

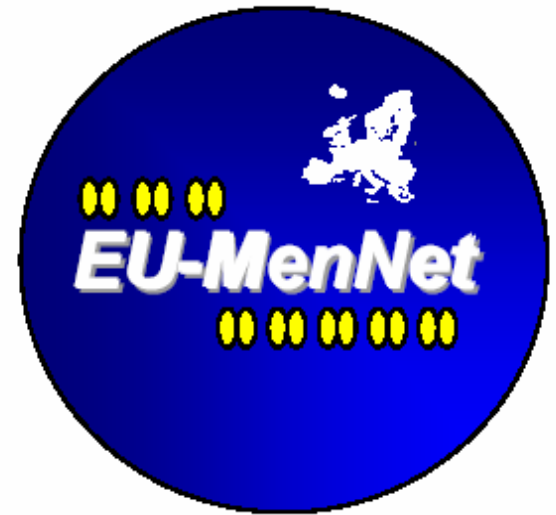
# EUMenNet: Genetic characterisation of European meningococcal disease isolates

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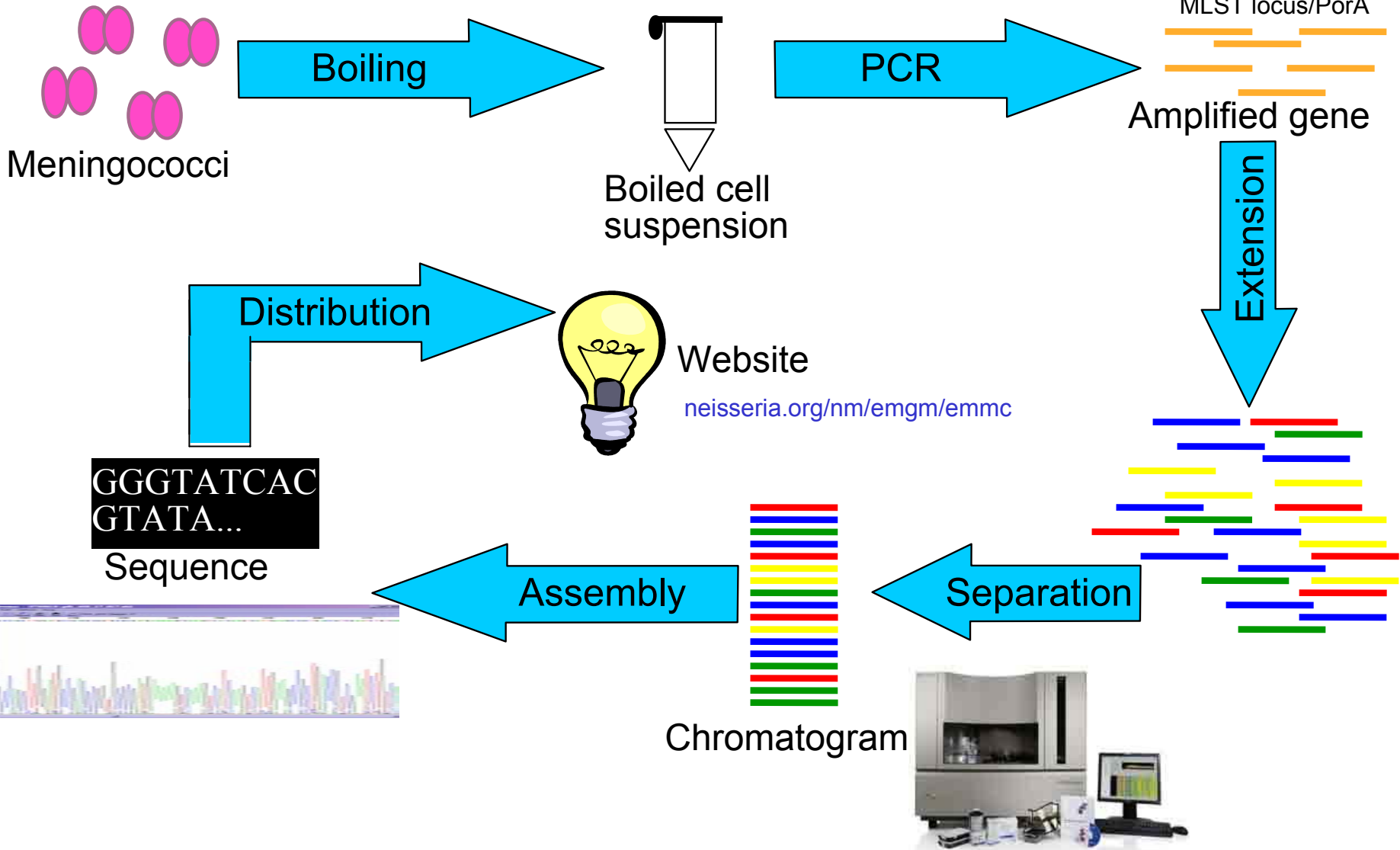
# Background

- European Meningococcal Multi-Locus Sequence Typing Centre (EMMC) – High-throughput low-cost MLST facility within EUMenNet project
- MLST/PorA typing
  - **Thanks to EUMenNet/EMGM Consortium**
- Overview of lineages and antigenic types involved in meningococcal disease Europe-wide



# The EMMC Infrastructure Model

From EMGM Paris 1997



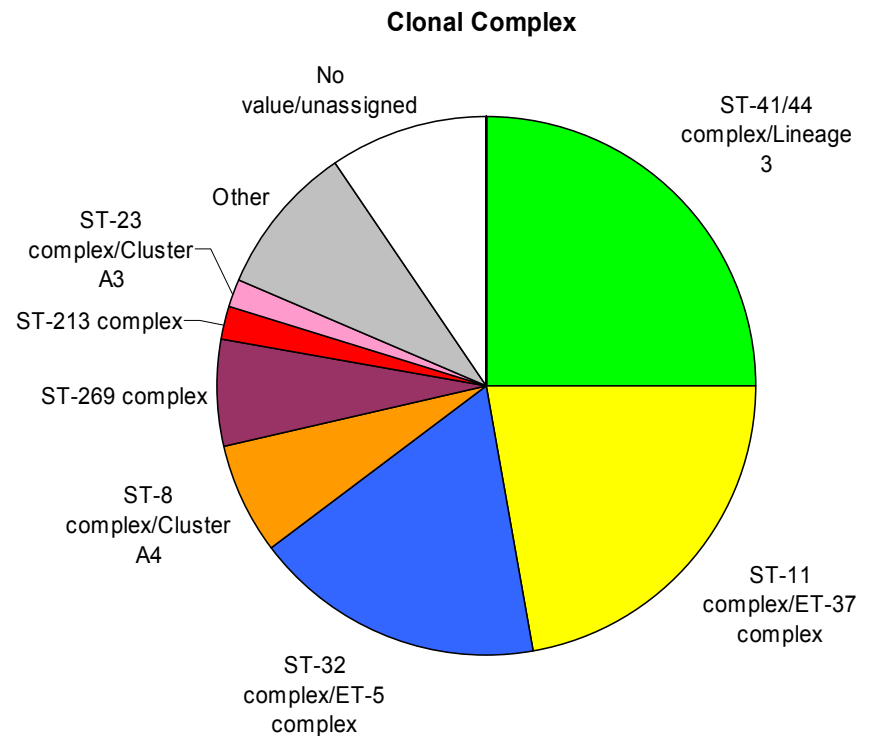
# Summary of results

- Disease isolates 18 European countries years 2000-2002
  - Countries with more than 80 isolates per year, every third isolate;
  - Countries with fewer than 80 isolates p/y, *all* isolates
  - England and Wales, every 10th isolate p/y
- MLST completed for 4053 isolates
- PorA completed for 2622 isolates
- Study database @  
<http://neisseria.org/nm/emgm/emmc>

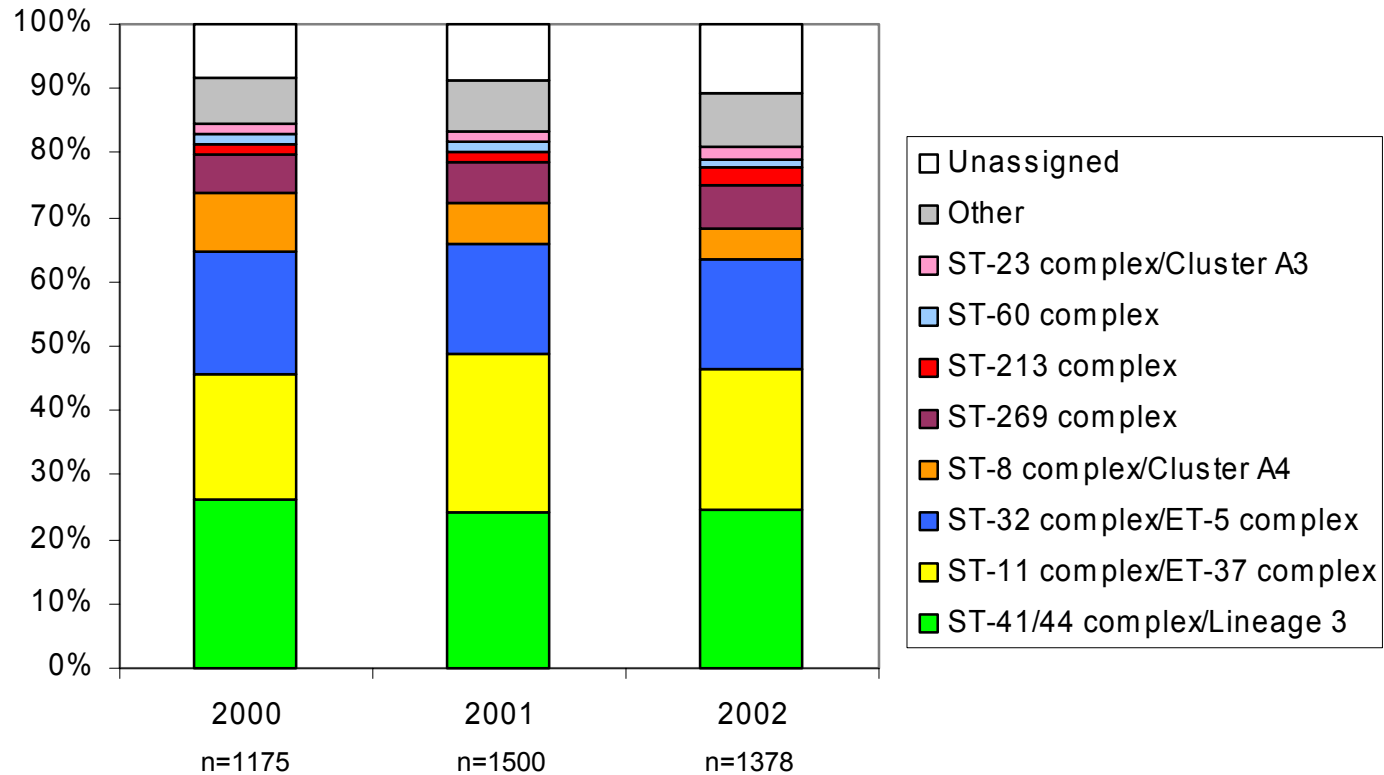


# Genetic diversity of disease isolates

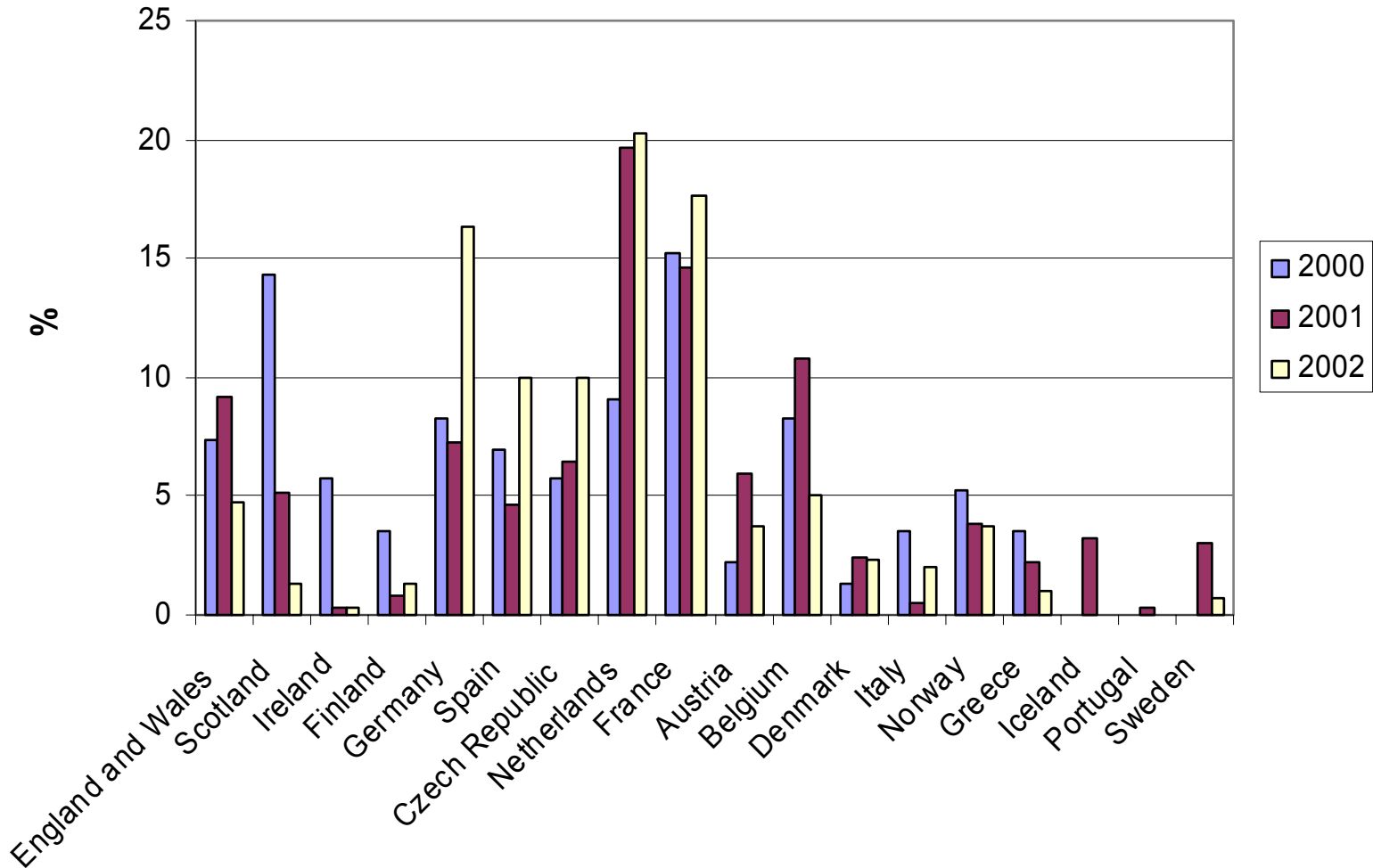
- 984 Sequence types (ST)
  - 5 major STs 40% of isolates: ST-11, 32, 41, 8 and 269
- 25 Clonal Complexes
  - 5 major clonal complexes 78% of isolates: ST-41/44, ST-11/ET-37 complex, ST-32/ET-5 complex, ST-8 complex/Cluster A4, ST-269 complex



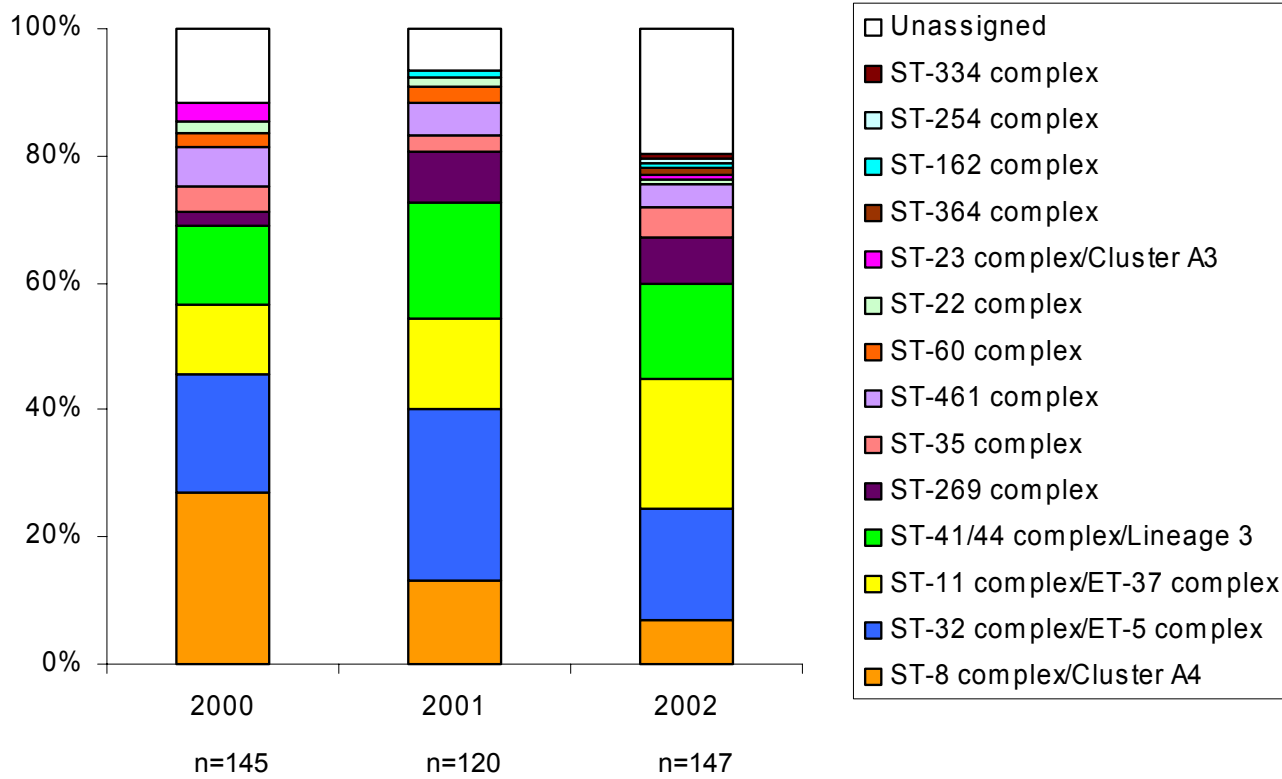
# Evidence for some minor changes in clonal complex distribution



# Changes in ST-11 complex in Europe

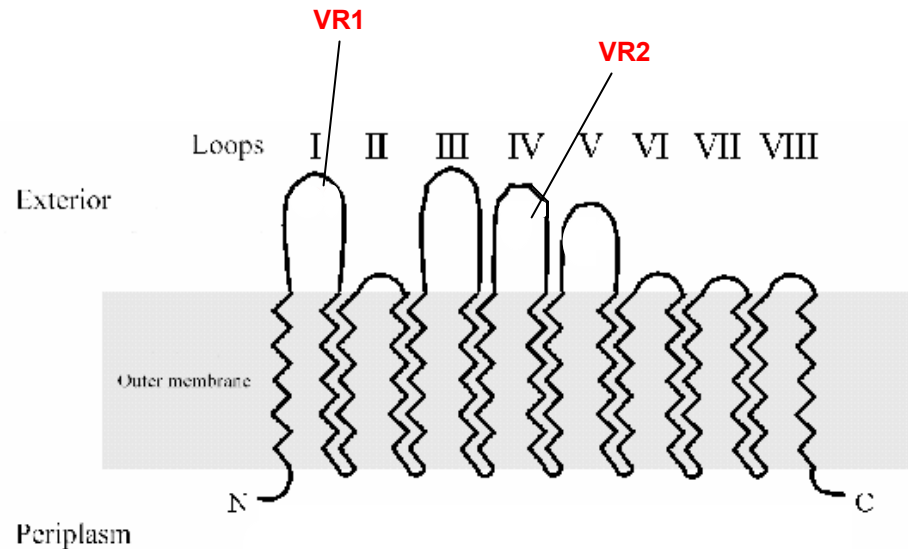


# Clonal complex prevalence change in Spain

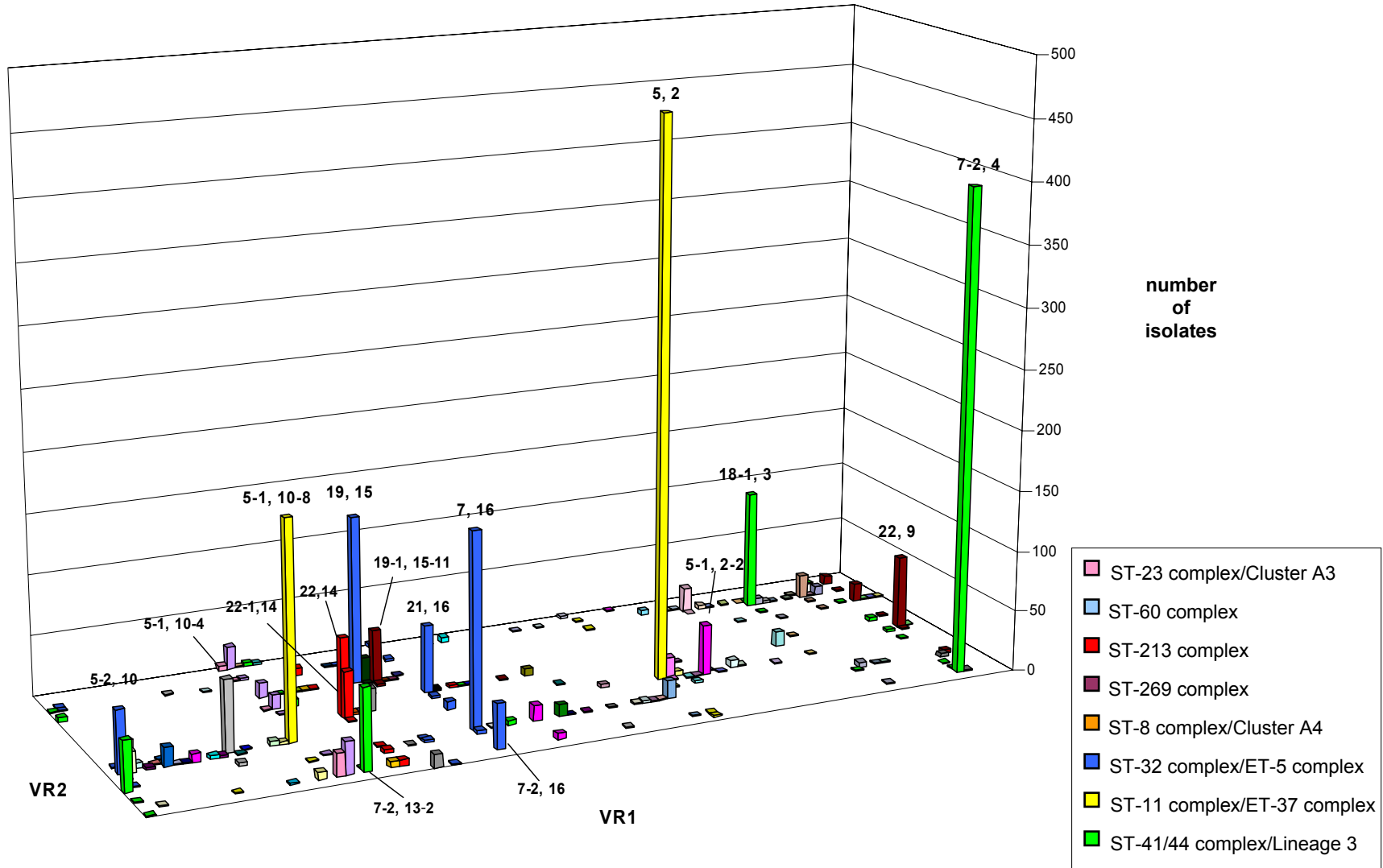


# PorA: No major changes over time

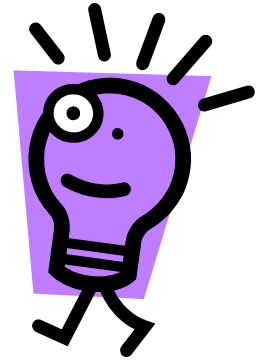
- Class 1 Outer-membrane protein (OMP)
- Vaccine candidate
- 8 surface-exposed loops
- Variable regions VR1 and VR2 used in PorA sub-typing
- EUMenNet: 200 PorA types
  - 40 VR1 types
  - 103 VR2 types
- 5 PorA types ~49% isolates i.e. 5,2  
7-2,4 5-1,10-8 7,16 19,15
- No major changes in distribution of major types over the three years
  - 5,2 19 to 13%
  - 5-1, 10-8 5 to 8%



# Structure of diversity of PorA types



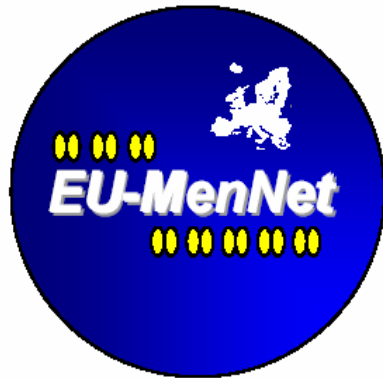
# Summary



- EMMC - functioning infrastructure for high-throughput isolate characterisation
- Despite genetic diversity but small number of STs, Clonal Complexes and PorA types account for most disease isolates
  - Types found throughout Europe broadly similar
- Minor changes in Clonal Complexes over the 3 years Europe-wide
  - Within countries some changes more noticeable
- Analysis and integration with other databases
  - Lineages and antigenic types involved in meningococcal disease Europe-wide
  - Design and implementation of public health measures e.g. vaccination

# Acknowledgments

- EUMenNet/EMGM Consortium



- MCJ Maiden
- KA Jolley
- Maiden Group
- Lynne Richardson and Becky Stack - Sequencing Facility

