



Portugal

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General information



Population size – 10,358,076	Category - National	
Structure of surveillance of meningococcal disease	Statutory notification of disease Enhanced surveillance Centralized Laboratory Surveillance	Yes Weekly match of datasets to actively request for samples or missing notifications Yes
NRL: repertoire of typing targets	Serogroup PorA antigen sequence typing FetA antigen sequence typing Vaccine Antigen sequence typing (e.g. fhbp) Antibiotic resistance gene typing MLST (7 loci) Genome sequencing	Yes Yes Yes No No Yes Occasionally
Meningococcal vaccine recommendation	Polysaccharide vaccines (not conjugated) MenC conjugate MenACWY conjugate Protein vaccines targeting MenB	No YES (it is included in the NIP) Risk group (travelers) > Jan 2017 Risk group
Uptake of Men WY vaccines	estimated % per target group size	Unknown %

Nov. 1st, 2016

EMGM Meeting on MenWY, Frankfurt

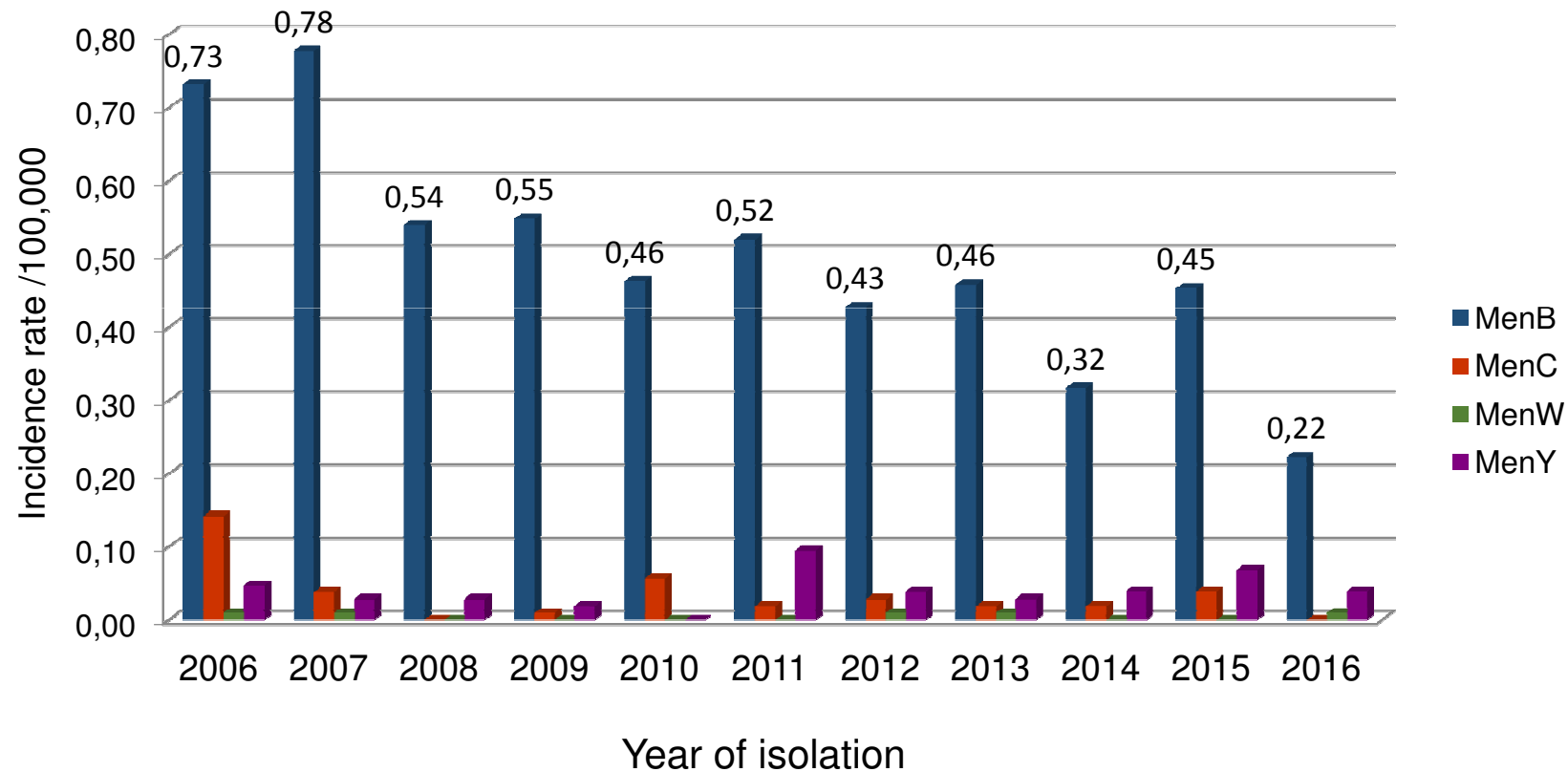
Basic numbers for 2015



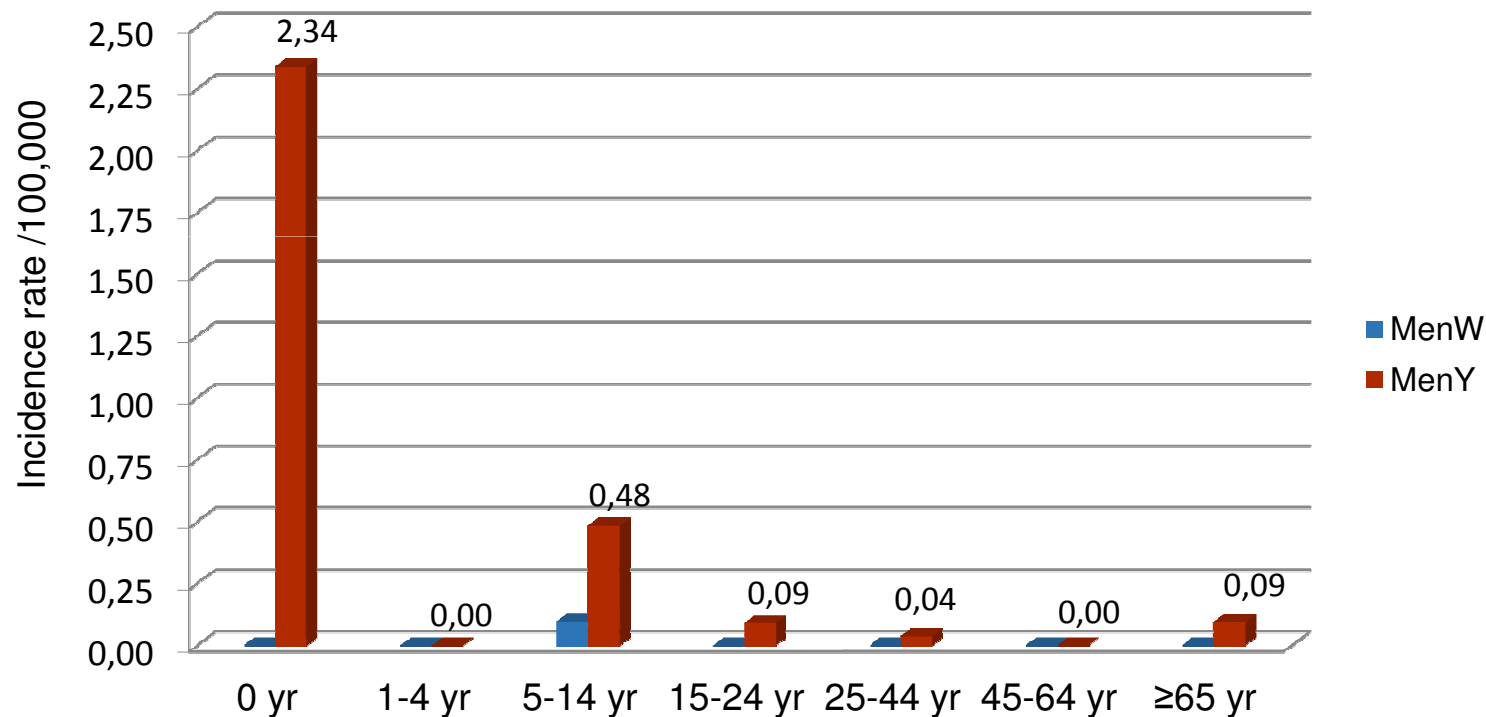
No of reported cases of invasive meningococcal disease * (incidence rate)	N= 65 confirmed cases + N=2 possible cases + N=1 probable case (0.63 /100,000)
Proportion of reported cases of invasive meningococcal disease, whose strains or samples were processed at NRL (<i>=laboratory surveillance coverage of reported cases</i>)	93.8 % (61/65)
MenW <ul style="list-style-type: none"> • no of cases, • incidence rate, • % of all cases 	N= 0 0 /100,000 0 %
MenY <ul style="list-style-type: none"> • no of cases, • incidence rate, • % of all cases 	N= 7 0.067/100,000 10.77% (7/65)

* please use [ECDC case definition](#)

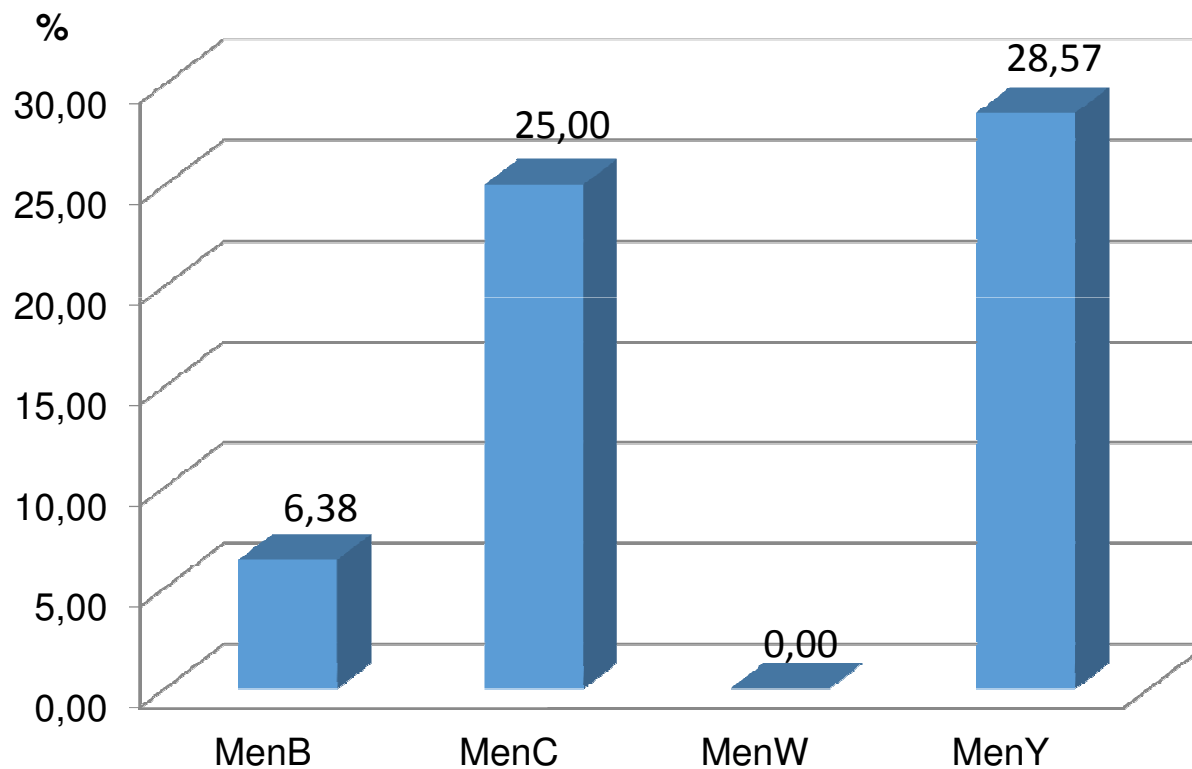
Incidence rates (N/100,000/a) for serogroups B, C, W, Y from 2006-2016



Age specific incidence rates 2015 and 2016 (N/100,000 of age group/a) for serogroups W and Y



Case fatality rates 2015 (in %) for serogroups B, C, W, Y



Sequence typing of **MenW** in 2016



Year 2016	
Dominant variant according to the typing method used	
Dominant variant according to the typing method used, in % of all MenW cases	%
cc11 in % of all serogroup W cases	%

1 isolate W:P1.18-1,3:F4-1:cc22

Outbreaks caused by serogroups W and Y **2012 - 2016**



	MenW	MenY
Number of outbreaks or clusters	0	0
Total number of patients involved	0	0
Settings		

Thank you



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