
Supplementary information

Antibiotic resistance genes in the gut microbiota of mothers and linked neonates with or without sepsis from low- and middle-income countries

In the format provided by the
authors and unedited

Supplementary Material Methods: Exploratory multivariable analyses performed

Association between WASH (water, sanitation and hygiene) related variables and maternal carriage of *bla*_{CTX-M-15} or *bla*_{NDM} or *bla*_{OXA-48}-like genes

Logistic regression models were fitted to each ARG (outcome), including the following explanatory variables:

- Residence water supply
- Drinking water
- Residence access to wastewater network
- Frequency of solid waste collection
- Access to soap
- Mother handwashing frequency
- Mother showering/bathing frequency → excluded due to high number of missing responses
- Type of residence*
- Type of toilet in residence
- Number of people living in residence*
- Number of bedrooms in residence*
- Household income equal or higher than country average
- Mother education status

*Models were fitted including and excluding these variables.

Association between the mother's handwashing frequency and maternal carriage of *bla*_{CTX-M-15} or *bla*_{NDM} or *bla*_{OXA-48}-like genes

Logistic regression models fitted to each ARG (outcome), included handwashing frequency as the explanatory variable and controlling for the following variables:

- Mother education status
- Household income equal or higher than country average
- Residence water supply
- Access to soap
- Frequency of solid waste collection
- Residence access to wastewater network
- Type of residence*

*Models were fitted including and excluding these variables.

Association between maternal infection in the three-months prior to enrolment in the study and maternal carriage of *bla*_{CTX-M-15} or *bla*_{NDM} or *bla*_{OXA-48}-like genes

Logistic regression models fitted to each ARG (outcome), included prior maternal infection as the explanatory variable and controlling for the following variables:

- Age of mother
- Mother use of antibiotics in the three months prior to enrolment*
- Mother visited hospital in the 12 months prior to enrolment
- Mother attended private healthcare in the three months prior to enrolment
- Mother visited traditional healer in the three months prior to enrolment
- Household income equal or higher than country average
- Mother education status
- Type of toilet in residence
- Mother handwashing frequency
- Residence access to wastewater network
- Frequency of solid waste collection
- Residence water supply
- Mother underlying diseases: immunocompromised
- Mother underlying diseases: diabetes

*Models were fitted with and without this variable due to the possibility of being a confounder and/or a mediator variable.

Association between maternal use of antibiotics in the three-months prior to enrolment in the study and maternal carriage of *bla*_{CTX-M-15} or *bla*_{NDM} or *bla*_{OXA-48}-like genes

Logistic regression model fitted to each ARG (outcome), included prior maternal use of antibiotics as the explanatory variable and controlling for the following variables:

- Maternal infection in the three months prior to enrolment
- Mother underlying diseases: immunocompromised
- Mother underlying diseases: diabetes
- Mother visited hospital in the 12 months prior to enrolment
- Mother attended private healthcare in the three months prior to enrolment
- Mother visited traditional healer in the three months prior to enrolment
- Household income equal or higher than country average
- Mother education status

Association between birth healthcare environment related variables and carriage of *bla*_{CTX-M-15} or *bla*_{NDM} or *bla*_{OXA-48}-like genes among neonates of the birth cohort

Logistic regression models were fitted to each ARG (outcome), including the following explanatory variables:

- Number of beds on ward
- Bathroom on ward
- Mother location on ward → excluded due to high number of missing responses
- Delivery type
- Timing of birth*
- Breech
- Perinatal asphyxia
- PPRM*

*Models were fitted either with “Timing of birth” or “PPROM” due to their collinear nature.

Association between age of infant at sample collection and carriage of *bla*_{CTX-M-15} or *bla*_{NDM} or *bla*_{OXA-48}-like genes among neonates of the birth cohort

Logistic regression model fitted to each ARG (outcome), included a categorised age at sample collection as the explanatory variable (0-72 hours; ≥72 hours - 60 days) and controlling for the following variables:

- Biological sepsis diagnosis
- Mother use of antibiotics in the three months prior to enrolment
- Residence water supply
- Drinking water
- Residence access to wastewater network
- Frequency of solid waste collection
- Access to soap
- Mother handwashing frequency
- Mother showering/bathing frequency → excluded due to high number of missing responses
- Type of residence*
- Type of toilet in residence
- Number of people living in residence*
- Number of bedrooms in residence*
- Household income equal or higher than country average

- Mother education status
- Delivery type
- Timing of birth**
- Breech
- Perinatal asphyxia
- PPRM**

* Models were fitted including and excluding these variables.

** Models were fitted either with “Timing of birth” or “PPROM” due to their collinear nature.

Supplementary Material Table 1 – World bank data for contextual analysis.

World bank data on mortality, poverty and sanitation in the countries included in BARNARDS (https://data.worldbank.org).							
World data indicator	Bangladesh	Ethiopia	India	Nigeria	Pakistan	Rwanda	South Africa
Pregnant women receiving pre-natal care (% population) [†]	64	62	79	67	86	98	94
Mortality rate under-5 (per 1,000 live births, 2018 data)	30	55	37	120	69	35	34
Number of neonatal deaths (2018 data)	50,244	99,275	549,227	267,227	251,484	6,215	12,717
Mortality rate attributed to unsafe water/sanitation and lack of hygiene (per 100,000 population, 2018 data)	11.9	43.7	18.6	68.6	19.6	19.3	13.7
International poverty* (less than \$1.90 per day) millions of population, %	23.3M, 14.8%	31.9M, 30.8%	268.7, 21.2%	84.7M, 53.5%	8M, 3.99%	6.6M, 55.5%	10.5M, 18.9%
Poverty at the national poverty line* Millions of population, %	38.4M, 24.3%	23.7M, 23.5%	273.8, 21.9%	71M, 46%	48.5M, 24.3%	4.5M, 38.2%	30.3M, 55.5%
GINI index*	32.4	35	37.8	43	33.5	43.7	63
People using at least basic sanitation services (% population, 2017 data)	48	7	60	39	60	67	76
People using at least basic sanitation services (% urban population, 2017 data)	51	20	72	48	77	52	76
People using at least basic sanitation services (% rural population, 2017 data)	47	4	53	31	50	70	75
People practicing open defecation (% population)	0	22	26	20	10	2	1
People using at least basic drinking water (% population, 2017 data)	97	41	93	71	91	58	93
People using at least basic drinking water (% urban population, 2017 data)	97	80	96	87	94	82	99
People using at least basic drinking water (% rural population, 2017 data)	97	31	91	56	90	53	81
People using safely managed drinking water (% population, 2017 data)	55	11	No data	20	35	No data	No data
People with basic handwashing facilities including soap and water (% population, 2017 data)	34.81	7.96	59.55	41.95	59.61	4.62	43.99
People with basic handwashing facilities including soap and water (% urban population, 2017 data)	51.09	23.55	79.76	52.85	83.25	13.42	52.56
People with basic handwashing facilities including soap and water (% rural population, 2017 data)	25.71	4.04	49.32	31.26	46.05	2.8	27.48
Diarrhoea treatment (% of children under 5 who received ORS packets)**	77	29.5	50.6	40	37.4	27.5	51.4

[†] Date of information: Bangladesh 2014, Ethiopia, 2016, India 2016, Nigeria 2018, Pakistan 2018, Rwanda 2017, South Africa 2016

*Date of information: Bangladesh 2016, Ethiopia 2015, India 2011, Nigeria 2009, Rwanda 2016, Pakistan 2015, South Africa 2014.

**Date of information: Bangladesh 2014, Ethiopia 2016, India 2016, Nigeria 2018, Pakistan 2018, Rwanda 2015, South Africa 2016.

Average household income reported by sites	US dollars
BC (Bangladesh)	\$150
BK (Bangladesh)	\$125
ES (Ethiopia)	\$130.5
IN (India)	\$717
NK (Nigeria)	\$500
NN (Nigeria)	\$1100
NW (Nigeria)	\$1100
PC (Pakistan)	\$180
PP (Pakistan)	\$500
RU (Rwanda)	\$500
RK (Rwanda)	\$200
ZAT (South Africa)	\$1331

Supplementary Material Table 2 – The country level ethical approval for the BARNARDS study and sample/data collection. The site, committee name, principal investigator (PI), ethics reference and approval date are listed.

BARNARDS ethics approval documents and references.				
Site	Committees	Named PI	Reference(s)	Approval date(s)
BC	Institute of Child Health	Samir Kumar Saha	BICH-ERC-4/3/2015	15/09/2015
BK	Institute of Child Health	Samir Kumar Saha	BICH-ERC-4/3/2015	15/09/2015
ES	Boston Children's Hospital	Grace Chan	IRB-P00023058	11/08/2016
IN	Institute of Cholera and Enteric Diseases and Institute of Post Graduate Medical Education and Research, IPGME&R Research Oversight Committee	Sulagna Basu	A-I/2016-IEC and Inst/IEC/2016/508	17/11/2016 and 04/11/2016
NK	Kano State Hospitals Management Board	Kenneth Iregbu	8/10/1437AH	13/07/2016
NN	Health Research Ethics Committee (HREC), National Hospital, Abuja	Kenneth Iregbu	NHA/EC/017/2015	27/04/2015
NW	Health Research Ethics Committee (HREC), National Hospital, Abuja	Kenneth Iregbu	NHA/EC/017/2015	27/04/2015
PC	University, Pakistan Institute of Medical Sciences (PIMS) Islamabad	Rabaab Zahra	NA, signed letter from Prof. Tabish Hazir	27/05/2015
PP	University, Pakistan Institute of Medical Sciences (PIMS) Islamabad	Rabaab Zahra	NA, signed letter from Prof. Tabish Hazir	27/05/2015
RK	Committee	Jean-Baptiste Mazarati	No342/RNEC/2015	10/11/2015
RU	Committee	Jean-Baptiste Mazarati	No342/RNEC/2015	10/11/2015
ZAT	Hospital, Research projects, Western Cape Government	Shaheen Mehtar	N15/07/063	04/12/2015 and 02/02/2016

Supplementary Material Table 3 – The primers used, PCR conditions and control strains for all PCRs performed within this study.

Primers, PCR conditions and control strains used in PCR experiments.						
a) Primers, amplicons and control strains						
Primers pair	Target	Sequence (5'-3')	Tan °C	Amplicon size (bp)	Reference	Control Strain
CTXM15- F CTXM15- R	<i>bla</i> CTX-M-15	ATGCGCAAACGGCGGACGTA CCCGTTGGCTGTCGCCCAAT	55	~600	Walsh group (Carvalho MJ)	<i>Escherichia coli</i> NCTC 13353
NDM-M-F NDM-M-R	<i>bla</i> NDM	AGCTGAGCACCGCATT CTCAGTGTGCGGCATCAC	52-58	648	Walsh group (Hassan B)	<i>Escherichia coli</i> X (in-house control strain)
KPC-M-F KPC-M-R	<i>bla</i> KPC	TAGTTCTGCTGTCTTGCTCTC CCGTCATGCCTGTTGTC	52-58	333	Walsh group (Hassan B)	<i>Klebsiella</i> sp. K10 (in-house control strain)
OXA-48-M-F OXA-48-M-R	<i>bla</i> OXA-48 (and OXA-48-like genes: <i>bla</i> OXA-162, -163, -181, and possibly -204 & -232)	GGCGTAGTTGTGCTCTG AAGACTTGGTGTTTCATCCTT	52-58	155	Walsh group (Hassan B)	<i>K. pneumoniae</i> NCTC 13442
b) PCR conditions for <i>bla</i> CTX-M-15 survey						
Number of cycles	Temperature	Time				
1x	95°C	5 min				
	94°C	30 s				
30x	52°C	1 min				
	72°C	1 min				
1x	72°C	10 min				
c) Multiplex-PCR conditions for <i>bla</i> NDM, <i>bla</i> KPC and <i>bla</i> OXA-48-like survey						
Number of cycles	Temperature	Time				
1x	95°C	5 min				
	95°C	30 s				
30x	61°C	30 s				
	72°C	30 s				
1x	72°C	10 min				

Supplementary Material Table 4 – Information relating to the antibiotic susceptibility testing performed within this study.

a) List of antibiotics tested using the Kirby-Bauer disk diffusion method, following the EUCAST guidelines (v9, 2019)

Antibiotic	Acronym	Disk content (µg)
Amoxicillin	AML	10
Amoxicillin/clavulanate	AMX	20/10
Piperacillin/tazobactam	TZP	30/6
Cefotaxime	CTX	5
Cefazidime	CAZ	10
Cefepime	FEP	30
Imipenem	IPM	10
Meropenem	MER	10
Ertapenem	ERT	10
Aztreonam	ATM	30
Gentamicin	GEN	10
Amikacin	AMK	30
Levofloxacin	LVX	5
Ciprofloxacin	CIP	5
Tigecycline	TGC	15
Trimethoprim/sulfamethoxazole	SxT	1.25/23.75
Nitrofurantoin	NIT	100
Fosfomycin	FOS	200 (50 glucose-6-phosphate)

Antibiotics disks from Liofilchem, Italy.

b) Quality control strains

Escherichia coli ATCC25922

Pseudomonas aeruginosa ATCC27853

Supplementary Material Table 4 (continued) – Information relating to the antibiotic susceptibility testing performed within this study.

Organisms	Amoxicillin	Amoxicillin/clavulanate	Piperacillin/tazobactam	Cefotaxime	Cefazidime	Cefepime
Enterobacteriaceae	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales
<i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Acinetobacter</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Stenotrophomonas maltophilia</i>	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Aeromonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; <i>Aeromonas</i> spp.	EUCAST V9; <i>Aeromonas</i> spp.
<i>Sphingomonas</i> sp.	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Shewanella</i> sp.	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Bordetella</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Brevundimonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Alcaligenes</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.

Organisms	Imipenem	Meropenem	Ertapenem	Aztreonam	Gentamicin	Amikacin
Enterobacteriaceae	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales
<i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Acinetobacter</i> spp.	EUCAST V9; <i>Acinetobacter</i> spp.	EUCAST V9; <i>Acinetobacter</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Acinetobacter</i> spp.	EUCAST V9; <i>Acinetobacter</i> spp.
<i>Stenotrophomonas maltophilia</i>	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Aeromonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; <i>Aeromonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales
<i>Sphingomonas</i> sp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Shewanella</i> sp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Bordetella</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Brevundimonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.
<i>Alcaligenes</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.

Organisms	Levofloxacin	Ciprofloxacin	Tigecycline	Trimethoprim-sulfamethoxazole	Nitrofurantoin	Fosfomycin
Enterobacteriaceae	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales - <i>E. coli</i>	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales - <i>E.</i>	EUCAST V9; Enterobacterales
<i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales - <i>E. coli</i>	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales - <i>E.</i>	EUCAST V9; Enterobacterales
<i>Acinetobacter</i> spp.	EUCAST V9; <i>Acinetobacter</i> spp.	EUCAST V9; <i>Acinetobacter</i> spp.	EUCAST V9; Enterobacterales - <i>E. coli</i>	EUCAST V9; <i>Acinetobacter</i> spp.	EUCAST V9; Enterobacterales - <i>E.</i>	EUCAST V9; Enterobacterales
<i>Stenotrophomonas maltophilia</i>	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales - <i>E. coli</i>	EUCAST V9; <i>Stenotrophomonas maltophilia</i>	EUCAST V9; Enterobacterales - <i>E.</i>	EUCAST V9; Enterobacterales
<i>Aeromonas</i> spp.	EUCAST V9; <i>Aeromonas</i> spp.	EUCAST V9; <i>Aeromonas</i> spp.	EUCAST V9; Enterobacterales - <i>E. coli</i>	EUCAST V9; <i>Aeromonas</i> spp.	EUCAST V9; Enterobacterales - <i>E.</i>	EUCAST V9; Enterobacterales
<i>Sphingomonas</i> sp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales - <i>E. coli</i>	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales - <i>E.</i>	EUCAST V9; Enterobacterales
<i>Shewanella</i> sp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales - <i>E. coli</i>	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales - <i>E.</i>	EUCAST V9; Enterobacterales
<i>Bordetella</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales - <i>E. coli</i>	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales - <i>E.</i>	EUCAST V9; Enterobacterales
<i>Brevundimonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales - <i>E. coli</i>	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales - <i>E.</i>	EUCAST V9; Enterobacterales
<i>Alcaligenes</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; <i>Pseudomonas</i> spp.	EUCAST V9; Enterobacterales - <i>E. coli</i>	EUCAST V9; Enterobacterales	EUCAST V9; Enterobacterales - <i>E.</i>	EUCAST V9; Enterobacterales

Supplementary Material Table 5 – Long read sequencing analysis QC metrics for isolates selected as the reference genome for ST based SNP analysis

Isolate Species		BC-BR1421-3 <i>Escherichia coli</i>	BC-BR228-2 <i>Escherichia coli</i>		
ST		405	4684		
Loci alleles		adk(35)	adk(6)		
		fumC(37)	fumC(604)		
		gyrB(29)	gyrB(3)		
		icd(25)	icd(16)		
		mdh(4)	mdh(11)		
		purA(5)	purA(8)		
		recA(73)	recA(6)		
Long read metrics	Number of reads	39,449.00	72,491.00		
	N50 long reads	15,375.00	18,155.00		
Hybrid assembly metrics	# contigs	6	3		
	Largest contig	5197174	4758536		
	Total length	5556123	4942260		
	GC (%)	50.61	50.8		
	N50	5197174	4758536		
Isolate Species		PP-BR254-2 <i>Klebsiella pneur</i>	PP-BR737-1 <i>Klebsiella pneum</i>	BC-MR44-1 <i>Klebsiella pneumoniae</i>	
ST		11	15	394	
Loci alleles		gapA(3)	gapA(1)	gapA(2)	
		infB(3)	infB(1)	infB(9)	
		mdh(1)	mdh(1)	mdh(2)	
		pgi(1)	pgi(1)	pgi(1)	
		phoE(1)	phoE(1)	phoE(13)	
		rpoB(1)	rpoB(1)	rpoB(1)	
		tonB(4)	tonB(1)	tonB(82)	
Long read metrics	Number of reads	37,492.00	81,332.00	26,187.00	
	N50 long reads	13,491.00	9,450.00	13,726.00	
Hybrid assembly metrics	# contigs	7	10	8	
	Largest contig	5381779	5332228	5325299	
	Total length	5828111	5914648	5738257	
	GC (%)	56.98	56.7	56.89	
	N50	5381779	5332228	5325299	
Isolate Species		BC-BR406-2 <i>Enterobacter clc</i>	BC-BR476-2 <i>Enterobacter hon</i>	BC-MR78-3 <i>Enterobacter hormaecl</i>	BK-BR752-3 <i>Enterobacter hormaechei</i>
ST		68	171	418	113
Loci alleles		dnaA(7)	dnaA(49)	dnaA(53)	dnaA(4)
		fusA(8)	fusA(21)	fusA(35)	fusA(22)
		gyrB(5)	gyrB(19)	gyrB(154)	gyrB(68)
		leuS(7)	leuS(44)	leuS(44)	leuS(69)
		pyrG(15)	pyrG(45)	pyrG(45)	pyrG(37)
		rplB(6)	rplB(12)	rplB(4)	rplB(4)
		rpoB(7)	rpoB(32)	rpoB(6)	rpoB(24)
Long read metrics	Number of reads	36,299.00	48,266.00	14,633.00	68,597.00
	N50 long reads	20,476.00	17,563.00	17,148.00	17,026.00
Hybrid assembly metrics	# contigs	4	4	5	10
	Largest contig	4775718	4616948	4696953	4516179
	Total length	4912294	5071364	4955331	4999801
	GC (%)	55.3	54.62	55.18	55.5
	N50	4775718	4616948	4696953	4516179

Supplementary Material Table 6 – Full list of BARNARDS consortium

Country	Forename	Surname	Position	Affiliation
Bangladesh	Samir	Saha	PI	Chittagong Medical College Hospital, Bangladesh
Bangladesh	Maksuda	Islam	scientist	Chittagong Medical College Hospital, Bangladesh
Bangladesh	Zabed	Bin-Ahmed	scientist	Chittagong Medical College Hospital, Bangladesh
Bangladesh	Wazir	Ahmed	clinician	Chittagong Medical College Hospital, Bangladesh
Bangladesh	Taslima	Begum	clinician	Chittagong Medical College Hospital, Bangladesh
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