluster size	9	0.137	-0.035, 0.309	0.101	26.91
% clusters with 2 cases	7	0.004	-0.007, 0.016	0.396	-2.39

^π Coefficients for the change in the proportion of clustering for each covariate. E.g. for a one-month increase in study duration, the proportion of clustering increases by 0.003.

[‡] The proportion of between-study variation explained by the univariate meta-regression.

Figure Caption

Figure 1: Results of systematic search, screening and data extraction.



Appendix: Medline/Embase search strategy

1. (tubercle adj3 (bacillus or bacilli)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
2. ((mycobacterium or mycobacteria) adj3 (bovis or africanum or microti or canetti)).mp.
3. exp tuberculosis/ or mycobacterium tuberculosis/ or tuberculosis.mp. or tb.mp. or Mtb.mp. or "M tuberculosis complex".mp.
4. or/1-3
5. Minisatellite Repeats/ or Genotype/ or Interspersed Repetitive Sequences/ or DNA Fingerprinting/ or Bacterial Typing Techniques/
6. "miru".mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
7. "vntr".mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
8. (miru adj3 vntr).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
9. (mycobacterial adj3 interspersed adj3 repetitive adj3 units).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
10. (dna adj3 fingerprinting).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
11. ((strain adj3 type) or (strain adj3 typing) or (strain adj3 types)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
12. ((molecular adj3 typing) or (molecular adj3 strain adj3 typ*)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
13. (genotype or genotyping or genotypes).ti,ab.
14. (minisatellite adj3 repeat*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
15. molecular epidemiology/mt or (molecular adj3 epidemiology).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
16. or/5-15
17. exp disease outbreaks/ or (outbreak adj3 analysis).mp. or (outbreak adj3 investigation).mp. or (outbreak adj3 management).mp. or (tuberculosis adj3 outbreak).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
18. exp contact tracing/ or (contact adj3 tracing).mp. or (contact* adj3 traced).mp. or (contact adj3 screen*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
19. exp case management/ or (case adj3 management).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
20. exp Risk Factors/
21. (risk adj3 factor*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
22. exp Epidemiologic Factors/
23. infectious disease transmission.mp. or exp Disease Transmission, Infectious/
24. exp case management/ or (case adj3 management).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
25. program evaluation/ or evaluation studies as topic/ or (program adj3 evaluation).mp. or (programme adj3 evaluation).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
26. public health practice/ or (public adj3 health).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
27. ((tuberculosis adj3 control) or (tb adj3 control)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
28. (molecular adj3 surveillance).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
29. exp cluster analysis/ or (cluster* adj3 rate*).mp. or (cluster* adj3 growth).mp. or (cluster* adj3 analysis).mp. or (cluster adj3 investigation).mp. or (proportion adj3 cluster*).mp. or (molecular adj3 cluster*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
30. ((recent adj3 transmission) or (transmission adj3 event*) or (transmission adj3 rate*) or (chain adj3 transmission) or (transmission adj3 setting*)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
31. or/17-30

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PRISMA 2009 Checklist

Section/topic	#	Checklist item	Reported on page #
TITLE			
Title	1	Identify the report as a systematic review, meta-analysis, or both.	1
ABSTRACT			
Structured summary	2	Provide a structured summary including, as applicable: background; objectives; data sources; study eligibility criteria, participants, and interventions; study appraisal and synthesis methods; results; limitations; conclusions and implications of key findings; systematic review registration number.	2
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of what is already known.	3
Objectives	4	Provide an explicit statement of questions being addressed with reference to participants, interventions, comparisons, outcomes, and study design (PICOS).	3
METHODS			
Protocol and registration	5	Indicate if a review protocol exists, if and where it can be accessed (e.g., Web address), and, if available, provide registration information including registration number.	n/a
Eligibility criteria	6	Specify study characteristics (e.g., PICOS, length of follow-up) and report characteristics (e.g., years considered, language, publication status) used as criteria for eligibility, giving rationale.	4
Information sources	7	Describe all information sources (e.g., databases with dates of coverage, contact with study authors to identify additional studies) in the search and date last searched.	4
Search	8	Present full electronic search strategy for at least one database, including any limits used, such that it could be repeated.	14
Study selection	9	State the process for selecting studies (i.e., screening, eligibility, included in systematic review, and, if applicable, included in the meta-analysis).	4
Data collection process	10	Describe method of data extraction from reports (e.g., piloted forms, independently, in duplicate) and any processes for obtaining and confirming data from investigators.	4
Data items	11	List and define all variables for which data were sought (e.g., PICOS, funding sources) and any assumptions and simplifications made.	5
Risk of bias in individual studies	12	Describe methods used for assessing risk of bias of individual studies (including specification of whether this was done at the study or outcome level), and how this information is to be used in any data synthesis.	4
Summary measures	13	State the principal summary measures (e.g., risk ratio, difference in means).	5
Synthesis of results	14	Describe the methods of handling data and combining results of studies, if done, including measures of consistency (e.g., I^2) for each meta-analysis.	5

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PRISMA 2009 Checklist

Section/topic	#	Checklist item	Reported on page #
Risk of bias across studies	15	Specify any assessment of risk of bias that may affect the cumulative evidence (e.g., publication bias, selective reporting within studies).	4
Additional analyses	16	Describe methods of additional analyses (e.g., sensitivity or subgroup analyses, meta-regression), if done, indicating which were pre-specified.	5
RESULTS			
Study selection	17	Give numbers of studies screened, assessed for eligibility, and included in the review, with reasons for exclusions at each stage, ideally with a flow diagram.	5
Study characteristics	18	For each study, present characteristics for which data were extracted (e.g., study size, PICOS, follow-up period) and provide the citations.	12
Risk of bias within studies	19	Present data on risk of bias of each study and, if available, any outcome level assessment (see item 12).	12
Results of individual studies	20	For all outcomes considered (benefits or harms), present, for each study: (a) simple summary data for each intervention group (b) effect estimates and confidence intervals, ideally with a forest plot.	12
Synthesis of results	21	Present results of each meta-analysis done, including confidence intervals and measures of consistency.	14
Risk of bias across studies	22	Present results of any assessment of risk of bias across studies (see Item 15).	12
Additional analysis	23	Give results of additional analyses, if done (e.g., sensitivity or subgroup analyses, meta-regression [see Item 16]).	14
DISCUSSION			
Summary of evidence	24	Summarize the main findings including the strength of evidence for each main outcome; consider their relevance to key groups (e.g., healthcare providers, users, and policy makers).	5
Limitations	25	Discuss limitations at study and outcome level (e.g., risk of bias), and at review-level (e.g., incomplete retrieval of identified research, reporting bias).	6
Conclusions	26	Provide a general interpretation of the results in the context of other evidence, and implications for future research.	6
FUNDING			
Funding	27	Describe sources of funding for the systematic review and other support (e.g., supply of data); role of funders for the systematic review.	7

From: Moher D, Liberati A, Tetzlaff J, Altman DG, The PRISMA Group (2009). Preferred Reporting Items for Systematic Reviews and Meta-Analyses: The PRISMA Statement. PLoS Med 6(6): e1000097. doi:10.1371/journal.pmed1000097

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BMJ Open

Effect of study design and setting on tuberculosis clustering estimates using Mycobacterial Interspersed Repetitive Units-Variable Number Tandem Repeats (MIRU-VNTR): A systematic review

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Keywords:	EPIDEMIOLOGY, Tuberculosis < INFECTIOUS DISEASES, MOLECULAR BIOLOGY

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1 Effect of study design and setting on tuberculosis clustering estimates using
2 Mycobacterial Interspersed Repetitive Units-Variable Number Tandem
3 Repeats (MIRU-VNTR): A systematic review

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18 **Word count: 2439**

Abstract

Objectives: To systematically review the evidence for the impact of study design and setting on the interpretation of TB transmission using clustering derived from Mycobacterial Interspersed Repetitive Units – Variable Number Tandem Repeats (MIRU-VNTR) strain typing.

Data sources: Medline, Embase, CINHAI, Web of Science and Scopus were searched for articles published before 21st October 2014.

Review methods: Studies in humans that reported the proportion of clustering of TB isolates by MIRU-VNTR were included in the analysis. Univariable meta-regression analyses were conducted to assess the influence of study design and setting on the proportion of clustering.

Results: The search identified 27 eligible articles reporting clustering between 0% and 63%. The number of MIRU-VNTR loci typed, requiring consent to type patient isolates (as a proxy for sampling fraction), the TB incidence and the maximum cluster size explained 14%, 14%, 27% and 48%, respectively, and had a significant association with the proportion of clustering .

Conclusions: Although MIRU-VNTR typing is being adopted worldwide there is a paucity of data on how study design and setting may influence estimates of clustering. We have highlighted study design variables for consideration in the design and interpretation of future studies.

Strengths and Limitations of Study

- This is a timely evaluation of the impact of study design on estimates of TB clustering using MIRU-VNTR strain typing because it has been incorporated into national typing services globally.
- The strength of this meta-analysis was limited by the lack of detail reported by the included studies, highlighting the need for better quality reporting in primary studies.

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44 **Introduction**

45 The introduction of molecular typing methods has improved our understanding of *Mycobacterium*
46 *tuberculosis* (TB) transmission and has changed local and national control policies [1–5]. The
47 proportion of cases that are clustered is often used to estimate the amount of ongoing transmission
48 within the population, based on the assumption that cases with indistinguishable strain types are
49 part of a chain of transmission. TB molecular typing methodology is changing rapidly and it is
50 important that we better understand how to interpret the outputs and thus act.

51 TB molecular typing methods include Spoligotyping [6], insertion sequence 6110 (IS6110) restriction
52 fragment length polymorphism (RFLP) analysis (the recent gold standard) [7], mycobacterial
53 interspersed repetitive units-variable number tandem repeats (MIRU-VNTR) typing [8], and whole
54 genome sequencing [9–11]. Published reviews have identified factors that might influence or bias
55 clustering by IS6110 RFLP [12,13]. No study has repeated this analysis using more up-to-date typing
56 methods, which is important for understanding of the epidemiology of TB and to shape the
57 application of molecular typing to improve TB control.

58 Published meta-analyses and modelling studies using IS6110 RFLP data show that the proportion of
59 clustering observed can be affected by 1) study design (affecting the proportion of eligible cases that
60 are included in the study); 2) features of the typing method (such as the ability to type isolates with
61 low copy numbers); and 3) study setting (such as characteristics of the study population). For
62 example, the proportion of clustering increases when the fraction of the total data sampled
63 increases [13–15] and when study duration increases [16].

64 MIRU-VNTR is currently the preferred method of molecular typing [17–21], and can be used
65 together with Spoligotyping [8]. Relative to IS6110 RFLP, MIRU-VNTR does not have to exclude
66 isolates with a low IS6110 copy number, has a faster turnaround time, is high throughput and the
67 numeric strain types are more easily compared. MIRU-VNTR strain typing is increasingly being
68 adopted worldwide [1,22–27], yet unlike IS6110 RFLP, the evidence for the interpretation of the
69 findings such as the impact of study design and setting on clustering have not been reviewed.
70 Although the two typing methods have been shown to have a similar discriminatory value, the
71 markers evolve independently and at different rates, resulting in a difference in clustering between
72 the two methods [28]. This suggests that there could be differences in the way study design, typing
73 method and setting affects clustering by the two methods. We conducted a systematic review to
74 assess the evidence for the impact of study design and setting on the interpretation of TB

transmission using clustering derived from MIRU-VNTR strain typing – as has been shown using IS6110 RFLP typing.

Methods

Five electronic databases were searched (EMBASE, ISI Web of Science, CINHALL, Scopus and Medline (Ovid)) up to 20th October 2014. The search strategy combined the following terms with Boolean operators: Tuberculosis, strain typing, and transmission. The search was limited to studies using the standard MIRU-VNTR method [8], in humans only, and in English.

All titles and abstracts from each of the searches were examined. The full text of each paper was obtained and reviewed if the study reported MIRU-VNTR strain typing of *M.tuberculosis* complex isolates with at least 15 of the standardised 24 loci (ETR A, B, C, D, E; MIRU 2, 10, 16, 20, 23, 24, 26, 27, 39, 40; VNTR 424, 1955, 2163b, 2347, 2401, 3171, 3690, 4052, 4156) [8,29,30].

Studies using fewer than 15 loci were not included because the level of discrimination is inadequate for epidemiological use (n=121) [8]. Studies that used loci different to the standardised 15 and 24 set were not included in the analysis in order to reduce the heterogeneity between studies (n=19). All publication types were included in this first screen to ensure that no relevant data were missed.

Reviews, letters, editorials, outbreaks or case reports (n=103) were excluded in the second screen. Studies that used incomplete sampling (e.g. random samples, studies using subsets of populations such as multidrug-resistant patients) (n=47) and studies that had a sample size of less than 50 (n=4) were also excluded.

A reviewer (JM) extracted the following data items from all included studies using a form developed in Excel (Microsoft 2010): publication details (year, authors, study country), study details (study duration, loci typed, secondary typing method, study population, whether participant consent was required (a characteristic of the study design that was used as proxy for sampling fraction, assuming that where consent was required the sampling fraction was low)), the number of clustered and unique isolates, and the covariates of interest: the maximum size of clusters; the proportion of clusters containing two cases; the proportion of the population that was culture positive; the proportion of culture positive isolates typed; risk factors for clustering; and the Hunter Gaston Discriminatory Index (HGDI) [31]. IA extracted data from 10% of the papers for external validity, disagreements were discussed and a consensus agreed upon.

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104 The main outcome measure – the proportion of TB isolates clustered by MIRU-VNTR strain typing –
105 was calculated as the number of clustered isolates/number of clustered+unique isolates. Where
106 there were uncertainties JM consulted with IA

107 Authors were contacted if TB incidence rate was not reported. Where no response was received
108 WHO country estimates of TB incidence for the study year were used [32]. As so few studies
109 reported the proportion coinfecting with TB/HIV, these estimates for the study country were taken
110 from an EU-wide survey and WHO country profiles.[33,34] Due to poor recording of the sampling
111 fraction (the number of isolates typed/ the total number of culture positive TB cases diagnosed
112 during the study period (n=19)), whether the study required the consent of participants (yes/no) was
113 included as a proxy for (high/low) sampling fraction. The risk of bias within each study was assessed
114 using the STROME-ID checklist. [35]

115 Data were analysed in Stata 12. Where studies reported data from more than one set of loci, the
116 method with the highest discriminatory value was included (i.e. MIRU-VNTR 24 would be chosen
117 over MIRU-VNTR 15, and MIRU-VNTR 15 plus Spoligotyping would be chosen over MIRU-VNTR 15
118 alone) (n=8). This review was not concerned with summary measures of clustering, but factors that
119 influenced clustering; therefore articles must have included at least one of the covariates.
120 Continuous variables were transformed where the distribution was skewed. The proportion
121 clustered was transformed using the Freeman Tukey transformation [36]. Study heterogeneity was
122 assessed using a forest plot and the chi² test of heterogeneity. Univariable meta-regression analyses
123 were carried out to determine the effect of the study design covariates on the proportion of
124 clustered isolates. All covariates in the analysis were hypothesised to influence the proportion
125 clustered *a priori*.

126 Sensitivity analyses were conducted to see the effect of removing studies reporting 0% clustering,
127 with only extra-pulmonary TB cases, only *M.bovis* cases, studies using the ‘old 12’ MIRU loci as part
128 of their 15 loci, and studies assessed as having a high likelihood of bias (STROME-ID score less than
129 20).

130 **Results**

131 The search identified 7274 references resulting in 27 studies (25 journal articles and 2 conference
132 abstracts) included after deduplication and title/abstract/full text screening (Figure 1). The main
133 characteristics of the included studies are shown in Table 1. Studies were published between 2007
134 and 2014 and the clustering reported varied from 0% [37] to 62.8% [38]. In all studies, clustered

isolates were defined as having identical strain types based on the MIRU-VNTR loci typed, with or without Spoligotyping. 17 studies included isolates from newly diagnosed TB cases, three studies reported including isolates from new and chronic cases of TB, and seven did not report this information. In addition, ten studies did not include repeat isolates from the same patient, one study included a repeat isolate from one patient, and the remaining 17 did not report whether repeat isolates were included or not. Furthermore, four studies included isolates with missing loci in the cluster analysis, whereas four excluded isolates with missing loci, and the remaining 20 did not report how they dealt with missing loci. The number of studies reporting each variable of interest is shown in Table 2.

A forest plot shows the spread of clustering reported by number of loci and additional typing method (Figure 2). Significant heterogeneity was identified between the studies ($p < 0.001$), suggesting that a meta-regression would be an appropriate analysis.

The univariable meta-regression shows evidence for the proportion of clustering to decrease as the number of MIRU-VNTR loci typed increased from 15 to 24 ($p = 0.04$; Table 3), accounting for 14% of the between study variation, and to increase when the study participants consented to being included in the study ($p = 0.03$), accounting for 14% of the between study variation. The proportion of clustering increased as the TB incidence in the population increased ($p = 0.007$, Adj $R^2 = 26.7$). There was also evidence for the proportion of clustering to increase as the maximum cluster size increased ($p = 0.001$), accounting for 48% of between study variation. There was no evidence of the other study design or study setting variables significantly influencing the proportion clustered. Though non-significant ($p > 0.05$), the TB/HIV coinfection rate in the population explained 2% of the between study variation. Too few studies included information on the proportion of clusters containing two cases, proportion of the study sample with previous TB or with pulmonary TB, and the proportion of the population with culture positive TB, so these could not be included in the analysis (Table 2).

Sensitivity analyses to examine the effect of excluding studies reporting 0% clustering,[37] only *M. bovis* cases,[39] studies using the 'old 12' MIRU loci,[39–44] and studies assessed as having a high risk of bias,[37,45–48] did not generally change the results. The proportion of culture positive TB in the population remained insignificant but explained 2.6% of the between study variation when excluding 0% clustering ($p = 0.278$ and Adj $R^2 = 2.62$). Similarly, the proportion of culture positive TB in the population remained insignificant but explained 2.6% of the between study variation when excluding studies with the highest risk of bias ($p = 0.278$ and Adj $R^2 = 2.62$). The number of loci typed became non-significant, but explained 9.6% and 10.5% of the between study variation when

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167 excluding studies using the 'old 12' loci and the highest risk of bias, respectively ($p=0.106$, Adj
168 $R^2=9.63$; $p=0.111$, Adj $R^2=10.51$, respectively).

169 **Discussion**

170 This review identified 27 studies that met the inclusion criteria. We illustrate that the interpretation
171 of studies using MIRU-VNTR to estimate clustering is subject to bias relating to study design and
172 setting; however, there were insufficient data available to fully explore this impact.

173 As expected, we found that the proportion of clustering decreased with a greater number of MIRU-
174 VNTR loci typed, with increasing TB incidence and with increasing maximum cluster size. We found
175 that requiring consent to type patient isolates reduced the proportion of clustering, which is
176 expected, given that the sampling fraction would be lower in these studies.

177 The other study design variables included in this analysis, such as study duration, did not significantly
178 influence the proportion of isolates that were clustered, contrary to previous findings [12]. This is
179 likely to be because of a lack of good quality evidence: of the 27 studies that met the inclusion
180 criteria for the review, none reported all the variables of interest, reducing the power of the analysis
181 and precluding multivariable meta-regression (Table 2). Importantly, key details of cluster analyses
182 were not reported consistently across the studies, such as whether repeat isolates from the same
183 patients were included, or typing profiles with missing loci were included, introducing new,
184 unmeasured biases. In addition, the range of the variables may have been too limited to show any
185 impact on clustering estimates. For example, the proportion of culture positive isolates typed ranged
186 from 34.5% to 100%, with 17 of the 19 studies reporting this variable from 81.9% to 100%.
187 Furthermore, most of the studies (17/27=63%) were from low TB burden settings and therefore may
188 be reflecting the rate at which imported cases have matching strain types by chance, rather than
189 rates of recent transmission.

190 The sensitivity analysis suggested that, when excluding the studies with the greatest risk of bias, the
191 culture-positivity in the population might explain a small amount of the between study variation.
192 This is counterintuitive and not consistent with estimates of the influence of sampling on the
193 proportion of clustering using IS6110 RFLP typing [49]. This may reflect the relationship between TB
194 burden and resource poor/rich settings and the consequent availability of culture diagnostic
195 laboratory services; i.e. in resource poor settings where there is a high burden of TB (and, therefore,
196 high rates of clustering) the prevalence of culture positive TB cases is low. The finding may also be
197 due to chance, with only 14 studies included in the analysis of this variable. In the sensitivity analysis

198 excluding studies that used the 'old 12' loci, the effect of the number of loci typed becomes non-
199 significant. This is likely because studies using the 'old 12' accounted for six out of ten studies
200 reporting 15 loci, reducing the number of studies and the power of the model.

201 This study is a timely evaluation of the impact of study design on estimates of TB clustering using
202 MIRU-VNTR strain typing because it has been incorporated into national typing services globally
203 [23,50]. The findings are relevant where strain typing is used to evaluate TB control systems across
204 different settings because the proportion of clustering is influenced by the number of loci typed, the
205 TB incidence and the maximum cluster size. Given that strain typing methods are advancing beyond
206 MIRU-VNTR typing and that the application of whole genome sequencing to TB control and public
207 health strategies has been demonstrated [9–11,51], it is important that the biases in the analysis of
208 such methods are explored and compared. Understanding how to design and compare research
209 studies for public health will greatly improve the benefit gained from newer technologies.

210 The strength of this meta-analysis was limited by (a lack of) detail reported by the included studies.
211 This review has highlighted the need for better quality reporting in primary studies to enable future
212 reviews to be more robust. Recently published standards for reporting of molecular epidemiology
213 for infectious diseases should improve the quality of reporting.[35] This review is further limited by
214 our inability to access 58 of the title/abstract screened articles for full text screening.

215 The use of TB strain typing as a public health tool in TB control programmes is increasing globally.
216 We have identified a lack of good quality studies that can contribute to our understanding in
217 interpreting the molecular typing of TB. We have also shown that the proportion of clustering
218 derived from MIRU-VNTR typing is influenced by the number of loci typed, whether consent is
219 required to type isolates, TB incidence in the study setting, and the maximum cluster size,
220 highlighting these as important considerations in the design and interpretation of future studies.

221 **Conflict of interest**

222 Nothing to declare.

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226 **Author contributions**

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Ethics

Ethical approval was not required as this review analyses data that is in the public domain.

Data sharing

No additional data are available

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450 [84878608813&partnerID=40&md5=babbd6d006ca64e327fb19e01b6bc697](http://www.scopus.com/inward/record.url?eid=2-s2.0-84878608813&partnerID=40&md5=babbd6d006ca64e327fb19e01b6bc697).
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Tables

Table 1: The study setting and design characteristics of the included articles

Ref	Study setting							Study design						Risk of bias ^d	Clustering (%) ^e	
	Study area and country	TB incidence (per 100,000)	TB/HIV (per 100,000) ^a	Previous TB treatment (%)	Pulmonary TB (%)	Maximum cluster size	Clusters of size 2 (%)	Study duration (months)	Study size (clustered + unique isolates)	Culture positive in study population (%)	Culture positive isolates typed (%)	Typing method ^b	Loci typed ^c	Consent required		
[52]	New South Wales, Australia	6.7	0.2	0.0	63.7	.	.	36	1128	.	.	m24	N	no	low	20.1
[40]	Tabriz and Orumieh, Azarbaijan	26.0	.	5.2	87.0	5	81.8	12	156	.	94.5	m15	O	no	low	32.7
[53]	Brussels-Capital Region, Belgium	35.2	5.1	10.8	.	23	64.2	24	530	86.1	87.9	m24	N	no	low	29.6
[54]	Brussels-Capital Region, Belgium	35.2	5.1	.	100	.	.	39	802	81.8	84.7	m24s	N	no	low	28.8
[55]	Ontario, Canada	4.8	0.4	.	.	18	58.8	65	2016	.	.	m24s	N	no	low	23.1
[37]	Changping District, Beijing, China	.	0.3	.	100	0	.	30	318	31.5	94.6	m24	N	no	high	0.0
[38]	Croatia	19.0	0.1	.	.	45	48.3	36	1587	.	.	m15	N	no	high	62.8
[56]	Amhara region, Northwest Ethiopia	.	24.0	17.6	100	13	.	5	244	.	.	m24	N	yes	low	45.1
[57]	Finland	5.0	0.0	.	.	20	.	48	1048	75.4	99.4	m15s	.	no	low	33.9
[58]	Hamburg, Germany	12.7	45.5	12	154	78.2	91.1	m24s	N	no	low	22.1
[46]	Schleswig-Holstein, Germany	3.2	0.1	.	.	22	44.4	48	277	.	.	m24s	N	no	high	27.1
[59]	South West Ireland	15.3	3.3	.	82.7	12	.	36	171	79.5	96.1	m24s	N	no	low	27.5
[60]	South Tawara, Kiribati	370.0	.	4.1	100	25	55.6	24	73	45.4	98.6	m24s	N	yes	low	75.3
[61]	Netherlands	6.5	0.2	.	.	.	57.2	60	3978	.	100.1	m24	N	no	low	46.7
[41]	Kharkiv, Russia	94.0	3.8	63.3	100	10	50.0	3	98	.	100	m15	O	yes	high	31.6
[62]	Eastern province, Saudi Arabia	4.0	.	.	73.1	24	19.0	24	522	.	.	m24s	N	no	low	40.2

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[63]	Singapore	40.5	1.2	.	.	21	48.0	24	1128	82.0	34.5	m24s	N	no	low	30.8
[64]	Slovenia	10.6	0.0	.	.	6	.	12	196	94.4	97.5	m24s	N	no	low	36.2
[48]	Almeria, Spain	26.0	6.0	.	.	8	.	27	281	.	81.9	m15	N	no	high	43.1
[65]	Sweden	4.8	0.1	.	.	10	.	36	406	.	.	m24s	N	no	low	21.2
[66]	Mubende, Uganda	.	86.0	31.1	87.8	11	70.0	6	67	21.5	90.5	m15s	N	yes	low	35.8
[42]	East Lancashire, UK	18.3	8.2	.	.	13	58.3	102	332	48.5	69.9	m15	O	no	low	42.8
[39]	UK	.	8.2	.	42.3	12	50.0	48	102	90.7	87.2	m15	O	no	low	30.4
[67]	London, UK	44.9	8.2	9	964	36.0	100	m24	N	no	.	37.0
[43]	Midlands, UK	15.0	8.2	48	4207	58.3	100	m15	O	no	.	61.2
[44]	Odessa and Nikolaev, Ukraine	80.4	3.9	34.2	100	.	.	4	225	.	.	m15	O	yes ^f	low	60.4
[68]	Hanoi, Vietnam	146.0	10.0	0.0	100	.	.	20	465	92.7	91.9	m15s	N	yes	low	55.3

^a Estimates from of the prevalence of TB/HIV co-infection in the study country [33,34]

^b 15=15 MIRU-VNTR loci (made up of the ‘old 12’ or ‘new 12’ defined in the footnote below), 24=24 MIRU-VNTR loci (ETR A, B, C, D, E; MIRU 2, 10, 16, 20, 23, 24, 26, 27, 39, 40; VNTR 424, 1955, 2163b, 2347, 2401, 3171, 3690, 4052, 4156), S=with Spoligotyping

^c O= old 12 MIRU loci (MIRU 2, 4, 10, 16, 20, 23, 24, 26, 27,30, 31, 39, 40), N=new 12 MIRU loci (MIRU 10, 16, 26, 31, 40 + Mtub 04, 21, 39 + ETR A C + QUB 11b, 26)

^d Risk of bias was assessed using the STROME-ID checklist. Studies scoring <20 were categorised as have a high risk of bias

^e The proportion of clustering was calculated as the number of clustered isolates/number of clustered + unique isolates

^f 11.3% did not consent to being part of the study. The other studies that required consent for isolates to be typed did not report the refusal rate

Table 2: The number of studies that reported the variables of interest

	Reported	Missing
<u>Study setting</u>		
TB incidence	8	15
TB/HIV co-infection	5	22
Previous TB treatment	9	18
Proportion pulmonary TB	14	13
Maximum cluster size	19	8
% clusters with 2 cases	14	13
<u>Study design</u>		
Study duration	27	0
Study size	27	0
% population that is culture positive	15	12
% culture positive typed	19	8
24 loci (compared to 15)	27	0
Repeat isolates	12	15
Missing loci	8	19
Double alleles	1	26
Consent required	6 ^a	21
Epidemiological information	6	21

^a Only one study reported the consent rate

Table 3: Univariable meta-regression showing the coefficients for change in the proportion of clustering and the percentage of between-study variation explained by variables describing the study design and setting.

	n	Coefficient ^a	CI	p	Adj R ² ^b
Study setting					
TB incidence	23	0.14	0.04-0.24	0.007	26.74
TB/HIV co-infection	23	0.04	-0.03-0.11	0.246	2.00
Maximum cluster size	19	0.20	0.09-0.30	0.001	48.20
Study design					
Study duration	27	-0.02	-0.09-0.06	0.677	-3.37
% population that is culture positive	15	0.34	-1.23-1.96	0.661	-5.92
% culture positive typed	19	0.22	-1.08-1.52	0.725	-5.41
Study size	27	0.03	-0.11-0.16	0.702	-3.31
24 loci (compared to 15)	27	-0.30	-0.59--0.01	0.04	13.58
Consent required	27	0.38	0.04-0.72	0.029	14.41

^a Coefficients for the change in the proportion of clustering for each covariate. E.g. for a one-month increase in study duration, the proportion of clustering increases by 0.003.

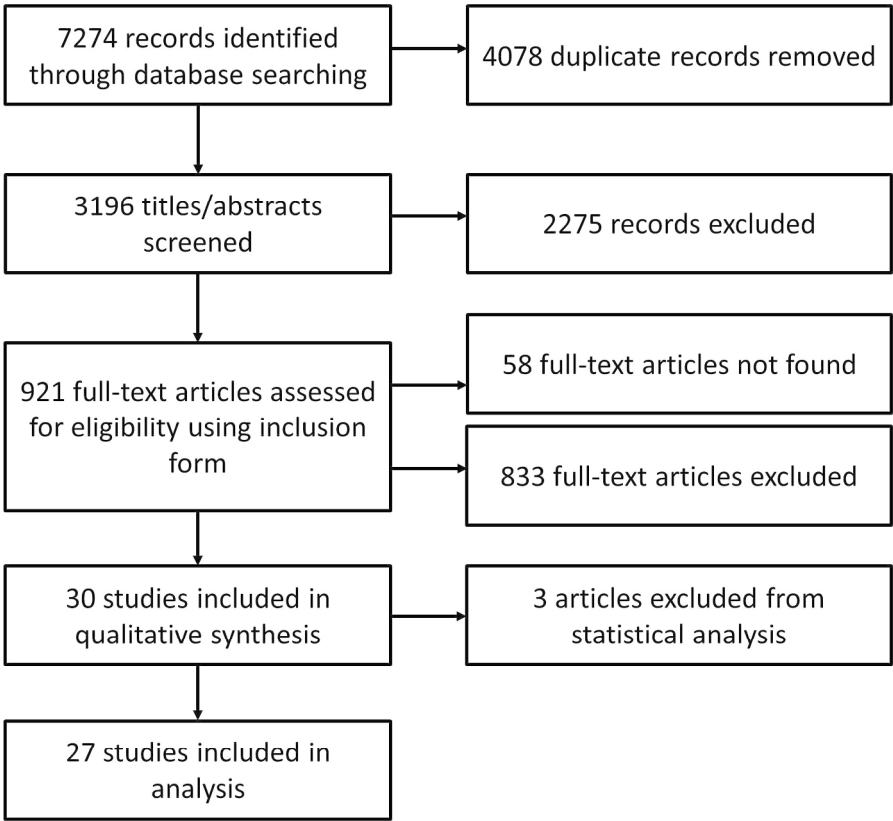
^b The proportion of between-study variation explained by the univariate meta-regression.

Figure Caption

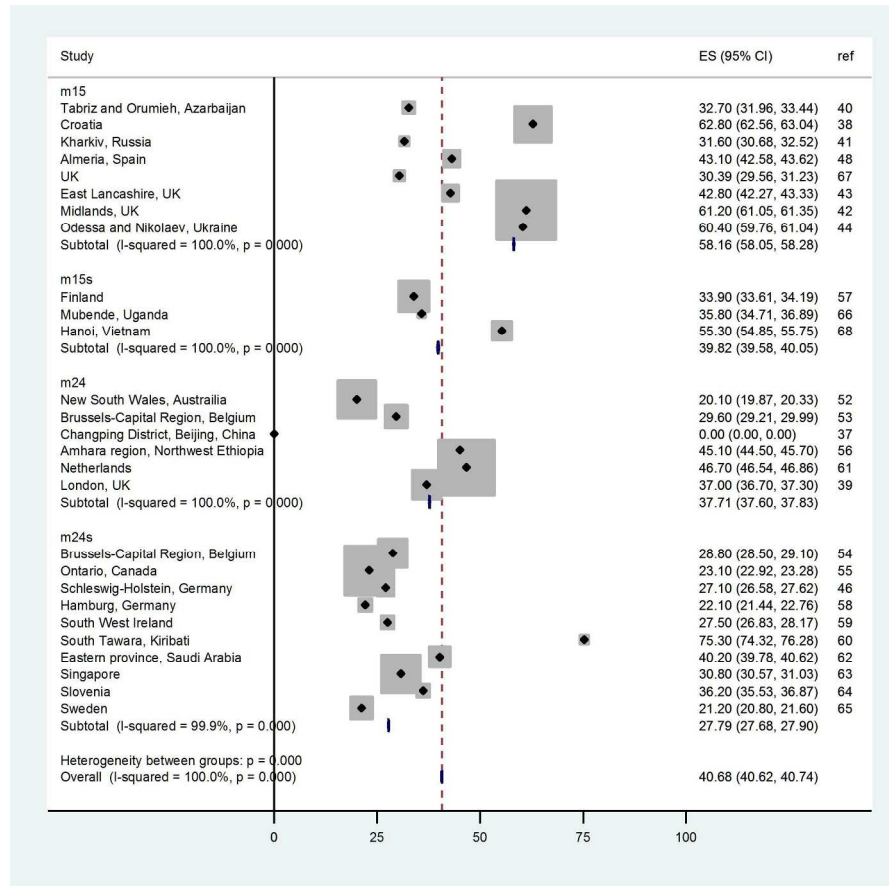
Figure 1: Results of systematic search, screening and data extraction.

Figure 2: Forest plot showing the proportion of clustering reported in each study by the number of MIRU-VNTR loci typed

The number of loci typed is categorised into 15 loci (m15), 15 loci with Spoligotyping (m15s), 24 loci (m24) and 24 loci with Spoligotyping (m24s). The study reference is shown in the right hand column.



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Appendix 1: Medline/Embase search strategy

1. (tubercle adj3 (bacillus or bacilli)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
2. ((mycobacterium or mycobacteria) adj3 (bovis or africanum or microti or canetti)).mp.
3. exp tuberculosis/ or mycobacterium tuberculosis/ or tuberculosis.mp. or tb.mp. or Mtb.mp. or "M tuberculosis complex".mp.
4. or/1-3
5. Minisatellite Repeats/ or Genotype/ or Interspersed Repetitive Sequences/ or DNA Fingerprinting/ or Bacterial Typing Techniques/
6. "miru".mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
7. "vntr".mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
8. (miru adj3 vntr).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
9. (mycobacterial adj3 interspersed adj3 repetitive adj3 units).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
10. (dna adj3 fingerprinting).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
11. ((strain adj3 type) or (strain adj3 typing) or (strain adj3 types)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
12. ((molecular adj3 typing) or (molecular adj3 strain adj3 typ*)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
13. (genotype or genotyping or genotypes).ti,ab.
14. (minisatellite adj3 repeat*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
15. molecular epidemiology/mt or (molecular adj3 epidemiology).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
16. or/5-15
17. exp disease outbreaks/ or (outbreak adj3 analysis).mp. or (outbreak adj3 investigation).mp. or (outbreak adj3 management).mp. or (tuberculosis adj3 outbreak).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
18. exp contact tracing/ or (contact adj3 tracing).mp. or (contact* adj3 traced).mp. or (contact adj3 screen*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
19. exp case management/ or (case adj3 management).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
20. exp Risk Factors/
21. (risk adj3 factor*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
22. exp Epidemiologic Factors/
23. infectious disease transmission.mp. or exp Disease Transmission, Infectious/
24. exp case management/ or (case adj3 management).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
25. program evaluation/ or evaluation studies as topic/ or (program adj3 evaluation).mp. or (programme adj3 evaluation).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
26. public health practice/ or (public adj3 health).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
27. ((tuberculosis adj3 control) or (tb adj3 control)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
28. (molecular adj3 surveillance).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
29. exp cluster analysis/ or (cluster* adj3 rate*).mp. or (cluster* adj3 growth).mp. or (cluster* adj3 analysis).mp. or (cluster adj3 investigation).mp. or (proportion adj3 cluster*).mp. or (molecular adj3 cluster*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
30. ((recent adj3 transmission) or (transmission adj3 event*) or (transmission adj3 rate*) or (chain adj3 transmission) or (transmission adj3 setting*)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
31. or/17-30

32. 4 and 16
33. 32 and 31
34. limit 33 to yr="1998-Current"
35. limit 34 to english language
36. animals/
37. humans/
38. 36 not 37
39. 35 not 38

Appendix 2: STROME-ID scores for the included studies

Author	STROME-ID score ^a
Aleksic, E	24
Allix-Beguec, C	32
Allix-Beguec, C	25
Alonso-Rodriguez, N	18
Asgharzadeh, M	28
Bidovec-Stojkovic, U	31
De Beer, JL	30
Dymova, MA	19
Evans, J	^b
Grujav, U	32
Guang-ming, DAI	19
Hamblion, E	^b
Hang, NTHL	31
Jonsson, J	22
Lim, LKY	30
Mandal, S	32
Muwonge, A	25
Nikolayevsky, V	23
Oelemann, M	34
Ojo, OO	36
Roetzer, A	16
Sails, A	23
Smit, PW	29
Tessema, B	26
Tuite, AR	31
Varghese, B	23
Zmak, L	19

^aIndividual studies score 1 for each element of checklist they had address

^bConference abstracts



PRISMA 2009 Checklist

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Section/topic	#	Checklist item	Reported on page #
TITLE			
Title	1	Identify the report as a systematic review, meta-analysis, or both.	1
ABSTRACT			
Structured summary	2	Provide a structured summary including, as applicable: background; objectives; data sources; study eligibility criteria, participants, and interventions; study appraisal and synthesis methods; results; limitations; conclusions and implications of key findings; systematic review registration number.	2
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of what is already known.	3
Objectives	4	Provide an explicit statement of questions being addressed with reference to participants, interventions, comparisons, outcomes, and study design (PICOS).	3
METHODS			
Protocol and registration	5	Indicate if a review protocol exists, if and where it can be accessed (e.g., Web address), and, if available, provide registration information including registration number.	n/a
Eligibility criteria	6	Specify study characteristics (e.g., PICOS, length of follow-up) and report characteristics (e.g., years considered, language, publication status) used as criteria for eligibility, giving rationale.	4
Information sources	7	Describe all information sources (e.g., databases with dates of coverage, contact with study authors to identify additional studies) in the search and date last searched.	4
Search	8	Present full electronic search strategy for at least one database, including any limits used, such that it could be repeated.	appendix
Study selection	9	State the process for selecting studies (i.e., screening, eligibility, included in systematic review, and, if applicable, included in the meta-analysis).	4
Data collection process	10	Describe method of data extraction from reports (e.g., piloted forms, independently, in duplicate) and any processes for obtaining and confirming data from investigators.	4
Data items	11	List and define all variables for which data were sought (e.g., PICOS, funding sources) and any assumptions and simplifications made.	5
Risk of bias in individual studies	12	Describe methods used for assessing risk of bias of individual studies (including specification of whether this was done at the study or outcome level), and how this information is to be used in any data synthesis.	5
Summary measures	13	State the principal summary measures (e.g., risk ratio, difference in means).	5
Synthesis of results	14	Describe the methods of handling data and combining results of studies, if done, including measures of consistency (e.g., I^2 for each meta-analysis).	5

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PRISMA 2009 Checklist

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Section/topic	#	Checklist item	Reported on page #
Risk of bias across studies	15	Specify any assessment of risk of bias that may affect the cumulative evidence (e.g., publication bias, selective reporting within studies).	5
Additional analyses	16	Describe methods of additional analyses (e.g., sensitivity or subgroup analyses, meta-regression), if done, indicating which were pre-specified.	5
RESULTS			
Study selection	17	Give numbers of studies screened, assessed for eligibility, and included in the review, with reasons for exclusions at each stage, ideally with a flow diagram.	Figure 1
Study characteristics	18	For each study, present characteristics for which data were extracted (e.g., study size, PICOS, follow-up period) and provide the citations.	15
Risk of bias within studies	19	Present data on risk of bias of each study and, if available, any outcome level assessment (see item 12).	15
Results of individual studies	20	For all outcomes considered (benefits or harms), present, for each study: (a) simple summary data for each intervention group (b) effect estimates and confidence intervals, ideally with a forest plot.	Figure 2
Synthesis of results	21	Present results of each meta-analysis done, including confidence intervals and measures of consistency.	18
Risk of bias across studies	22	Present results of any assessment of risk of bias across studies (see Item 15).	15
Additional analysis	23	Give results of additional analyses, if done (e.g., sensitivity or subgroup analyses, meta-regression [see Item 16]).	18
DISCUSSION			
Summary of evidence	24	Summarize the main findings including the strength of evidence for each main outcome; consider their relevance to key groups (e.g., healthcare providers, users, and policy makers).	7
Limitations	25	Discuss limitations at study and outcome level (e.g., risk of bias), and at review-level (e.g., incomplete retrieval of identified research, reporting bias).	7-8
Conclusions	26	Provide a general interpretation of the results in the context of other evidence, and implications for future research.	8
FUNDING			
Funding	27	Describe sources of funding for the systematic review and other support (e.g., supply of data); role of funders for the systematic review.	8

From: Moher D, Liberati A, Tetzlaff J, Altman DG, The PRISMA Group (2009). Preferred Reporting Items for Systematic Reviews and Meta-Analyses: The PRISMA Statement. PLoS Med 6(6): e1000097. doi:10.1371/journal.pmed1000097

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BMJ Open

Effect of study design and setting on tuberculosis clustering estimates using Mycobacterial Interspersed Repetitive Units-Variable Number Tandem Repeats (MIRU-VNTR): A systematic review

Journal:	BMJ Open
Manuscript ID:	bmjopen-2014-005636.R2
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Complete List of Authors:	Mears, Jessica; University College London, Department of Infection and Population Health Abubakar, Ibrahim; University College London, Department of Infection and Population Health; Public Health England, Centre for Infectious Disease Surveillance and Control Cohen, Ted; Harvard School of Public Health, Harvard University, Division of Global Health Equity, Brigham and Women's Hospital and Department of Epidemiology McHugh, Timothy; Centre for Clinical Microbiology, Research Department of Infection, Royal Free Campus, University College London Sonnenberg, Pamela; University College London, Department of Infection and Population Health
Primary Subject Heading:	Research methods
Secondary Subject Heading:	Infectious diseases, Public health
Keywords:	EPIDEMIOLOGY, Tuberculosis < INFECTIOUS DISEASES, MOLECULAR BIOLOGY

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1 Effect of study design and setting on tuberculosis clustering estimates using
2 Mycobacterial Interspersed Repetitive Units-Variable Number Tandem
3 Repeats (MIRU-VNTR): A systematic review

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18 **Word count: 2392**

Abstract

Objectives: To systematically review the evidence for the impact of study design and setting on the interpretation of TB transmission using clustering derived from Mycobacterial Interspersed Repetitive Units – Variable Number Tandem Repeats (MIRU-VNTR) strain typing.

Data sources: Medline, Embase, CINHAI, Web of Science and Scopus were searched for articles published before 21st October 2014.

Review methods: Studies in humans that reported the proportion of clustering of TB isolates by MIRU-VNTR were included in the analysis. Univariable meta-regression analyses were conducted to assess the influence of study design and setting on the proportion of clustering.

Results: The search identified 27 eligible articles reporting clustering between 0% and 63%. The number of MIRU-VNTR loci typed, requiring consent to type patient isolates (as a proxy for sampling fraction), the TB incidence and the maximum cluster size explained 14%, 14%, 27% and 48% of between-study variation, respectively, and had a significant association with the proportion of clustering.

Conclusions: Although MIRU-VNTR typing is being adopted worldwide there is a paucity of data on how study design and setting may influence estimates of clustering. We have highlighted study design variables for consideration in the design and interpretation of future studies.

Strengths and Limitations of Study

- This is a timely evaluation of the impact of study design on estimates of TB clustering using MIRU-VNTR strain typing because it has been incorporated into national typing services globally.
- The strength of this meta-analysis was limited by the lack of detail reported by the included studies, highlighting the need for better quality reporting in primary studies.

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45 **Introduction**

46 The introduction of molecular typing methods has improved our understanding of *Mycobacterium*
47 *tuberculosis* (TB) transmission and has changed local and national control policies [1–5]. The
48 proportion of cases that are clustered is often used to estimate the amount of ongoing transmission
49 within the population, based on the assumption that cases with indistinguishable strain types are
50 part of a chain of transmission. TB molecular typing methodology is changing rapidly and it is
51 important that we better understand how to interpret the outputs and thus act.

52 TB molecular typing methods include Spoligotyping [6], insertion sequence 6110 (IS6110) restriction
53 fragment length polymorphism (RFLP) analysis (the recent gold standard) [7], mycobacterial
54 interspersed repetitive units-variable number tandem repeats (MIRU-VNTR) typing [8], and whole
55 genome sequencing [9–11]. Published reviews have identified factors that might influence or bias
56 clustering by IS6110 RFLP [12,13]. No study has repeated this analysis using more up-to-date typing
57 methods, which is important for understanding of the epidemiology of TB and to shape the
58 application of molecular typing to improve TB control.

59 Published meta-analyses and modelling studies using IS6110 RFLP data show that the proportion of
60 clustering observed can be affected by 1) study design (affecting the proportion of eligible cases that
61 are included in the study); 2) features of the typing method (such as the ability to type isolates with
62 low copy numbers); and 3) study setting (such as characteristics of the study population). For
63 example, the proportion of clustering increases when the fraction of the total data sampled
64 increases [13–15] and when study duration increases [16].

65 MIRU-VNTR is currently the preferred method of molecular typing [17–21], and can be used
66 together with Spoligotyping [8]. Relative to IS6110 RFLP, MIRU-VNTR does not have to exclude
67 isolates with a low IS6110 copy number, has a faster turnaround time, is high throughput and the
68 numeric strain types are more easily compared. MIRU-VNTR strain typing is increasingly being
69 adopted worldwide [1,22–27], yet unlike IS6110 RFLP, the evidence for the interpretation of the
70 findings such as the impact of study design and setting on clustering have not been reviewed.
71 Although the two typing methods have been shown to have a similar discriminatory value, the
72 markers evolve independently and at different rates, resulting in a difference in clustering between
73 the two methods [28]. This suggests that there could be differences in the way study design, typing
74 method and setting affects clustering by the two methods. We conducted a systematic review to
75 assess the evidence for the impact of study design and setting on the interpretation of TB

transmission using clustering derived from MIRU-VNTR strain typing – as has been shown using IS6110 RFLP typing.

Methods

Five electronic databases were searched (EMBASE, ISI Web of Science, CINHALL, Scopus and Medline (Ovid)) up to 20th October 2014. The search strategy combined the following terms with Boolean operators: Tuberculosis, strain typing, and transmission (Appendix 1). The search was limited to studies using the standard MIRU-VNTR method [8], in humans only, and in English.

All titles and abstracts from each of the searches were examined. The full text of each paper was obtained and reviewed if the study reported MIRU-VNTR strain typing of *M.tuberculosis* complex isolates with at least 15 of the standardised 24 loci (ETR A, B, C, D, E; MIRU 2, 10, 16, 20, 23, 24, 26, 27, 39, 40; VNTR 424, 1955, 2163b, 2347, 2401, 3171, 3690, 4052, 4156) [8,29,30].

Studies using fewer than 15 loci were not included because the level of discrimination is inadequate for epidemiological use (n=121) [8]. Studies that used loci different to the standardised 15 and 24 set were not included in the analysis in order to reduce the heterogeneity between studies (n=19). All publication types were included in this first screen to ensure that no relevant data were missed.

Reviews, letters, editorials, outbreaks or case reports (n=103) were excluded in the second screen. Studies that used incomplete sampling (e.g. random samples, studies using subsets of populations such as multidrug-resistant patients) (n=47) and studies that had a sample size of less than 50 (n=4) were also excluded.

A reviewer (JM) extracted the following data items from all included studies using a form developed in Excel (Microsoft 2010): publication details (year, authors, study country), study details (study duration, loci typed, secondary typing method, study population, whether participant consent was required (a characteristic of the study design that was used as proxy for sampling fraction, assuming that where consent was required the sampling fraction was low)), the number of clustered and unique isolates, and the covariates of interest: the maximum size of clusters; the proportion of clusters containing two cases; the proportion of the population that was culture positive; the proportion of culture positive isolates typed; risk factors for clustering; and the Hunter Gaston Discriminatory Index (HGDI) [31]. IA extracted data from 10% of the papers for external validity, disagreements were discussed and a consensus agreed upon.

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105 The main outcome measure – the proportion of TB isolates clustered by MIRU-VNTR strain typing –
106 was calculated as the number of clustered isolates/number of clustered+unique isolates. Where
107 there were uncertainties JM consulted with IA.

108 Authors were contacted if TB incidence rate was not reported. Where no response was received
109 WHO country estimates of TB incidence for the study year were used.[32] As so few studies reported
110 the proportion coinfecting with TB/HIV, these estimates for the study country were taken from an
111 EU-wide survey and WHO country profiles.[33,34] Due to poor recording of the sampling fraction
112 (the number of isolates typed/the total number of culture positive TB cases diagnosed during the
113 study period (n=19)), whether the study required the consent of participants (yes/no) was included
114 as a proxy for (low/high) sampling fraction. The risk of bias within each study was assessed using the
115 STROME-ID checklist.[35]

116 Data were analysed in Stata 12. Where studies reported data from more than one set of loci, the
117 method with the highest discriminatory value was included (i.e. MIRU-VNTR 24 would be chosen
118 over MIRU-VNTR 15, and MIRU-VNTR 15 plus Spoligotyping would be chosen over MIRU-VNTR 15
119 alone) (n=8). This review was not concerned with summary measures of clustering, but factors that
120 influenced clustering; therefore articles must have included at least one of the covariates.
121 Continuous variables were transformed where the distribution was skewed. The proportion
122 clustered was transformed using the Freeman Tukey transformation [36]. Study heterogeneity was
123 assessed using a forest plot and the chi² test of heterogeneity. Univariable meta-regression analyses
124 were carried out to determine the effect of the study design covariates on the proportion of
125 clustered isolates. All covariates in the analysis were hypothesised to influence the proportion
126 clustered *a priori*.

127 Sensitivity analyses were conducted to see the effect of removing studies reporting 0% clustering,
128 with only extra-pulmonary TB cases, only *M.bovis* cases, studies using the ‘old 12’ MIRU loci as part
129 of their 15 loci, and studies assessed as having a high likelihood of bias (STROME-ID score less than
130 20).

131 **Results**

132 The search identified 7274 references resulting in 27 studies (25 journal articles and 2 conference
133 abstracts) included after deduplication and title/abstract/full text screening (Figure 1). The main
134 characteristics of the included studies are shown in Table 1. Studies were published between 2007
135 and 2014 and the clustering reported varied from 0% [37] to 62.8% [38]. In all studies, clustered

isolates were defined as having identical strain types based on the MIRU-VNTR loci typed, with or without Spoligotyping. 17 studies included isolates from newly diagnosed TB cases, three studies reported including isolates from new and chronic cases of TB, and seven did not report this information. In addition, ten studies did not include repeat isolates from the same patient, one study included a repeat isolate from one patient, and the remaining 17 did not report whether repeat isolates were included or not. Furthermore, four studies included isolates with missing loci in the cluster analysis, whereas four excluded isolates with missing loci, and the remaining 20 did not report how they dealt with missing loci. The number of studies reporting each variable of interest is shown in Table 2. STROME-ID scores can be found in Appendix 2.

A forest plot shows the spread of clustering reported by number of loci and additional typing method (Figure 2). Significant heterogeneity was identified between the studies ($p < 0.001$), suggesting that a meta-regression would be an appropriate analysis.

The univariable meta-regression shows evidence for the proportion of clustering to decrease as the number of MIRU-VNTR loci typed increased from 15 to 24 ($p = 0.04$; Table 3), accounting for 14% of the between study variation, and to increase when the study participants consented to being included in the study ($p = 0.03$), accounting for 14% of the between study variation. The proportion of clustering increased as the TB incidence in the population increased ($p = 0.007$, Adj $R^2 = 26.7$). There was also evidence for the proportion of clustering to increase as the maximum cluster size increased ($p = 0.001$), accounting for 48% of between study variation. There was no evidence of the other study design or study setting variables significantly influencing the proportion clustered. Though non-significant ($p > 0.05$), the TB/HIV coinfection rate in the population explained 2% of the between study variation. Too few studies included information on the proportion of clusters containing two cases, proportion of the study sample with previous TB or with pulmonary TB, so these could not be included in the analysis (Table 2).

Sensitivity analyses to examine the effect of excluding studies reporting 0% clustering,[37] only *M. bovis* cases,[39] studies using the 'old 12' MIRU loci,[39–44] and studies assessed as having a high risk of bias,[37,45–48] did not generally change the results. The proportion of culture positive TB in the population remained insignificant but explained 2.6% of the between study variation when excluding 0% clustering ($p = 0.278$ and Adj $R^2 = 2.62$). Similarly, the proportion of culture positive TB in the population remained insignificant but explained 2.6% of the between study variation when excluding studies with the highest risk of bias ($p = 0.278$ and Adj $R^2 = 2.62$). The number of loci typed became non-significant, but explained 9.6% and 10.5% of the between study variation when

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168 excluding studies using the ‘old 12’ loci and the highest risk of bias, respectively ($p=0.106$, Adj
169 $R^2=9.63$; $p=0.111$, Adj $R^2=10.51$, respectively).

170 **Discussion**

171 This review identified 27 studies that met the inclusion criteria. We illustrate that the interpretation
172 of studies using MIRU-VNTR to estimate clustering is subject to bias relating to study design and
173 setting; however, there were insufficient data available to fully explore this impact.

174 As expected, we found that the proportion of clustering decreased with a greater number of MIRU-
175 VNTR loci typed, with increasing TB incidence and with increasing maximum cluster size. We found
176 that requiring consent to type patient isolates increased the proportion of clustering, which is not
177 expected, given that the sampling fraction would be lower in these studies.

178 The other study design variables included in this analysis, such as study duration, did not significantly
179 influence the proportion of isolates that were clustered, contrary to previous findings [12]. This is
180 likely to be because of a lack of good quality evidence: of the 27 studies that met the inclusion
181 criteria for the review, none reported all the variables of interest, reducing the power of the analysis
182 and precluding multivariable meta-regression (Table 2). Importantly, key details of cluster analyses
183 were not reported consistently across the studies, such as whether repeat isolates from the same
184 patients were included, or typing profiles with missing loci were included, introducing new,
185 unmeasured biases. In addition, the range of the variables may have been too limited to show any
186 impact on clustering estimates. For example, the proportion of culture positive isolates typed ranged
187 from 34.5% to 100%, with 17 of the 19 studies reporting this variable from 81.9% to 100%.
188 Furthermore, most of the studies (17/27=63%) were from low TB burden settings and therefore may
189 be reflecting the rate at which imported cases have matching strain types by chance, rather than
190 rates of recent transmission.

191 The sensitivity analysis suggested that, when excluding the studies with the greatest risk of bias, the
192 culture-positivity in the population might explain a small amount of the between study variation.
193 This is consistent with estimates of the influence of sampling on the proportion of clustering using
194 /S6110 RFLP typing [49]. In the sensitivity analysis excluding studies that used the ‘old 12’ loci, the
195 effect of the number of loci typed becomes non-significant. This is likely because studies using the
196 ‘old 12’ accounted for six out of ten studies reporting 15 loci, reducing the number of studies and
197 the power of the model.

198 This study is a timely evaluation of the impact of study design on estimates of TB clustering using
199 MIRU-VNTR strain typing because it has been incorporated into national typing services globally
200 [23,50]. The findings are relevant where strain typing is used to evaluate TB control systems across
201 different settings because the proportion of clustering is influenced by the number of loci typed, the
202 TB incidence and the maximum cluster size. Given that strain typing methods are advancing beyond
203 MIRU-VNTR typing and that the application of whole genome sequencing to TB control and public
204 health strategies has been demonstrated [9–11,51], it is important that the biases in the analysis of
205 such methods are explored and compared. Understanding how to design and compare research
206 studies for public health will greatly improve the benefit gained from newer technologies.

207 The strength of this meta-analysis was limited by (a lack of) detail reported by the included studies.
208 This review has highlighted the need for better quality reporting in primary studies to enable future
209 reviews to be more robust. Recently published standards for reporting of molecular epidemiology
210 for infectious diseases should improve the quality of reporting.[35] This review is further limited by
211 our inability to access 58 of the title/abstract screened articles for full text screening.

212 The use of TB strain typing as a public health tool in TB control programmes is increasing globally.
213 We have identified a lack of good quality studies that can contribute to our understanding in
214 interpreting the molecular typing of TB. We have also shown that the proportion of clustering
215 derived from MIRU-VNTR typing is influenced by the number of loci typed, whether consent is
216 required to type isolates, TB incidence in the study setting, and the maximum cluster size,
217 highlighting these as important considerations in the design and interpretation of future studies.

218 **Conflict of interest**

219 Nothing to declare.

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222 advice on meta-regression.

223 **Author contributions**

224 All authors made substantial contributions to the conception and design of the review, and the
225 analysis and interpretation of data. JM drafted the article and PS, IA, TM and TC revised it critically
226 for important intellectual content. All authors approved the final version for publication.

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230 **Ethics**

231 Ethical approval was not required as this review analyses data that is in the public domain.

232 **Data sharing**

233 No additional data are available

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Tables

Table 1: The study setting and design characteristics of the included articles

Ref	Study setting							Study design						Risk of bias ^d	Clustering (%) ^e	
	Study area and country	TB incidence (per 100,000)	TB/HIV (per 100,000) ^a	Previous TB treatment (%)	Pulmonary TB (%)	Maximum cluster size	Clusters of size 2 (%)	Study duration (months)	Study size (clustered + unique isolates)	Culture positive in study population (%)	Culture positive isolates typed (%)	Typing method ^b	Loci typed ^c	Consent required		
[52]	New South Wales, Australia	6.7	0.2	0.0	63.7	.	.	36	1128	.	.	m24	N	no	low	20.1
[40]	Tabriz and Orumieh, Azarbaijan	26.0	.	5.2	87.0	5	81.8	12	156	.	94.5	m15	O	no	low	32.7
[53]	Brussels-Capital Region, Belgium	35.2	5.1	10.8	.	23	64.2	24	530	86.1	87.9	m24	N	no	low	29.6
[54]	Brussels-Capital Region, Belgium	35.2	5.1	.	100	.	.	39	802	81.8	84.7	m24s	N	no	low	28.8
[55]	Ontario, Canada	4.8	0.4	.	.	18	58.8	65	2016	.	.	m24s	N	no	low	23.1
[37]	Changping District, Beijing, China	.	0.3	.	100	0	.	30	318	31.5	94.6	m24	N	no	high	0.0
[38]	Croatia	19.0	0.1	.	.	45	48.3	36	1587	.	.	m15	N	no	high	62.8
[56]	Amhara region, Northwest Ethiopia	.	24.0	17.6	100	13	.	5	244	.	.	m24	N	yes	low	45.1
[57]	Finland	5.0	0.0	.	.	20	.	48	1048	75.4	99.4	m15s	.	no	low	33.9
[58]	Hamburg, Germany	12.7	45.5	12	154	78.2	91.1	m24s	N	no	low	22.1
[46]	Schleswig-Holstein, Germany	3.2	0.1	.	.	22	44.4	48	277	.	.	m24s	N	no	high	27.1
[59]	South West Ireland	15.3	3.3	.	82.7	12	.	36	171	79.5	96.1	m24s	N	no	low	27.5
[60]	South Tawara, Kiribati	370.0	.	4.1	100	25	55.6	24	73	45.4	98.6	m24s	N	yes	low	75.3
[61]	Netherlands	6.5	0.2	.	.	.	57.2	60	3978	.	100.1	m24	N	no	low	46.7
[41]	Kharkiv, Russia	94.0	3.8	63.3	100	10	50.0	3	98	.	100	m15	O	yes	high	31.6
[62]	Eastern province, Saudi Arabia	4.0	.	.	73.1	24	19.0	24	522	.	.	m24s	N	no	low	40.2

[63]	Singapore	40.5	1.2	.	.	21	48.0	24	1128	82.0	34.5	m24s	N	no	low	30.8
[64]	Slovenia	10.6	0.0	.	.	6	.	12	196	94.4	97.5	m24s	N	no	low	36.2
[48]	Almeria, Spain	26.0	6.0	.	.	8	.	27	281	.	81.9	m15	N	no	high	43.1
[65]	Sweden	4.8	0.1	.	.	10	.	36	406	.	.	m24s	N	no	low	21.2
[66]	Mubende, Uganda	.	86.0	31.1	87.8	11	70.0	6	67	21.5	90.5	m15s	N	yes	low	35.8
[42]	East Lancashire, UK	18.3	8.2	.	.	13	58.3	102	332	48.5	69.9	m15	O	no	low	42.8
[39]	UK	.	8.2	.	42.3	12	50.0	48	102	90.7	87.2	m15	O	no	low	30.4
[67]	London, UK	44.9	8.2	9	964	36.0	100	m24	N	no	.	37.0
[43]	Midlands, UK	15.0	8.2	48	4207	58.3	100	m15	O	no	.	61.2
[44]	Odessa and Nikolaev, Ukraine	80.4	3.9	34.2	100	.	.	4	225	.	.	m15	O	yes ^f	low	60.4
[68]	Hanoi, Vietnam	146.0	10.0	0.0	100	.	.	20	465	92.7	91.9	m15s	N	yes	low	55.3

^a Estimates from of the prevalence of TB/HIV co-infection in the study country [33,34]

^b 15=15 MIRU-VNTR loci (made up of the 'old 12' or 'new 12' defined in the footnote below), 24=24 MIRU-VNTR loci (ETR A, B, C, D, E; MIRU 2, 10, 16, 20, 23, 24, 26, 27, 39, 40; VNTR 424, 1955, 2163b, 2347, 2401, 3171, 3690, 4052, 4156), S=with Spoligotyping

^c O= old 12 MIRU loci (MIRU 2, 4, 10, 16, 20, 23, 24, 26, 27, 30, 31, 39, 40), N=new 12 MIRU loci (MIRU 10, 16, 26, 31, 40 + Mtub 04, 21, 39 + ETR A C + QUB 11b, 26)

^d Risk of bias was assessed using the STROME-ID checklist. Studies scoring <20 were categorised as have a high risk of bias. See Appendix 2 for STROME-ID scores

^e The proportion of clustering was calculated as the number of clustered isolates/number of clustered + unique isolates

^f 11.3% did not consent to being part of the study. The other studies that required consent for isolates to be typed did not report the refusal rate

Table 2: The number of studies that reported the variables of interest

	Reported	Missing
<u>Study setting</u>		
TB incidence	8	15
TB/HIV co-infection	5	22
Previous TB treatment	9	18
Proportion pulmonary TB	14	13
Maximum cluster size	19	8
% clusters with 2 cases	14	13
<u>Study design</u>		
Study duration	27	0
Study size	27	0
% population that is culture positive	15	12
% culture positive typed	19	8
24 loci (compared to 15)	27	0
Repeat isolates	12	15
Missing loci	8	19
Double alleles	1	26
Consent required	6 ^a	21
Epidemiological information	6	21

^a Only one study reported the consent rate

Table 3: Univariable meta-regression showing the coefficients for change in the proportion of clustering and the percentage of between-study variation explained by variables describing the study design and setting.

	n	Coefficient ^a	CI	p	Adj R ² ^b
Study setting					
TB incidence	23	0.14	0.04-0.24	0.007	26.74
TB/HIV co-infection	23	0.04	-0.03-0.11	0.246	2.00
Maximum cluster size	19	0.20	0.09-0.30	0.001	48.20
Study design					
Study duration	27	-0.02	-0.09-0.06	0.677	-3.37
% population that is culture positive	15	0.34	-1.23-1.96	0.661	-5.92
% culture positive typed	19	0.22	-1.08-1.52	0.725	-5.41
Study size	27	0.03	-0.11-0.16	0.702	-3.31
24 loci (compared to 15)	27	-0.30	-0.59--0.01	0.04	13.58
Consent required	27	0.38	0.04-0.72	0.029	14.41

^a Coefficients for the change in the proportion of clustering for each covariate. E.g. for a one unit increase in maximum cluster size, the proportion of clustering increases by 0.2.

^b The proportion of between-study variation explained by the univariate meta-regression.

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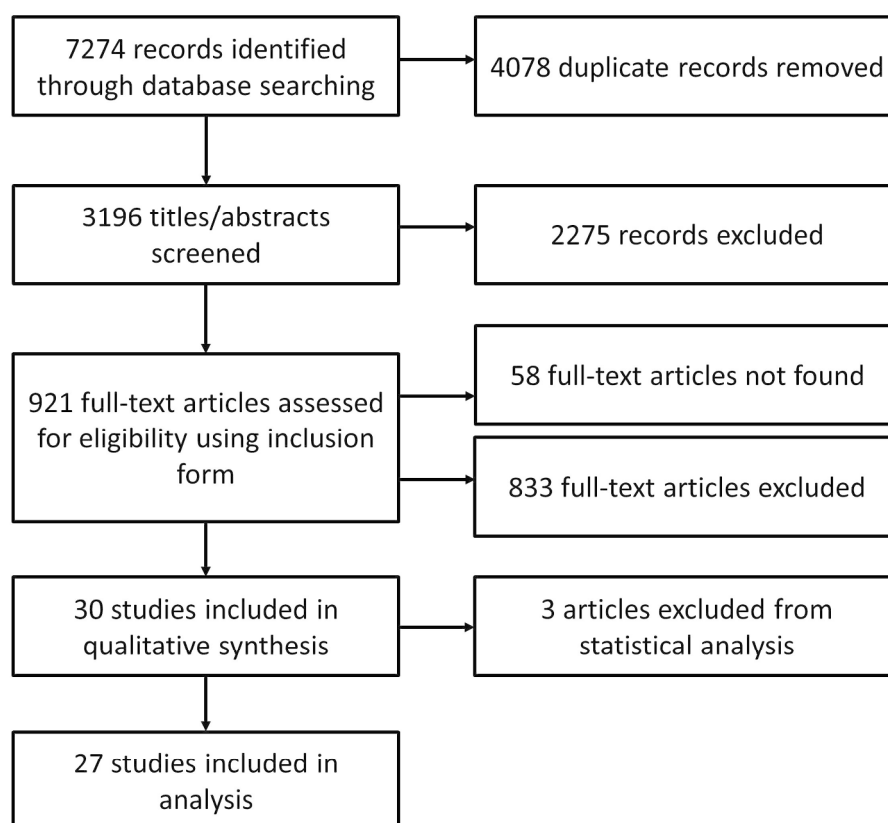
Figure Caption

Figure 1: Results of systematic search, screening and data extraction.

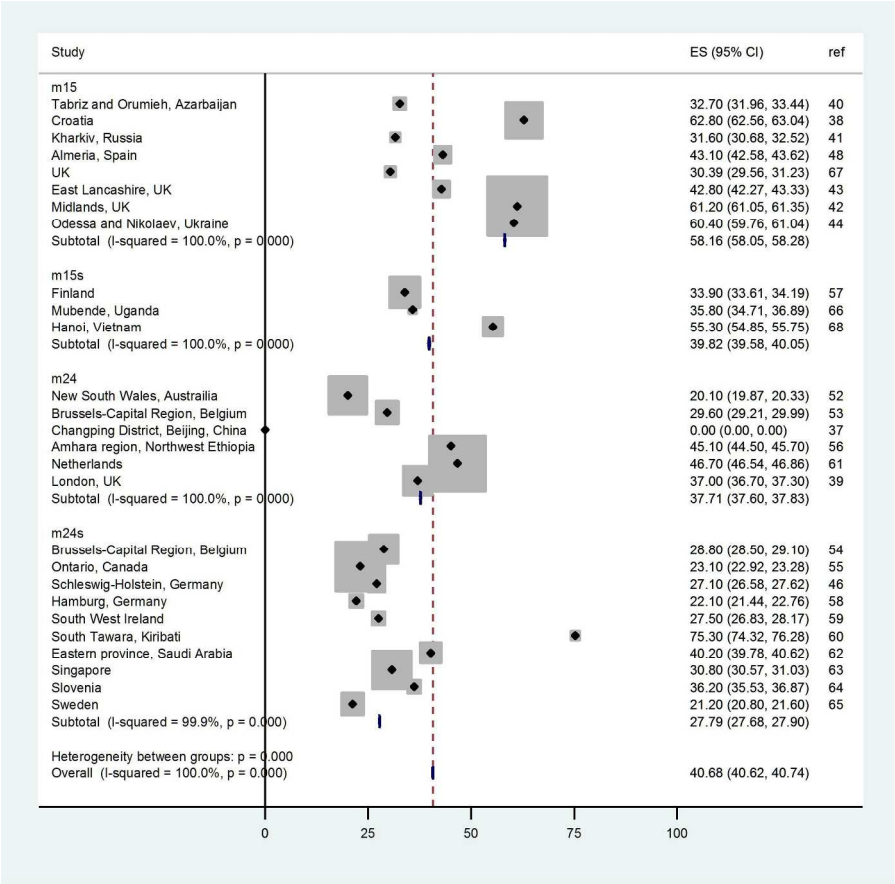
Figure 2: Forest plot showing the proportion of clustering reported in each study by the number of MIRU-VNTR loci typed

The number of loci typed is categorised into 15 loci (m15), 15 loci with Spoligotyping (m15s), 24 loci (m24) and 24 loci with Spoligotyping (m24s). The study reference is shown in the right hand column.

For peer review only



190x254mm (300 x 300 DPI)



190x254mm (300 x 300 DPI)

Appendix 1: Medline/Embase search strategy

1. (tubercle adj3 (bacillus or bacilli)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
2. ((mycobacterium or mycobacteria) adj3 (bovis or africanum or microti or canetti)).mp.
3. exp tuberculosis/ or mycobacterium tuberculosis/ or tuberculosis.mp. or tb.mp. or Mtb.mp. or "M tuberculosis complex".mp.
4. or/1-3
5. Minisatellite Repeats/ or Genotype/ or Interspersed Repetitive Sequences/ or DNA Fingerprinting/ or Bacterial Typing Techniques/
6. "miru".mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
7. "vntr".mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
8. (miru adj3 vntr).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
9. (mycobacterial adj3 interspersed adj3 repetitive adj3 units).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
10. (dna adj3 fingerprinting).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
11. ((strain adj3 type) or (strain adj3 typing) or (strain adj3 types)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
12. ((molecular adj3 typing) or (molecular adj3 strain adj3 typ*)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
13. (genotype or genotyping or genotypes).ti,ab.
14. (minisatellite adj3 repeat*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
15. molecular epidemiology/mt or (molecular adj3 epidemiology).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
16. or/5-15
17. exp disease outbreaks/ or (outbreak adj3 analysis).mp. or (outbreak adj3 investigation).mp. or (outbreak adj3 management).mp. or (tuberculosis adj3 outbreak).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
18. exp contact tracing/ or (contact adj3 tracing).mp. or (contact* adj3 traced).mp. or (contact adj3 screen*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
19. exp case management/ or (case adj3 management).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
20. exp Risk Factors/
21. (risk adj3 factor*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
22. exp Epidemiologic Factors/
23. infectious disease transmission.mp. or exp Disease Transmission, Infectious/
24. exp case management/ or (case adj3 management).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
25. program evaluation/ or evaluation studies as topic/ or (program adj3 evaluation).mp. or (programme adj3 evaluation).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
26. public health practice/ or (public adj3 health).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
27. ((tuberculosis adj3 control) or (tb adj3 control)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
28. (molecular adj3 surveillance).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
29. exp cluster analysis/ or (cluster* adj3 rate*).mp. or (cluster* adj3 growth).mp. or (cluster* adj3 analysis).mp. or (cluster adj3 investigation).mp. or (proportion adj3 cluster*).mp. or (molecular adj3 cluster*).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
30. ((recent adj3 transmission) or (transmission adj3 event*) or (transmission adj3 rate*) or (chain adj3 transmission) or (transmission adj3 setting*)).mp. [mp=title, original title, abstract, name of substance word, subject heading word, unique identifier]
31. or/17-30

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332. 4 and 16
433. 32 and 31
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634. limit 33 to yr="1998-Current"
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835. limit 34 to english language
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1137. humans/
1238. 36 not 37
1339. 35 not 38
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Appendix 2: STROME-ID scores for the included studies

Author	STROME-ID score ^a
Aleksic, E	24
Alliex-Beguec, C	32
Allix-Beguec, C	25
Alonso-Rodriguez, N	18
Asgharzadeh, M	28
Bidovec-Stojkovic, U	31
De Beer, JL	30
Dymova, MA	19
Evans, J	^b
Grujav, U	32
Guang-ming, DAI	19
Hamblion, E	^b
Hang, NTHL	31
Jonsson, J	22
Lim, LKY	30
Mandal, S	32
Muwonge, A	25
Nikolayevsky, V	23
Oelemann, M	34
Ojo, OO	36
Roetzer, A	16
Sails, A	23
Smit, PW	29
Tessema, B	26
Tuite, AR	31
Varghese, B	23
Zmak, L	19

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^aIndividual studies score 1 for each element of checklist they had address

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^bConference abstracts



PRISMA 2009 Checklist

Section/topic	#	Checklist item	Reported on page #
TITLE			
Title	1	Identify the report as a systematic review, meta-analysis, or both.	1
ABSTRACT			
Structured summary	2	Provide a structured summary including, as applicable: background; objectives; data sources; study eligibility criteria, participants, and interventions; study appraisal and synthesis methods; results; limitations; conclusions and implications of key findings; systematic review registration number.	2
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of what is already known.	3
Objectives	4	Provide an explicit statement of questions being addressed with reference to participants, interventions, comparisons, outcomes, and study design (PICOS).	3
METHODS			
Protocol and registration	5	Indicate if a review protocol exists, if and where it can be accessed (e.g., Web address), and, if available, provide registration information including registration number.	n/a
Eligibility criteria	6	Specify study characteristics (e.g., PICOS, length of follow-up) and report characteristics (e.g., years considered, language, publication status) used as criteria for eligibility, giving rationale.	4
Information sources	7	Describe all information sources (e.g., databases with dates of coverage, contact with study authors to identify additional studies) in the search and date last searched.	4
Search	8	Present full electronic search strategy for at least one database, including any limits used, such that it could be repeated.	appendix
Study selection	9	State the process for selecting studies (i.e., screening, eligibility, included in systematic review, and, if applicable, included in the meta-analysis).	4
Data collection process	10	Describe method of data extraction from reports (e.g., piloted forms, independently, in duplicate) and any processes for obtaining and confirming data from investigators.	4
Data items	11	List and define all variables for which data were sought (e.g., PICOS, funding sources) and any assumptions and simplifications made.	5
Risk of bias in individual studies	12	Describe methods used for assessing risk of bias of individual studies (including specification of whether this was done at the study or outcome level), and how this information is to be used in any data synthesis.	5
Summary measures	13	State the principal summary measures (e.g., risk ratio, difference in means).	5
Synthesis of results	14	Describe the methods of handling data and combining results of studies, if done, including measures of consistency (e.g., I^2 for each meta-analysis).	5

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PRISMA 2009 Checklist

Section/topic	#	Checklist item	Reported on page #
Risk of bias across studies	15	Specify any assessment of risk of bias that may affect the cumulative evidence (e.g., publication bias, selective reporting within studies).	5
Additional analyses	16	Describe methods of additional analyses (e.g., sensitivity or subgroup analyses, meta-regression), if done, indicating which were pre-specified.	5
RESULTS			
Study selection	17	Give numbers of studies screened, assessed for eligibility, and included in the review, with reasons for exclusions at each stage, ideally with a flow diagram.	Figure 1
Study characteristics	18	For each study, present characteristics for which data were extracted (e.g., study size, PICOS, follow-up period) and provide the citations.	15
Risk of bias within studies	19	Present data on risk of bias of each study and, if available, any outcome level assessment (see item 12).	15
Results of individual studies	20	For all outcomes considered (benefits or harms), present, for each study: (a) simple summary data for each intervention group (b) effect estimates and confidence intervals, ideally with a forest plot.	Figure 2
Synthesis of results	21	Present results of each meta-analysis done, including confidence intervals and measures of consistency.	18
Risk of bias across studies	22	Present results of any assessment of risk of bias across studies (see Item 15).	15
Additional analysis	23	Give results of additional analyses, if done (e.g., sensitivity or subgroup analyses, meta-regression [see Item 16]).	18
DISCUSSION			
Summary of evidence	24	Summarize the main findings including the strength of evidence for each main outcome; consider their relevance to key groups (e.g., healthcare providers, users, and policy makers).	7
Limitations	25	Discuss limitations at study and outcome level (e.g., risk of bias), and at review-level (e.g., incomplete retrieval of identified research, reporting bias).	7-8
Conclusions	26	Provide a general interpretation of the results in the context of other evidence, and implications for future research.	8
FUNDING			
Funding	27	Describe sources of funding for the systematic review and other support (e.g., supply of data); role of funders for the systematic review.	8

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