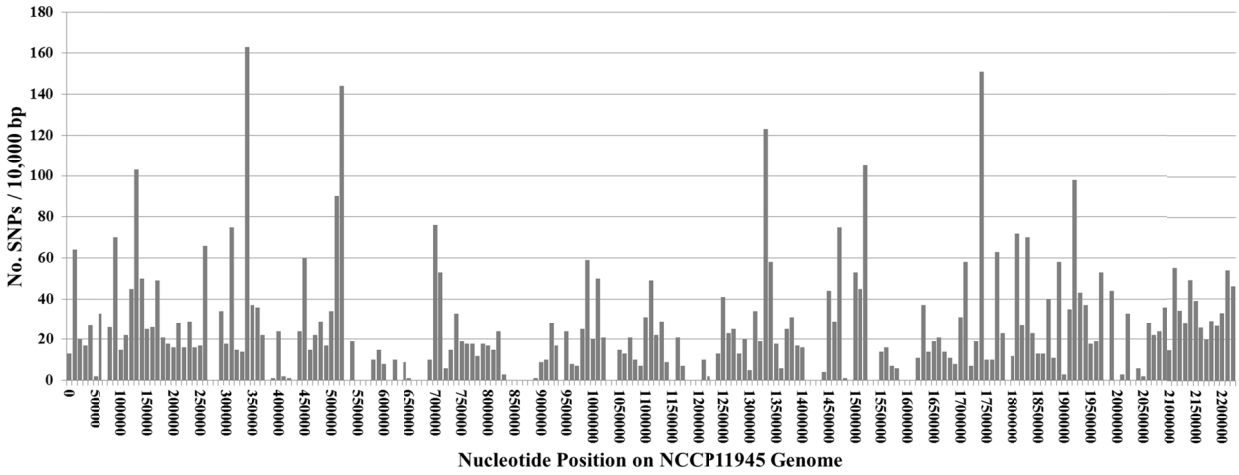

Supplemental Figure S1: Single Nucleotide Polymorphism (SNP) density of 179 *N. gonorrhoeae* strains across the NCCP11945 genome. Regions with > 90 SNPs/10000 base pairs (except the *porB* region) were removed from downstream SNP analysis and are listed in Supplemental Table S1.

Supplemental Table S1: Suspected recombination events removed from the core SNP phylogenomic analysis.

Start[(a)]	Stop[(a)]	Locus
344095	348876	#NGK_0419-IgA-specific metalloendopeptidase (148 SNPs) [(b)]
517391	518794	#NGK_0622-replicative DNA helicase (31 SNPs)
519086	519324	#intergenic (23 SNPs)
519746	520360	#NGK_0624-putative type IV pilus assembly protein PilV (15 SNPs)
520357	521316	#NGK_0625-hypothetical protein (25 SNPs)
521908	522381	#NGK_0627-Putative type IV pilin-like protein (37 SNPs)
523126	523407	#NGK_0630-AzlC-like protein (25 SNPs)
523408	523561	#intergenic (18 SNPs)
995192	995844	#intergenic (33 SNPs)
1741076	1742944	#NGK_2108-putative trans-acylase protein (81 SNPs)

[(a)] Start and stop locations are positions of loci on the *N. gonorrhoeae* NCCP11945 genome with SNP density >90 SNPs/10,000 bp.

[(b)] Total SNPs in the specified NCCP11945 locus of all isolates.

Supplementary Table S2: SNP matrix of *N. gonorrhoeae* showing the number of SNPs between all pairs of isolates (MS-Excel).

Supplementary Table S3: Epidemiological metadata information associated with *N. gonorrhoeae* strains in the analysis (MS-Excel)

Supplementary Table S4: Comparisons of novel *penA* types of *N. gonorrhoeae* isolates

penA Type[a]	Isolate No.	Amino Acid Sequence of PenA[b]
		3471111122222222222333333333333333333333333333344444444444444444444455555555555555555 5100046700001367889111222222333344444577778880001113445666667788800111134445555567 7 0140312344029581126346789012512356346783691470238488235690314625136732360236775 6
WT[c]	M32091[d]	MCAKDDVNYGEDQQAADRRAIVAGTDLNERLQPSPR.SRGAEFEITLNRRPAVLQIFESRENPTTAFANVAAHGGAPPKII.A
X*[e]	H041[d]	....E.ASHAGEE..VEKQVMPS.V.TTDTFLSATQ.TMTPK.DVSV.K..VEVKVIA.KKEASI.LVY...N.ST.VQVVNV
X		....E.ASHAGEE..VEKQ.MTS.V.ATDTFLSATQ.TMTPK.DV..S.QKVEVKVIA.KKEA...LVY...N.ST.VQVVNV
XXXIV		....E.ASHAGEE..VEKQ.MTS.V.ATDTFLSATQ.TMTPK.DV..S.QKVEVKVIA.KKEA..LVY...N.S.....
XXXIV*	F89(34842)[f]	....E.ASHAGEE..VEKQ.MTS.V.ATDTFLSATQ.TMTPK.DV..S.QKVEVKVIA.KKEA..PLVY...N.S.....
XXXV[g]		IGT.E...HAGE.K......MTS.V.ATDTFL.ATQ.TMTPK.DV........V.............I.....
V		.........HAGEE.....D.....LV..G..S.....VNV
V*	Clade B[h]	.........HAGEE.....D.....LV..G..S.....VNV
I		.....D.....S.....
I*	23693	.....D.....S.....
II		.....D.....LV..G.....V.....
II*	883218	.....D.....LV..G.....V.....
II**	27920,35317	.....D.....VLV..G.....

[a] *penA* types depicted in bold font correspond to a mosaic *penA* allele.
[b] Positions are depicted in vertical orientation.
[c] WT = Wild Type *penA* allele.
[d] Strains M32091 and H041 are as described by Ohnishi *et al*. 2011 (1).
[e] An asterisk (*)indicates a novel *penA* type.
[f] Isolate F89 is a highly ESC-DS isolate from France as described by Unemo *et al*., 2012 (2).
[g] The *penA* mosaic type XXXV is present in a sub-clade of 3 isolates in Clade A that is predominated by ST1407-like isolates with *penA* mosaic type XXXIV alleles and is shown in the table to demonstrate the variations between these *penA* types.
[h] Clade B isolates include isolate numbers 33756, 32849, 33386.

Supplemental References:

1. **Ohnishi M, Golparian D, Shimuta K, Saika T, Hoshina S, Iwasaku K, Nakayama S-, Kitawaki J, Unemo M.** 2011. Is *Neisseria gonorrhoeae* initiating a future era of untreatable gonorrhea?: Detailed characterization of the first strain with high-level resistance to ceftriaxone. Antimicrob. Agents Chemother. **55:**3538-3545. 10.1128/AAC.00325-11.

2. **Unemo M, Golparian D, Nicholas R, Ohnishi M, Gallay A, Sednaouie P.** 2012. High-level cefixime- and ceftriaxone-resistant *Neisseria gonorrhoeae* in France: Novel *penA* mosaic allele in a successful international clone causes treatment failure. Antimicrob. Agents Chemother. **56:**1273-1280. 10.1128/AAC.05760-11.