The clinical notification of meningococcal disease (MD) has been carried out in Portugal since 1939. In October 2002 the General-Directorate of Health implemented a laboratory based surveillance of MD turning mandatory the clinical and laboratory notification of all cases. The National Reference Laboratory (NRL) of Neisseria meningitidis at the National Institute of Health Dr. Ricardo Jorge, Lisbon (NIH) has been managing a hospital laboratory network implemented throughout the country in 2002, which supports the laboratory component of the surveillance. Laboratories should send meningococcal isolates as well as negative culture clinical samples from suspected cases for lab confirmation and genotyping to the NRL. Voluntary vaccination against MenC started in 2002. In 2006 the MenC vaccine was introduced in the national immunization programme, addressed to children under one year of age (3 doses). During 2006 and 2007 a catch-up campaign was addressed to children under 15 years old. In 2012 the MenC vaccination schedule changed to one dose at 12 months of age. Since 2007 the number of invasive C strains became residual. In April 2014 the multi-component vaccine 4CMenB was introduced in the Portuguese market. Since January 2017 this vaccine has been freely given to individuals with increased risk of MD.

The aim of this work is to present data of MD surveillance referring to the period 2007-2016.

In the last decade 764 cases of MD were reported in Portugal (677 confirmed and 87 possible/probable). Incidence rate of MD decreased from 1.11/100,000 inhabitants in 2007 to 0.41/100,000 in 2016 (Figure 1). The highest incidence rate occurred in children younger than one year old, decreasing significantly for the 1-4 years age group, decreasing even further and maintaining at very low levels for the other age groups. Although this pattern was observed since 2007-2010, the decrease observed in the 1-4 years age group was particularly significant for the past two years, greatly contributing to the overall decrease in the incidence.

Serogroup B meningococci

From 2009 to 2016, 236 out of 367 invasive B strains (64.3%) were genotyped. They presented great genotype diversity (Figure 5). The most common clonal complexes (cc) were cc44 (28.1%), cc213 (13.8%) cc269 (11.9%), cc162 (8.5%) and cc461 (6.8%) (Figure 5). A particular attention was given to clonal complexes cc4461 and cc213 since they have been identified only in B strains and they’re estimated coverage by meningococcal multicomponent vaccine (4CMenB) was low (1% and 20%, respectively) (7). An increasing trend in the number of strains from these clonal complexes was observed (Figure 7).

Proteins PorA from families 22 and 7-2 were present in 57.2% of B strains isolated between 2009 and 2016, and were mostly associated with cc213, cc269 and cc4414. These proteins remained the most in the last two years (Figure 8). Protein FimA presented a great genetic diversity, the most predominantly being F1-5 (22.1%) and F5-5 (15.3%). A weak association between FimA variants and ST was observed, exception to cc461 associated to F5-9 and cc52 associated to F1-1 (Figure 9).

Serogroup Y meningococci

Serogroup Y strains were mostly characterized as cc23 (59.4%) (Figure 10).