

INTRODUCTION

In the past decades *Streptococcus agalactiae* (group B streptococcus, GBS) has been increasingly associated with invasive disease in adults.

We analyzed all GBS recovered from invasive infections in adults in Iceland, between 1978 and 2012, with the aim of documenting the prevalence of serotypes, genetic lineage and antimicrobial resistance.

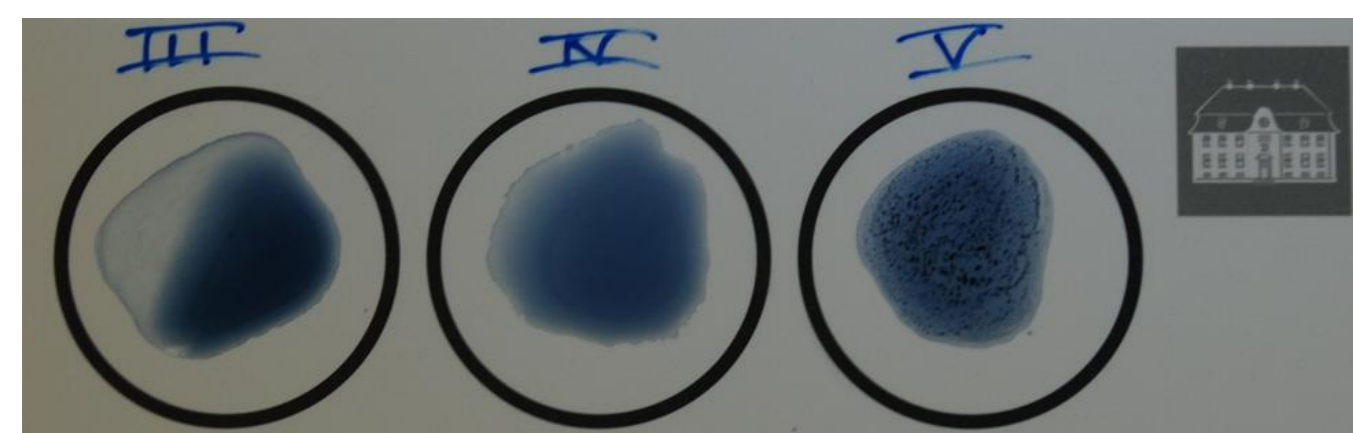
MATERIAL AND METHODS

All 134 invasive isolates were serotyped with latex agglutination test (SSI) and assigned to clones ($n \geq 3$ isolates) according to their pulsed-field gel electrophoretic (PFGE) profiles and MLST-based sequence types (STs). Susceptibility to penicillin, erythromycin and clindamycin was tested by disk diffusion according to the CLSI guidelines. Presence of the surface protein genes *bca*, *alp2*, *alp3*, *alp4*, *eps* and *rib* and of pilus islands PI-1, PI-2a and PI-2b was tested by PCR.

RESULTS

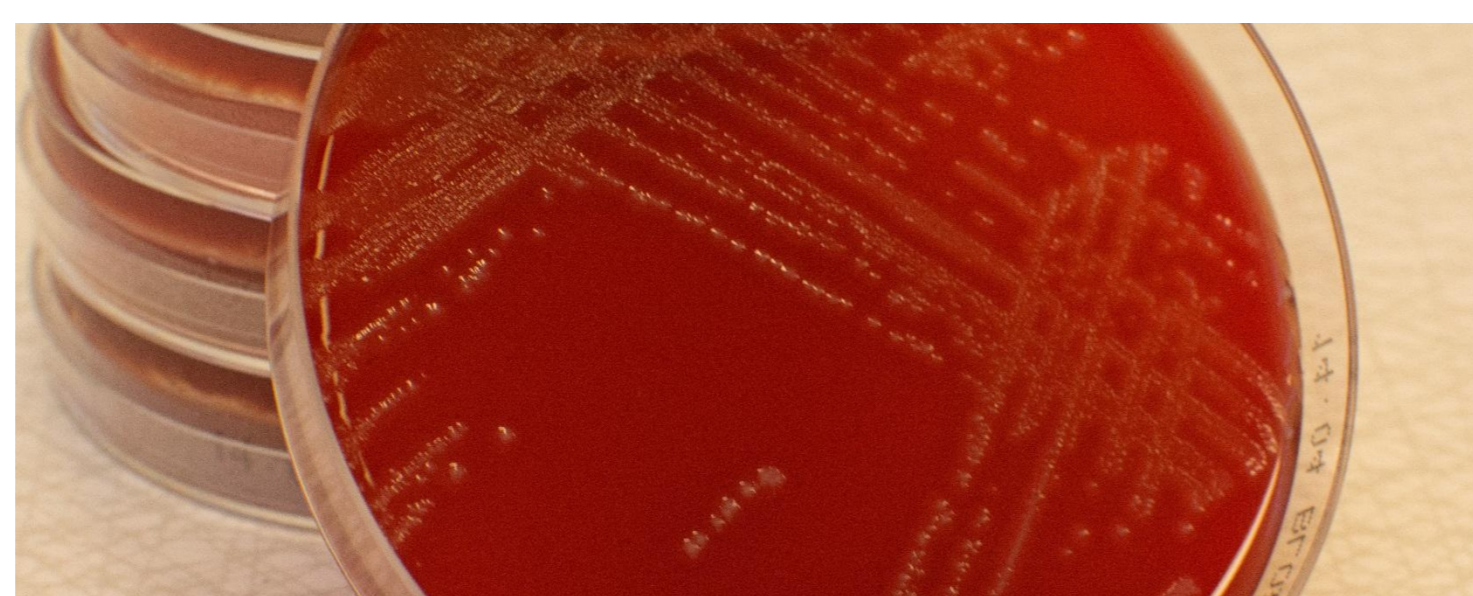
Serotype Ia was most frequently found (23%) but was closely followed by serotypes V, III, Ib and II, all showing similar prevalence (14-19%).

The combination PI-1+PI-2a was found in 66% of all isolates.

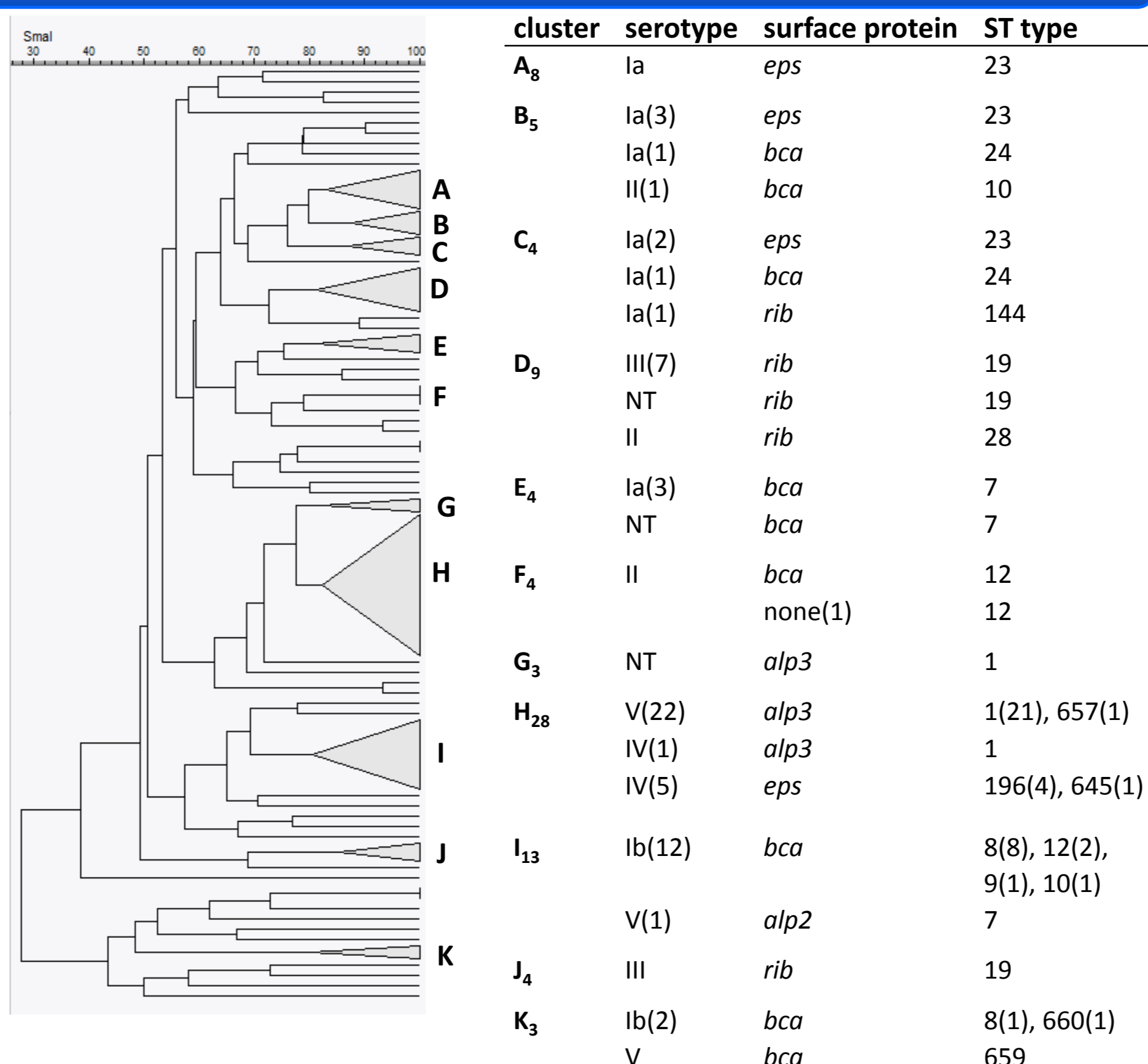


serotype(%)	PI-1+PI-2a	PI-1+PI-2b	PI-2a	PI-2b	total
Ia (23)	2	7	21	1	31
Ib (15)	18		2		20
II (14)	15		4		19
III (16)	16	6			22
IV (7)	9			1	10
V (19)	25				25
NT (5)	4	2	1		7
total	89	15	28	2	134

The isolates were grouped into 11 PFGE clusters. Although serotype V was not dominant, it was represented mainly by a single PFGE cluster defined by ST1/*alp3*. The more frequent serotype Ia isolates were distributed across several PFGE clusters and genetic lineages, mainly ST23/*eps*. But also ST24/*bca*.



All isolates were susceptible to penicillin. The rate of resistance to erythromycin was 6% and to clindamycin 9% and a over-representation of erythromycin resistance was observed in serotype V/ST1/*alp3* genetic lineage ($p < 0.05$).



CONCLUSION

The population of invasive infections in Iceland revealed that several distinct lineages were present over the last 25 years. In Iceland there is no significant dominance of a particular serotype or genetic lineage, but instead several serotypes and genetic lineages cause invasive disease.

Our data emphasizes the need for continued surveillance of GBS invasive infection in adults in Iceland to determine the reasons behind the diversity of the circulating genetic lineages.

