



# Italy

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# General information



Population size	Category	
Structure of surveillance of meningococcal disease	Statutory notification of disease	Yes
	Enhanced surveillance	Yes
	Centralized Laboratory Surveillance	Yes
NRL: repertoire of typing targets	Serogroup	Yes
	PorA antigen sequence typing	Yes
	FetA antigen sequence typing	Yes
	Vaccine Antigen sequence typing (e.g. fhbp)	Yes
	Antibiotic resistance gene typing	Yes
	MLST (7 loci)	Yes
Meningococcal vaccine recommendation	Genome sequencing	Yes
	Polysaccharide vaccines (not conjugated)	No
	MenC conjugate	YES
	MenACWY conjugate	YES
Uptake of MenWY vaccines	Protein vaccines targeting MenB	YES
	estimated % per target group size	%

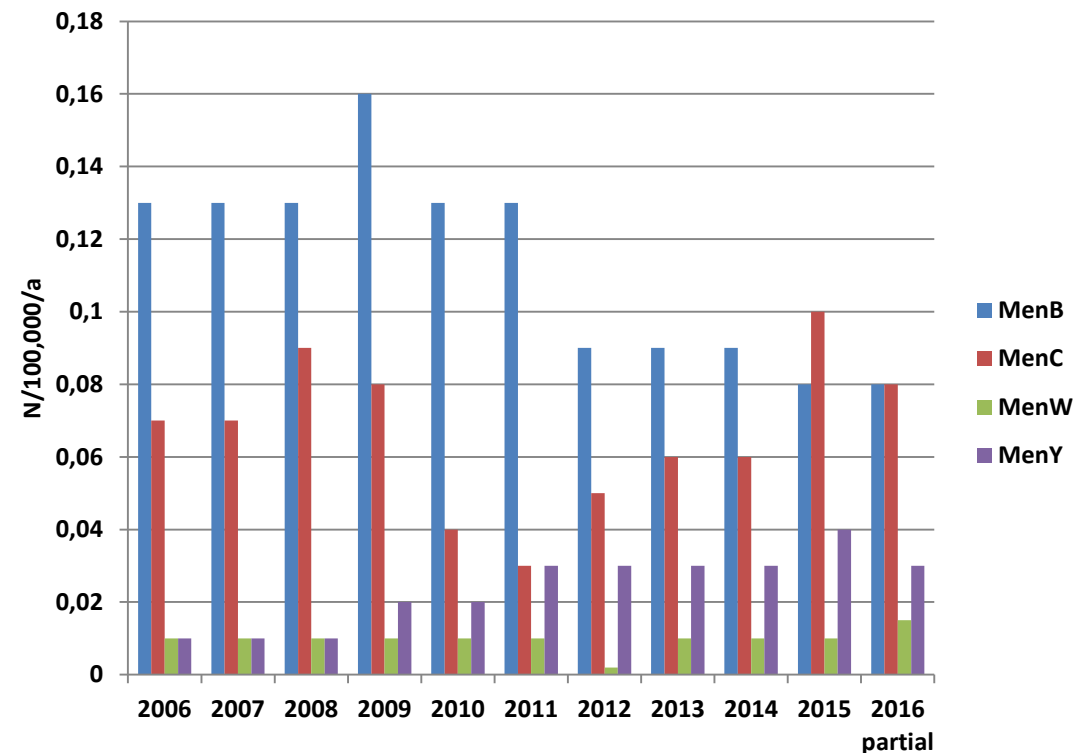
# Basic numbers for 2015



No of reported cases of <b>invasive meningococcal disease</b> * (incidence rate)	N= 168 (0.28 /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> )	70%
MenW <ul style="list-style-type: none"><li>• no of cases,</li><li>• incidence rate,</li><li>• % of all cases</li></ul>	N= 7 0.01/100,000 5 %
MenY <ul style="list-style-type: none"><li>• no of cases,</li><li>• incidence rate,</li><li>• % of all cases</li></ul>	N= 22 0.036/100,000 16%

\* please use [ECDC case definition](#)

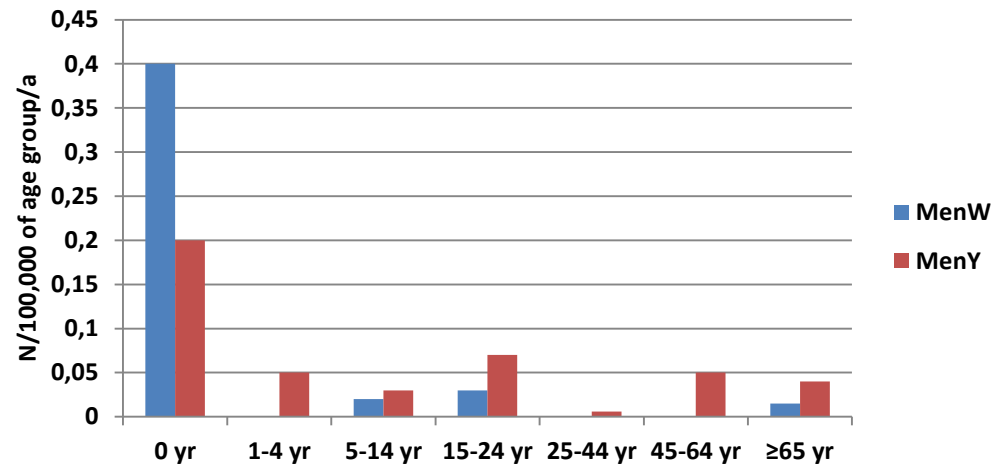
# Incidence rates (N/100,000/a) for serogroups B, C, W, Y from 2006-2016



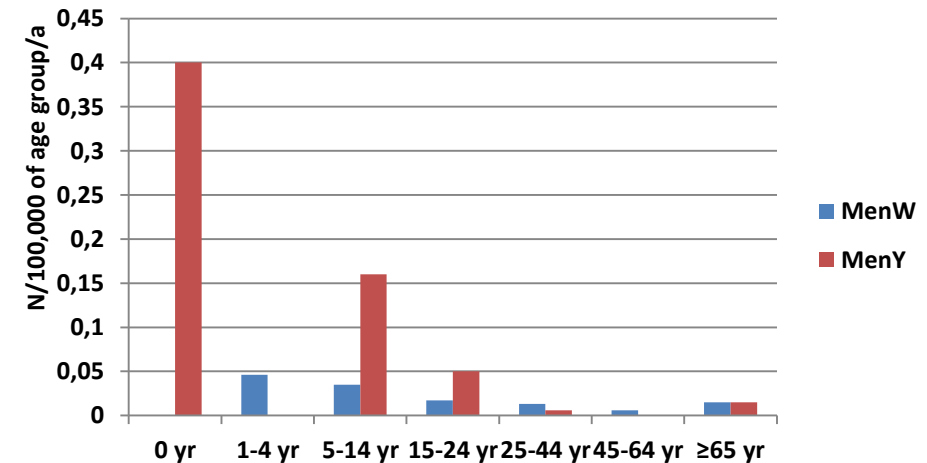
# Age specific incidence rates 2015 and/or 2016 (N/100,000 of age group/a) for serogroups W and Y



2015



2016



# Sequence typing of **MenW** in 2015 and 2016



Year	2015	2016
Dominant variant according to the typing method used	cc11 (finetype P1.5,2:F1-1:ST-11)	cc11 (finetype P1.5,2:F1-1:ST-11)
<b>Dominant variant</b> according to the typing method used, in % of all MenW cases	60% (finetype P1.5,2:F1-1:ST-11)	67% (finetype P1.5,2:F1-1:ST-11)
<b>cc11</b> in % of all serogroup W cases	60% (finetype P1.5,2:F1-1:ST-11)	67% (finetype P1.5,2:F1-1:ST-11)

# Sequence typing of **MenW** in 2015 and / or 2016



Year	2015
Dominant variant according to the typing method used	cc11
<b>Dominant variant</b> according to the typing method used, in % of all MenW cases	cc11 60%
<b>cc11</b> in % of all serogroup W cases	60%

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



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

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