

Introduction to Exercise 3

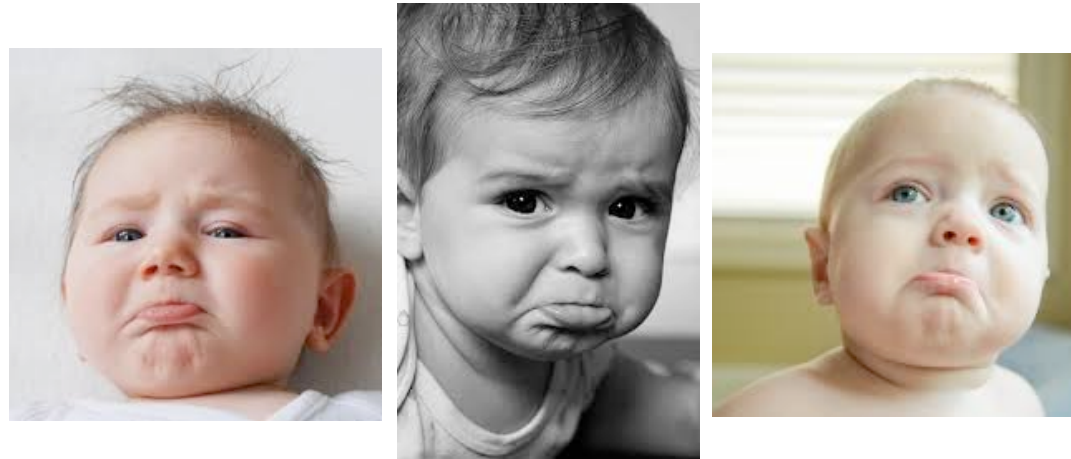
Phylogeny (NDtree and CSIPhylogeny)

Whole-genome sequencing for analysis of an outbreak of meticillin-resistant *Staphylococcus aureus*: a descriptive study

Simon R Harris*, Edward J P Cartwright*, M Estée Török, Matthew T G Holden, Nicholas M Brown, Amanda L Ogilvy-Stuart, Matthew J Ellington, Michael A Quail, Stephen D Bentley, Julian Parkhill†, Sharon J Peacock†

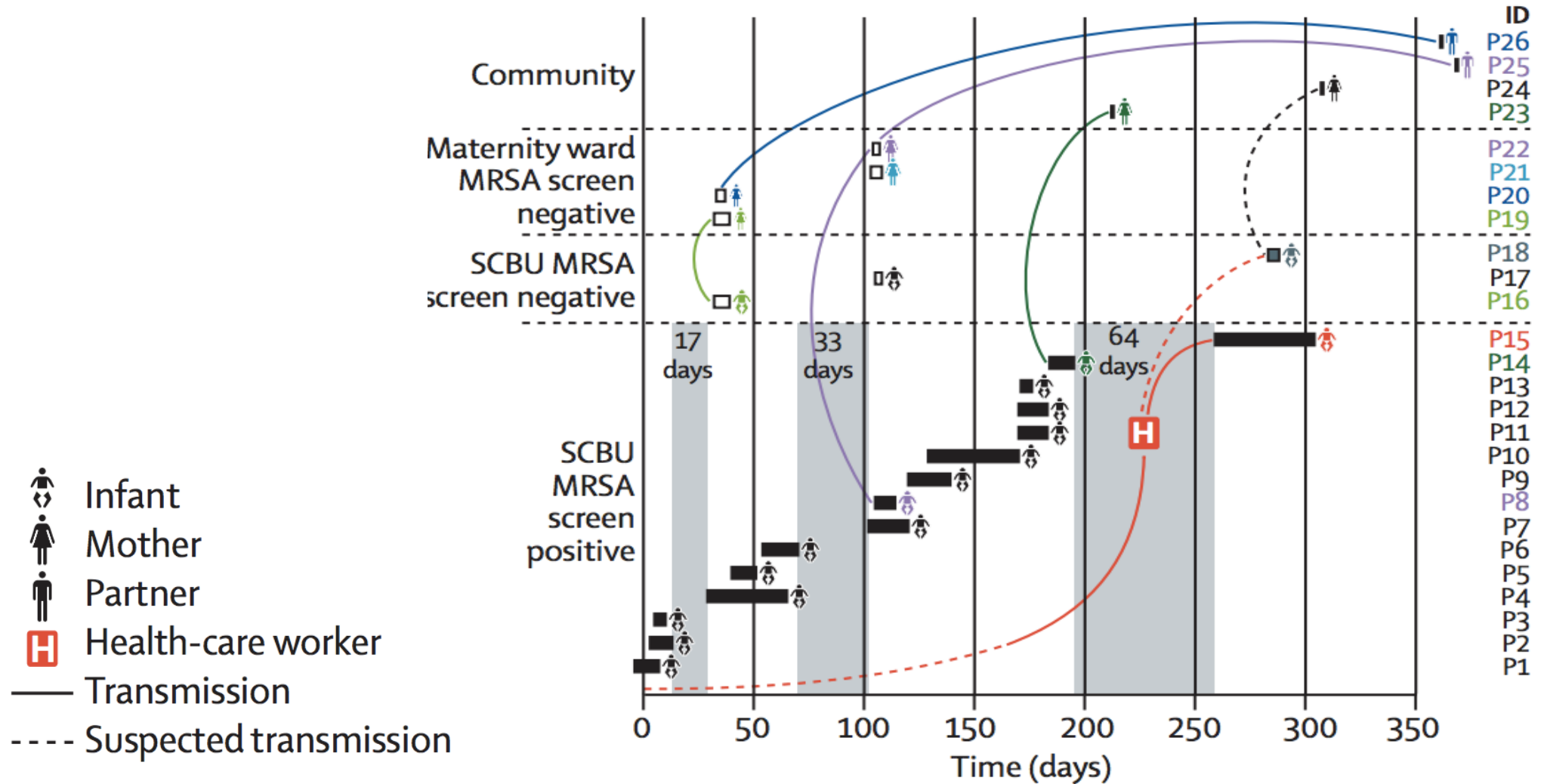
Lancet Infect Dis 2013;
13: 130–36

It all starts with 3 babies that at the same time have an MRSA infection: P11, P12, and P13



- A systematic review of all MRSA isolates from the ward from the preceding 6 months is initiated
- The possible outbreak is initially analysed using conventional methods
- Later Whole Genome Sequencing is also conducted.

Epidemiological map, incl. 11 cases outside the SCBU and one employee



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