

Molecular epidemiology of invasive meningococcal disease in the Czech Republic

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Objectives

Enhanced surveillance of invasive meningococcal disease has been conducted in the Czech Republic since 1993, when a new hyperinvasive clonal complex, cc11, emerged and caused increase in incidence and morbidity of invasive meningococcal disease. Molecular methods for the characterization of *Neisseria meningitidis* which have been used continuously in the National Reference Laboratory

for Meningococcal Infections (NRL) allow precise assessment of the epidemiological situation. The aims of this study were to identify possible epidemiological links between cases of invasive meningococcal disease across districts of the country, to detect secondary cases, and to assess possible epidemiological links between patients and healthy contacts.

Methods

Epidemiological and microbiological data from the surveillance database for 2007 were analysed. All meningococcal isolates from cases of invasive meningococcal disease (43 isolates) and healthy contacts (36 isolates) referred to the NRL were characterized by serogrouping, *PorA* and *FetA* sequencing (<http://neisseria.org/nm/typing/>) and multilocus sequence typing (MLST) (<http://pubmlst.org/neisseria/>).

Conclusion

- No secondary case of invasive meningococcal disease has been detected in the Czech Republic.
- The measures taken in foci of invasive meningococcal disease are efficacious and need to be targeted at close contacts only.

Results

Invasive meningococcal disease in the Czech Republic in 2007 was caused mainly by serogroup B (67.5 %), followed by serogroups C (20.9 %), Y (9.3 %) and X (2.3 %) – **Figure 1, Table 1**. The following clonal complexes were most frequently associated with invasive meningococcal disease: cc11 (18.6 %), cc18 (13.9 %), cc41/44 (9.3 %), cc32 (9.3 %) and cc35 (9.3 %) – **Figure 2, Table 1**. Most isolates from healthy contacts were either serogroup B (61.1 %) or non-

groupable (33.3 %) – **Figure 3, Table 2**. They showed high heterogeneity in clonal complexes, with the prevalence of cc41/44 (19.4 %) and a high proportion of strains unassigned to clonal complex (36.1 %) – **Figure 4, Table 2**. In 2007, invasive meningococcal disease occurred in 49 out of 86 districts. A single case was reported in 30 districts, two or more cases occurred in 19 districts. No secondary case of invasive meningococcal disease was detected by the analysis

of epidemiological data and isolate genotypes. Genotypes were identified for 7 clusters of pair case/contact isolates. The case and contact isolates had identical genotypes in 3 clusters, the former differed in genotype from the latter in one cluster and mixed genotypes were observed in 3 clusters – **Figure 5, Table 3**. All pair case/close contact isolates had identical genotypes in contrast to most pair case/non-close contact isolates that differed in genotype.

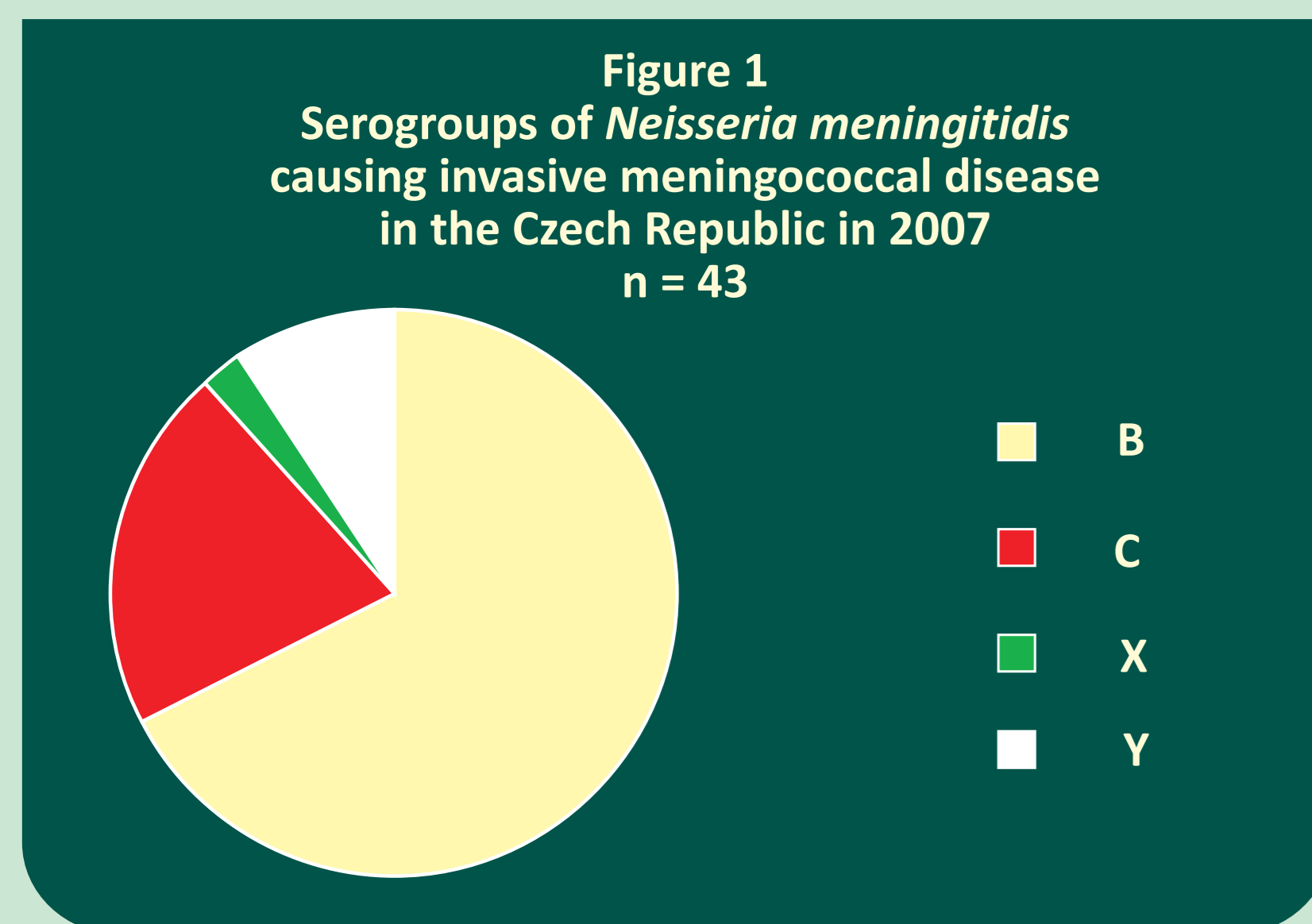


Table 1. Serogroups and clonal complexes of *N. meningitidis* causing invasive meningococcal disease in the Czech Republic in 2007 n=43

Clonal complex	Serogroup				Total
	B	C	X	Y	
cc11	1	7			8
cc18	6				6
cc32	4				4
cc35	4				4
cc41/44	3	1			4
cc103	1				1
cc1157	1				1
cc116					1
cc167		1		1	1
cc23				1	1
cc269	1				1
cc60	2				2
Unassigned	6			2	9
Total	29	9	1	4	43

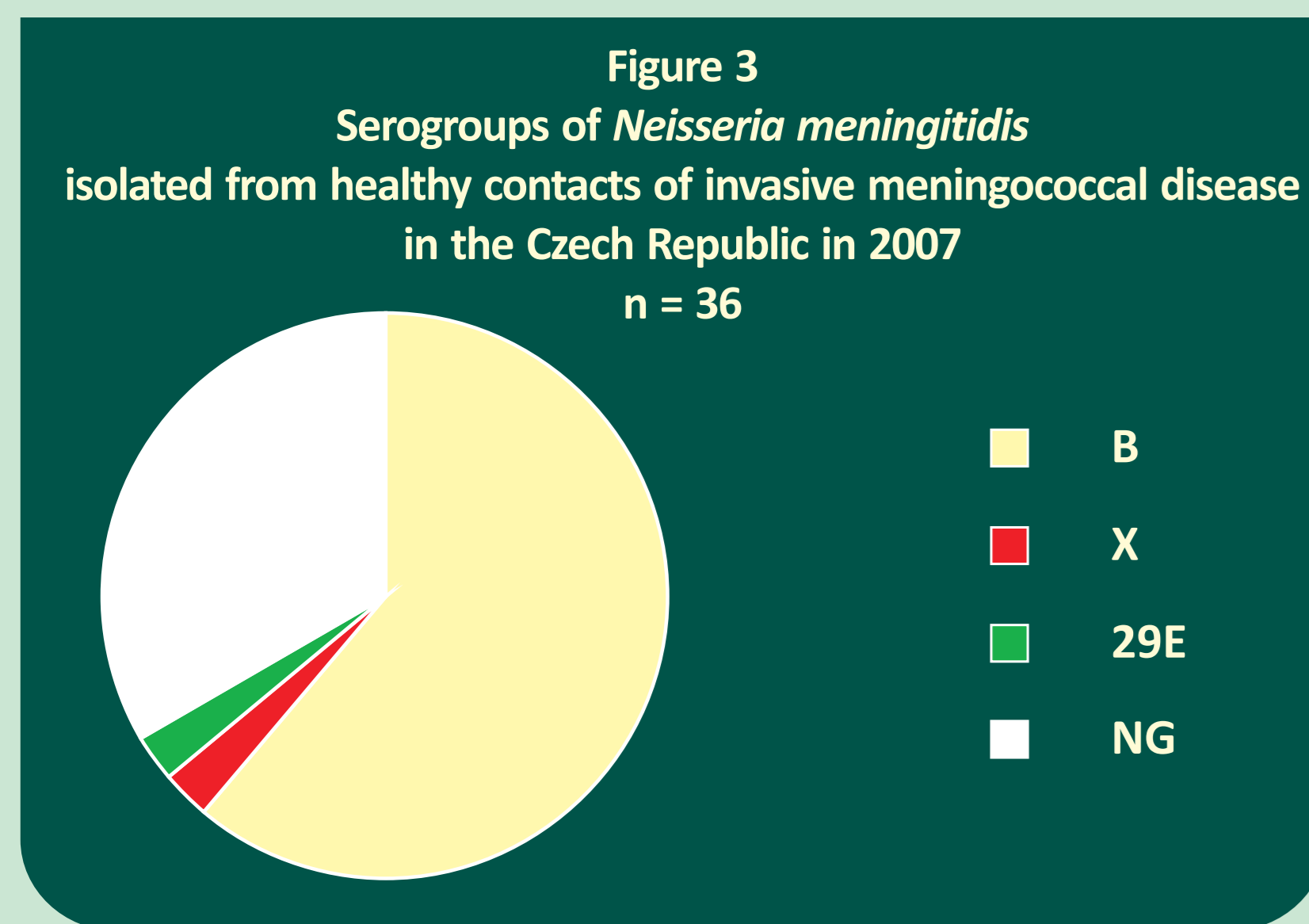
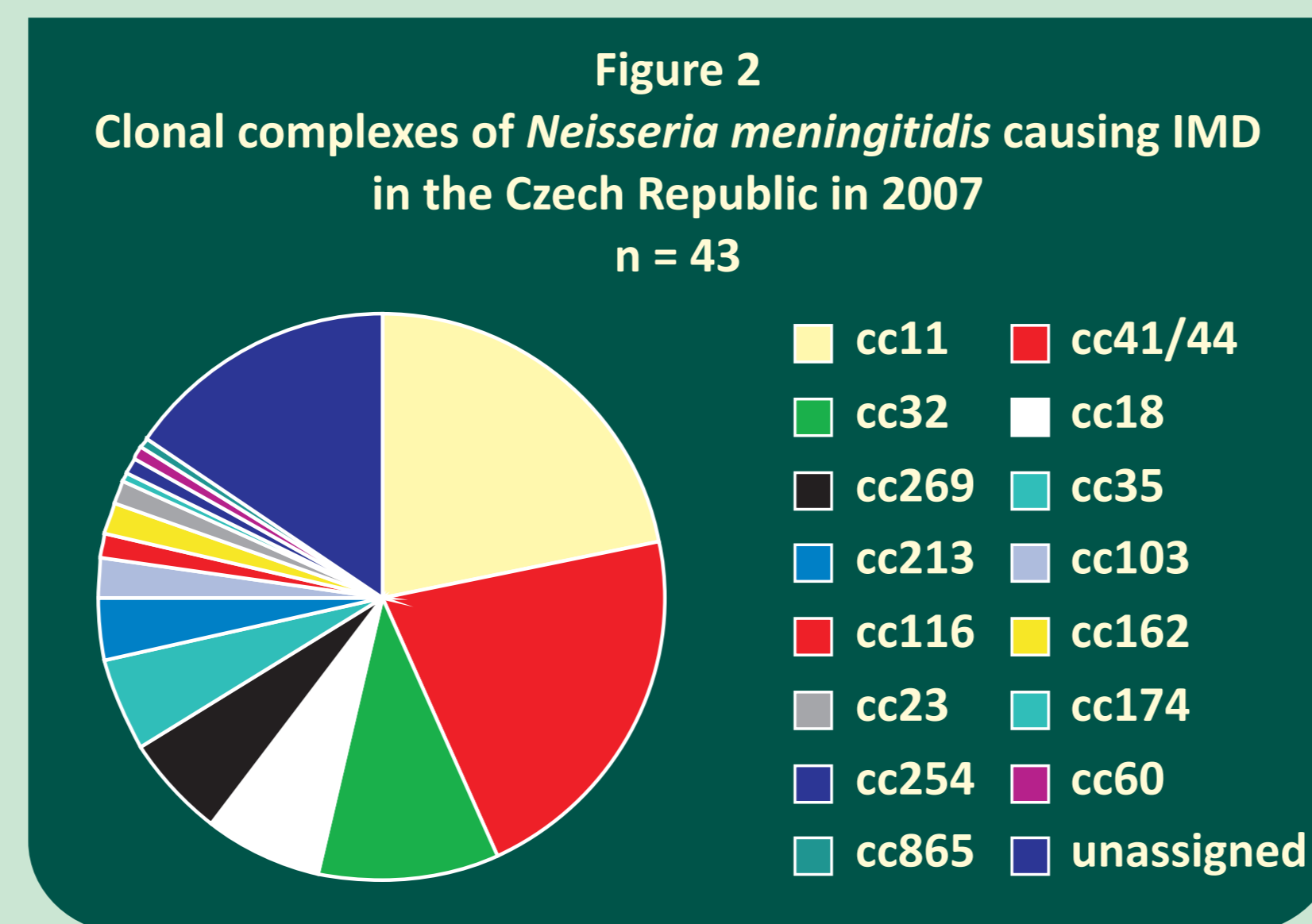
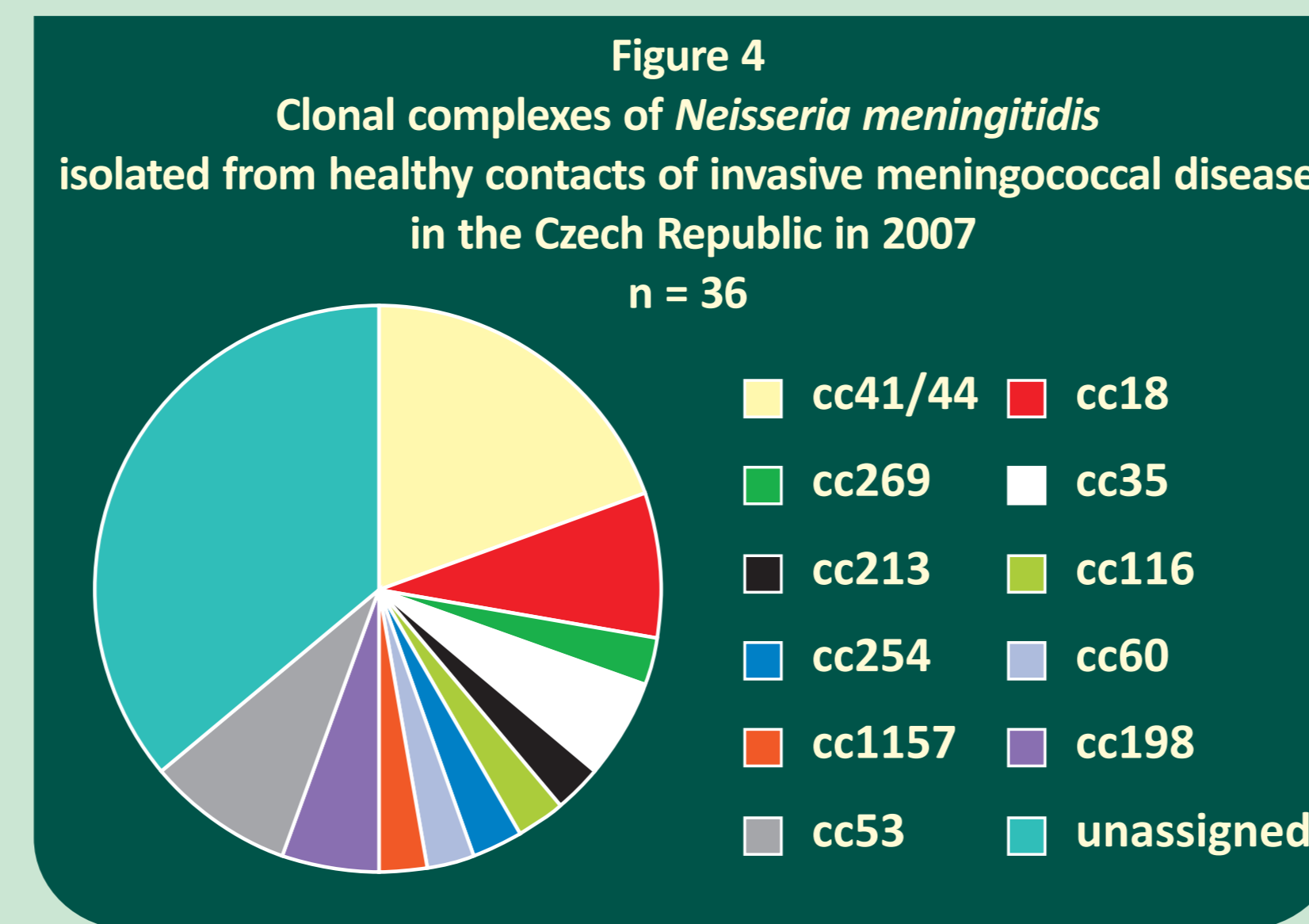
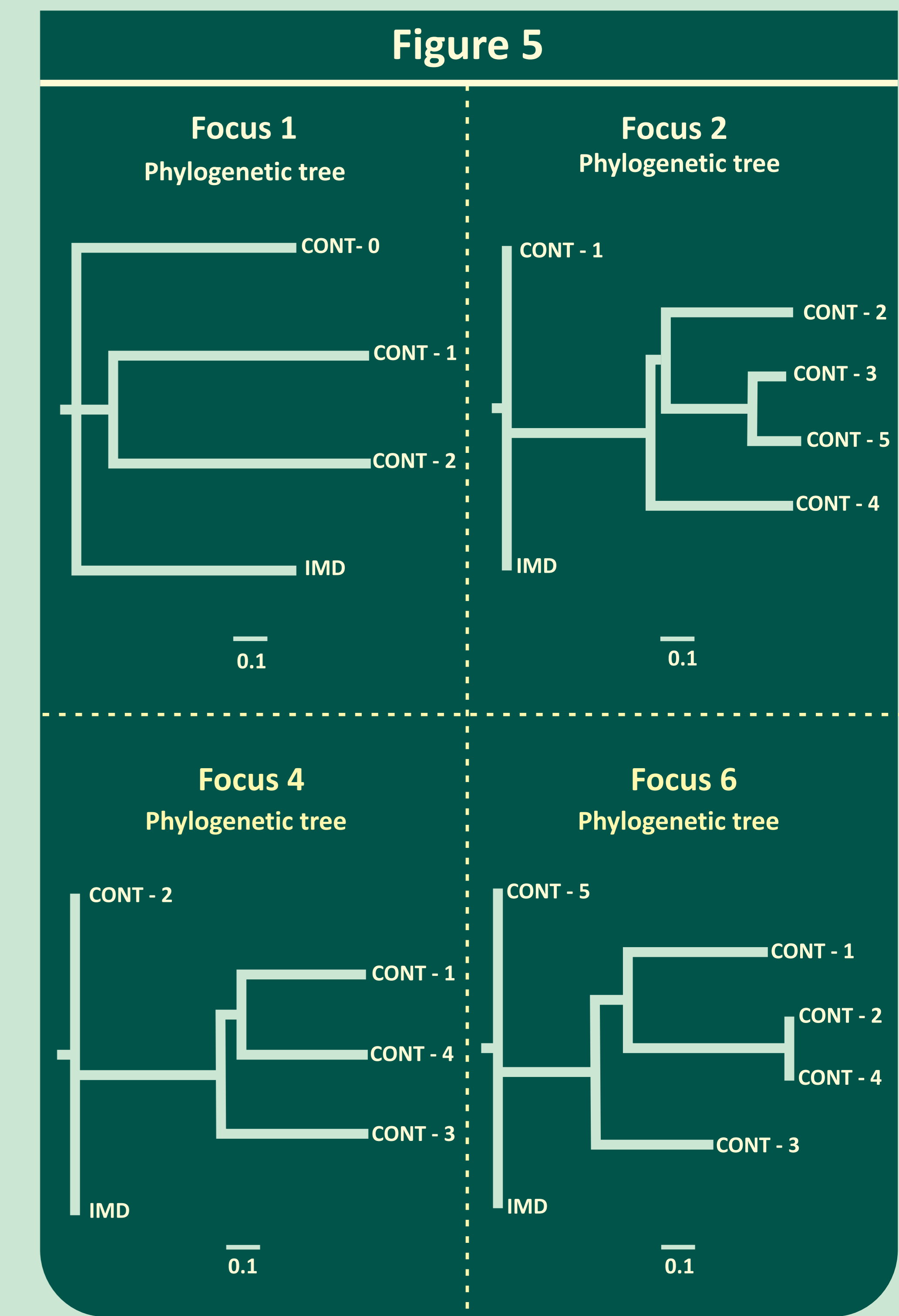


Table 2. Serogroups and clonal complexes of *N. meningitidis* isolated from healthy contacts of invasive meningococcal disease in the Czech Republic in 2007 n=36

Clonal complex	Serogroup				Total
	B	X	29E	NG	
cc18	2			1	3
cc35	2				2
cc41/44	3			4	7
cc1157	1				1
cc116				1	1
cc198				2	2
cc213	1				1
cc254			1		1
cc269	1				1
cc53		1		2	3
cc60	1				1
Unassigned	11			2	13
Total	22	1	1	12	36



Focus	Isolate	Phenotype	Sequence type	Clonal complex	Epidemiological relationship
F 1	IMD	B:4:P1.15	ST-34	cc32	non-close contact
	CONT-1	NG:NT:P1.15	ST-110	cc41/44	
	CONT-2	X:21:P1.7	ST-53	cc53	
	CONT-3	B:4:P1.14	ST-35	cc35	
F 2	IMD	B:4,21:P1.22,14	ST-35	cc35	close contact
	CONT-1	B:4,21:P1.22,14	ST-35	cc35	
	CONT-2	NG:21:P1.7,P1.30	ST-53	cc53	
	CONT-3	B:4:P1.17,P1.16	ST-5940	cc41/44	
	CONT-4	B:22:P1.22,P1.14	ST-18	cc18	
CONT-5	NG:4:P1.19,P1.15	ST-110	cc41/44		
F 3	IMD	B:NT:P1.5,P1.2	ST-1383	cc60	close contact
	CONT	B:NT:P1.5,P1.2	ST-1383	cc60	
F 4	IMD	B:22:P1.22,P1.14	ST-18	cc18	non-close contact
	CONT-1	NG:21:P1.7,P1.30	ST-53	cc53	
	CONT-2	B:22:P1.22,P1.14	ST-18	cc18	
	CONT-3	B:21:P1.18,P1.25	ST-823	cc198	
CONT-4	B:4:P1.19,P1.15	ST-669	UA	non-close contact	
F 5	IMD	B:NT:P1.21,P1.16	ST-1157	cc1157	close contact
	CONT	B:NT:P1.21,P1.16	ST-1157	cc1157	
F 6	IMD	B:nd:P1.5,P1.2	ST-1383	cc60	non-close contact
	CONT-1	NG:nd:P1.18,P1.13	ST-2878	cc22	
	CONT-2	NG:nd:P1.18,P1.25	ST-823	cc198	
	CONT-3	NG:nd:P1.14,P1.15	ST-2395	UA	
	CONT-4	NG:nd:P1.18,P1.25	ST-823	cc198	
CONT-5	B:nd:P1.5,P1.2	ST-1383	cc60	close contact	
F 7	IMD	B:4:P1.14	ST-35	cc35	close contact
	CONT	B:4:P1.14	ST-35	cc35	



Acknowledgement
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IMD = invasive meningococcal disease NG = non-groupable NST = non-subtypable
UA = clonal complex unassigned NT = non-typable nd = not done

NG = non-groupable