**Supplementary Information**

**Appendix 1. Bayesian multinomial mixture model description**

Our model describes the empirical distribution of isolates of different groups (STs, AMRs profiles) *y* as a mixture of *K* different sampled origins noted *x*1, *x*2, ..., *xK* with corresponding mixture coefficient  *α*1, *α*2, ..., *αK* (with *α*1 + *α*2 + ... + *αK* = 1). These coefficients are weights describing the contributions of each origin to the observed distribution of interest. We noted *n*1, *n*2, ..., *nK* the sample sizes of the origins, and *n* the sample size of *y*. Assuming that all origins contribute independently to *y*, the distribution of *y* is defined as:

*y* ~ Multinomial(*α*1 *φ*1, *α2**φ*2, ..., *αK**φK*, *n*)

where *φi*is the frequency distribution of the groups in origin *i*. Similiary, the empirical distribution within any origin *i* is defined as:

*xi* ~ Multinomial(*φi*, *ni*)

Given these distributions, we can write the posterior distribution of our model as:

*p*(y, *x*1, *x*2, ..., *xK* | *α*1 *φ*1, *α2**φ*2, ..., *αK**φK*) =

( *p*(y, *x*1, *x*2, ..., *xK* | *α*1 *φ*1, *α2**φ*2, ..., *αK**φK*) *p*(*α*1 *φ*1, *α2**φ*2, ..., *αK**φK*) ) / *p*(y, *x*1, *x*2, ..., *xK*)

where *p*(y, *x*1, *x*2, ..., *xK*) is a constant representing the marginal probability of the data. This posterior distribution is then proportional to:

 *p*(y, *x*1, *x*2, ..., *xK* | *α*1 *φ*1, *α2**φ*2, ..., *αK**φK*) *p*(*α*1 *φ*1, *α2**φ*2, ..., *αK**φK*)

where the first term is the likelihood of our model, and the second term represents the priors. The likelihood is written as a product of independent terms:

 *p*(y, *x*1, *x*2, ..., *xK* | *α*1 *φ*1, *α2**φ*2, ..., *αK**φK*) =

*p*(y | *α*1 *φ*1, *α2**φ*2, ..., *αK**φK*) *p*(*x*1 | *α*1 *φ*1) *p*(*x*2 | *α2**φ*2) ... *p*(*xK*| *αK**φK*) =

*FM*(y, *α*1 *φ*1, *α2**φ*2, ..., *αK**φK, n*) *FM*(*x*1, *φ*1, *n*1) *FM*(*x*2, *φ2*, *n*2) ... *FM*(*xK*, *φK*, *nK*)

where *FM* refers to the Multinomial probability mass function.

The joint prior distribution is rewritten as a product of independent components:

*p*(*α*1 *φ*1, *α2**φ*2, ..., *αK**φK*) =

*p*(*α*1, *α2*, ..., *αK*) *p*(*φ*1, *φ*2, ..., *φK*) =

*p*(*α*1, *α2*, ..., *αK*) *p*(*φ*1) *p*(*φ*2) ... *p*(*φK*)

We assume no prior information on the mixture coefficients or the group frequencies so that these priors can be modelled by a constant Dirichlet distribution, and are effectively treated as constants in the estimation procedure.

The model above can be easily extended to incorporate an *unsampled* origin, by adding a new origin *xunsampled* containing only 0s and with sample size *nunsampled* = 0, and frequencies *φunsampled*.

**Estimation**

Markov Chain Monte Carlo can be used to derive samples of the parameters from the posterior distribution. We use a simple Metropolis algorithm for all parameters, using Dirichlet proposals for the mixture coefficients and for the group frequencies. In theory, both the contribution coefficients and the frequencies could be estimated simultaneously. However, for computational efficiency frequencies of groups in the different origins *φi*can also be fixed to their Maximum Likelihood estimates so that *φi* = *xi* / *ni.*Note that if the model includes an unsampled origin, group frequencies *φunsampled* have to be estimated, whether or not other frequency distributions *φi*are estimated or fixed. Convergence is assessed by ensuring stationarity of the different parameters from visual inspection of their traces.

**Availability**

The Bayesian Mixture model has been implemented in the R package *bmmix* available from CRAN and github:

CRAN: <https://cran.r-project.org/web/packages/bmmix/index.html>

github (development version): <https://github.com/thibautjombart/bmmix>

*bmmix* is distributed under Gnu General Public License (GPL) ≥ 2.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Study name** | **Period** | **Location** | **Study type** | **Study population** | **Study aims** |
| The Vietnam Initiative on Zoonotic Infections (VIZIONs). | Not specified (5 years of retrospective and 5 years of prospective data from provincial hospitals) and high risk-cohorts. | Provincial hospitals in Dong Thap, Ho ChiMinh City, Dak Lak, Khanh Hoa, Hue, Hanoi, and Ba Vi; and high risk cohorts in Dong Thap, DakLak, and Ba Vi. | Hospital-based surveillance program + longitudinal cohort study | 1) Disease surveillance in provincial hospitals: ongoing enrollment of patients (>12,000 over 5 years) with diarrhea, respiratory tract infections, aundice/hepatitis, and central nervous system infections. 2) High-risk cohort and social studies: Animal baseline sampling in three provinces; enrolment of 852 cohort members (farmers, animal health workers, butchers, market traders); follow-up sampling every 12 months. | 1. To establish international collaborative consortium with an integrated approach to human and animal health research;2. To estimate the burden of zoonotic diseases disease and investigate the disease epidemiology in hospitalized patients and individuals occupationally exposed to animals;3. To characterize genetic diversity and describe disease transmission;4. To identify socio-demographic, environmental, and behavioral drivers for disease emergence. |
| The bacterial etiology and antimicrobial susceptibility profile of bloodstream infections at the Hospital for Tropical Diseases in Ho Chi Minh City. | January 2010-December 2013 | Hospital for Tropical Diseases (HTD), Ho Chi Minh City, Vietnam | Retrospective hospital-based study | Patients at HTD with a positive bacterial culture from a blood sample from the 1st January 2010 to 31st December 2013 | To understand the main causes of bacteremia and their associated antimicrobial susceptibility profiles at HTD. |
| The aetiology diarrheal disease in children in Hoi Chi Minh City | May 2009-April 2010 | Children’s Hospital 1 (CH1), Children’s Hospital 2 (CH2), and the Hospital for Tropical Diseases (HTD), Ho Chi Minh City, Vietnam | Prospective hospital-based study | Patients at CH1, CH2, and HTD with a positive bacterial culture from stool | To understand the aetiology of diarrhea in Southern Vietnam |
| The Vietnam Bacterial Resistance (VIBRE). | March 2012 to April 2013 | Tien Giang | Cross-sectional study | 204 backyard chicken farms, 204 farmers and 306 matched individuals not exposed to chicken farming. | To investigate the risk of NTS colonization in humans as a result of direct animal exposure. |

**Table S1.** Characteristics of the studies included in our analyses

**Table S2.** The distribution of NTS serovars and corresponding sequence types among human blood isolates in Vietnam.

|  |  |  |
| --- | --- | --- |
| Serovar/ Sequence type | No. | % |
| Enteritidis | 62 | 41.89 |
|  ST 11 | 62 | 100 |
| Typhimurium | 44 | 29.73 |
|  ST 34 | 28 | 63.64 |
|  ST 19 | 14 | 31.82 |
|  ST 1544 | 2 | 4.55 |
| Choleraesuis | 15 | 10.14 |
|  ST 68 | 14 | 93.33 |
|  ST 139 | 1 | 6.67 |
| Paratyphi B var Java | 3 | 2.03 |
|  ST 42 | 1 | 33.33 |
|  ST 135 | 1 | 33.33 |
|  ST 423 | 1 | 33.33 |
| Rissen | 3 | 2.03 |
|  ST 469 | 3 | 100 |
| Stanley | 3 | 2.03 |
|  ST 29 | 3 | 100 |
| Corvallis | 2 | 1.35 |
|  ST 1541  | 2 | 100 |
| Give | 2 | 1.35 |
|  ST 516 | 2 | 100 |
| Sub species IV | 2 | 1.35 |
|  ST 958 | 2 | 100 |
| Albany | 1 | 0.68 |
|  ST 292 | 1 | 100 |
| Brandenburg | 1 | 0.68 |
|  ST 20 | 1 | 100 |
| Derby | 1 | 0.68 |
|  ST 40 | 1 | 100 |
| Indiana | 1 | 0.68 |
|  ST 17 | 1 | 100 |
| Montevideo | 1 | 0.68 |
|  ST 1531 | 1 | 100 |
| Newport | 1 | 0.68 |
|  ST 31 | 1 | 100 |
| Schwarzengrund | 1 | 0.68 |
|  ST 96  | 1 | 100 |
| Weltevreden | 1 | 0.68 |
|  ST 365 | 1 | 100 |
| N/A | 4 | 2.70 |
|  ST 48 | 2 | 50 |
|  ST 1864 | 1 | 25 |
|  ST 1873 | 1 | 25 |
| **Total** | **148** | **100** |

**Table S3.** The distribution of NTS serovars and corresponding sequence types among human stool isolates in Vietnam.

|  |  |  |  |
| --- | --- | --- | --- |
| Serovar/Sequence type | No. | % |  |
| Typhimurium | 46 | 21.8 |  |
|  ST 19 | 21 | 45.65 |  |
|  ST 34 | 20 | 43.48 |  |
|  ST 36 | 2 | 4.35 |  |
|  ST 99 | 1 | 2.17 |  |
|  ST 313 | 1 | 2.17 |  |
|  ST 1544 | 1 | 2.17 |  |
| Weltevreden | 41 | 19.43 |  |
|  ST 365 | 33 | 80.49 |  |
|  ST 1500 | 8 | 19.51 |  |
| Newport | 11 | 5.21 |  |
|  ST 46 | 9 | 81.82 |  |
|  ST 31 | 2 | 18.18 |  |
| Derby | 10 | 4.74 |  |
|  ST 40 | 10 | 100 |  |
| Stanley | 9 | 4.27 |  |
|  ST 29 | 8 | 88.89 |  |
|  ST 1550 | 1 | 11.11 |  |
| Rissen | 8 | 3.79 |  |
|  ST 469 | 8 | 100 |  |
| Enteritidis | 6 | 2.84 |  |
|  ST 11 | 6 | 100 |  |
| Litchfield | 5 | 2.37 |  |
|  ST 1499 | 3 | 60 |  |
|  ST 214 | 2 | 40 |  |
| Corvallis | 4 | 1.9 |  |
|  ST 1541 | 4 | 100 |  |
| Paratyphi B var Java monophasic | 4 | 1.9 |  |
|  ST 423 | 4 | 100 |  |
| Give | 3 | 1.42 |  |
|  ST 516 | 3 | 100 |  |
| Virchow | 3 | 1.42 |  |
|  ST 359 | 2 | 66.67 |  |
|  ST 197 | 1 | 33.33 |  |
| Anatum | 2 | 0.95 |  |
|  ST 64 | 2 | 100 |  |
| Braenderup | 2 | 0.95 |  |
|  ST 22 | 2 | 100 |  |
| Bredeney | 2 | 0.95 |  |
|  ST 1543 | 2 | 100 |  |
| Hadar | 2 | 0.95 |  |
|  ST 33 | 2 | 100 |  |
| Kentucky | 2 | 0.95 |  |
|  ST 314 | 2 | 100 |  |
| London | 2 | 0.95 |  |
|  ST 155 | 2 | 100 |  |
| Mbandaka | 2 | 0.95 |  |
|  ST 413 | 2 | 100 |  |
| Ohio | 2 | 0.95 |  |
|  ST 329 | 2 | 100 |  |
| Bareilly | 1 | 0.47 |  |
|  ST 203 | 1 | 100 |  |
| Cerro var. Siegburg | 1 | 0.47 |  |
|  ST 367 | 1 | 100 |  |
| Indiana | 1 | 0.47 |  |
|  ST 17 | 1 | 100 |  |
| Meleagridis | 1 | 0.47 |  |
|  ST 463 | 1 | 100 |  |
| Muenchen | 1 | 0.47 |  |
|  ST 82 | 1 | 100 |  |
| Orientalis | 1 | 0.47 |  |
|  ST 558 | 1 | 100 |  |
| Pomona | 1 | 0.47 |  |
|  ST 451 | 1 | 100 |  |
| Rubislaw | 1 | 0.47 |  |
|  ST 820 | 1 | 100 |  |
| Saintpaul | 1 | 0.47 |  |
|  ST 50 | 1 | 100 |  |
| Subspecies IIIb | 1 | 0.47 |  |
|  ST 430 | 1 | 100 |  |
| Worthington | 1 | 0.47 |  |
|  ST 592 | 1 | 100 |  |
| N/A | 34 | 16.11 |  |
|  ST 1542 | 10 | 29.41 |  |
|  ST 292 | 7 | 20.59 |  |
|  ST 48 | 3 | 8.82 |  |
|  ST 74 | 2 | 5.88 |  |
|  ST 1546 | 2 | 5.88 |  |
|  ST 909 | 1 | 2.94 |  |
|  ST 1545 | 1 | 2.94 |  |
|  ST 1547 | 1 | 2.94 |  |
|  ST 1548 | 1 | 2.94 |  |
|  ST 1549 | 1 | 2.94 |  |
|  ST 1561 | 1 | 2.94 |  |
|  ST 1562 | 1 | 2.94 |  |
|  ST 1867 | 1 | 2.94 |  |
|  ST 1871 | 1 | 2.94 |  |
|  ST 1874 | 1 | 2.94 |  |
| **Total** | **211** | **100** |  |

**Table S4.** The distribution of NTS serovars and corresponding sequence types among NTS animal isolates in Vietnam.

|  |  |  |
| --- | --- | --- |
| **Serovar/ Sequence type** | **No.** | **%** |
| Weltevreden | 43 | 13.74 |
|  ST 1500 | 41 | 95.35 |
|  ST 365 | 2 | 4.65 |
| Typhimurium | 32 | 10.22 |
|  ST 1544 | 14 | 43.75 |
|  ST 19 | 9 | 28.13 |
|  ST 34 | 7 | 21.88 |
|  ST 36 | 2 | 6.25 |
| Paratyphi B var Java monophasic | 26 | 8.31 |
|  ST 423 | 13 | 50 |
|  ST 42 | 8 | 30.77 |
|  ST 135 | 4 | 15.38 |
|  ST 43 | 1 | 3.85 |
| Indiana | 18 | 5.75 |
|  ST 17 | 18 | 100 |
| Newport | 17 | 5.43 |
|  ST 31 | 11 | 64.71 |
|  ST 46 | 6 | 35.29 |
| Enteritidis | 16 | 5.11 |
|  ST 11 | 14 | 87.5 |
|  ST 180 | 1 | 6.25 |
|  ST 1863 | 1 | 6.25 |
| Derby | 14 | 4.47 |
|  ST 40 | 14 | 100 |
| Rissen | 10 | 3.19 |
|  ST 469 | 10 | 100 |
| Anatum | 8 | 2.56 |
|  ST 64 | 8 | 100 |
| Hadar | 8 | 2.56 |
|  ST 33 | 8 | 100 |
| Oslo | 8 | 2.56 |
|  ST 1370 | 8 | 100 |
| Give | 7 | 2.24 |
|  ST 516 | 7 | 100 |
| Kentucky | 7 | 2.24 |
|  ST 314 | 6 | 85.71 |
|  ST 1865 | 1 | 14.29 |
| Meleagridis | 6 | 1.92 |
|  ST 463 | 6 | 100 |
| London | 5 | 1.6 |
|  ST 155 | 5 | 100 |
| Albany | 4 | 1.28 |
|  ST 292 | 4 | 100 |
| Senftenberg | 4 | 1.28 |
|  ST 14 | 4 | 100 |
| Stanley | 4 | 1.28 |
|  ST 29 | 2 | 50 |
|  ST 182 | 2 | 50 |
| Tennessee | 4 | 1.28 |
|  ST 319 | 4 | 100 |
| Braenderup | 3 | 0.96 |
|  ST 22 | 3 | 100 |
| Litchfield | 3 | 0.96 |
|  ST 1499 | 3 | 100 |
| Sandiego | 3 | 0.96 |
|  ST 1568 | 3 | 100 |
| Virchow | 3 | 0.96 |
|  ST 359 | 3 | 100 |
| Bareilly | 2 | 0.64 |
|  ST 203 | 2 | 100 |
| Corvallis | 2 | 0.64 |
|  ST 1541 | 2 | 100 |
| Bovismorbificans | 1 | 0.32 |
|  ST 1058 | 1 | 100 |
| Heidelberg | 1 | 0.32 |
|  ST 15 | 1 | 100 |
| Mbandaka | 1 | 0.32 |
|  ST 413 | 1 | 100 |
| Saintpaul | 1 | 0.32 |
|  ST 50 | 1 | 100 |
| Tananarive | 1 | 0.32 |
|  ST 1794 | 1 | 100 |
| Urbana | 1 | 0.32 |
|  ST 512 | 1 | 100 |
| N/A | 50 | 15.97 |
|  ST 1547 | 13 | 26 |
|  ST 74 | 9 | 18 |
|  ST 1546 | 9 | 18 |
|  ST 1562 | 7 | 14 |
|  ST 292 | 4 | 8 |
|  ST 1861 | 3 | 6 |
|  ST 1867 | 3 | 6 |
|  ST 1866 | 1 | 2 |
|  ST 1868 | 1 | 2 |
| **Total** | **313** | **100** |

**Table S5.** Distribution of 40 antimicrobial susceptibility profiles among human blood NTS isolates in Vietnam.

|  |  |  |  |
| --- | --- | --- | --- |
| Antimicrobial susceptibility profilea | No. of antimicrobial agents | No. of isolates | % |
| Fully susceptible | 0 | 28 | 18.92 |
| Gen | 1 | 1 | 0.68 |
| Cip | 1 | 18 | 12.16 |
| Amp | 1 | 19 | 12.84 |
| ChlCip | 2 | 2 | 1.35 |
| CtxCip | 2 | 1 | 0.68 |
| AmpSxt | 2 | 7 | 4.73 |
| AmpGen | 2 | 1 | 0.68 |
| AmpCip | 2 | 7 | 4.73 |
| AmpChl | 2 | 3 | 2.03 |
| AmpGenSxt | 3 | 1 | 0.68 |
| AmpCpSxt | 3 | 1 | 0.68 |
| AmpChlSxt | 3 | 4 | 2.7 |
| AmpChlGen | 3 | 1 | 0.68 |
| AmpChlCip | 3 | 3 | 2.03 |
| AmpCipGenSxt | 4 | 4 | 2.7 |
| AmpChlGenSxt | 4 | 3 | 2.03 |
| AmpChlCipSxt | 4 | 4 | 2.7 |
| AmpChlCipGen | 4 | 2 | 1.35 |
| AmpAkChlSxt | 4 | 1 | 0.68 |
| AmpAkChlCip | 4 | 2 | 1.35 |
| AmpChlCipGenSxt | 5 | 16 | 10.81 |
| AmpAkCipGenSxt | 5 | 1 | 0.68 |
| AmpAkChlGenSxt | 5 | 2 | 1.35 |
| AmpAkChlCipSxt | 5 | 2 | 1.35 |
| AmpAkChlCipGen | 5 | 2 | 1.35 |
| AmpCfzCtxChlGenSxt | 6 | 1 | 0.68 |
| AmpAkChlCipGenSxt | 6 | 9 | 6.08 |
| AmpAkCtxChlCipGenSxt | 7 | 1 | 0.68 |
| AmpAkCfzCtxChlCipGenSxt | 8 | 1 | 0.68 |
| **Total** |  | **148** | **100** |

aAbbreviated antimicrobial agents: Amp, ampicillin; Ak, amikacin; Caz, ceftazidime, Ctx, ceftriaxone; Chl, chloramphenicol, Cip, ciprofloxacin; Gen, gentamicin; Stx, trimethoprim-sulfamethoxazole

**Table S6.** The distribution of 30 antimicrobial susceptibility profiles among human stool NTS isolates in Vietnam.

|  |  |  |  |
| --- | --- | --- | --- |
| **Antimicrobial susceptibility profilea** | **No. of antimicrobial agents** | **No. of isolates** | **%** |
| Fully susceptible | 0 | 111 | 52.61 |
| Sxt | 1 | 8 | 3.79 |
| Gen | 1 | 5 | 2.37 |
| Cip | 1 | 6 | 2.84 |
| Chl | 1 | 5 | 2.37 |
| Amp | 1 | 16 | 7.58 |
| CipSxt | 2 | 1 | 0.47 |
| ChlSxt | 2 | 1 | 0.47 |
| AkChl | 2 | 1 | 0.47 |
| AmpSxt | 2 | 4 | 1.9 |
| AmpAk | 2 | 3 | 1.42 |
| ChlCipSxt | 3 | 1 | 0.47 |
| CfzChlCip | 3 | 1 | 0.47 |
| AmpGenSxt | 3 | 2 | 0.95 |
| AmpChlSxt | 3 | 16 | 7.58 |
| AmpChlGen | 3 | 3 | 1.42 |
| AmpChlGenSxt | 4 | 7 | 3.32 |
| AmpChlCipSxt | 4 | 1 | 0.47 |
| AmpAkGenSxt | 4 | 1 | 0.47 |
| AmkAkChlSxt | 4 | 3 | 1.42 |
| AmpAkChlGen | 4 | 2 | 0.95 |
| AmkAkChlCip | 4 | 1 | 0.47 |
| AmpAkCfzCtx | 4 | 2 | 0.95 |
| AmpChlCipGenSxt | 5 | 2 | 0.95 |
| AmpAkChlGenSxt | 5 | 1 | 0.47 |
| AmkAkChlCipSxt | 5 | 1 | 0.47 |
| AmkAkChlCipGen | 5 | 2 | 0.95 |
| AmkAkCfzCtxGenSxt | 6 | 1 | 0.47 |
| AmkAkCfzCtxChlSxt | 6 | 2 | 0.95 |
| AmpAkCfzCtxChlCipGenSxt | 8 | 1 | 0.47 |
| **Total**  |  | **211** | **100** |

aAbbreviated antimicrobial agents: Amp, ampicillin; Ak, amikacin; Caz, ceftazidime, Ctx, ceftriaxone; Chl, chloramphenicol, Cip, ciprofloxacin; Gen, gentamicin; Stx, trimethoprim-sulfamethoxazole

**Table S7.** The distribution of 34 antimicrobial susceptibility profiles among animal NTS isolates in Vietnam.

|  |  |  |  |
| --- | --- | --- | --- |
| Antimicrobial susceptibility profilea | No. of antimicrobial agents | No. of isolates | % |
| Fully susceptible | 0 | 167 | 53.35 |
| Sxt | 1 | 10 | 3.19 |
| Gen | 1 | 3 | 0.96 |
| Cip | 1 | 29 | 9.27 |
| Chl | 1 | 8 | 2.56 |
| Cfz | 1 | 1 | 0.32 |
| Ak | 1 | 1 | 0.32 |
| Amp | 1 | 15 | 4.79 |
| CipSxt | 2 | 1 | 0.32 |
| CipGen | 2 | 1 | 0.32 |
| ChlSxt | 2 | 14 | 4.47 |
| ChlCip | 2 | 1 | 0.32 |
| CtxChl | 2 | 1 | 0.32 |
| AkCip | 2 | 1 | 0.32 |
| AmpSxt | 2 | 4 | 1.28 |
| AmpCip | 2 | 2 | 0.64 |
| AmpChl | 2 | 3 | 0.96 |
| AmpAk | 2 | 4 | 1.28 |
| ChlCipSxt | 3 | 1 | 0.32 |
| AkChlSxt | 3 | 1 | 0.32 |
| AkChlCip | 3 | 1 | 0.32 |
| AmpGenSxt | 3 | 1 | 0.32 |
| AmpCipSxt | 3 | 1 | 0.32 |
| AmpChlSxt | 3 | 12 | 3.83 |
| AmpChlGenSxt | 4 | 3 | 0.96 |
| AmpChlCipSxt | 4 | 9 | 2.88 |
| AmpAkCipSxt | 4 | 1 | 0.32 |
| AmpAkChlSxt | 4 | 2 | 0.64 |
| AmpChlCipGenSxt | 5 | 5 | 1.6 |
| AmpAkChlCipSxt | 5 | 4 | 1.28 |
| AmpAkChlCipGen | 5 | 1 | 0.32 |
| AmpAkCfzCtxChl | 5 | 1 | 0.32 |
| AmpAkChlCipGenSxt | 6 | 3 | 0.96 |
| AmpAkCfzCtxChlGen | 6 | 1 | 0.32 |
| **Total** |  | **313** | **100** |

aAbbreviated antimicrobial agents: Amp, ampicillin; Ak, amikacin; Caz, ceftazidime, Ctx, ceftriaxone; Chl, chloramphenicol, Cip, ciprofloxacin; Gen, gentamicin; Stx, trimethoprim-sulfamethoxazole

**Table S8.** The distribution of 66 ST-AMR profiles among human blood NTS isolates in Vietnam.

|  |  |  |  |
| --- | --- | --- | --- |
| ST\_Antimicrobial susceptibility profilea | No. of antimicrobial agents | No. of isolates | % |
| 11\_Fully susceptible | 0 | 19 | 12.84 |
| 11\_Cip | 1 | 9 | 6.08 |
| 11\_Amp | 1 | 18 | 12.16 |
| 11\_AmpSxt | 2 | 5 | 3.38 |
| 11\_AmpGen | 2 | 1 | 0.68 |
| 11\_AmpCip | 2 | 5 | 3.38 |
| 11\_AmpChl | 2 | 1 | 0.68 |
| 11\_AmpCipSxt | 3 | 1 | 0.68 |
| 11\_AmpChlSxt | 3 | 1 | 0.68 |
| 11\_AmpChlCip | 3 | 2 | 1.35 |
| 17\_AmpAkChlCipGenSxt | 6 | 1 | 0.68 |
| 19\_Fully susceptible | 0 | 2 | 1.35 |
| 19\_Gen | 1 | 1 | 0.68 |
| 19\_AmpCipGenSxt | 4 | 2 | 1.35 |
| 19\_AmpChlCipSxt | 4 | 3 | 2.03 |
| 19\_AmpAkChlCip | 4 | 2 | 1.35 |
| 19\_AmpAkChlSxt | 4 | 1 | 0.68 |
| 19\_AmpChlCipGen | 4 | 1 | 0.68 |
| 19\_AmpChlCipGenSxt | 5 | 1 | 0.68 |
| 19\_AmpAkCipGenSxt | 5 | 1 | 0.68 |
| 20\_Fully susceptible | 0 | 1 | 0.68 |
| 29\_Fully susceptible | 0 | 1 | 0.68 |
| 29\_Cip | 1 | 1 | 0.68 |
| 29\_Amp | 1 | 1 | 0.68 |
| 31\_CtxCip | 2 | 1 | 0.68 |
| 34\_Cip | 1 | 1 | 0.68 |
| 34\_ChlCip | 2 | 1 | 0.68 |
| 34\_AmpCip | 2 | 2 | 1.35 |
| 34\_AmpChl | 2 | 1 | 0.68 |
| 34\_AmpChlSxt | 3 | 1 | 0.68 |
| 34\_AmpChlCip | 3 | 1 | 0.68 |
| 34\_AmpChlGen | 3 | 1 | 0.68 |
| 34\_AmpChlGenSxt | 4 | 1 | 0.68 |
| 34\_AmpChlCipGen | 4 | 1 | 0.68 |
| 34\_AmpChlCipGenSxt | 5 | 5 | 3.38 |
| 34\_AmpAkChlGenSxt | 5 | 2 | 1.35 |
| 34\_AmpAkChlCipSxt | 5 | 1 | 0.68 |
| 34\_AmpAkChlCipGen | 5 | 2 | 1.35 |
| 34\_AmpAkChlCipGenSxt | 6 | 7 | 4.73 |
| 34\_AmpAkCtxChlCipGenSxt | 7 | 1 | 0.68 |
| 40\_AmpChl | 2 | 1 | 0.68 |
| 42\_Cip | 1 | 1 | 0.68 |
| 48\_AmpChlGenSxt | 4 | 1 | 0.68 |
| 48\_AmpChlCipGenSxt | 5 | 1 | 0.68 |
| 68\_AmpChlSxt | 3 | 1 | 0.68 |
| 68\_AmpGenSxt | 3 | 1 | 0.68 |
| 68\_AmpCipGenSxt | 4 | 2 | 1.35 |
| 68\_AmpChlGenSxt | 4 | 1 | 0.68 |
| 68\_AmpChlCipGenSxt | 5 | 8 | 5.41 |
| 68\_AmpAkCfzCtxChlCipGenSxt | 8 | 1 | 0.68 |
| 96\_AmpChlCipGenSxt | 5 | 1 | 0.68 |
| 135\_Gen | 1 | 1 | 0.68 |
| 139\_AmpCfzCtxChlGenSxt | 6 | 1 | 0.68 |
| 292\_AmpAkChlCipSxt | 5 | 1 | 0.68 |
| 365\_Cip | 1 | 1 | 0.68 |
| 423\_Cip | 1 | 1 | 0.68 |
| 469\_AmpSxt | 2 | 2 | 1.35 |
| 469\_AmpChlSxt | 3 | 1 | 0.68 |
| 516\_ChlCip | 2 | 1 | 0.68 |
| 516\_AmpChlCipSxt | 4 | 1 | 0.68 |
| 958\_Fully susceptible | 0 | 2 | 1.35 |
| 1531\_Cip | 1 | 1 | 0.68 |
| 1541\_Cip | 1 | 2 | 1.35 |
| 1544\_Fully susceptible | 0 | 2 | 1.35 |
| 1864\_Fully susceptible | 0 | 1 | 0.68 |
| 1873\_AmpAkChlCipGenSxt | 6 | 1 | 0.68 |
| **Total** |  | **148** | **100** |

aAbbreviated antimicrobial agents: Amp, ampicillin; Ak, amikacin; Caz, ceftazidime, Ctx, ceftriaxone; Chl, chloramphenicol, Cip, ciprofloxacin; Gen, gentamicin; Stx, trimethoprim-sulfamethoxazole

**Table S9.** The distribution of 110 ST-AMR profiles among human stool NTS isolates in Vietnam.

|  |  |  |  |
| --- | --- | --- | --- |
| ST\_Antimicrobial susceptibility profilea | No. of antimicrobial agents | No. of isolates | % |
| 11\_Fully susceptible | 0 | 1 | 0.47 |
| 11\_Amp | 1 | 5 | 2.37 |
| 17\_AmpAkChlCipGen | 5 | 1 | 0.47 |
| 19\_Fully susceptible | 0 | 3 | 1.42 |
| 19\_Sxt | 1 | 2 | 0.95 |
| 19\_Chl | 1 | 1 | 0.47 |
| 19\_Amp | 1 | 1 | 0.47 |
| 19\_AmpSxt | 2 | 2 | 0.95 |
| 19\_AmpGenSxt | 3 | 1 | 0.47 |
| 19\_AmpChlSxt | 3 | 7 | 3.32 |
| 19\_AmpChlGenSxt | 4 | 1 | 0.47 |
| 19\_AmpAkChlGen | 4 | 1 | 0.47 |
| 19\_AmpAkChlCipSxt | 5 | 1 | 0.47 |
| 19\_AmpAkCfzCtxGenSxt | 6 | 1 | 0.47 |
| 22\_CipSxt | 2 | 1 | 0.47 |
| 22\_AmpAk | 2 | 1 | 0.47 |
| 29\_Fully susceptible | 0 | 5 | 2.37 |
| 29\_Gen | 1 | 1 | 0.47 |
| 29\_AmpChlSxt | 3 | 2 | 0.95 |
| 31\_Fully susceptible | 0 | 1 | 0.47 |
| 31\_ChlCipSxtCtx | 4 | 1 | 0.47 |
| 33\_AmpAk | 2 | 2 | 0.95 |
| 34\_Fully susceptible | 0 | 1 | 0.47 |
| 34\_Amp | 1 | 8 | 3.79 |
| 34\_AmpChlSxt | 3 | 1 | 0.47 |
| 34\_AmpChlGen | 3 | 1 | 0.47 |
| 34\_AmpAkChlGen | 4 | 1 | 0.47 |
| 34\_AmpAkCfzCtx | 4 | 1 | 0.47 |
| 34\_AmpChlGenSxt | 4 | 2 | 0.95 |
| 34\_AmpChlCipGenSxt | 5 | 1 | 0.47 |
| 34\_AmpAkChlGenSxt | 5 | 1 | 0.47 |
| 34\_AmpAkChlCipGen | 5 | 1 | 0.47 |
| 34\_AmpAkCfzCtxChlSxt | 6 | 1 | 0.47 |
| 34\_AmpAkCfzCtxChlCipGenSxt | 8 | 1 | 0.47 |
| 36\_Fully susceptible | 0 | 2 | 0.95 |
| 40\_Fully susceptible | 0 | 3 | 1.42 |
| 40\_Chl | 1 | 3 | 1.42 |
| 40\_AkChl | 2 | 1 | 0.47 |
| 40\_AmpGenSxt | 3 | 1 | 0.47 |
| 40\_AmpChlGenSxt | 4 | 1 | 0.47 |
| 40\_AmpChlCipGenSxt | 5 | 1 | 0.47 |
| 46\_Fully susceptible | 0 | 7 | 3.32 |
| 46\_Cip | 1 | 1 | 0.47 |
| 46\_AmpAkCfzCtx | 4 | 1 | 0.47 |
| 48\_AmpChlGen | 3 | 1 | 0.47 |
| 48\_AmpChlGenSxt | 4 | 2 | 0.95 |
| 50\_Fully susceptible | 0 | 1 | 0.47 |
| 64\_AmpSxt | 2 | 1 | 0.47 |
| 64\_AmpAkGenSxt | 4 | 1 | 0.47 |
| 74\_Fully susceptible | 0 | 2 | 0.95 |
| 82\_Fully susceptible | 0 | 1 | 0.47 |
| 99\_Fully susceptible | 0 | 1 | 0.47 |
| 155\_Fully susceptible | 0 | 2 | 0.95 |
| 197\_Fully susceptible | 0 | 1 | 0.47 |
| 203\_Fully susceptible | 0 | 1 | 0.47 |
| 214\_Fully susceptible | 0 | 1 | 0.47 |
| 214\_AmpChlSxt | 3 | 1 | 0.47 |
| 292\_Sxt | 1 | 2 | 0.95 |
| 292\_AmpChlSxt | 3 | 1 | 0.47 |
| 292\_AmpAkChlSxt | 4 | 3 | 1.42 |
| 292\_AmpAkCfzCtxChlSxt | 6 | 1 | 0.47 |
| 313\_Fully susceptible | 0 | 1 | 0.47 |
| 314\_Fully susceptible | 0 | 2 | 0.95 |
| 329\_Cip | 1 | 1 | 0.47 |
| 329\_CfzChlCip | 3 | 1 | 0.47 |
| 359\_Fully susceptible | 0 | 2 | 0.95 |
| 365\_Fully susceptible | 0 | 27 | 12.8 |
| 365\_Sxt | 1 | 2 | 0.95 |
| 365\_Gen | 1 | 1 | 0.47 |
| 365\_Cip | 1 | 1 | 0.47 |
| 365\_Amp | 1 | 1 | 0.47 |
| 365\_AmpChlSxt | 3 | 1 | 0.47 |
| 367\_Gen | 1 | 1 | 0.47 |
| 413\_Fully susceptible | 0 | 2 | 0.95 |
| 423\_Fully susceptible | 0 | 4 | 1.9 |
| 430\_Fully susceptible | 0 | 1 | 0.47 |
| 451\_Fully susceptible | 0 | 1 | 0.47 |
| 463\_Fully susceptible | 0 | 1 | 0.47 |
| 469\_Fully susceptible | 0 | 7 | 3.32 |
| 469\_AmpSxt | 2 | 1 | 0.47 |
| 516\_Cip | 1 | 1 | 0.47 |
| 516\_AmpChlSxt | 3 | 1 | 0.47 |
| 516\_AmpChlCipSxt | 4 | 1 | 0.47 |
| 558\_Cip | 1 | 1 | 0.47 |
| 592\_Sxt | 1 | 1 | 0.47 |
| 820\_AmpAkChlCip | 4 | 1 | 0.47 |
| 909\_Fully susceptible | 0 | 1 | 0.47 |
| 1499\_Fully susceptible | 0 | 1 | 0.47 |
| 1499\_Chl | 1 | 1 | 0.47 |
| 1499\_AmpChlSxt | 3 | 1 | 0.47 |
| 1500\_Fully susceptible | 0 | 6 | 2.84 |
| 1500\_Sxt | 1 | 1 | 0.47 |
| 1500\_Cip | 1 | 1 | 0.47 |
| 1541\_Fully susceptible | 0 | 4 | 1.9 |
| 1542\_Fully susceptible | 0 | 9 | 4.27 |
| 1542\_Gen | 1 | 1 | 0.47 |
| 1543\_AmpChlGen | 3 | 1 | 0.47 |
| 1543\_AmpChlGenSxt | 4 | 1 | 0.47 |
| 1544\_Fully susceptible | 0 | 1 | 0.47 |
| 1545\_Amp | 1 | 1 | 0.47 |
| 1546\_Fully susceptible | 0 | 2 | 0.95 |
| 1547\_Fully susceptible | 0 | 1 | 0.47 |
| 1548\_ChlSxt | 2 | 1 | 0.47 |
| 1549\_Fully susceptible | 0 | 1 | 0.47 |
| 1550\_AmpChlSxt | 3 | 1 | 0.47 |
| 1561\_Fully susceptible | 0 | 1 | 0.47 |
| 1562\_Gen | 1 | 1 | 0.47 |
| 1867\_Fully susceptible | 0 | 1 | 0.47 |
| 1871\_Fully susceptible | 0 | 1 | 0.47 |
| 1874\_Fully susceptible | 0 | 1 | 0.47 |
| **Total** |  | **211** | **100** |

aAbbreviated antimicrobial agents: Amp, ampicillin; Ak, amikacin; Caz, ceftazidime, Ctx, ceftriaxone; Chl, chloramphenicol, Cip, ciprofloxacin; Gen, gentamicin; Stx, trimethoprim-sulfamethoxazole

**Table S10.** The distribution of 133 ST-AMR profiles among animal NTS isolates in Vietnam.

|  |  |  |  |
| --- | --- | --- | --- |
| ST\_Antimicrobial susceptibility profilea | No. of antimicrobial agents | No. of isolates | % |
| 11\_Fully susceptible | 0 | 7 | 2.24 |
| 11\_Cip | 1 | 2 | 0.64 |
| 11\_Amp | 1 | 4 | 1.28 |
| 11\_AmpCipSxt | 3 | 1 | 0.32 |
| 14\_Fully susceptible | 0 | 3 | 0.96 |
| 14\_AmpChlGenSxt | 4 | 1 | 0.32 |
| 15\_Fully susceptible | 0 | 1 | 0.32 |
| 17\_Fully susceptible | 0 | 2 | 0.64 |
| 17\_Sxt | 1 | 4 | 1.28 |
| 17\_ChlSxt | 2 | 6 | 1.92 |
| 17\_AkChlSxt | 3 | 1 | 0.32 |
| 17\_AmpAkChlSxt | 4 | 1 | 0.32 |
| 17\_AmpChlCipGenSxt | 5 | 3 | 0.96 |
| 17\_AmpAkChlCipGenSxt | 6 | 1 | 0.32 |
| 19\_Fully susceptible | 0 | 3 | 0.96 |
| 19\_AmpSxt | 2 | 1 | 0.32 |
| 19\_AmpChl | 2 | 1 | 0.32 |
| 19\_AmpChlSxt | 3 | 3 | 0.96 |
| 19\_AmpChlGenSxt | 4 | 1 | 0.32 |
| 22\_Cip | 1 | 3 | 0.96 |
| 29\_Fully susceptible | 0 | 2 | 0.64 |
| 31\_Fully susceptible | 0 | 5 | 1.6 |
| 31\_Sxt | 1 | 1 | 0.32 |
| 31\_Cip | 1 | 2 | 0.64 |
| 31\_CipSxt | 2 | 1 | 0.32 |
| 31\_ChlSxt | 2 | 1 | 0.32 |
| 31\_ChlCipSxtCtx | 4 | 1 | 0.32 |
| 33\_Fully susceptible | 0 | 5 | 1.6 |
| 33\_Amp | 1 | 1 | 0.32 |
| 33\_AmpAk | 2 | 2 | 0.64 |
| 34\_Amp | 1 | 2 | 0.64 |
| 34\_AmpGenSxt | 3 | 1 | 0.32 |
| 34\_AmpChlCipGenSxt | 5 | 1 | 0.32 |
| 34\_AmpAkChlCipGen | 5 | 1 | 0.32 |
| 34\_AmpAkChlCipGenSxt | 6 | 1 | 0.32 |
| 34\_AmpAkCfzCtxChlGen | 6 | 1 | 0.32 |
| 36\_Fully susceptible | 0 | 1 | 0.32 |
| 36\_AmpChlSxt | 3 | 1 | 0.32 |
| 40\_Fully susceptible | 0 | 5 | 1.6 |
| 40\_Chl | 1 | 3 | 0.96 |
| 40\_ChlSxt | 2 | 1 | 0.32 |
| 40\_AmpChl | 2 | 1 | 0.32 |
| 40\_AmpChlSxt | 3 | 1 | 0.32 |
| 40\_AmpChlGenSxt | 4 | 1 | 0.32 |
| 40\_AmpChlCipSxt | 4 | 1 | 0.32 |
| 40\_AmpChlCipGenSxt | 5 | 1 | 0.32 |
| 42\_Fully susceptible | 0 | 6 | 1.92 |
| 42\_Cip | 1 | 1 | 0.32 |
| 42\_CtxChl | 2 | 1 | 0.32 |
| 43\_Fully susceptible | 0 | 1 | 0.32 |
| 46\_Fully susceptible | 0 | 5 | 1.6 |
| 46\_Cip | 1 | 1 | 0.32 |
| 50\_Cip | 1 | 1 | 0.32 |
| 64\_Fully susceptible | 0 | 2 | 0.64 |
| 64\_Chl | 1 | 1 | 0.32 |
| 64\_ChlSxt | 2 | 3 | 0.96 |
| 64\_AmpSxt | 2 | 1 | 0.32 |
| 64\_AmpAkCipSxt | 4 | 1 | 0.32 |
| 74\_Fully susceptible | 0 | 8 | 2.56 |
| 74\_Cip | 1 | 1 | 0.32 |
| 135\_Fully susceptible | 0 | 4 | 1.28 |
| 155\_Fully susceptible | 0 | 2 | 0.64 |
| 155\_AmpChlSxt | 3 | 3 | 0.96 |
| 180\_Cip | 1 | 1 | 0.32 |
| 182\_Fully susceptible | 0 | 2 | 0.64 |
| 203\_Sxt | 1 | 1 | 0.32 |
| 203\_AmpAk | 2 | 1 | 0.32 |
| 292\_Sxt | 1 | 1 | 0.32 |
| 292\_AmpAk | 2 | 1 | 0.32 |
| 292\_AmpChlSxt | 3 | 1 | 0.32 |
| 292\_AmpAkChlSxt | 4 | 1 | 0.32 |
| 292\_AmpAkChlCipSxt | 5 | 4 | 1.28 |
| 314\_Fully susceptible | 0 | 5 | 1.6 |
| 314\_AmpChl | 2 | 1 | 0.32 |
| 319\_Fully susceptible | 0 | 3 | 0.96 |
| 319\_ChlCip | 2 | 1 | 0.32 |
| 359\_Fully susceptible | 0 | 3 | 0.96 |
| 365\_Fully susceptible | 0 | 1 | 0.32 |
| 365\_Cip | 1 | 1 | 0.32 |
| 413\_CipGen | 2 | 1 | 0.32 |
| 423\_Fully susceptible | 0 | 10 | 3.19 |
| 423\_Cip | 1 | 2 | 0.64 |
| 423\_Ak | 1 | 1 | 0.32 |
| 463\_Fully susceptible | 0 | 6 | 1.92 |
| 469\_Fully susceptible | 0 | 5 | 1.6 |
| 469\_Chl | 1 | 1 | 0.32 |
| 469\_Amp | 1 | 1 | 0.32 |
| 469\_AmpSxt | 2 | 2 | 0.64 |
| 469\_AmpChlSxt | 3 | 1 | 0.32 |
| 512\_Fully susceptible | 0 | 1 | 0.32 |
| 516\_Fully susceptible | 0 | 2 | 0.64 |
| 516\_Chl | 1 | 1 | 0.32 |
| 516\_AkChlCip | 3 | 1 | 0.32 |
| 516\_AmpChlCipSxt | 4 | 3 | 0.96 |
| 1058\_Fully susceptible | 0 | 1 | 0.32 |
| 1370\_Fully susceptible | 0 | 6 | 1.92 |
| 1370\_Sxt | 1 | 1 | 0.32 |
| 1370\_Cip | 1 | 1 | 0.32 |
| 1499\_Fully susceptible | 0 | 2 | 0.64 |
| 1499\_Amp | 1 | 1 | 0.32 |
| 1500\_Fully susceptible | 0 | 25 | 7.99 |
| 1500\_Sxt | 1 | 2 | 0.64 |
| 1500\_Cip | 1 | 8 | 2.56 |
| 1500\_Cfz | 1 | 1 | 0.32 |
| 1500\_Amp | 1 | 1 | 0.32 |
| 1500\_ChlSxt | 2 | 1 | 0.32 |
| 1500\_AmpCip | 2 | 2 | 0.64 |
| 1500\_AmpAkChlCipGenSxt | 6 | 1 | 0.32 |
| 1541\_Chl | 1 | 1 | 0.32 |
| 1541\_ChlSxt | 2 | 1 | 0.32 |
| 1544\_Fully susceptible | 0 | 8 | 2.56 |
| 1544\_Gen | 1 | 3 | 0.96 |
| 1544\_Amp | 1 | 3 | 0.96 |
| 1546\_Fully susceptible | 0 | 1 | 0.32 |
| 1546\_Cip | 1 | 3 | 0.96 |
| 1546\_AkCip | 2 | 1 | 0.32 |
| 1546\_AmpChlCipSxt | 4 | 4 | 1.28 |
| 1547\_Fully susceptible | 0 | 11 | 3.51 |
| 1547\_Cip | 1 | 1 | 0.32 |
| 1547\_AmpChlCipSxt | 4 | 1 | 0.32 |
| 1562\_Fully susceptible | 0 | 7 | 2.24 |
| 1568\_Amp | 1 | 1 | 0.32 |
| 1568\_AmpChlSxt | 3 | 1 | 0.32 |
| 1568\_AmpAkCfzCtxChl | 5 | 1 | 0.32 |
| 1794\_Amp | 1 | 1 | 0.32 |
| 1861\_Fully susceptible | 0 | 2 | 0.64 |
| 1861\_ChlSxt | 2 | 1 | 0.32 |
| 1863\_Fully susceptible | 0 | 1 | 0.32 |
| 1865\_Fully susceptible | 0 | 1 | 0.32 |
| 1866\_AmpChlSxt | 3 | 1 | 0.32 |
| 1867\_Fully susceptible | 0 | 1 | 0.32 |
| 1867\_Cip | 1 | 2 | 0.64 |
| 1868\_Fully susceptible | 0 | 1 | 0.32 |
| **Total** |  | **313** | **100** |

aAbbreviated antimicrobial agents: Amp, ampicillin; Ak, amikacin; Caz, ceftazidime, Ctx, ceftriaxone; Chl, chloramphenicol, Cip, ciprofloxacin; Gen, gentamicin; Stx, trimethoprim-sulfamethoxazole

**Table S11.** Source attribution models of NTS in human blood and human stool by ST, AMR, and ST-AMR profile

|  |
| --- |
| **1. Model with observed sources** |
|  | **Human blood (n=148)** |  |  | **Human stool (n=211)** |  |
|  |  Mixture coefficient α (x 100)a (95% CrI)b |  |  | Mixture coefficient α (x 100)a (95% CrI)b |  |
|  | Human stool (n=211) | Chicken (n=136) | Duck (n=75) | Pig (n=65) | Rodent (n=37) |  |  | Human blood (n=148) | Chicken (n=136) | Duck (n=75) | Pig (n=65) | Rodent (n=37) |  |
| **ST** | 55.7 (41.3-67.6) | 38.7(26.4-51.0) | 2.6 (0.2-7.7) | 1.4 (0.1-6.7) | 0.7 (0.0-3.8) |  |  | 26.7 (16.9-36.1) | 19.7 (10.9-28.6) | 2.1 (0.1-7.3) | 25.6 (16.4-34.8) | 25.1 (18.3-32.8) |  |
| **AMR** | 17 (4.9-29.8) | 36.5 (23.9-48.5) | 12.2 (2.3-26.2) | 30.3 (16.9-46.1) | 2.8 (0.1-11) |  |  | 7.8 (1.7-16.4) | 7.3 (0.4-20.7) | 24.0 (11.8-39.9) | 45.2(30.5-58.7) | 13.5 (2.2-27.4) |  |
| **ST-AMR** | 31.8 (18.6-46.4) | 53.5 (39.9-66.1) | 3.8 (0.7-9.6) | 7.4 (2.3-16.0) | 1.9 (0.2-6.3) |  |  | 11.0 (5.8-18.2) | 10.8 (4.4-19.3) | 7.5 (3.2-14.0) | 40.2 (31.7-49.4) | 29.6 (22.0-37.4) |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **2. Model with unobserved sources** |
|  | **Human blood (n=148)** |  | **Human stool (n=211)** |
|  | Mixture coefficient α (x 100)a(95% CrI)b |  | Mixture coefficient α (x 100)a (95% CrI)b |
|  | Human stool (n=211) | Chicken (n=136) | Duck (n=75) | Pig (n=65) | Rodent (n=37) | Unobserved source |  | Human blood (n=148) | Chicken (n=136) | Duck (n=75) | Pig (n=65) | Rodent (n=37) | Unobserved source |
| **ST** | 44.1 (31.8-59.7) | 36.0 (20.9-48.2) | 2.2 (0.1-7.3) | 1.8 (0.0-7.0) | 0.7 (0.0-3.5) | 12.8(7.7-24.8) |   | 2.8 (0.2-11.3) | 34.4 (20.5-47) | 2.5 (0.2-8.5) | 2.0(0.1-8.4) | 1.2 (0.0-4.9) | 54.7 (42.7-67.3) |
| **AMR** | 6.2 (0.3-25.2) | 19.4 (3.0-37.6) | 4.9 (0.1-20.1) | 31.2 (13.4-46.5) | 12.3 (0.6-26.8) | 21.9 (14.6-31.0) |  | 2.3 (0.1-10.3) | 5.7 (0.3-18.5) | 21.7(8.0-38.2) | 45.3(32.1-58.5) | 16.8 (3.1-30.6) | 5.4 (2.4-9.7) |
| **ST-AMR** | 2.8 (0.2-11.3) | 34.4 (20.5-47) | 2.5 (0.2-8.5) | 2.0 (0.1-8.4) | 1.2(0.0-4.9) | 54.7 (42.7-67.3) |  | 2.6 (0.3-7.6) | 6.2 (0.6-15.2) | 2.4 (0.1-8.1) | 28.4 (20.9-35.8) | 6.1 (0.7-15.7) | 52.9 (44.8-61.4) |

aExpressed as percentage

b95% credibility interval

****

**Figure S1. Distribution of sequence types by the source of isolate**

**A. B.**

**Figure S2. Source attribution of human NTS isolates in Vietnam by sequence type.**

****

**Figure S3. Distribution of AMR profiles by the source of isolate.**



**Figure S4. Number and proportion of unique and shared AMR profiles among human and animal NTS isolates in Vietnam.**

**A B**

**Figure S5. Source attribution of NTS isolates in humans by AMR profile in Vietnam.**

**A B**

**Figure S6. Source attribution of NTS isolates in humans by ST-AMR profile in Vietnam.**