



POLAND

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General information



Population size: 38 478 602*	Category	
Structure of surveillance of meningococcal disease	Statutory notification of disease Enhanced surveillance Centralized Laboratory Surveillance	Yes No Yes, but voluntary based
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 occasionally occasionally Yes occasionally
Meningococcal vaccine recommendation	Polysaccharide vaccines (not conjugated) MenC conjugate MenACWY conjugate Protein vaccines targeting MenB	All Men vaccines are recommended but not reimbursed
Uptake of MenWY vaccines	estimated % per target group size	NA

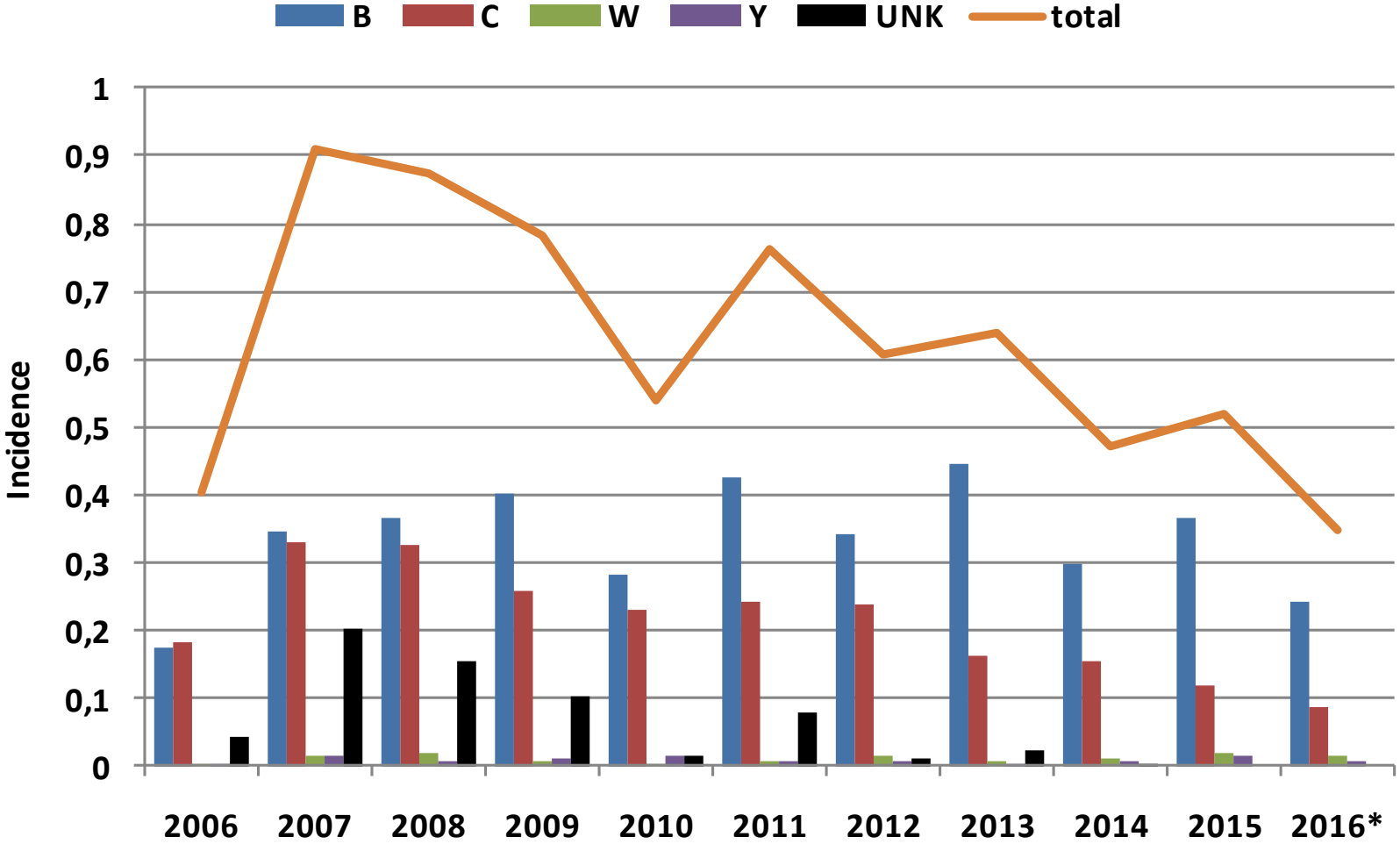
Basic numbers for 2015



No of reported cases of invasive meningococcal disease * (incidence rate)	N = 218 (0.57 /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>	200/218 91.7 %
MenW <ul style="list-style-type: none"> • no of cases, • incidence rate, • % of all cases 	N = 7 0.018/100,000 3.5 %
MenY <ul style="list-style-type: none"> • no of cases, • incidence rate, • % of all cases 	N = 6 0.016 /100,000 3.0 %

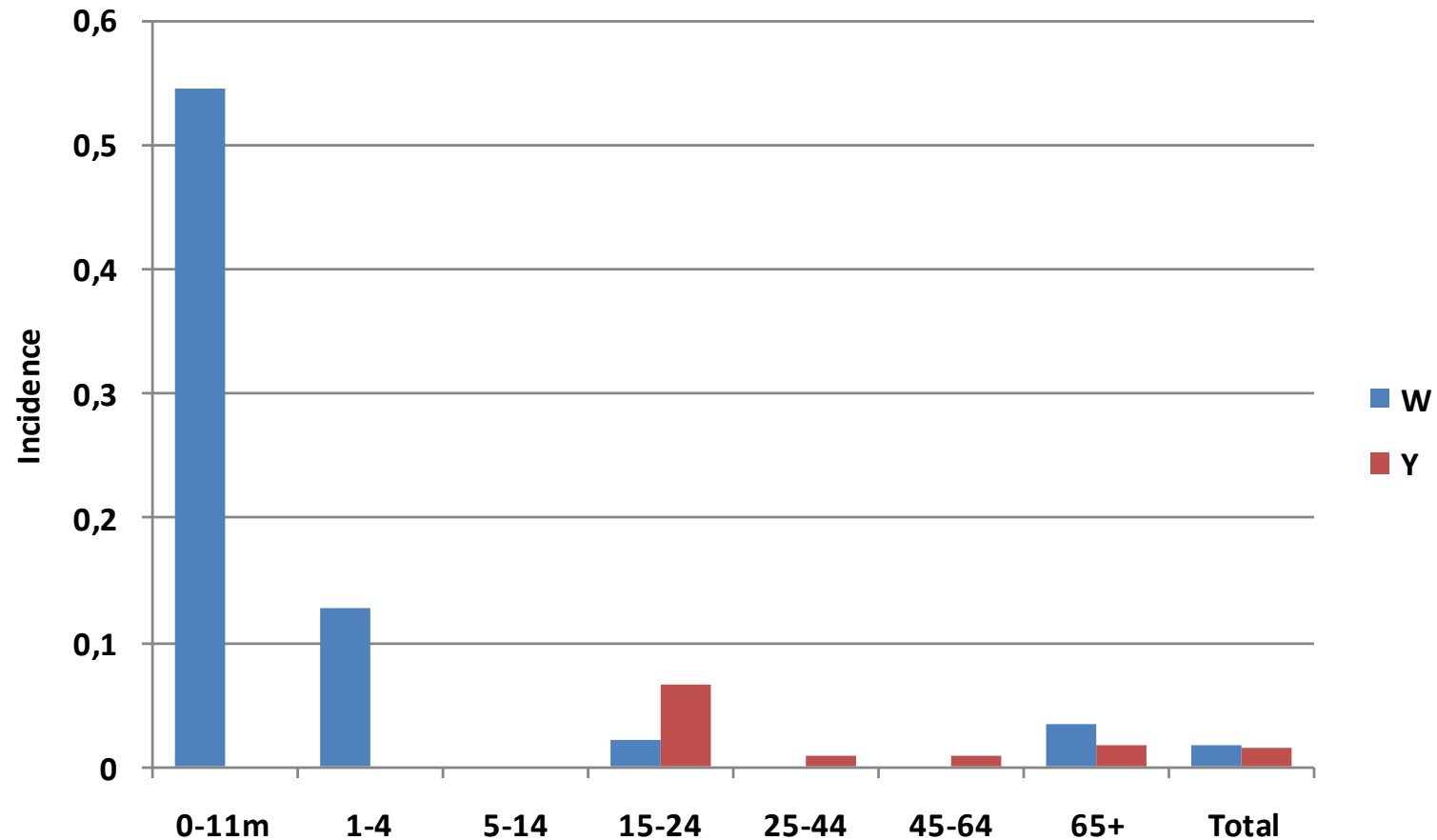
* please use [ECDC case definition](#)

Incidence rates for serogroups B, C, W, Y (2006-2016)

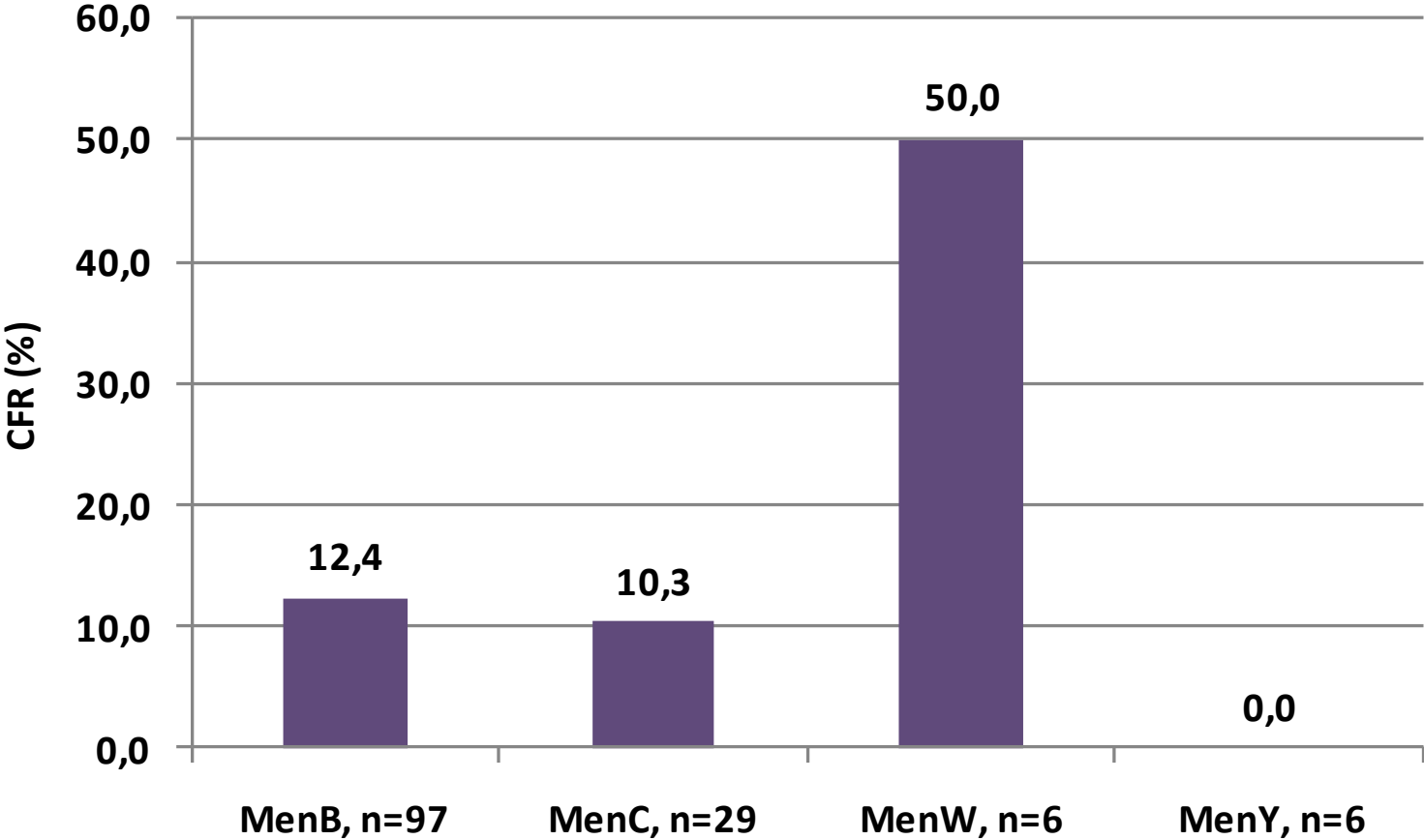


*2016 – until 31.10.16

Age specific incidence rates for serogroups W and Y, 2015



Case fatality rates in 2015 for serogroups B, C, W, Y (cases with known outcome only, 138/200)



Sequence typing of MenW in 2015 and 2016



Year	2015 (n=7, incl. 6 isolates)	2016* (n=5, incl. 3 isolates)
Dominant variant according to the typing method used	<ul style="list-style-type: none"> • ST-9316 (n=4); • including 3 x (5-2/10-1, F5-8) 	<ul style="list-style-type: none"> • ST-9316; 5-2/10-1, F5-8 • ST-9316 or its slv; 5-2/10-1, F5-8 • CSF: four common alleles with ST-9316, three unknown
Dominant variant according to the typing method used, in % of all MenW cases	ST-9316 57% (4/7)	ST-9316 50% or 75% (2/4 or 3/4)
cc11 in % of all serogroup W cases	29% (2/7)	25% (1/4)

*until 31.10.2016

Outbreaks caused by MenW and MenY, 2012 - 2016



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