

Comparative analysis of *Streptococcus agalactiae* isolates causing infections in cattle and humans in Iceland

E. S. Björnsdóttir¹, E. R. Martins², H. Erlendsdóttir¹, G. Haraldsson¹, J. Melo-Cristino³, M. Ramirez², and K. G. Kristinsson¹

¹Dept. of Microbiology, Landspítali University Hospital and Faculty of Medicine, University of Iceland

²Unidade de Microbiologia Molecular e Infecção, Instituto de Medicina Molecular, Faculdade de Medicina da Universidade de Lisboa

³Instituto de Microbiologia, Faculdade de Medicina da Universidade de Lisboa

INTRODUCTION

Streptococcus agalactiae (Group B streptococcus, GBS) was first described as a causative agent of bovine mastitis and only later acknowledged as a leading cause of neonatal disease and associated with invasive infections in adults. Our aim was to compare GBS isolates recovered from human infections and bovine mastitis in Iceland.

We compared 24 isolates recovered from cases of bovine mastitis with 134 GBS isolates recovered from invasive infections in adults.

MATERIAL AND METHODS

All 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. The 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.

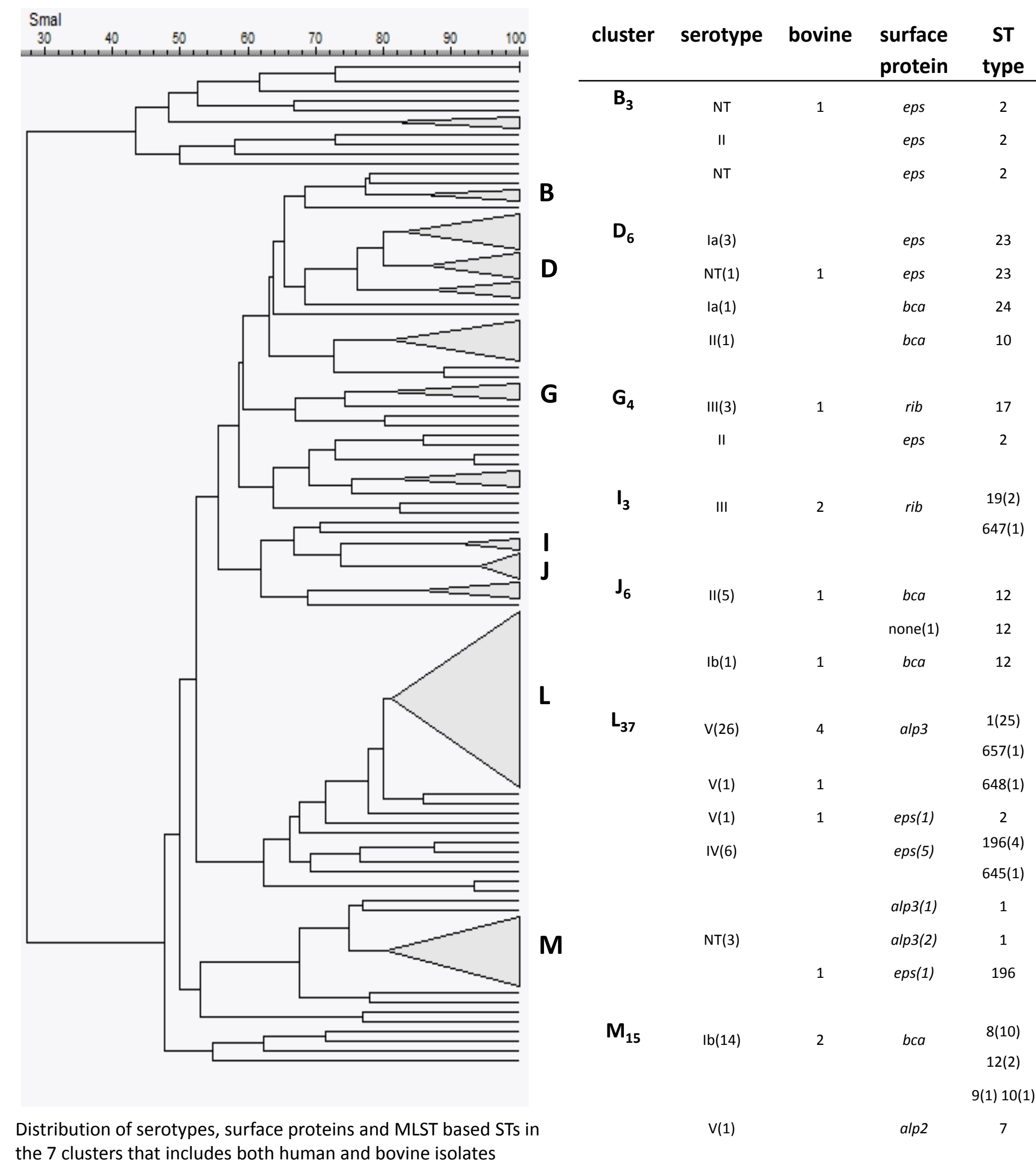
RESULTS

The most frequent serotype among the isolates recovered from bovine mastitis was V (29%) and non-typeable isolates which were equally prevalent. No isolates of serotype Ia were identified in this collection, in contrast to the human isolates among which it was the most frequent serotype (23%). In the bovine isolates the combination PI-1+PI-2a was predominant (92%) similarly to human isolates (66%).

serotype	PI-1+PI-2a		PI-1+PI-2b		PI-2a		PI-2b	
	human	bovine	human	bovine	human	bovine	human	bovine
Ia	2		7		21		1	
Ib	18	3			2			
II	15	1			4			
III	16	4	6	1				
IV	9						1	
V	25	7						
IX		1						
NT	4	6	2		1	1		
Total	89	22	15	1	28	1	2	

All isolates were susceptible to penicillin and erythromycin resistance was significantly associated with the serotype V/ST1/*alp3* genetic lineage ($p < 0.05$) in both human and bovine isolates.

The isolates were grouped into 13 PFGE clusters, where 7 of the clusters have both human and bovine isolates. Of the 24 bovine isolates 16 of them grouped into clones together with human isolates and the remaining 8 were included in minor PFGE groups or had unique profiles. No clones contained bovine isolates exclusively.



Distribution of serotypes, surface proteins and MLST based STs in the 7 clusters that includes both human and bovine isolates



CONCLUSION

Over half of the bovine isolates clustered together with those causing invasive infections in humans. Our data indicates there is only limited differentiation between the two GBS populations, raising the possibility of ongoing GBS transmission between humans and cattle. Continuous surveillance is needed to clarify this possibility.

