Encapsulated Bacteria Session 5: Genome upload and annotation

Genomics and Clinical Microbiology 2025
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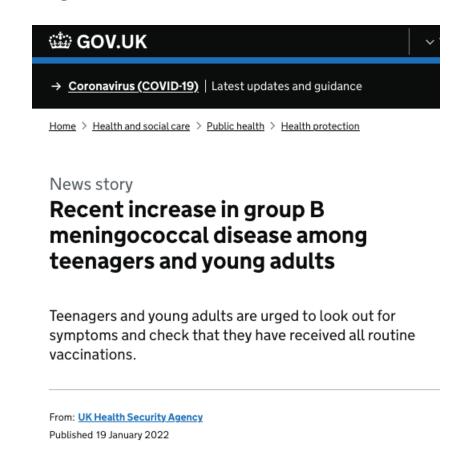
Scenario recap: fine typing results

specimen	age	town	serogroup	abcZ	adk	aroE	fumC	gdh	pdhC	pgm	ST	СС	PorA	FetA
6	6 mo	А	В	3	6		24	11	6			41/44	P1.7-2,4	F1-21
7	5 mo	Α	В	3	6	9	24	11	6	9	6697	41/44	P1.7-2,4	F1-21
8	5 mo	А	В	3	6	9	24	11	6	9	6697	41/44	P1.7-2,4	F5-12
9	10 mo	В	В	4	5	2				20				
2	15 mo	А	В	3	6	9	24	11	6	9	6697	41/44	P1.7-2,4	F5-12
5	3 yrs	Α	В		6	9	24	-	6			41/44	P1.7-2,4	
non- typeable	9 mo	В	-	-	-	-	-	-	-	-	-	-	-	-

Meningococcal disease: still with us Peltola, H. (1983). *Rev Infect Dis* **5**, 71-91.



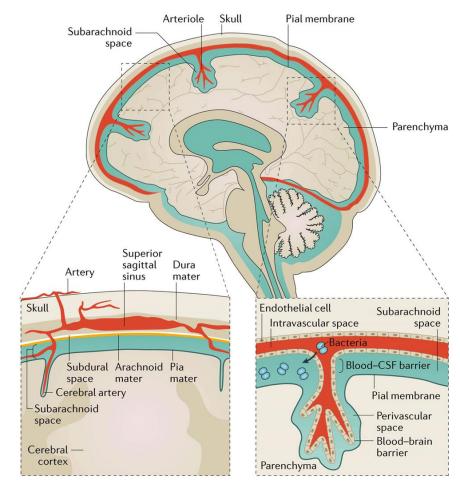
Vieusseux, G. (1806). Mémoire sur la maladie qui a regné a Genêve au printemps de 1805. *J Med Chir Pharm* **11**, 163-182.



https://www.gov.uk/government/news/recent-increase-in-group-b-meningococcal-disease-among-teenagers-and-young-adults
Accessed 26th January 2022.

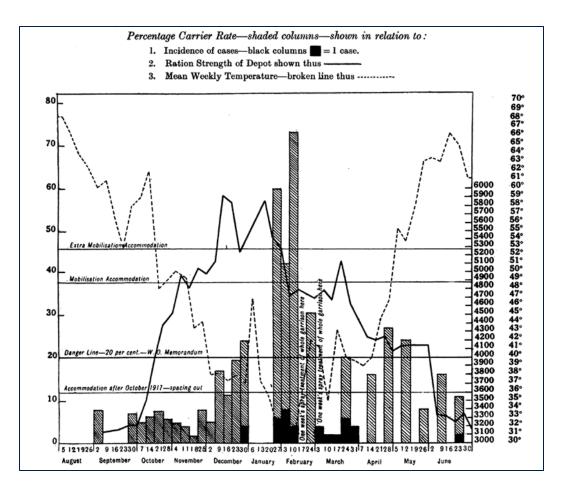
Meningitis and Invasive Meningococcal Disease

- Meningitis:
 - Inflammation of the meninges (tissues around the brain).
- Invasive Meningocococcal Disease (IMD):
 - Invasion by the bacterium Neisseria meningitidis (the meningococcus);
 - Can be meningitis or septicaemia (blood poisoning).
- Severe and frequently fatal:
 - Survivors frequently suffer squelae,
 - Digit or limb loss
 - Brain damage, deafness.

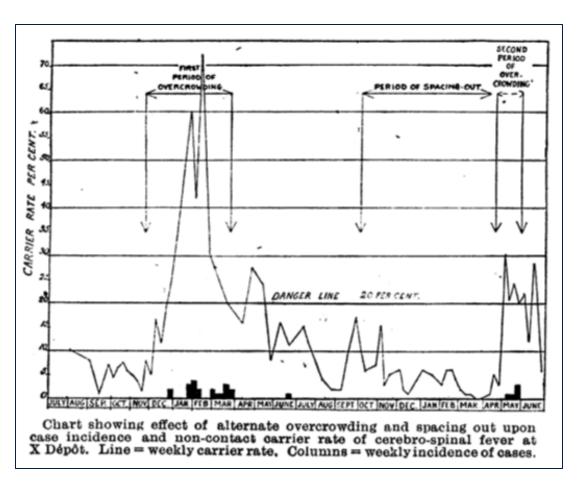


Rodrigues, C. M. C. & Maiden, M. C. J. (2018). A world without bacterial meningitis: how genomic epidemiology can inform vaccination strategy. *F1000Res* **7,** 401.

Carriage, disease, and social distancing, 1917



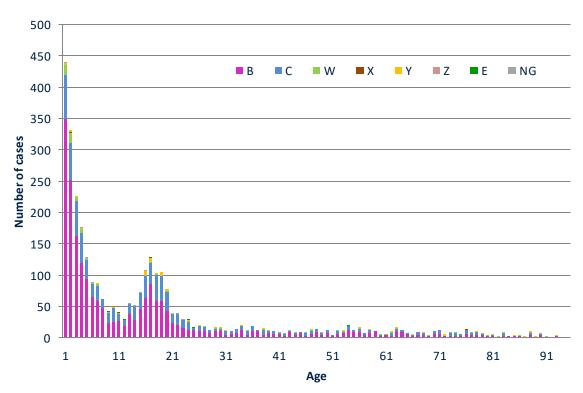
Glover, J. A. (1918). The Cerebro-Spinal Fever Epidemic of 1917 at X Depot. *J Hyg (Lond)* **17**, 350-365.



Glover, J. A. (1918). "Spacing out" in the Prevention of Military Epidemics of Cerebro-Spinal Fever. *Br Med J.* **2**, 509-512.

Meningococcal Disease and carriage

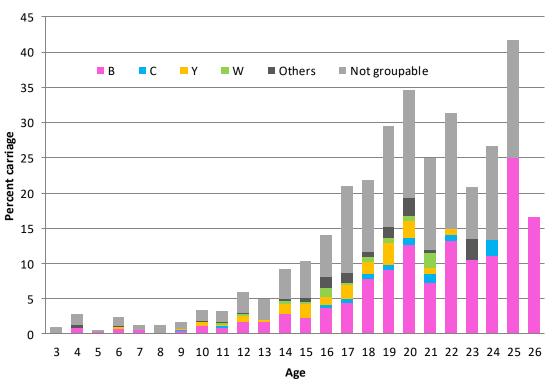
IMD Europe 2000-2002



Frosch, M. & Maiden, M. C. (2007). The European networking for combating meningococcal disease. *FEMS Microbiol Rev* **31**, 1-2.

Brehony, C., Jolley, K. A. & Maiden, M. C. (2007). Multilocus sequence typing for global surveillance of meningococcal disease. *FEMS Microbiol Rev* **31**, 15-26.

Carriage Germany 1999-2001



Claus, H., Maiden, M. C., Wilson, D. J., McCarthy, N. D., Jolley, K. A., Urwin, R., Hessler, F., Frosch, M. & Vogel, U. (2005). Genetic analysis of meningococci carried by children and young adults. *J Infect Dis* **191**, 1263-1271.

Carriage Studies



UK Meningococcal Carriage Study								
Today's Date /								
Q2 amx male female								
Q3 What is your home postcode?								
Q5 Do you <u>currently</u> have a cold or sore throat? NO NO YES								
Q6 Are you <u>currently</u> taking or have you recently stopped taking antibiotics? not taken in the stopped in the stopped in the yes, currently taking past month last month last week.								
Q7 How many cigarettes do you smoke in a typical day? 0 1-5 6-10 11-20 more than 20								
Q8 How many times have you smoked an e-cigarette <u>in the last week?</u> 0 1-2 3-6 7 or more								
Q9 How many times have you smoked a waterpipe (shisha, hookah, hubbly bubbly) <u>in the last month?</u> 0 1 2 3-4 5 or more								
Q10 Does any other person at home smoke cigarettes? NO YES, outside the house YES, inside the house								
Q11 How many days <u>in the last week</u> have you been to a party, pub, bar or night club?								
Q12 How many people have you kissed (kissing with tongues, not just lips or cheeks) in the last week? 0 1 2-3 4 or more								
Q13a Do you have a regular girlfriend or boyfriend? NO NO YES								
Q13b If YES: do they smoke cigarettes? NO YES do they smoke shisha? NO YES								
Q14 What is your ethnic group? White Asian/Asian British Black/African/Caribbean/Black British Mixed/multiple ethnic Other ethnic group								
Thank you for completing this questionnaire								
UKMENCAR4 Questionnaire v1.2 11/08/14 REC REF 14/SC/1163								

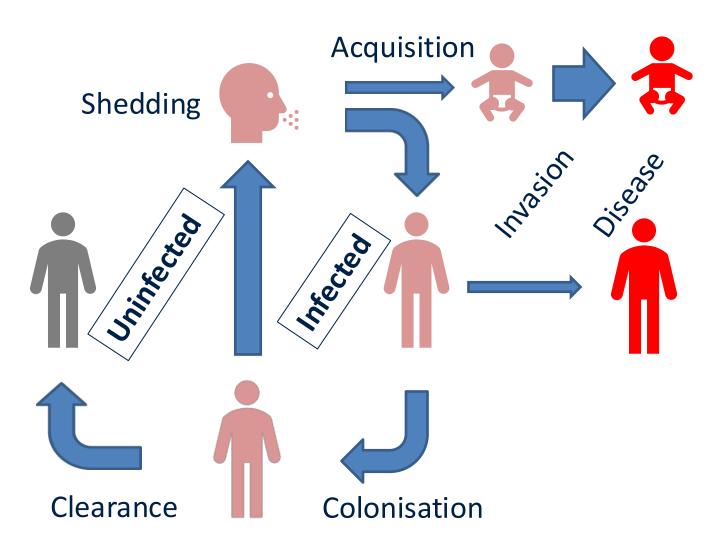
Bratcher, H. B., Rodrigues, C. M. C., Finn, A., Wootton, M., Cameron, J. C., Smith, A., Heath, P., Ladhani, S., Snape, M. D., Pollard, A. J., Cunningham, R., Borrow, R., Trotter, C., Gray, S. J., Maiden, M. C. J. & MacLennan, J. M. (2019). UKMenCar4: A cross-sectional survey of asymptomatic meningococcal carriage amongst UK adolescents at a period of low invasive meningococcal disease incidence. *Wellcome Open Res* 4, 118.

IMD: the 'tip of the iceberg'

- For the meingococcus the great majority infections are not observed:
 - an 'accidental' pathogen.
- Asymptomatic infections, carriage, are major drivers of transmission.
- Eliminating disease requires knowledge of transmission,
 - and in its absence disease control is difficult or impossible.



Meningococcal Transmission, Infection, and Invasion



The meningococcus is ordinarily a commensal, causing disease rarely.

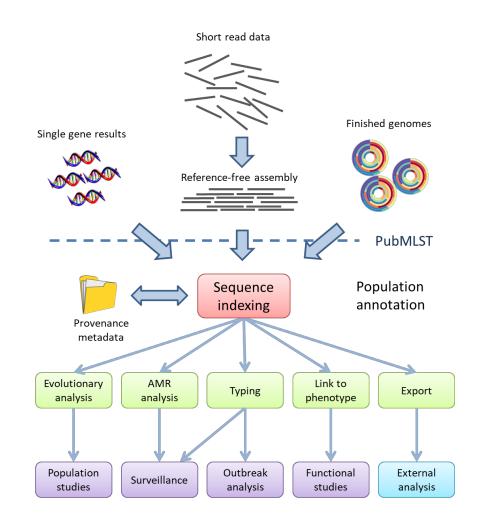
Invasion plays no role in transmission, so it can be thought of as an **accidental pathogen**.

Trotter, C. L. & Maiden, M. C. (2009). Meningococcal vaccines and herd immunity: lessons learned from serogroup C conjugate vaccination programs. *Expert Rev Vaccines* 8, 851-861.

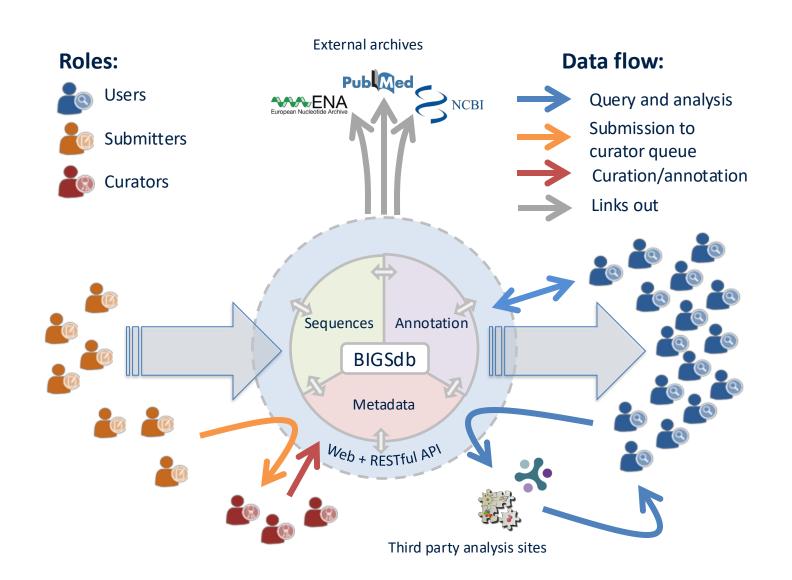
BIGSdb and Population genomics

- Open source
- Web-based
- Links:
 - Sequence data (all types);
 - Provenance information (what, where);
 - Phenotype information (how).
- Contains:
 - Sequence bins;
 - Allele/scheme databases;
 - Isolate records;
 - Links to literature.

Jolley, K. A. & Maiden, M. C. (2010). BIGSdb: Scalable analysis of bacterial genome variation at the population level. *BMC Bioinformatics* **11**, *595*.



BIGSdb and the PubMLST platform



Jolley, K. A., Bray, J. E. & Maiden, M. C. J. (2018). Openaccess bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. *Wellcome Open Res* **3**, 124.

The of the outbreak and its context

- Five months after the specimen 9 was submitted, a further specimen (specimen 10) from another case of meningococcal septicaemia was received.
- This was from a 6 month-old child, a relative of all the previous cases.
- Following this case, a carriage study (throat swabs) was carried out of the extended family (n=112) from which all the reported cases emanated.
 - 14 meningococci were cultured and one PCR positive was obtained (carriage rate 13.4%)
- Following subculture, DNA was extracted and sequenced for the chromosomal DNA obtained from eight B:P1.7-2,4:ST-6697(cc41/44) meningococci (carriage rate 7.14%) obtained in the carriage study. This was also done for the isolates from specimens 7 and 10.
 - These data have been assembled.

Exercise

- The PubMLST database contains:
 - the outbreak specimens (genome and other sequence data);
 - the 8 carried isolates from the outbreak strain obtained from the extended family;
 - reference and and historical isolates;
 - a range of analysis tools.
- Upload your assembled genomes and annotate them for comparative analysis.
- Discussion Points:
 - What do these data tell you about the relationships between carried and diseaseassociated meningococci?
 - What additional information would be useful, in addition to the microbiological/genomic data?
 - What public health action, if any, is required?
 - What is your understanding of this outbreak now?

