Laboratory surveillance of invasive isolates of *Neisseria meningitidis*. Argentina 2015-2022

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Background

Invasive meningococcal disease (IMD) is a serious and potentially fatal condition. The incidence in Argentina is 0,2/100,000 inhabitants. In 2017 the Argentine National Immunisation Program (NIP) implemented MenACWY-CRM197 vaccine for 3-5-15 months and 11 years old. Since 2020 the NIP has recommended a combined vaccination MenACWY- 4CMenB for high-risk groups. The aim of this study was to describe the clinical presentations and capsular groups distributions and characterize through Whole Genome Sequencing (WGS) invasive isolates of *Neisseria meningitidis* (Men) circulating in Argentina.

Methods

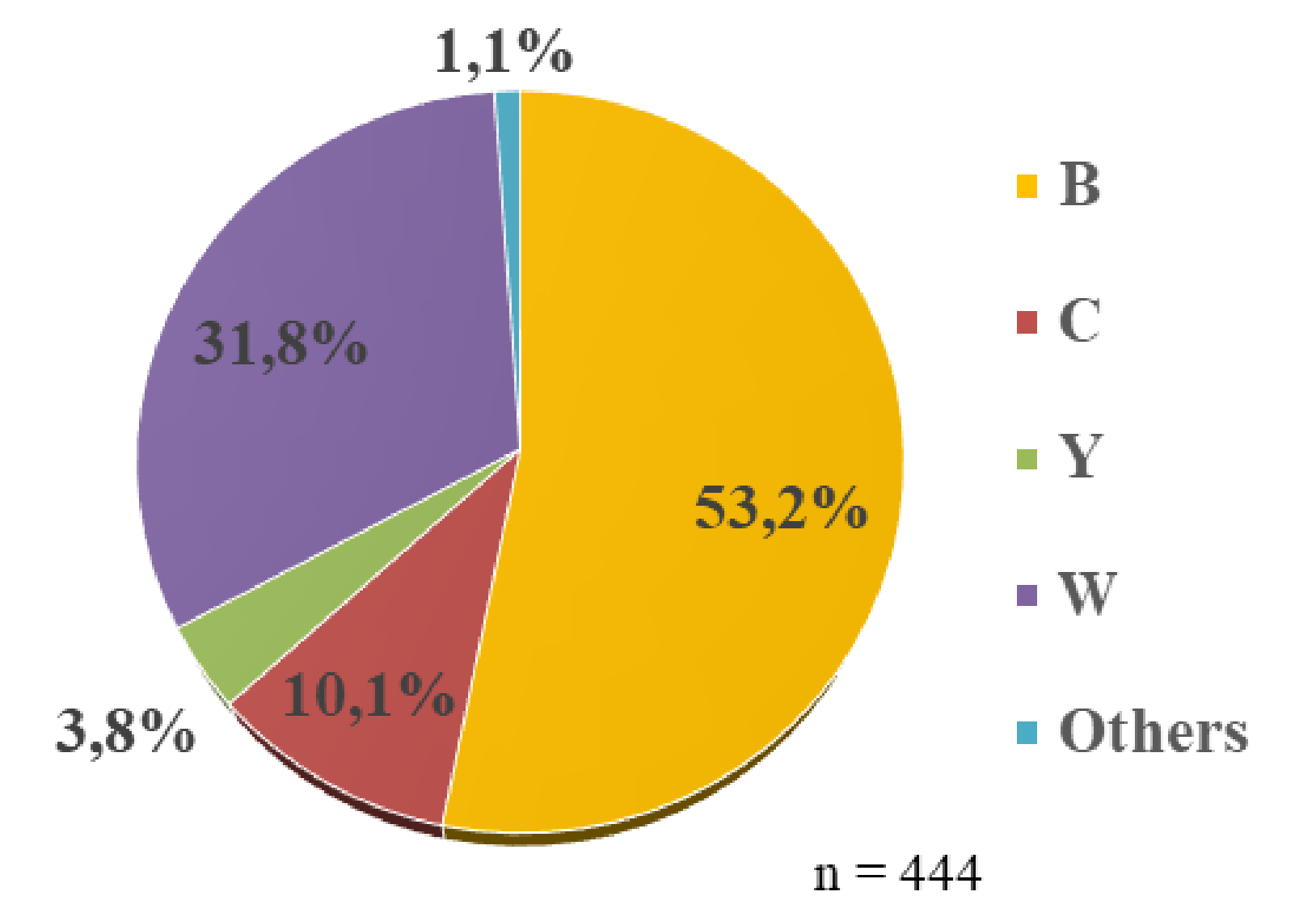
A total of 444 Men isolates recovered from children and adults with IMD during 2015-2022 were received at the National Reference Laboratory to confirm the capsular group using PCR and characterize through WGS (344 available).
Libraries were sequenced with NovaSeq (Illumina) platform and the assembled genomes (Unicycler) were analyzed with PubMLST website.

Results

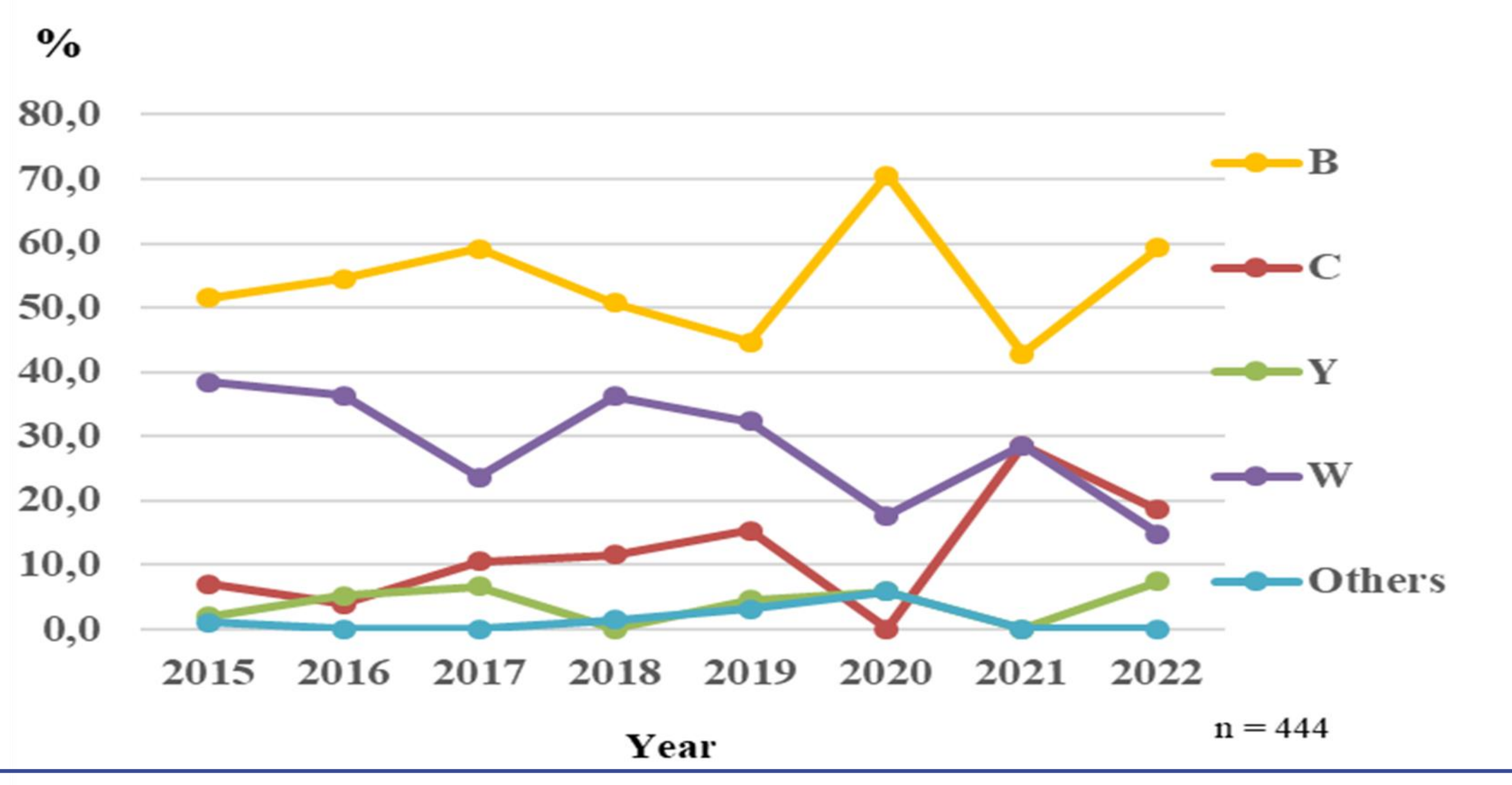
Clinical presentations distribution

Clinical presentation	n	%
Meningitis	239	53,8
Meningococcemia	82	18,5
Mening- Meningococ.	59	13,3
Bacteremia	42	9,5
Arthritis	9	2,0
Pneumonia	8	1,8
Other	5	1,1

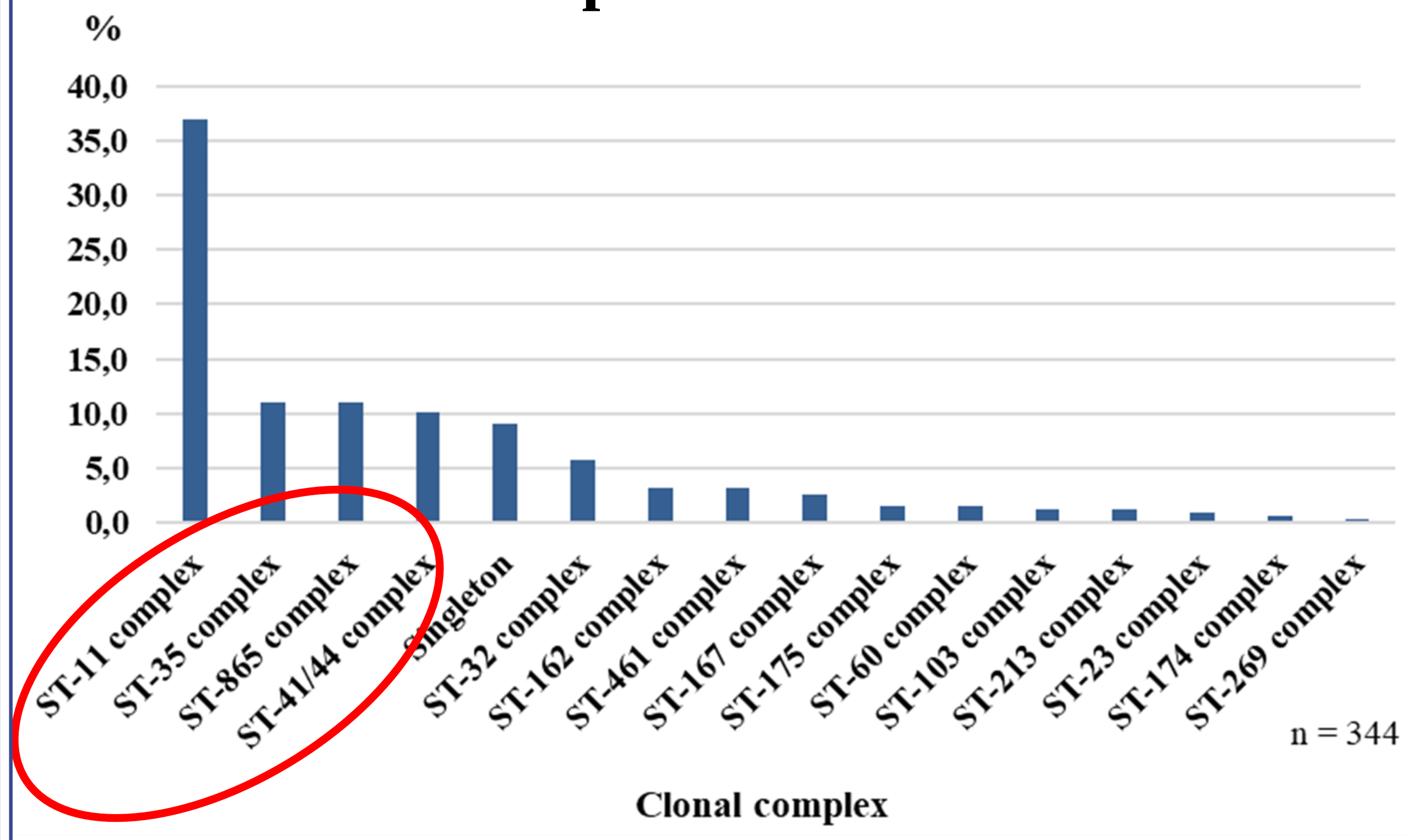
Capsular groups distribution



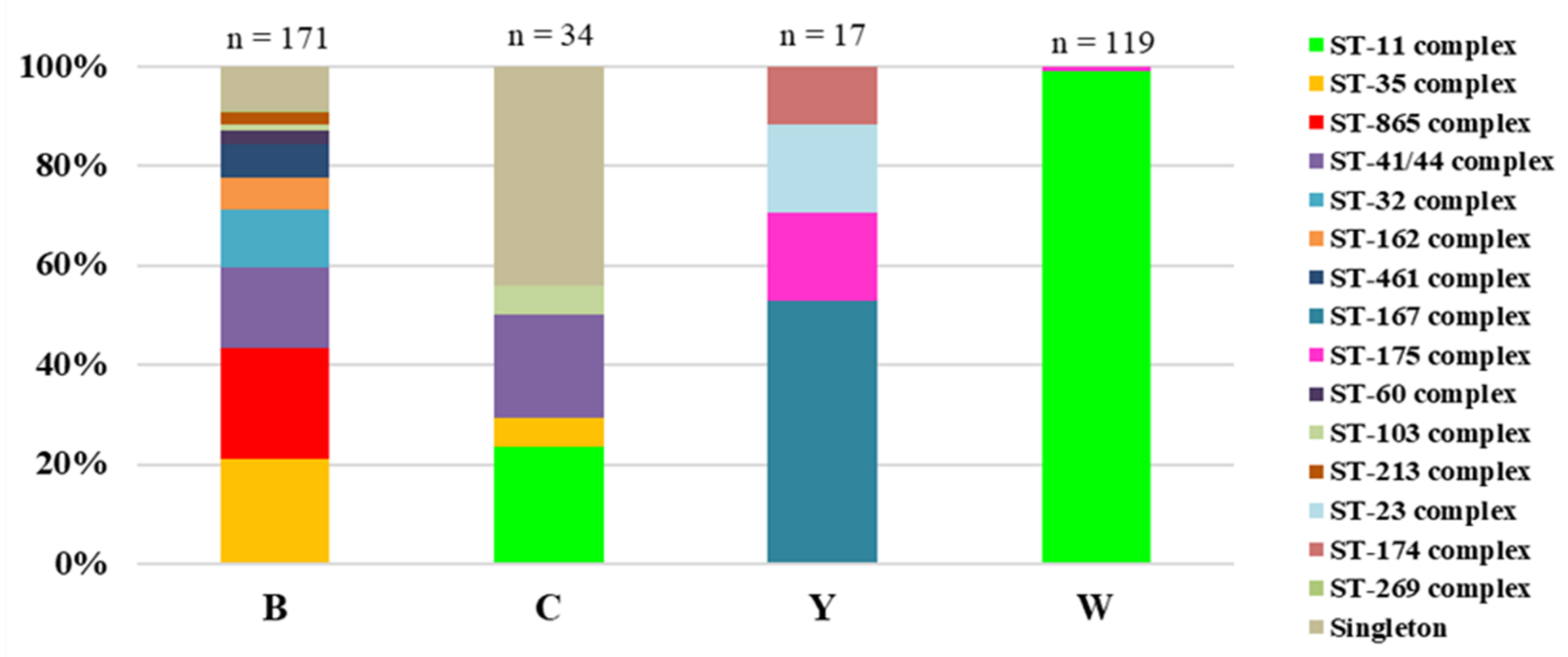
Annual relative frequency of capsular groups



Clonal complexes distribution

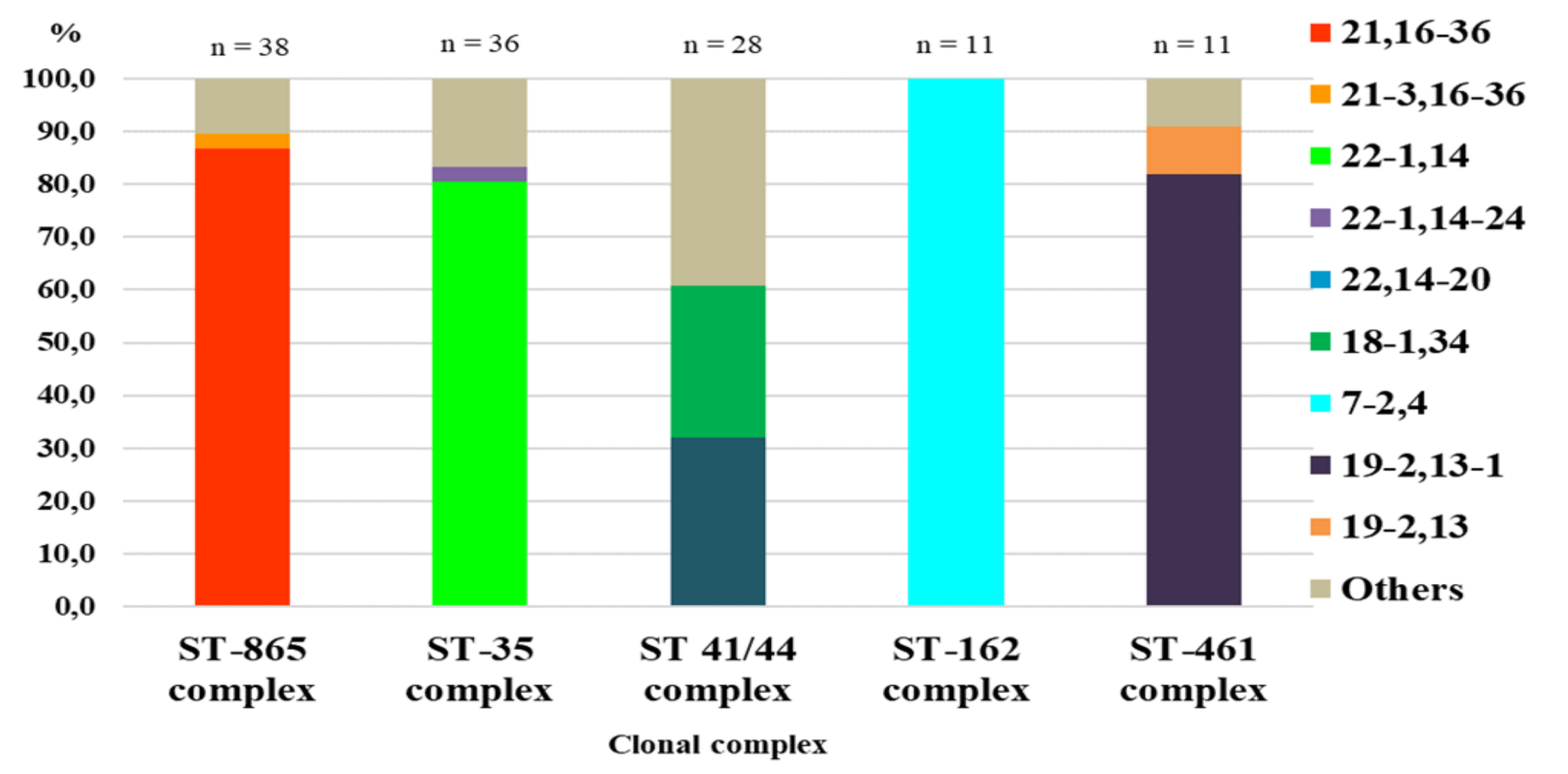


Clonal complexes distribution according to capsular group

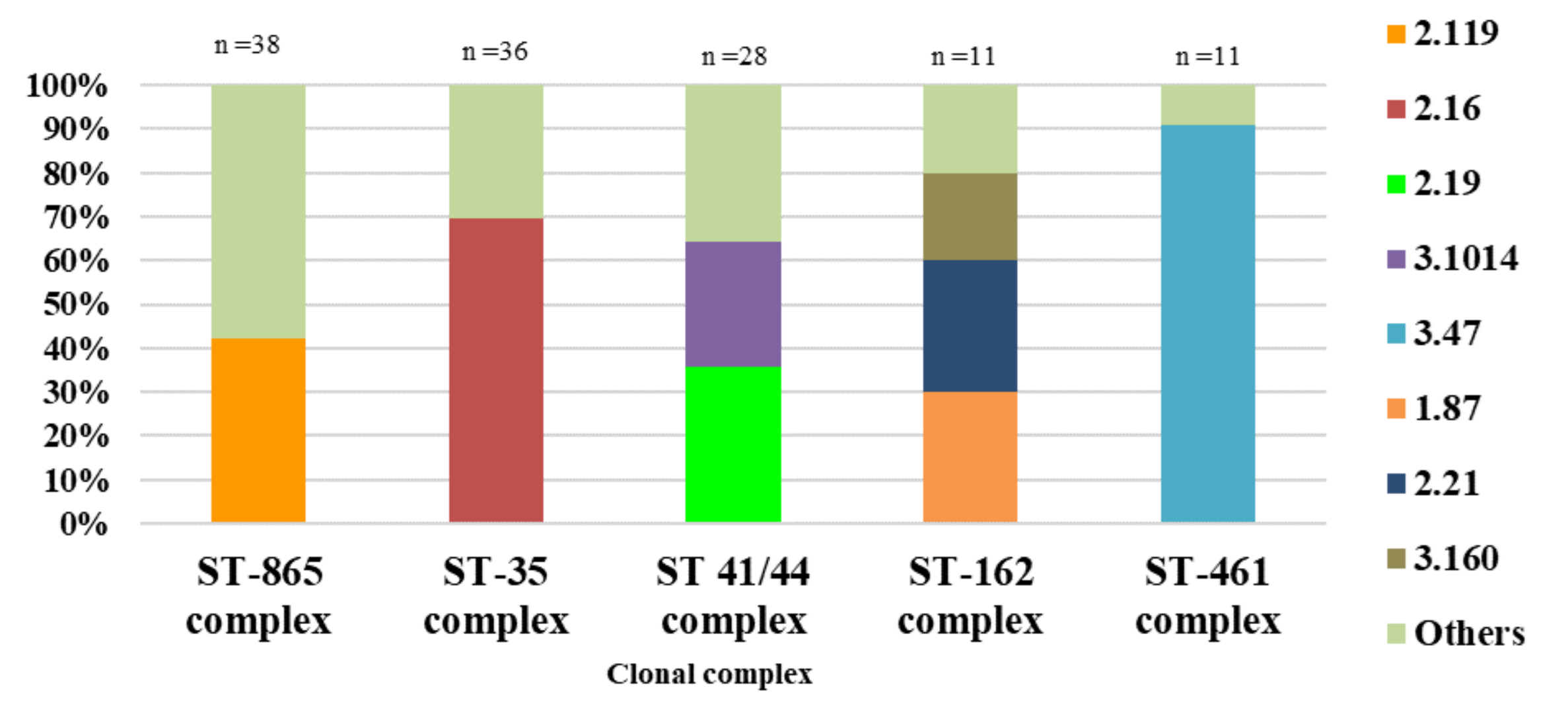


Capsular group C was mostly associated with singleton ST-2196, 44.1% (14/34), endemic in Chaco Province.

Main associations between PorA peptides (VR1,VR2) and clonal complexes in MenB

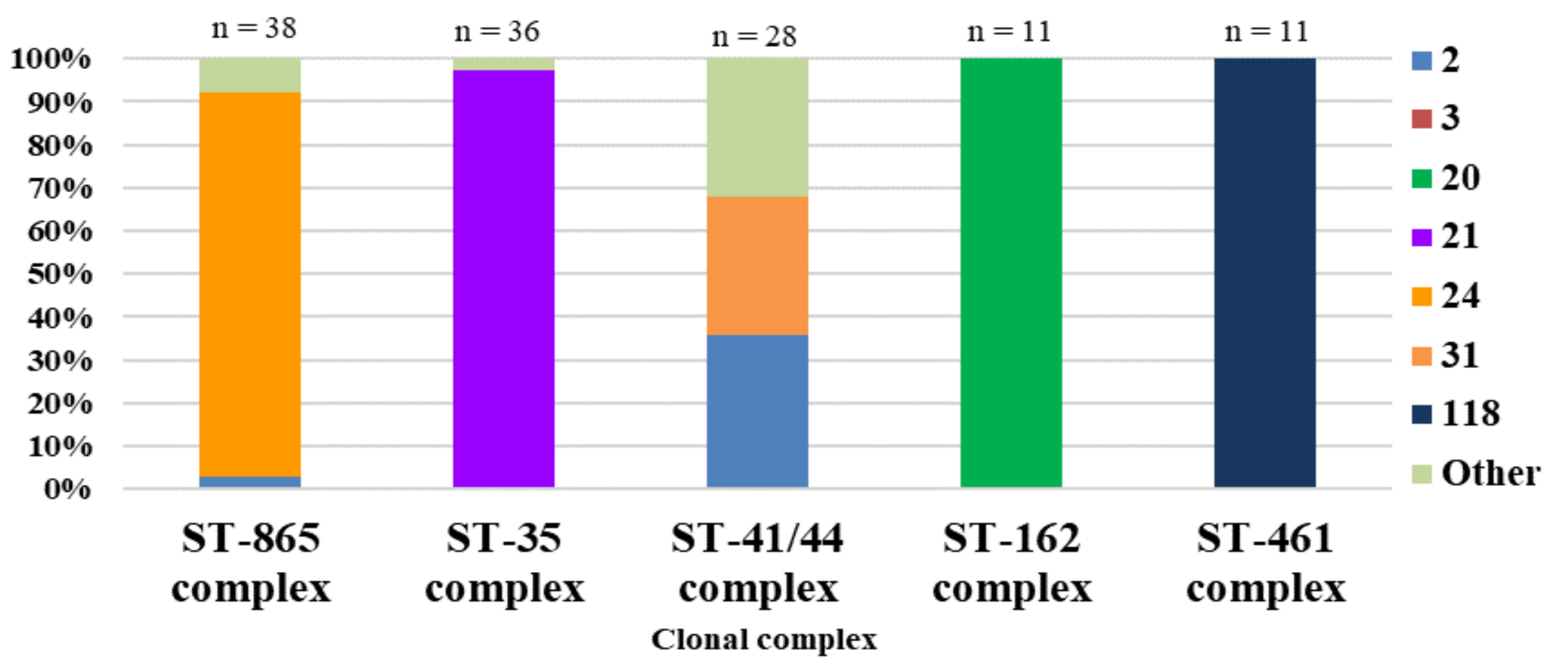


Main associations between FHbp peptides and clonal complexes in MenB



NadA peptide was present only in 13.5% MenB isolates

Main associations between NHBA peptides and clonal complexes in MenB



MenDeVar Index in MenB

MenDeVar Index	Bexsero		Trumemba	
	n	%	n	%
Exact match	25	14,6	1	0,6
Cross reactive	7	4,1	64	37,4
Insufficient data	136	79,5	106	62,0
None	3	1,8	0	0,0

Among **W ST-11 complex**, more than 95% of the isolates exhibited the same antigenic profile: fHbp peptide 2.22, NHBA peptide 29, PorA 5,2 and NadA peptide 6 (variant 2/3 4CMenB vaccine).

Conclusions

- **B was the most prevalent capsular group, associated mainly with ST-865 complex and ST-35 complex.**
- **WGS of ST-865 complex isolates could help clarify why these strains that are uncommon in other regions became the leading cause of IMD in Argentina.**
- **The presence of NadA peptide 6 in W strains could suggest that they exhibit cross-reactivity with 4CMenB vaccine, according to our previous study of serum bactericidal activity (hSBA)**
- **MenDeVar results must be carefully analyzed taking into account our previous hSBA assays and the same MenB clonal complexes distribution regarding to the precedent period.**

Acknowledgments: Argentinian National Laboratory Network

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