Niehus et al. – MICRO guidelines [Turner *et al. BMC Medicine* 2019]

Item	Number	Recommendation	Addressed where
Methods			
Study design	1	Specimen types: Describe the types of specimen included, i.e. clinical (e.g. blood cultures) or non-diagnostic surveillance (e.g. admission and other screening swabs to diagnose carriage). If specimens were obtained for diagnostic reasons, clinical syndromes should be described where possible, and specimens/isolates stratified by clinical syndrome.	Described in "Identification of ESBL producing organism carriers" under **Methods and Materials.**
	2	Sampling period: State the collection timeframe for specimens yielding isolates for which data is reported, e.g. from MM/YY to MM/YY to be able to identify variability between seasons.	Period given in Table 1.
	3	Sampling strategy: Describe the strategy for specimen collection, e.g. asymptomatic screening, sampling of all febrile patients, sampling at clinician discretion, sampling of specific patient groups and convenience sampling (e.g. use of isolates from an existing sample repository). Specify whether sampling followed routine clinical practice or was protocol driven. Classify specimens as from community-acquired (CAI) or hospital-acquired (HAI) infections. The definition of HAI used (e.g. HAI defined by specimen collection > 48 h after hospital admission) should be provided and should use ideally an international standard (e.g. US Centers for Disease Control).	Sampling strategy described in "Study participants and follow-up", classification of specimens is described in "Identification of ESBL producing organism carriers" in **Methods and Materials.**
	4	Target organisms: Explicitly state which organisms/organism groups were included in the report. Nomenclature should follow international standards (i.e. using approved genus/species names as summarised in the International	Target organisms are specified in "Identification of ESBL producing organism carriers" in **Methods and Materials.**

		Journal of Systematic and Evolutionary Microbiology). Lists of approved bacterial names can be downloaded from Prokaryotic Nomenclature Up-to-Date (https://www.dsmz.de/bacterial-diversity/prokaryotic-nomenclature-up-to-date.html) and the List of Prokaryotic Names with Standing in Nomenclature (http://www.bacterio.net/). Organisms considered contaminants should be listed, if appropriate (e.g. coagulase negative staphylococci or Corynebacterium spp.).	Throughout the manuscript we follow standard nomenclature for naming prokaryotic organisms.
Setting	5	Geographical setting: Describe the geographical distribution of specimens/patients from which isolates were obtained, at least to a country level, but preferably to a sub-national level or a geoposition.	Setting is described in "Study participants and follow-up" under **Methods and Materials**
	6	Clinical setting: Describe the type and level of the healthcare facilities (e.g. primary, secondary, tertiary) from which specimens were obtained. If stating a microbiology laboratory, the centres served by the laboratory should be specified.	"Study participants and follow-up" (**Methods and Materials**) describes the countries and the types of hospital wards included.
Laboratory work	7	Specimen processing: If applicable, describe specimen collection and handling, processing and sub-culture methods for all types of specimen included. For example, if reporting AST results for blood culture and cerebrospinal fluid culture isolates, the processing of these specimens by the laboratory should be briefly explained, including how specimens are sub-cultured, the media used, incubation conditions and duration. A summary of specimen processing steps (e.g. pre-processing steps, nucleic acid extraction method (if applicable), amplification platform, contamination avoidance strategy) should be provided for molecular-only workflows (e.g. to detect	Specimen processing described in "Identification of ESBL producing organism carriers" and "Quantitative PCR" in **Methods and Materials.**

		Mycobacterium tuberculosis and rifampicin resistance using the Cepheid Xpert MTB/RIF system).	
	8	Target organism identification: Details of identification methodology should be reported briefly. Where identification databases were used (e.g. bioMerieux API/bioMerieux VITEK-MS/Bruker Biotyper), the version should be specified. In general, all pathogens should be identified to species level. In the case of Salmonella species, organisms should be identified to at least the S. Typhi, S. Paratyphi, or non-typhoidal Salmonella (NTS) level. Strain subtyping methods should be reported according to STROME-ID	ESBL producing organisms were not identified to the species level since study focuses on carriage and not on pathogen infections. "Identification of ESBL producing organism carriers" (**Methods and Materials**) discusses which group of organisms can be detected with our methods.
	9	Antimicrobial susceptibility testing: Describe the antimicrobial susceptibility testing methods used, internal quality control processes and their interpretation, with reference to a recognised international standard, e.g. CLSI, EUCAST. Where an international standard was followed, the specific edition(s) of guidelines used should be referenced. Deviations from standard methodology should be described, along with evidence of validation. Handling of any changes to interpretative criteria during the sampling period should be documented. State whether the raw AST data (zone diameters and/or minimum inhibitory concentrations) were re-categorised with updated breakpoints or left as-is.	Described in "Identification of ESBL producing organism carriers" in **Methods and Materials.**
	10	Additional tests performed to identify resistance mechanisms: Describe the testing methods used for adjunctive/ confirmatory antimicrobial susceptibility tests, such as enzymatic/molecular assays (e.g. Xpert MTB/RIF, mecA PCR) and	"Quantitative PCR" (**Methods and Materials**) describes the qPCR method targeting the bla_{CTX-M} resistance gene and

		inducible resistance assays, with reference to a recognised international standard, where available. Where an international standard was followed, the specific edition of guidelines used should be referenced. Deviations from standard methodology should be described, along with evidence of validation.	the use of internal standards.
	11	Antimicrobial resistance definitions: Define resistance for each antimicrobial class (i.e. are isolates in the 'intermediate' category included within 'susceptible' or 'resistant' or analysed as a distinct category). If using the term, define MDR (e.g. ≥ 1 agent in ≥ 3 classes tested). For each organism type, an MDR test panel must be defined, consisting of the minimum panel of individual antimicrobial agents/classes against which an isolate must be tested for that isolate to be considered tested for MDR status. Antimicrobials to which an organism is intrinsically resistant cannot be part of the test panel or contribute to MDR status	Described in "Identification of ESBL producing organism carriers" in **Methods and Materials.**
Quality assurance	12	External quality assurance: State whether the microbiology laboratory participates in an external quality control programme and, if so, provide scheme details. Examples include the UK National External Quality Assurance Scheme (www.ukneqasmicro.org.uk) and the American College of Pathologists External Quality Assurance/Proficiency Testing Program (https://www.cap.org/)	Laboratory quality validation described in "Identification of ESBL producing organism carriers" in **Methods and Materials.**
	13	Accreditation: State whether the laboratory is accredited through a national or international body (e.g. the International Standards Organisation, ISO) and specify which assays are covered in the accreditation.	Described in "Identification of ESBL producing organism carriers" in **Methods and Materials.**
Bias	14	Duplicate and sequential isolates: The strategy for accounting for duplicate	Duplicated and sequential

		and sequential isolates from the same patient should be clearly detailed. Duplicate isolates are multiple isolates of the same phenotypic organism (i.e. same species and same resistance profile) from the same patient on the same date cultured either from the same clinical specimen, or from two separate clinical specimens, such as blood and CSF. Sequential isolates are isolates of the same phenotypic organism from the same patient at different dates, such as blood cultures taken on different dates. Various strategies for the handling of duplicate and sequential isolates exist [11], and the strategy used should be transparent as it will bias pooled resistance results. For example, inclusion of all isolates (the 'all isolate strategy') has been shown to shift pooled resistance proportions toward greater resistance, whilst inclusion of only the first isolate per patient (the 'first isolate strategy') or only the first isolate per infection episode (the 'episode-based strategy') will shift pooled results toward susceptibility.	observations are accounted for in the dynamic model described in "Dynamic within-host model" in **Methods and Materials.**
Results			
	15	Population: Describe the demographics of the population from which clinical specimens and subsequent isolates have been obtained, disaggregating age and gender data.	"Study participants and follow-up" (**Methods and Materials**) describes the study setting with regard to abundance of EBSL resistance and the population served by the hospitals.
	16	Denominators: Patient and isolate denominators should be used appropriately to ensure clarity regarding the numbers included in each analysis. Of particular importance is the reporting of resistance where first- and second-line	Not applicable.

		AST panels were used (i.e. not all isolates of a particular species were tested against all agents). For drugs where only a subset of isolates was tested, reporting of a percentage without the numbers of isolates tested/resistant may be highly misleading.	
	17	Site/place of acquisition: AST data from CAI and HAI should be reported and analysed separately.	All ESBL producing organisms are considered CAI.
	18	Reporting resistance proportions for single agent and class resistance: Proportions of resistant isolates should be reported as number of isolates susceptible or resistant to a given antimicrobial agent/class out of actual number of isolates tested for susceptibility to that agent/class.	Not applicable.
	19	Reporting multidrug resistance proportions: If defined, the proportion of MDR isolates should be expressed as the number of MDR isolates out of the number of isolates tested (i.e. the number undergoing the MDR test panel specific to that organism). Single agent/class resistance should be always be reported, regardless of MDR reporting.	Not applicable.
Discussion			
Limitations	20	Discuss any reasons why bias may have been introduced into the reported data, due to patient/specimen selection, isolation of organisms, or otherwise. Consider factors which may have either introduced bias into the types of organisms isolated or the antimicrobial susceptibility profiles, e.g. receipt of antimicrobials prior to specimen collection will reduce the yield of certain species and also select for more resistant organisms.	Sources for bias and transportability is discussed in **Discussion and Conclusion.**