Whole-Genome Characterization of Epidemic *Neisseria meningitidis* Serogroup C and Resurgence of Serogroup W, Niger, 2015

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In 2015, Niger reported the largest epidemic of *Neisseria meningitidis* serogroup C (NmC) meningitis in sub-Saharan Africa. The NmC epidemic coincided with serogroup W (NmW) cases during the epidemic season, resulting in a total of 9,367 meningococcal cases through June 2015. To clarify the phylogenetic association, genetic evolution, and antibiotic determinants of the meningococcal strains in Niger, we sequenced the genomes of 102 isolates from this epidemic, comprising 81 NmC and 21 NmW isolates. The genomes of 82 isolates were completed, and all 102 were included in the analysis. All NmC isolates had sequence type 10217, which caused the outbreaks in Nigeria during 2013–2014 and for which a clonal complex has not yet been defined. The NmC isolates from Niger were substantially different from other NmC isolates collected globally. All NmW isolates belonged to clonal complex 11 and were closely related to the isolates causing recent outbreaks in Africa.

Neisseria meningitidis commonly causes meningitis in the African meningitis belt, where periodic meningococcal epidemics have contributed to the highest reported incidence of meningococcal meningitis in the world (*1*). Most meningococcal disease historically has been caused by *N. meningitidis* serogroup A (NmA); however, NmA disease dramatically decreased after the preventative MenAfriVac vaccination campaign was initiated in 2010 (*2*). Serogroup W (NmW) has been the major cause of meningococcal disease in the region since then (*2*).

N. meningitidis serogroup C (NmC) disease has rarely been reported in the meningitis belt; it has not been detected in many molecular studies of invasive isolates (*3*,*4*) and is rarely found in carriage studies (*5*,*6*). The last large NmC epidemic in Africa occurred in Burkina Faso (then Upper Volta) in 1979 (*7*). During 2013 and 2014, NmC outbreaks were reported in Nigeria (*8*). The Nigerian outbreaks were caused by a novel NmC strain with a previously undescribed sequence type, 10217 (ST-10217), which does not belong to a defined clonal complex. In 2015, an epidemic of 9,367 meningococcal meningitis cases occurred in Niger, with NmC disease comprising most laboratory-confirmed cases (*9*).

NmW disease has been reported in the meningitis belt since the 1980s (*10*,*11*), and NmW from clonal complex 11 (CC11) has been a major concern in the region since 2001 (*12*). The first large epidemic of disease caused by CC11 NmW occurred during 2002 in Burkina Faso (*13*). Subsequently, NmW disease outbreaks were reported in Niger during 2010 and 2011, both involving CC11 (*14*). These outbreaks were followed by another large epidemic caused by CC11 NmW in Burkina Faso during 2012 (*15*). Whole-genome sequencing (WGS) analysis of diverse NmW isolates from around the world has demonstrated that a clone within CC11, commonly associated with NmC, became globally dispersed after it switched to serogroup W (*16*,*17*). WGS analyses also provided sufficient resolution to assign isolates from the meningitis belt to a long-standing regional

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population and to a clone that became globally dispersed after an outbreak during the 2000 Hajj pilgrimage (*16*,*17*; A. Retchless, unpub. data).

In addition to distinguishing among closely related strains, WGS provides information about allelic variation in genes that may affect antibiotic susceptibility and the coverage of protein-based vaccines. Two vaccines designed for serogroup B meningococcus have been approved for use in the United States and Europe: Trumenba and Bexsero. Trumenba targets the factor H–binding protein (FHbp), and includes components belonging to FHbp subfamilies A and B (*18*). Bexsero includes 4 different components: an FHbp of variant 1 (subfamily B); a *Neisseria* adhesion A protein (NadA); a neisserial heparin-binding antigen (NhbA); and outer membrane vesicles from a serogroup B strain containing PorA P1.4 (*19*). Recognizing the diversity of these genes among strains can aid in evaluating whether these vaccines may provide protection. Likewise, whole-genome sequences can be rapidly screened for indications of antibiotic resistance when the genetic determinants are well characterized, as with genes *penA*, *gyrA,* and *rpoB*, which are involved in reduced susceptibility to penicillin, ciprofloxacin, and rifampin, respectively. To clarify the meningococcal population in Niger during the 2015 epidemic season, we completed genomic analysis on the 102 NmC and NmW invasive isolates collected during this period.

Materials and Methods

Strain Collection

A total of 102 isolates from the Centre de Recherche Médicale et Sanitaire (CERMES; Niamey, Niger; online Technical Appendix Table 1, http://wwwnc.cdc.gov/EID/article/22/10/16-0468-Techapp1.pdf) were received at the World Health Organization Collaborating Centres for Meningitis at the following sites: Centers for Disease Control and Prevention (CDC; Atlanta, GA, USA), the Institut Pasteur (Paris, France); and the Norwegian Institute of Public Health (Oslo, Norway). These isolates originated from 12 districts (Figure 1). Species and serogroup of 102 viable isolates were confirmed by culture, PCR, and slide agglutination (*20*) at the 3 World Health Organization Collaborating Centres. The results were 100% in concordance with the laboratory testing performed at CERMES. Conventional PCR-based molecular typing was performed on 9 cerbrospinal fluid specimens for which no associated isolates were available (3 NmW, 6 NmC); all ST, PorA, FetA, and *penA* sequences matched those of isolates that were fully sequenced. An additional 30 NmC isolates from 20 countries and 94 NmW isolates from 15 countries, representing the diversity of the 2 serogroups in the CDC culture collection, were selected and sequenced to compare with the Niger isolates (online Technical Appendix Table 1).

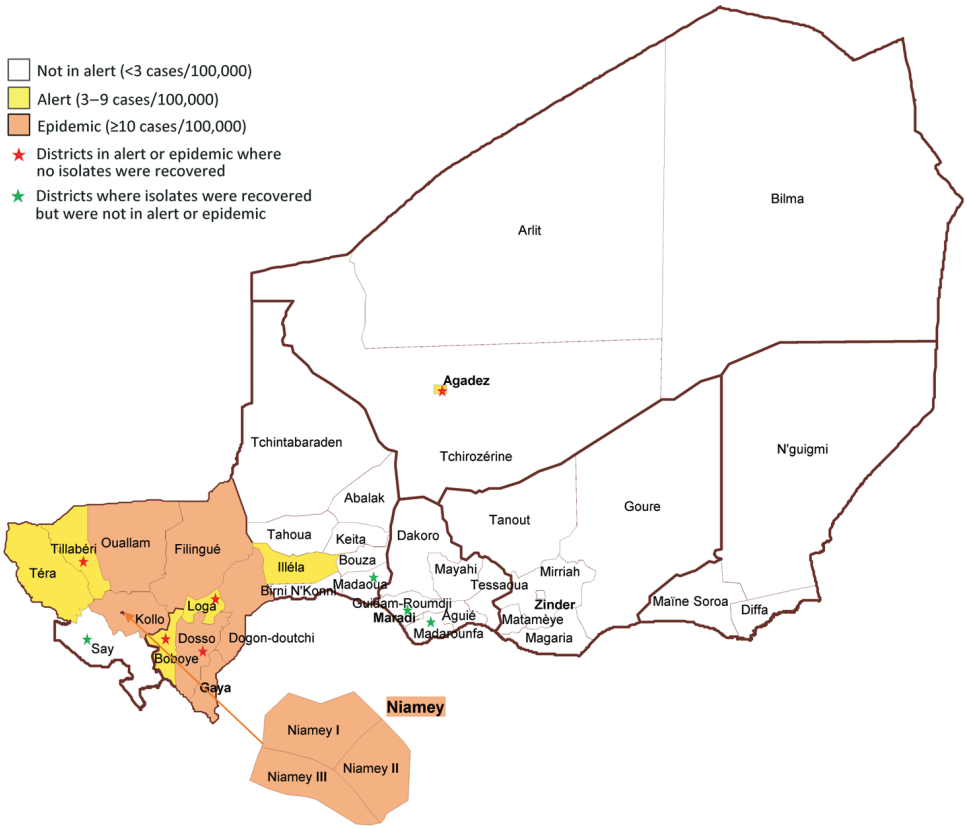

Figure 1. Distribution of *Neisseria meningitidis* isolates by district in Niger during the 2015 epidemic. Dogon-doutchi: 23 (NmC 15; NmW 8); Filingue: 2 (NmC 2); Gaya 2 (NmC 1; NmW 1); Guidan-Roumji: 1 (NmW 1); Illela: 1 (NmC 1); Kollo: 10 (NmC 5; NmW 5); Madaoua: 1 (NmW 1); Madarounfa: 1 (NmW 1); Niamey: 39 (NmC 37; NmW 2); Ouallam: 3 (NmC 2; NmW 1); Say: 3 (NmC 2; NmW 1); Téra: 11 (NmC 11).

Genome Sequencing

Genome sequencing data for each isolate were generated with both the Pacific Biosystems (PacBio; Menlo Park, CA, USA) RSII instrument and the Illumina HiSeq 2500 (San Diego, CA, USA). DNA was extracted from plated isolates by using ArchivePure DNA purification kit (5prime, Gaithersburg, MD, USA). PacBio sequences were generated by using P4-C2 sequencing chemistry and assembled using PacBio's Hierarchical Genome Assembly Process version 3 (HGAP) (*21*). HGAP produces linear DNA sequences, so we identified circular, complete chromosome sequences on the basis of the existence of reads that bridged the 2 ends of the chromosome after 1 copy of the terminal repeat produced by the assembler was removed. These assemblies were corrected with 250-bp, paired-end Illumina read data generated with TruSeq Rapid SBS chemistry (Illumina) from 600-bp libraries prepared with NEBNext Ultra DNA library preparation kits (New England BioLabs, Ipswich, MA, USA). The Illumina reads were trimmed with Trim Galore version 0.3.7 (Babraham Bioinformatics, Cambridge, UK) to remove reads below Q28, 100 bp, and an error rate of 0.03, then mapped with bowtie version 2.1.0 (*22*) and used to identify base-calling errors and indels by using freebayes version 0.9.16 (https://github.com/ekg/freebayes) with base quality >20, alternate count >20, and coverage >100. The PubMLST (http://pubmlst.org/neisseria/) identifier for the sequences are in online Technical Appendix Table 1 and genome coverage information and statistics on each genome in online Technical Appendix Table 2.

Molecular Characterization

We identified multilocus sequence typing (MLST) alleles on the basis of a BLAST (https://blast.ncbi.nlm.nih.gov/Blast.cgi) search of the assembled genomes compared with the PubMLST allele lists (*23*). We also identified potential antibiotic susceptibility based on PubMLST alleles for *gyrA, penA,* and *rpoB* genes. Protein sequences were likewise typed according to PubMLST sequence collection. PorA, PorB, and FetA were classified according to their respective variable regions, NadA was categorized by the Novartis convention of variant and peptide identifier (*24*), NhbA was identified by PubMLST peptide identifier, and FHbp was identified by the PubMLST peptide identifier and the Pfizer peptide identifier (subfamilies A and B).

Comparative Genomics

For each comparison of genome-wide similarity, we identified single nucleotide polymorphisms (SNPs) using kSNP version 3 software (*25*), with a kmer length of 25. We then built a maximum-likelihood phylogenic tree based on the core SNPs using MEGA6 (*26*), with the Tamura-Nei substitution model and 500 bootstrap iterations.

Results

Genomic Characterization and Diversity of NmC Isolates

We sequenced the genomes of 81 Niger NmC isolates using PacBio and Illumina sequencing. PacBio sequencing allowed reconstruction of the complete circular chromosome for 68 isolates. All 81 isolates had the same molecular profile (PorA P1.21–15,16, PorB 3–463, FetA F1–7, and ST-10127, which is not assigned to a known clonal complex; Table). The genome of the ST-10217 isolates were compared with the genomes of NmC isolates from 8 different clonal complexes, collected from countries in North and South America, Europe, Asia, and Africa as far back as 1976. We identified 13,746 core SNPs, with a difference of 0–32 core SNPs between the ST-10217 isolates and a difference of >4,400 core SNPs between ST-10217 and other NmC isolates. The ST-10217 isolates formed a distinct phylogenetic cluster, relative to the other NmC isolates (Figure 2).

Genomic Characterization and Diversity of NmW Isolates

We sequenced the genomes of 21 Niger NmW isolates; 20 were complete circular chromosomes. They all belonged to CC11/ST-11 and had a PorA P1.5,2 (Table). However, they differed in the PorB and FetA sequences. Fourteen NmW isolates had PorB 2–2, six had PorB 2–277, and 1 had PorB 2–60. Fifteen isolates had FetA F1–1, and 6 had FetA F1–84. When we compared the genomes of a collection of African

Table. Summary of molecular typing and serogroups of *Neisseria meningitidis* isolates, Niger, 2015*

Serogroup	No. isolates	ST/CC	PorA†	PorB†	FetA†	NadA‡	NhbA§	FHbp¶	*gyrA*§	*penA*§	*rpoB*§
C	81	ST-10217/NA	P1.21–15,16	3–463	1–7	Not present	798	27/A106	2	22	1
W	14	ST-11/CC11	P1.5,2	2–2	1–1	2/3.6	96	9/B45	4	1	9
W	6	ST-11/CC11	P1.5,2	2–277	1–84	2/3.6	96	9/B45	4	1	9
W	1	ST-11/CC11	P1.5,2	2–60	1–1	2/3.6	96	841/B#	4	1	9

*ST and CC are derived from multilocus sequence typing. CC, clonal complex; NA, not assigned; ST, sequence type.
†PorA, PorB, and FetA are typed according to their respective variable regions.
‡NadA is categorized by Novartis conventions of variant and peptide identifier.
§The alleles for *gyrA*, *penA*, and *rpoB* are identified by PubMLST DNA allele identifiers (http://pubmlst.org/). NhbA is identified by PubMLST peptide identifier.
¶FHbp is identified by the PubMLST peptide identifier and the Pfizer peptide identifier (subfamilies A and B). Assignment of Pfizer peptide identifier is pending for peptide 841.

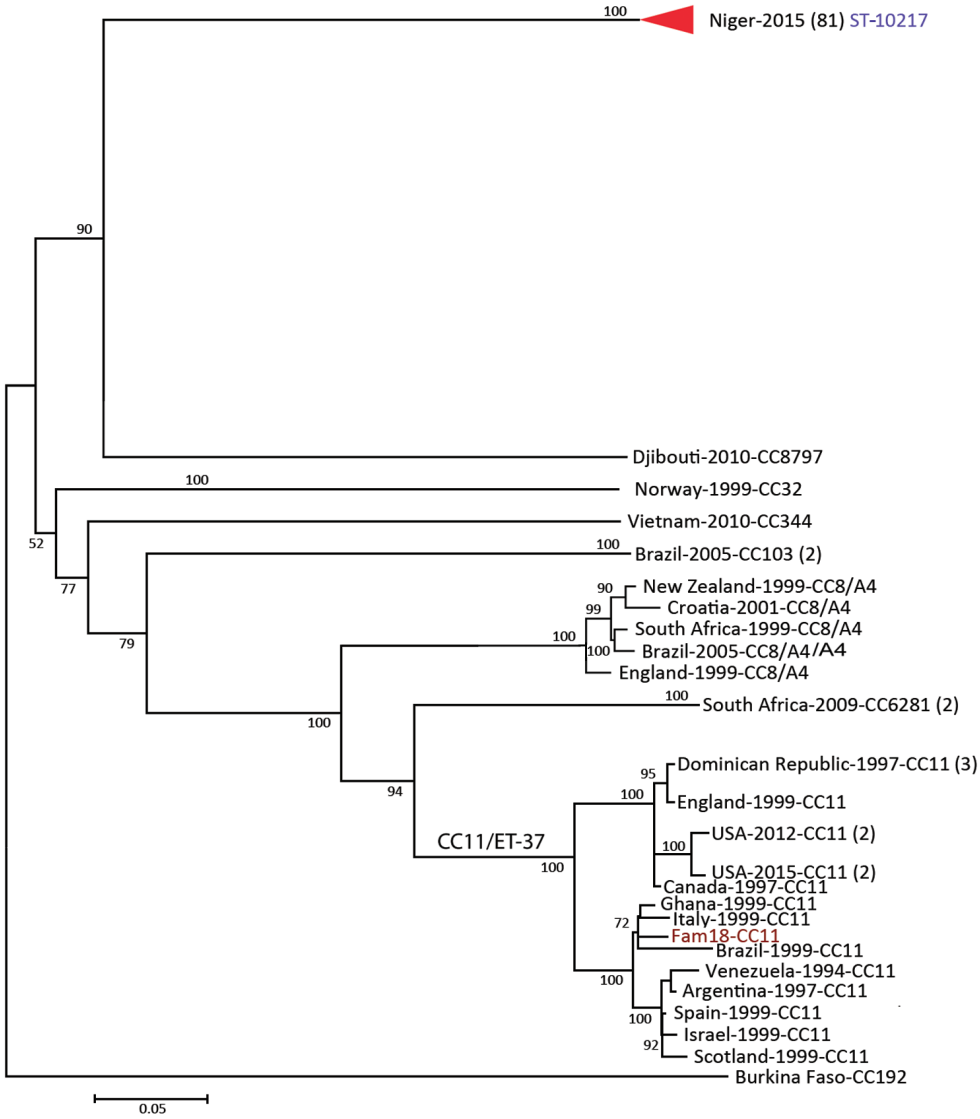

Figure 2. Phylogenetic tree of the *Neisseria meningitidis* serogroup C isolates, labeled with country of origin, year of isolation, and multilocus sequence typing (MLST) group (clonal complex or sequence type). Internal nodes are labeled with bootstrap values. The scale bar is based on the 13,746 positions in the core single nucleotide polymorphism (SNP) matrix and indicates nucleotide substitutions per site.

NmW isolates, including CC22 and CC175, we identified 11,324 core SNPs, with a difference of 0–122 SNPs among the isolates from Niger 2015. These isolates were closely related to NmW isolates collected from Burkina Faso and Mali in 2012, with 1–147 SNP differences (Figure 3). Moreover, the Niger CC11 NmW isolates showed 93–157 SNP differences when compared with an isolate collected in Saudi Arabia during the Hajj-related outbreak in 2000.

Antibiotic-Resistance Genes and Meningococcal Antigen-Encoding Genes

All NmC isolates had *gyr*A allele 2, *pen*A allele 22, and *rpo*B allele 1, whereas all NmW genomes contain *gyr*A 4, *pen*A 1, and *rpo*B 9 (Table). None of these alleles had the mutations associated with resistance to the respective antibiotic (*27*,*28*). The NmC ST-10127 isolates contained FHbp peptide 27, belonging to subfamily A and with 5 aa substitutions relative to peptide 19, against which Trumenba is likely effective on the basis of serum bactericidal activity using human complement (hSBA) (*18*). The NmW isolates contained FHbp peptides 9 or 841 of subfamily B, with 1 aa difference between them and another 13 aa differences relative to peptide 1 (B24), which was susceptible to hSBA (*18*) and is also the FHbp component of the Bexsero vaccine (*19*). None of the NmC isolates contained a *nadA* gene, but the NmW isolates contained NadA peptide 6, which belongs to variant group 2/3 and has 4 aa differences from the Bexsero vaccine component (peptide 8 belonging to variant group 2/3). The NhbA-encoding gene was found in ST-10127 NmC (peptide 798) and ST-11 NmW (peptide 96). Peptide 798 had 68 aa differences relative to the Bexsero component (peptide 2), in addition to being 69 aa longer. Peptide 96 had 85 aa differences, 13 aa missing, and an additional 8 aa relative to peptide 2. No isolate from

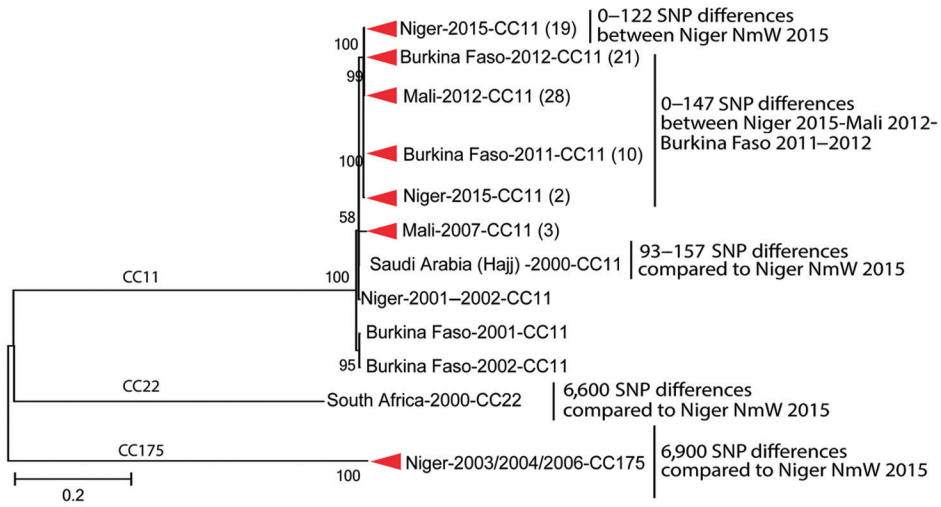

Figure 3. Phylogenetic tree of a subset of the *Neisseria meningitidis* serogroup W (NmW) isolates, labeled with country of origin, year of isolation, and clonal complex (CC). Clades comprising isolates from a single country and year are collapsed, with the isolate count in parentheses. Internal nodes are labeled with bootstrap values, and the number of single nucleotide polymorphisms (SNPs) distinguishing different groups is provided at right. The scale bar is based on the 11,324 positions in the core SNP matrix and indicates nucleotide substitutions per site.

this epidemic contained PorA P1.4, one of the components of Bexsero.

Discussion

This study provides a genomic analysis of 102 invasive NmC and NmW strains collected from Niger during a large epidemic in 2015. The isolates within each serogroup (C and W) were closely related and formed a distinct phylogenetic cluster, with identical ST and little variability in the rest of the genome, suggesting a recent emergence, recent clonal expansion, or both. No mutations involved in reduced antibiotic susceptibility were found, suggesting that these isolates are likely susceptible to penicillin, ciprofloxacin, and rifampin. The NmC isolates were not closely related to the reference NmC strain FAM18 or to any of the NmC isolates that were selected from the United States and 20 countries but had the same ST as the strain that caused the outbreaks in Nigeria during 2013–2014 (*8*). The NmW isolates were closely related to isolates collected in the neighboring countries Burkina Faso (2011 and 2012) and Mali (2012). All of these isolates belonged to a clade defined by an isolate from the Hajj-related outbreak in Saudi Arabia in 2000 (A. Retchless, unpub. data), suggesting that the Niger NmW strains may have recently diverged from prior circulating strains in the region. Recent WGS studies have shown that NmW isolates from CC11 form several clades (with 1 harboring the Hajj-related isolates), suggesting a multifocal emergence of the CC11 NmW strains (*16*,*17*; A. Retchless, unpub. data). Researchers may need to analyze larger numbers of NmW isolates from several countries of the meningitis belt to gain knowledge regarding the recent emergence and spread of these strains.

The scale of the epidemic in Niger (>8,500 cases), along with recent NmC outbreaks and sporadic cases in neighboring countries, highlights the risk for resurgent meningococcal meningitis in the meningitis belt, in the form of a newly emergent lineage (*2*). The novelty of this serogroup C lineage is especially concerning, raising questions about how long it has been present in the meningitis belt and why it has not been associated with prior outbreaks. Examination of the PubMLST database revealed only 2 observations of meningococcus with similar profiles: the same ST was observed in serogroup C strains from Nigeria during 2013–2014, and a similar ST (ST-9367, matching at 6 of 7 MLST loci) was represented by a nongroupable isolate from a carriage study in Burkina Faso during 2011. Although comparison between the ST-10127 NmC isolates from Niger 2015 and Nigeria 2013–2014 would reveal recent evolution of ST-10127 lineage, close comparison between ST-10127 and ST-9367 may illuminate recent evolution of the capsule locus. The origin of ST-10127 is unclear due to the limited number of genetically closely related strains. Additional invasive and carriage meningococcal strains that were collected from Africa and other countries in the past few decades should be examined at the genomic level to identify closely related strains and assess the genetic variations that have led to the emerging ST-10127 NmC.

This resurgence of meningococcal disease is not solely due to the novel NmC lineage; laboratory-confirmed NmW cases in Niger increased from 10 in 2013 (*29*) and 14 in 2014 (*2*) to 206 in 2015. The recurrence of non-NmA meningococcal disease after mass vaccination against NmA disease raises questions regarding whether serogroup replacement has occurred and is somehow related to vaccination against NmA, similar to the serotype replacement that was observed after the implementation of pneumococcal vaccines (*30*). Although NmW meningococcal disease continued to resurge after the MenAfriVac campaign in meningitis belt countries began in 2010 (*29*), and NmC subsequently emerged in Nigeria in 2013,

neither of these occurrences were likely to be a side-effect of mass vaccination because NmW epidemics had occurred before MenAfriVac (*14*,*31*), and the NmC outbreaks occurred in districts that had not yet been vaccinated. Reemergence of NmC epidemics may have been fueled by the population being immunologically naive to the causative strain. Evaluation of the serogroup replacement hypothesis, and of competing hypotheses such as variation in environmental characteristics (*32*), will greatly benefit from the routine collection of representative molecular surveillance data across the region.

The epidemiologic changes in the meningitis belt underscore the importance of continuous effort to develop vaccines against infectious disease caused by nonvaccine serogroups. Although polysaccharide-based vaccines should provide protection against the NmW and NmC strains, protection may also be provided by recently approved serogroup B meningococcus vaccines that are used in Europe and the United States and target surface proteins that are also found in non-B meningococcal strains (*33*). FHbp-based vaccines can provide protection against strains expressing alleles from the same subfamily of the protein (*34*). The ST-10127 NmC strain contain a FHbp of subfamily A, which is included in the Trumenba bivalent FHbp vaccine, but not the Bexsero multicomponent vaccine (*18*,*19*). This strain lacks NadA but does include a gene encoding NhbA. The ST-11 NmW genomes contain an FHbp of subfamily B, which is included in both Trumenba and Bexsero. Of interest, 3 of the polymorphic residues in FHbp are involved in hydrogen bonding of peptide 1 to human factor H (*35*,*36*). NadA and NhbA are also found in the ST-11 NmW isolates, which suggests that these vaccines may provide protection against ST-11 NmW disease. The antigenicity of these vaccine targets remains to be analyzed to precisely evaluate the coverage of these strains by Trumenba and Bexsero, as has been effectively done for emerging clonal complex 181 serogroup X isolates from the meningitis belt (*37*).

In addition to vaccination, natural immunity could be conferred by prior exposure to *N. meningitidis* strains carrying similar antigens. Because NmC has, until now, been very rare in Africa, immunity against serogroup C is unlikely to exist among the African population, which highlights the urgent need to prepare a response for potential NmC outbreaks and epidemics in the upcoming seasons.

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Whole-Genome Characterization of Epidemic *Neisseria meningitidis* Serogroup C and Resurging Serogroup W, Niger, 2015

Technical Appendix

Technical Appendix Table 1. Details regarding 102 *Neisseria meningitidis* isolates from the Centre de Recherche Médicale et sanitaire (Niamey, Niger) that were confirmed at World Health Organization Collaborating Centres for Meninigitis. An additional 30 NmC isolates from 20 countries and 94 NmW isolates from 15 countries, representing the diversity of the 2 serogroups in the CDC culture collection, were selected and sequenced to compare with the Niger isolates.

															gyrA¶		penA¶		rpoB¶		PubMLST
Niger ID	Lab_ID	sAsG	PCR sG	Year	Country	District	ST*	CC*	PorA†	PorB†	FetA†	NadA§	NhbA¶	FHbp#	allele	meaning	allele	meaning	allele	meaning	ID
19-15	M37531	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39587
82-15	M37609	W	NmW	2015	Niger	KOLLO	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6‡	p0096	B45	4	Sus	1	Sus	9	Sus	39628
83-15	M37610	W	NmW	2015	Niger	KOLLO	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39629
111-15	M37611	W	NmW	2015	Niger	KOLLO	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39630
126-15	M37532	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39631
171-15	M37612	W	NmW	2015	Niger	OuALLAM	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39632
179-15	M37613	W	NmW	2015	Niger	sAY	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39633
583-15	M37614	W	NmW	2015	Niger	MADAOuA	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39634
587-15	M37533	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39635
606-15	M37534	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39636
645-15	M37535	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39637
666-15	M37615	W	NmW	2015	Niger	GuIDAN ROuMJI	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39638
685-15	M37536	C	NmC	2015	Niger	ILLELA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39639
982-15	NA	C	NmC	2015	Niger	NA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39640
1010-15	M37616	W	NmW	2015	Niger	DOGONDOuTCHI	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39641
1024-15	M37537	C	NmC	2015	Niger	OuALLAM	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39642
1025-15	M37538	C	NmC	2015	Niger	OuALLAM	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39643
1063-15	M37540	C	NmC	2015	Niger	KOLLO	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39644
1064-15	M37617	W	NmW	2015	Niger	KOLLO	11	CC11/ET-37	P1.5,2	2-277	1-84	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39645
1077-15	M37541	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39646
1082-15	M37618	W	NmW	2015	Niger	DOGONDOuTCHI	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39647

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Niger ID	Lab_ID	sAsG	PCR sG	Year	Country	District	ST*	CC*	PorA†	PorB†	FetA†	NadA§	NhbA¶	FHbp#	allele	meaning	allele	meaning	allele	meaning	ID
1078-15	M37542	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39648
1083-15	M37619	W	NmW	2015	Niger	DOGONDOuTCHI	11	CC11/ET-37	P1.5,2	2-277	1-84	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39649
1090-15	M37620	W	NmW	2015	Niger	DOGONDOuTCHI	11	CC11/ET-37	P1.5,2	2-277	1-84	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39650
1096-15	M37621	W	NmW	2015	Niger	DOGONDOuTCHI	11	CC11/ET-37	P1.5,2	2-60	1-1	NadA-2/3.6	p0096	B#	4	Sus	1	Sus	9	Sus	39651
1098-15	M37543	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39652
1099-15	M37544	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39653
1103-15	M37545	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39654
1168-15	NA	C	NmC	2015	Niger	NA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39655
1169-15	M37546	C	NmC	2015	Niger	TERA	10217	Unassigned	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39656
1172-15	M37547	C	NmC	2015	Niger	TERA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39657
1173-15	M37548	C	NmC	2015	Niger	KOLLO	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39658
1174-15	M37549	C	NmC	2015	Niger	TERA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39659
1376-15	M37550	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39767
1385-15	M37551	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39768
1395-15	NA	C	NmC	2015	Niger	NA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39769
1396-15	M37552	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39770
1434-15	M37553	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39771
1437-15	M37554	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39772
1640-15	M37555	C	NmC	2015	Niger	KOLLO	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39773
1641-15	M37556	C	NmC	2015	Niger	KOLLO	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39774
1658-15	M37622	W	NmW	2015	Niger	NIAMEY	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39775
1659-15	M37557	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39776
1660-15	M37558	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39777
1661-15	M37559	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39778
1662-15	M37560	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39779
1663-15	M37561	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39780
1847-15	M37623	W	NmW	2015	Niger	NIAMEY	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39781

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Niger ID	Lab_ID	sAsG	PCR sG	Year	Country	District	ST*	CC*	PorA†	PorB†	FetA†	NadA§	NhbA¶	FHbp#	allele	meaning	allele	meaning	allele	meaning	ID
1898-15	M37562	C	NmC	2015	Niger	KOLLO	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39782
1945-15	M37563	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39783
1946-15	M37564	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39784
1947-15	M37565	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39785
1956-15	M37566	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39786
2007-15	M37567	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39787
2014-15	M37568	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39788
2015-15	M37569	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39789
2023-15	M37570	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39790
2029-15	M37624	W	NmW	2015	Niger	DOGONDOuTCHI	11	CC11/ET-37	P1.5,2	2-277	1-84	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39791
2043-15	M37571	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39792
2081-15	M37572	C	NmC	2015	Niger	FILINGuE	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39793
2085-15	M37573	C	NmC	2015	Niger	FILINGuE	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39794
2099-15	M37625	W	NmW	2015	Niger	KOLLO	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39795
2137-15	M37574	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39796
2143-15	M37626	W	NmW	2015	Niger	DOGONDOuTCHI	11	CC11/ET-37	P1.5,2	2-277	1-84	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39797
2146-15	M37627	W	NmW	2015	Niger	DOGONDOuTCHI	11	CC11/ET-37	P1.5,2	2-277	1-84	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39798
2380-15	M37575	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39799
2385-15	M37576	C	NmC	2015	Niger	TERA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39800
2398-15	M37578	C	NmC	2015	Niger	TERA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39801
2399-15	M37579	C	NmC	2015	Niger	TERA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39802
2400-15	M37580	C	NmC	2015	Niger	TERA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39803
2401-15	M37581	C	NmC	2015	Niger	TERA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39804
2404-15	M37582	C	NmC	2015	Niger	TERA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39805
2405-15	M37583	C	NmC	2015	Niger	TERA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39806
2441-15	M37584	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39807

															gyrA¶		penA¶		rpoB¶		PubMLST
Niger ID	Lab_ID	sAsG	PCR sG	Year	Country	District	ST*	CC*	PorA†	PorB†	FetA†	NadA§	NhbA¶	FHbp#	allele	meaning	allele	meaning	allele	meaning	ID
2464-15	M37585	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39808
2491-15	M37586	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39809
2548-15	M37587	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39810
2586-15	NA	C	NmC	2015	Niger	KOLLO	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39811
2749-15	M37628	W	NmW	2015	Niger	MADAROuNFA	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39812
3180-15	M37589	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39813
3217-15	M37590	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39814
3411-15	M37591	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39815
3412-15	M37592	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39816
3422-15	M37593	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39817
3479-15	M37594	C	NmC	2015	Niger	DOGONDOuTCHI	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39818
3641-15	M37595	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39819
3642-15	M37596	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39820
3643-15	M37597	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39821
3644-15	M37598	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39822
3645-15	M37599	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39823
3769-15	M37600	C	NmC	2015	Niger	sAY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39824
3772-15	M37601	C	NmC	2015	Niger	sAY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39825
3828-15	M37602	C	NmC	2015	Niger	GAYA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39826
3833-15	M37629	W	NmW	2015	Niger	GAYA	11	CC11/ET-37	P1.5,2	2-2	1-1	NadA-2/3.6	p0096	B45	4	Sus	1	Sus	9	Sus	39827
3882-15	M37603	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39828
3884-15	M37604	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39829
3949-15	M37605	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39830
3962-15	M37606	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39831
4019-15	M37607	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39832

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Niger ID	Lab_ID	sAsG	PCR sG	Year	Country	District	ST*	CC*	PorA†	PorB†	FetA†	NadA§	NhbA¶	FHbp#	allele	meaning	allele	meaning	allele	meaning	ID
4036-15	M37608	C	NmC	2015	Niger	NIAMEY	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39833
4064-15	M37539	C	NmC	2015	Niger	NA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39834
2395-15	M37577	C	NmC	2015	Niger	NA	10217	Unassigned CC for 10217	P1.21-15,16	3-463	1-7	Not present	P00798	A106	2	Sus	22	Sus	1	Sus	39835
NA	M03473	C	NmC	1995	Argentina	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39836
NA	M05730	C	NmC	1976	Brazil	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39837
NA	M13970	C	NmC	2005	Brazil	NA	8	CC8/cluster A4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39838
NA	M13973	C	NmC	2005	Brazil	NA	5122	CC103	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39839
NA	M14431	C	NmC	2005	Brazil	NA	3779	CC103	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39840
NA	M09596	C	NG	NA	Burkina Faso	NA	192	Unassigned CC for 192	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39841
NA	M04874	C	NmC	1997	Canada	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39842
NA	M08566	C	NmC	2001	Croatia	NA	66	CC8/cluster A4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39843
NA	M22236	C	NmC	2010	Djibouti	NA	8797	Unassigned CC for 8797	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39844
NA	M03564	C	NmC	1997	Dominican Republic	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39845
NA	M05451	C	NmC	1998	Dominican Republic	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39846
NA	M05831	C	NmC	1998	Dominican Republic	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39847
NA	M05721	C	NmC	1996	England	NA	8	CC8/Cluster A4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39848
NA	M05731	C	NmC	1993	England	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39849
NA	M05732	C	NmC	1984	Ghana	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39850
NA	M05733	C	NmC	1988	Israel	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39851
NA	M05734	C	NmC	1984	Italy	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39852
NA	M05726	C	NmC	1994	New Zealand	NA	66	CC8/cluster A4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39853
NA	M05749	C	NmC	1987	Norway	NA	32	CC32/ET-5	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39854
NA	M05737	C	NmC	1990	Scotland	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39855
NA	M05729	C	NmC	1990	South Africa	NA	8	CC8/cluster A4	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39856
NA	M14217	C	NmC	2005	South Africa	NA	6281	Unassigned CC for 6281	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39857
NA	M19586	C	NmC	2009	South Africa	NA	6281	Unassigned CC for 6281	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39858
NA	M05738	C	NmC	1985	Spain	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39859
NA	M28679	C	NmC	2014	United Kingdom	NA	467	CC269	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39860
NA	M00601	C	NmC	1994	Venezuela	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39861
NA	M22440	C	NmC	2010	Vietnam	NA	344	Unassigned CC for 344	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	39862
NA	M37654	C	NmC	2015	USA	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

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Niger ID	Lab_ID	sAsG	PCR sG	Year	Country	District	ST*	CC*	PorA†	PorB†	FetA†	NadA§	NhbA¶	FHbp#	allele	meaning	allele	meaning	allele	meaning	ID
NA	M37398	C	NmC	2015	USA	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25683	C	NmC	2012	USA	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25684	C	NmC	2012	USA	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22722	W	NmW	2001	Algeria	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22790	W	NmW	2004	Benin	NA	2881	CC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22809	W	NmW	2006	Benin	NA	2881	CC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22819	W	NmW	2007	Benin	NA	2881	CC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M07999	W	NmW	2001	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M08000	W	NmW	2001	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M08001	W	NmW	2001	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M09261	W	NmW	2002	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M09293	W	NmW	2002	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22797	W	NmW	2004	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22828	W	NmW	2008	Burkina Faso	NA	2881	CC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M23413	W	NmW	2011	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M23414	W	NmW	2011	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M23415	W	NmW	2011	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M23422	W	NmW	2011	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M23423	W	NmW	2011	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M23426	W	NmW	2011	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M24705	W	NmW	2010	Burkina Faso	NA	8638	CC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M24730	W	NmW	2011	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M24731	W	NmW	2011	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M24734	W	NmW	2011	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25430	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25431	W	NmW	2012	Burkina Faso	NA	2881	CC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25432	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

Niger ID	Lab_ID	sAsG	PCR sG	Year	Country	District	ST*	CC*	PorA†	PorB†	FetA†	NadA§	NhbA¶	FHbp#	gyrA¶		penA¶		rpoB¶		PubMLST
															allele	meaning	allele	meaning	allele	meaning	ID
NA	M25433	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25434	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25435	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25436	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25438	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25440	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25456	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25459	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25462	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25467	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25468	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25469	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25470	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25471	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25472	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25473	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25474	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25476	W	NmW	2012	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M27559	W	NmW	2011	Burkina Faso	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22740	W	NmW	2001	Cameroon	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22747	W	NmW	2001	Central African Republic	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22748	W	NmW	2001	Central African Republic	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22803	W	NmW	2005	Chad	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22801	W	NmW	2004	Djibouti	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M07165	W	NmW	1995	Gambia	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

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Niger ID	Lab_ID	sAsG	PCR sG	Year	Country	District	ST*	CC*	PorA†	PorB†	FetA†	NadA§	NhbA¶	FHbp#	allele	meaning	allele	meaning	allele	meaning	ID
NA	M07161	W	NmW	1994	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M07162	W	NmW	1994	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M12752	W	NmW	NA	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22160	W	NmW	2007	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22189	W	NmW	2007	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22191	W	NmW	2007	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25070	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25073	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25074	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25075	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25076	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25077	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25078	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25079	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25080	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25081	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25082	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25086	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25087	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25088	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25089	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25093	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25094	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25100	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25101	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25102	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25103	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25104	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25106	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25107	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25108	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25109	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25110	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25111	W	NmW	2012	Mali	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22718	W	NmW	2001	Mauritius	Candos	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22759	W	NmW	2001	Niger	Niamey	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22769	W	NmW	2002	Niger	Niamey	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22783	W	NmW	2003	Niger	Niamey	2881	CC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22804	W	NmW	2005	Niger	Niamey	2881	CC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22811	W	NmW	2006	Niger	Dosso	2881	CC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M07149	W	NmW	2000	Saudi Arabia	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22772	W	NmW	2002	Senegal	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M07293	W	NmW	2000	South Africa	NA	22	CC22	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M25419	W	NmW	2012	South Africa	NA	11	CC11/ET-37	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
NA	M22822	W	NmW	2007	Togo	NA	2881	CC175	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

															gyrA¶		penA¶		rpoB¶		PubMLST
Niger ID	Lab_ID	sAsG	PCR sG	Year	Country	District	ST*	CC*	PorA†	PorB†	FetA†	NadA§	NhbA¶	FHbp#	allele	meaning	allele	meaning	allele	meaning	ID

*CC, clonal complex; CDC, Centers for Disease Control and Prevention; ID, identifier; NA, not applicable; n.a., not assigned; NmC, *N. meningitidis* serogroup C; NmW, *N. meningitidis* serogroup W; Sus, susceptible; ST, sequence type. ST and CC are derived from multilocus sequence typing. The CC for sT-10217 is Not assigned (n.a.).
†PorA, PorB, and FetA are typed according to their respective variable regions.
§NadA is categorized by Novartis conventions of variant and peptide ID.
¶The alleles for gyrA, penA, and rpoB are identified by PubMLsT DNA allele IDs. NhbA is identified by PubMLsT peptide ID..
#FHbp is identified by the PubMLsT peptide ID and the Pfizer peptide ID (subfamilies A and B). Assignment of Pfizer peptide ID is pending for peptide 841.

Technical Appendix Table 2. Genome coverage information and statistics for each *Neisseria meningitidis* isolate analyzed, Niger, 2015

Isolate	Synonym	Bases in contigs	Contig counts	PacBio depth of coverage	Illumina depth of coverage	Circular assembly
M37531	19-15	2175296	1	146.7	464.93	Yes
M37532	126-15	2170282	1	100.2	469.54	Yes
M37533	587-15	2174310	1	120.23	720.66	Yes
M37534	606-15	2174329	1	93.1	662.60	Yes
M37535	645-15	2174366	1	165.83	632.19	Yes
M37536	685-15	2174321	1	140.76	507.78	Yes
M37537	1024-15	2174294	1	189.7	531.74	Yes
M37538	1025-15	2169856	1	176.19	485.66	Yes
M37539	4064_15	2172023	1	133.52	402.72	No
M37540	1063-15	2174321	1	144.12	363.56	Yes
M37541	1077-15	2183924	1	134.68	457.09	Yes
M37542	1078-15	2175816	1	171.5	481.52	Yes
M37543	1098-15	2174300	1	151.45	504.09	Yes
M37544	1099-15	2174220	1	151	425.30	Yes
M37545	1103-15	2174310	1	133.56	457.55	Yes
M37546	1169-15	2174333	1	166.45	523.45	Yes
M37547	1172-15	2174332	1	170.96	369.55	Yes
M37548	1173-15	2174303	1	166.44	337.75	Yes
M37549	1174-15	2172497	1	173.99	415.62	Yes
M37550	1376-15	2174309	1	102.32	402.26	Yes
M37551	1385-15	2174223	1	125.71	434.52	Yes
M37552	1396-15	2168525	1	82.93	564.00	Yes
M37553	1434-15	2166229	1	159.33	668.59	Yes
M37554	1437-15	2166233	1	198.32	523.45	Yes
M37555	1640-15	2174308	1	153.76	417.93	Yes
M37556	1641-15	2173021	1	117.79	401.80	No
M37557	1659-15	2190989	1	144.39	496.26	No
M37558	1660-15	2174302	1	147.05	289.37	Yes
M37559	1661-15	2174328	1	112.79	401.34	Yes
M37560	1662-15	2174310	1	97.41	470.46	Yes
M37561	1663-15	2174326	1	88.62	429.45	Yes
M37562	1898-15	2175143	1	80.88	506.86	Yes
M37563	1945-15	2174332	1	89.62	407.79	Yes
M37564	1946-15	2173715	1	140.09	349.73	Yes
M37565	1947-15	2174336	1	67.39	434.52	Yes
M37566	1956-15	2184360	1	87.51	393.97	No
M37567	2007-15	2175750	1	55.45	935.85	Yes
M37568	2014-15	2185943	1	103.56	415.62	No
M37569	2015-15	2174259	1	91.17	385.67	Yes
M37570	2023-15	2176087	1	118.92	448.34	Yes
M37571	2043-15	2173673	1	112.45	421.15	No
M37572	2081-15	2174241	1	80.19	351.58	Yes
M37573	2085-15	2186255	1	90.36	446.50	No
M37574	2137-15	2174196	1	99.14	417.93	Yes