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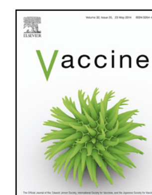

Genetic stability of pneumococcal isolates during 35 days of human experimental carriage

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ABSTRACT

Background: Pneumococcal carriage is a reservoir for transmission and a precursor to pneumococcal disease. The experimental human pneumococcal carriage model provides a useful tool to aid vaccine licensure through the measurement of vaccine efficacy against carriage (VEcol). Documentation of the genetic stability of the experimental human pneumococcal carriage model is important to further strengthen confidence in its safety and conclusions, enabling it to further facilitate vaccine licensure through providing evidence of VEcol.

Methods: 229 isolates were sequenced from 10 volunteers in whom experimental human pneumococcal carriage was established, sampled over a period of 35 days. Multiple isolates from within a single volunteer at a single time provided a deep resolution for detecting variation. HiSeq data from the isolates were mapped against a PacBio reference of the inoculum to call variable sites.

Results: The observed variation between experimental carriage isolates was minimal with the maximum SNP distance between any isolate and the reference being 3 SNPs.

Conclusion: The low-level variation described provides evidence for the stability of the experimental human pneumococcal carriage model over 35 days, which can be reliably and confidently used to measure VEcol and aid future progression of pneumococcal vaccination.

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1. Introduction

Pneumococcal conjugate vaccines (PCV) have been introduced across the globe since 2000 to combat pneumococcal disease. The indirect effect of pneumococcal vaccination, through reduction of vaccine-type carriage, has been a key contributor to conjugate vaccine cost effectiveness [1–3]. However, carriage, which is necessary for both person-to-person transmission and spread within the body, is not part of the current pneumococcal vaccine licensure process [4]. Therefore, the impact of vaccination on nasopharyngeal carriage is of growing interest and has been presented as a vaccine implementation and licensing aid [5]. Experimental human pneumococcal carriage offers a model to measure vaccine efficacy against carriage (VEcol) in a small, controlled population where carriage can be monitored weekly, either as presence/absence or by density and duration [6]. The model involves inoculating the nasopharynx of healthy adult volunteers with a known quantity of serotype 6B. Serotype 6B was selected for the experimental human pneumococcal carriage model as it was a PCV vaccine type, had an odds ratio of <1 for assessing invasive disease potential and had previously been used to investigate the immunizing effect of a carriage episode [7–10]. It is important to understand the genomic stability of the pneumococcal inoculum to further assess the safety of the experimental carriage model and consider any potential impact this could have on measuring VEcol. To this end, 229 experimental carriage isolates recovered from multiple volunteers and time-points, were sequenced to document the number of variable sites.

2. Methods

2.1. Recruitment and ethics

Healthy volunteers were enrolled with informed consent to an Experimental Human Pneumococcal Carriage trial [7]. All participants were non-smoking adults aged 18–60 who had no close contact with at risk individuals, including young children and the elderly. Ethical approval was obtained from the National Health

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Table 1
Number of isolates per volunteer and time-point.

	Days since inoculation (SNPs observed)						
Volunteer	***2***	***7***	***14***	***21***	***28***	***35***	***Total***
362/172	10	10	10	10	7		47
382/193	8	8	8	7	8		39
381/192	8		2	8	8		26
391/203	8	8	8	1	1		26
368/178		2	10		3	8	23
366/176	1	10*	10				21
364/174	10	10					20
380/191		8	8				16
384/196	1			8			9
376/186	2						2

*collected on day 8

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Service Research Ethics Committee (11/NW/0592) and the study was sponsored by the Royal Liverpool and Broadgreen University Hospitals Trust.

2.2. Experimental carriage

Pneumococcal stock preparation, inoculation and nasal wash were done as previously described [7]. Nasal washes were performed one week prior to pneumococcal challenge to determine natural carriage status. Twenty-four volunteers that were negative for natural pneumococcal carriage were inoculated with a serotype 6B strain, multi locus sequence type ST138, and nasal washes were taken on days 2, 7, 14, 21, 28 and 35 post-inoculation [11]. Carriage positive volunteers $n = 10$ received amoxicillin 500 mg T.D.S. for 3 days after day 28 in order to ensure 6B colonisation clearance. One volunteer (368/178, Table 1) did not have antibiotics until after day 35.

In carriage positive volunteers, up to ten individual pneumococcal colonies (where available) were taken from a blood agar plate following overnight incubation, added to 1 ml of Todd Hewitt broth containing 0.5% yeast extract and incubated at 37 °C, 5% CO_2 for 7 h. The broth was then centrifuged at 17,000 × *g* for 3 min and the pellet was resuspended in 200 μl sterile PBS and 40 μl of 10 mg/ml of RNAse A (Qiagen) and stored at −20 °C until extraction. DNA was extracted from the isolates using a modification of the QIAamp DNA Mini Kit (Qiagen). Briefly, the sample was added to 100 μl of TE buffer containing 0.04 g/ml lysozyme and 75 U/ml mutanolysin (Sigma) and incubated for 1 h at 37 °C. Following incubation, proteinase K was added and the sample was incubated for 30 min at 56 °C. Next, Buffer AL was added, the sample was incubated at room temperature for 10 min and then 260 μl of ethanol was added. All subsequent steps were as outlined in the kit protocol.

2.3. Sequencing

Sequencing was performed at the Wellcome Trust Sanger Institute, on the Illumina HiSeq2000 platform. The inoculum was sequenced using the PacBio platform to provide a reference genome. Pacbio sequencing of the inoculum provided 335,112 filtered sub-reads. De novo assembly was performed with the Hierarchical Genome Assembly Process HGAP.2, using PacBio's smrtanalysis version 2.1. The assembly was blasted against itself and inspected in Artemis Comparison Tool (ACT), 3 small spurious contigs covered elsewhere in the assembly were removed and the reads mapped back against the new assembly to create a final consensus fasta sequence using the PacBio SMRT Portal version v2.2.0 build 133,335. The resultant assembly had 6 contigs with a N50 of 1.15 Mb (accession CTRR01000001–CTRR01000006). Supplementary Table 1 includes the ENA accession numbers for the sequence data.

Illumina reads were mapped to the PacBio assembly of the inoculum to identify single nucleotide polymorphisms (SNPs) using SMALT [12] with GATK indel realignment [13] and filtered with a minimum base call quality of 50 and minimum mapping quality of 30 as previously described [14]. The SNP calling was replicated with reduced minimum base call quality of 30 and minimum mapping quality of 20. This was to assess the potential numbers of false negatives and indicate whether variation was missed used the stringent SNP calling, both approaches gave identical results. SNP alignments were used to construct a maximum likelihood phylogenetic tree with 100 bootstrap replicates of RAxML v7.0.4 [15] and combined with temporal data to detect root to tip divergence in Path-O-Gen [16].

3. Results

Of the 24 challenged volunteers, 10 were carriage positive for serotype 6B ST138. From these 10 volunteers, 229 isolates from multiple time-points were sequenced (Table 1).

3.1. Sequence variation

A total of 37 positions in the reference sequence contained a SNP in at least one isolate (variable sites) and 232 SNPs were identified within the 229 isolates. No SNPs were detected for 59/229 isolates. The greatest number of SNP differences from the reference sequence for a single isolate was 3 ($n = 8/229$). No more than 11 variable sites were observed for all isolates taken from a single volunteer. Seven or less variable sites were observed within any volunteers time-point. Between 1 and 3 variable sites could be observed at the primary time-point of 2 days for all volunteers with the exception of 376/186. For 376/186 only two isolates identical to the reference could be retrieved at day 2 and no isolates at later time-points. Furthermore the variation observed within the most comprehensive set of isolates from volunteer 362/172 was only detected on day 2. All remaining 362/172 isolates ($n = 37$) were identical to the reference sequence.

One shared SNP was detected in multiple isolates from two separate volunteers 380/191 (16/16 isolates) and 384/196 (4/9 isolates). The gene annotation for this SNP site in the reference was DNA replication initiation control protein YabA. The C to A transversion resulted in a non-synonymous change from Threonine to Asparagine.

Horizontal exchange of genetic material (homologous recombination), introducing multiple SNPs within a localised area of the genome was not detected in this dataset with an average distance of 55,694 base pairs (bp) and a minimum of 1319 bp between SNPs. Full SNP profiles can be found in Supplementary Table 1.

The correlation between sampling time and different genetic distances from the root to the tips of the phylogenetic tree was assess using Path-O-Gen root to tip phylogenetic divergence. No

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