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Differences in molecular epidemiology of *Staphylococcus aureus* and *Escherichia coli* in nursing home residents and people in unassisted living situations

M. Olofsson [a,b,*], A. Matussek [c,d,e], R. Ehricht [f,g,h], P-E. Lindgren [c,i], C.J. Östgren [a,b]

[a] *Ödeshög Health Care Centre, Ödeshög, Sweden*
[b] *Division of Community Medicine, Department of Medical and Health Sciences, Linköping University, Linköping, Sweden*
[c] *Department of Laboratory Medicine, Region Jönköping County, Sweden*
[d] *Division of Clinical Microbiology, Department of Laboratory Medicine, Karolinska Institute, Stockholm, Sweden*
[e] *Karolinska University Laboratory, Stockholm, Sweden*
[f] *Abbott (Alere Technologies GmbH), Jena, Germany*
[g] *InfectoGnostics Research Campus, Jena, Germany*
[h] *Leibniz Institute of Photonic Technology, Jena, Germany*
[i] *Division of Medical Microbiology, Department of Clinical and Experimental Medicine, Linköping University, Linköping, Sweden*

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SUMMARY

Background: The usefulness of colonization pressure as a working model and proxy for infection transmission is limited due to the inability to grade or quantify the specific risk within environments that are subject to change.

Aim: To elaborate on the colonization pressure model by comparing the molecular epidemiology of two bacteria, *Staphylococcus aureus* and *Escherichia coli*, among residents in a nursing home and people in unassisted living situations.

Methods: A cross-sectional study of 73 elderly residents from a village in south-central Sweden was conducted. Of these, 35 were residents of a nursing home, and 34 lived in an own place of residence in the same geographical area. Samples of two representative bacterial species were collected from multiple body sites and analysed for molecular diversity.

Findings: Combining all body sites, 47% of the participants were colonized with *S. aureus* and 93% with *E. coli*. The nursing home group, the group in unassisted living situations, and both units combined, held 16, 17, and 29 different *S. aureus* spa types, respectively. The corresponding numbers of different *E. coli* serogenotypes were 34, 28, and 48. Diabetes mellitus was associated with more frequent colonization with *S. aureus*.

Conclusion: The molecular diversity of bacteria found within different forms of accommodation was within the same range. Hospital quality hygiene might have contributed to the absence of homogenization of the molecular diversity within the nursing home group.

* Corresponding author. Address: Ödeshög Health Care Centre, Skolgatan 3-7, SE-599 32, Ödeshög, Sweden. Tel.: +46 10 1048720; fax: +46 10 1048712.
E-mail address: magnus.olofsson@regionostergotland.se (M. Olofsson).

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Diabetes mellitus might have played a role in a patient selection characterized by advanced age.

Introduction

Employing microbial surveillance to prevent nosocomial infections requires that efforts should be guided to the areas of greatest medical interest. Rising antimicrobial resistance increases the complexity of this issue since both commensals and pathogenic agents demonstrate a dynamic range of antimicrobial resistance [1–3]. Colonization pressure, that is the physical proximity of infectious agents in a specific situation, plays a role in spreading multidrug-resistant organisms [4,5]. However, the usefulness of colonization pressure as a working model and proxy for infection transmission is limited due to the inability to grade or quantify the specific risk within environments, i.e. those that are subject to change when moving patients between healthcare institutions.

Nursing homes have been proposed as logical target areas for microbial surveillance, since risk factors for infection transmission accumulate when patients are crowded, physically frail, often moved between healthcare institutions, or frequently treated with antibacterials [6–8]. Our research group has recently added to this discussion some estimates of colonization and antimicrobial resistance by applying active microbial surveillance methods in Swedish nursing homes [9–11].

Pursuing a more adaptable working model and proxy for infection transmission, we theorized that colonization pressure in a nursing home — provided that it is maintained by continual reciprocal transference of infectious agents — would result in a gradual homogenization of the molecular diversity. Further, we postulated that the presence of a homogenization of this sort might pose a risk by favouring not only bacterial strains that are numerous, but also those that are more virulent.

Thus, this study set out to employ active microbial surveillance methods, combined with techniques for molecular analysis, to investigate whether the molecular diversity is, in fact, lower in two common bacteria: *Staphylococcus aureus* and *Escherichia coli* [12–15]. Residents in a nursing home were compared with people in unassisted living situations.

Methods

Study population

The study was conducted within the confines of the primary healthcare centre in Ödeshög, a village of about 5000 inhabitants in the south-central part of Sweden. We created a cross-sectional and non-experimental design, our purpose being to collect original data. We turned to the municipality and a nationwide quality register titled 'Senior Alert' for potential participants (Figure 1) [16]. Consequently, we approached 101 individuals for participation during the autumn of 2014. The recruitment process was in part judgemental (i.e. the non-random process of actively seeking persons whose eligibility was established in advance) and in part consecutive (i.e. including as many individuals as possible from the eligible group). The criterion for exclusion lay in an inability to co-operate due to either terminal illness and/or severe dementia.

Overall, the nursing home residents suffered from poor general health and disability, whereas those in unassisted living situations enjoyed relatively good health. The study was approved by the Regional Ethical Review Board in Linköping (date: August 13th, 2014; case number: 2014/211-31). Written informed consent was obtained from all participants or, when appropriate, persons legally responsible for them.

Bacterial samples and background parameters

Upon inclusion, a study nurse asked the participants to fill in a questionnaire and to allow bacterial sample collection. The samples were collected between September 2014 and January 2015. Six body sites were sampled: nasal mucosa, pharyngeal mucosa, groin, rectum, urine, and any chronic skin lesions. The bacterial samples were obtained using either an ESwab™ liquid-based collection and transport system (Copan Diagnostics, Murietta, CA, USA) or a plastic urine collection vial. The method of urine collection depended on patients' mental and physical conditions. In addition to the bacterial samples,

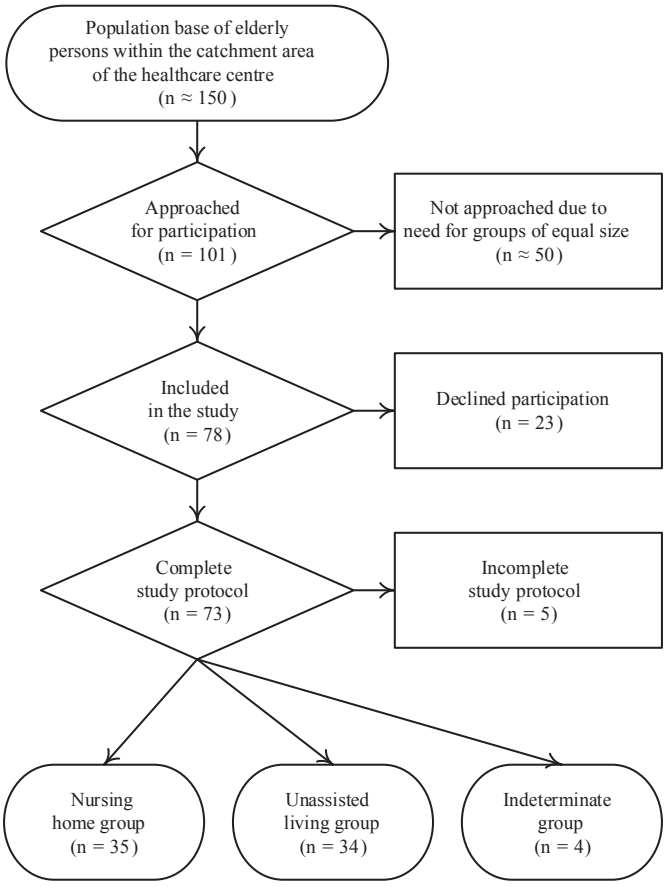

Figure 1. The recruitment process.

Table I
Baseline characteristics of the participants and the main subgroups as divided by accommodation[a]

Characteristics	All participants ($N = 73$)		Nursing home (NH) ($N = 35$)		Unassisted living (UL) ($N = 34$)		*P* for NH vs UL
	Value	95% CI	Value	95% CI	Value	95% CI	
Anthropometrics							
Male gender	25 (34%)	17–34	15 (44%)	9–21	9 (26%)	4–15	0.15
Age (years), mean (SD)	84.9 (6.5)	–	86.6 (7.4)	–	83.7 (5.3)	–	0.062
Body mass index (kg/m^2), mean (SD)	27.8 (4.8)	–	27.1 (4.8)	–	29.1 (4.4)	–	0.084
Past or chronic illness							
Dementia	12 (16%)	7–20	12 (34%)	7–18	0 (0%)	0–4	<0.001
Fracture of femur or pelvis	12 (16%)	7–20	9 (26%)	4–15	3 (9%)	1–8	0.064
Stroke	13 (18%)	7–21	8 (23%)	4–14	4 (12%)	1–10	0.22
Diabetes mellitus	28 (38%)	20–37	13 (37%)	8–19	15 (44%)	9–21	0.56
Physical impairment							
Urinary incontinence	17 (23%)	11–25	13 (37%)	8–19	2 (6%)	0–7	0.002
Mobility impairment	30 (41%)	22–39	22 (63%)	16–27	5 (15%)	2–11	<0.001
Antibacterials in the past							
36 months	49 (67%)	40–57	27 (77%)	21–31	19 (56%)	13–25	0.061
12 months	32 (44%)	24–41	17 (49%)	11–23	12 (35%)	7–18	0.26
6 months	20 (27%)	13–29	9 (26%)	4–15	8 (24%)	4–14	0.83
Hospitalization in the past							
36 months	43 (59%)	34–51	26 (74%)	20–31	13 (38%)	8–19	0.003
12 months	23 (32%)	16–32	12 (34%)	7–18	7 (21%)	3–13	0.20
6 months	11 (15%)	6–19	5 (14%)	2–11	2 (6%)	0–7	0.25

CI, confidence interval; SD, standard deviation.
[a] The subgroup with indeterminate forms of accommodation has been removed due to its small size.

archival data were collected on previous healthcare encounters, medical treatment, confirmed diagnoses, and antibacterial treatment from the county council's electronic patient records. The participants' impairments regarding urinary incontinence and mobility impairment were also registered. The severity of the impairments was rated according to a modified four-stage scale adopted by the Swedish National Study on Ageing and Care (SNAC) [17]. Mobility impairment meant that the individual was dependent upon walking aids or wheelchairs for limited indoors movement or was dependent on others for movement.

Microbial analyses

Cultivation of S. aureus

The *S. aureus* specimens were pre-incubated for 16–20 h in a MAMSA broth for enrichment (Proteose Peptone LP0085B, Liver Digest Neutralised LP0027B, and Yeast Extract Powder LP0021B, Oxoid Ltd, Basingstoke, UK; sodium chloride 2.5% and mannitol 1.0% with the addition of aztreonam 8.0 mg/mL) [18]. The enriched broth was cultured on blood agar base plates. The plates were incubated for 16–20 h at 36°C by Swedish reference methods [19]. The presence of *S. aureus* was determined by testing for DNase activity. A small number of *S. aureus* colonies (three or four) were taken from the blood agar plates, dissolved in 0.9% saline solution, smeared on iso-tryptophan plates (Iso-Sensitest Agar CM0471B, Oxoid; and L-tryptophan), and incubated for antimicrobial susceptibility tests (first for 30 min at room temperature, then overnight at 36°C).

Cultivation of E. coli

Similarly, the *E. coli* specimens (mucosal swabs or 10 μL of urine) were cultured on both a CPS ID 3 plate and a chromID extended-spectrum β-lactam (ESBL) plate (both bioMérieux, Marcy l'Etoile, France). The plates were incubated for 16–20 h at 36°C by Swedish reference methods [19]. A small number of pink *E. coli* colonies (three or four) were taken from the CPS ID 3 plates and incubated for antimicrobial susceptibility tests in the same manner as described above.

Antimicrobial susceptibility

NordicAST minimum inhibitory concentration (MIC) breakpoints were used for interpreting the zone diameters (all testing discs were from Oxoid) [20]. For the *S. aureus* isolates, the 15 tested antibacterials were: amikacin, cefoxitin, ciprofloxacin, clindamycin, erythromycin, fusidic acid, gentamicin, linezolid, norfloxacin, oxacillin, rifampicin, sulphamethoxazole and trimethoprim (SMZ/TMP), tetracycline, tobramycin, and vancomycin. For the *E. coli* isolates, the 17 tested antibacterials were: amikacin, ampicillin, cefadroxil, cefotaxime, ceftazidime, ceftibuten, cefuroxime, chloramphenicol, ciprofloxacin, gentamicin, mecillinam, meropenem, nitrofurantoin, piperacillin–tazobactam (PIP/TAZ), sulphamethoxazole and trimethoprim (SMZ–TMP), tobramycin, and trimethoprim.

Molecular typing

The *S. aureus* isolates were classified using *spa* typing as a genetic fingerprinting technique [21,22]. The *E. coli* isolates were classified using DNA microarray-based analysis (*E. coli* PanType AS-2 Kit and *E. coli* SeroGenoTyping AS-1 Kit, both Abbott, Alere Technologies GmbH, Jena, Germany) [23,24].

Statistical analysis

PASW statistical package, version 24 (SPSS Inc., Chicago, IL, USA), was used. The analyses were focused on differences in

the prevalence of colonization and molecular diversity among the subgroups as divided by a series of patient-level variables. Student's *t*-test was used for continuous variables and Pearson's χ^2-test for dichotomous variables. $P < 0.05$ was considered statistically significant.

Results

A total of 73 participants were included, of which 25 (34%) were males. Baseline characteristics are outlined in Table I. The study population was divided primarily by the type of accommodation, leaving 35 (48%) participants in the nursing home group, 34 (47%) in the unassisted living group, and four (5%) in an indeterminate group due to ambiguous information regarding their residence. Combining all records, 859 days of hospitalization, 5055 primary healthcare encounters, and 1940 days of treatment with antibacterials were registered. All day counts were trimmed to a 36-month window preceding inclusion, thus discarding older data.

Staphylococcus aureus susceptibility and spa typing

There were 69/256 (27%, 95% confidence interval (CI): 21–33) positive *S. aureus* cultures. The prevalence of colonization in each of the four body sites relevant to *S. aureus* was: nasal mucosa: 25/73 (34%; 95% CI: 24–46); pharyngeal mucosa: 19/73 (26%; 17–38); groin: 15/73 (21%; 12–32); skin lesion: 5/15 (33%; 15–59). The aggregated prevalence of colonization in any body site was 34/73 (47%; 35–58).

Only one (1%; 95% CI: 0–8) *S. aureus* isolate was antibiotic resistant, being resistant to ciprofloxacin, clindamycin, erythromycin, and norfloxacin. There were no meticillin-resistant *S. aureus* (MRSA) isolates. There were 16 different *S. aureus spa* types in the nursing home group, 17 in the unassisted living group and 29 when the units were combined. Comparing the *spa* types in the nursing home group and the unassisted living group, the proportion of *spa* types as represented in only one instance was lower in the nursing home group (Table IIa). Eighteen out of 73 (25%; 95% CI: 16–36) participants had colonization in multiple body sites with *S. aureus* isolates that belonged to the same *spa* type.

Escherichia coli susceptibility and serogenotyping

Overall, there were 136/250 (54%; 95% CI: 48–61) positive *E. coli* cultures. The prevalence of colonization in each of the four relevant body sites or fluids was: groin: 30/73 (41%; 30–53); rectum: 68/73 (93%; 84–98); urine: 36/67 (54%; 41–66); skin lesion: 2/15 (13%; 3–38). The aggregated prevalence of colonization in any body site or fluid was 68/73 (93%; 84–98).

Nineteen out of 136 (14%; 95% CI: 9–21) *E. coli* isolates were antibiotic resistant. The isolates were variably resistant to nine antibacterials: ampicillin: 17 isolates; cefadroxil: five isolates; cefotaxime: five isolates; cefuroxime: five isolates; ciprofloxacin: six isolates; mecillinam: three isolates; nitrofurantoin: one isolate; trimethoprim: two isolates; SMZ/TMP: one isolate. Among the individuals studied, the prevalence of carrying an *E. coli* isolate resistant to any antibacterial was 14/73 (19%; 11–30). There were five ESBL-producing isolates; these were recovered from two participants, both of whom were found to

Table IIa
Molecular diversity among all *Staphylococcus aureus* isolates and the main subgroups as divided by accommodation[a]

Serial no.	*spa* type	Frequency	Proportion of isolates within grouping	95% CI
All *Staphylococcus aureus* isolates ($N = 69$)				
1	t5593	7	10	5–20
2	t085	6		
3	t160	6		
4	t14905	6	26	17–38
5	t026	4	6	2–14
6	t008	3		
7	t095	3		
8	t252	3		
9	t304	3		
10	t342	3	22	13–33
11	t015	2		
12	t084	2		
13	t5545	2		
14	t14817	2		
15	t14904	2		
16	t14906	2	17	10–28
17	t018	1		
18	t089	1		
19	t094	1		
20	t127	1		
21	t189	1		
22	t382	1		
23	t383	1		
24	t493	1		
25	t550	1		
26	t772	1		
27	t1328	1		
28	t5745	1		
29	t12153	1	19	11–30
Total		69	100	
Isolates in the nursing home subgroup ($N = 41$)				
1	t160	6		
2	t14905	6	29	17–45
3	t026	4		
4	t085	4		
5	t5593	4	29	17–45
6	t304	3	7	2–20
7	t008	2		
8	t095	2		
9	t14817	2		
10	t14904	2	20	10–35
11	t089	1		
12	t094	1		
13	t383	1		
14	t1328	1		
15	t5745	1		
16	t12153	1	15	6–29
Total		41	100	
Isolates in the unassisted living group ($N = 28$)				
1	t252	3		
2	t342	3		
3	t5593	3	32	17–51
4	t015	2		

(*continued on next page*)

Table IIa (*continued*)

Serial no.	*spa* type	Frequency	Proportion of isolates within grouping	95% CI
5	t084	2		
6	t085	2		
7	t5545	2		
8	t14906	2	36	20–55
9	t008	1		
10	t018	1		
11	t095	1		
12	t127	1		
13	t189	1		
14	t382	1		
15	t493	1		
16	t550	1		
17	t772	1	32	17–51
Total		28	100	

CI, confidence interval.

[a] The subgroup with indeterminate forms of accommodation has been removed due to its small size. The omission has left zero *Staphylococcus aureus* isolates unaccounted for.

be ESBL negative at a subsequent follow-up. There were 34 different *E. coli* serogenotypes in the nursing home group, 28 in the unassisted living group, and 48 when the units were combined. Comparing the serogenotypes in the nursing home group and the unassisted living group, the proportion of serogenotypes as represented in only one instance was within the same range (Table IIb). Thirty-six out of 73 (49%; 38–61) participants had colonization in multiple body sites with *E. coli* isolates belonging to the same serogenotype.

Colonization and patient-level factors

There were few notable differences in colonization as indicated by patient-level factors. The mean body mass index (BMI) was higher among the participants diagnosed with diabetes mellitus ($P = 0.004$). The mean BMI was lower among the participants diagnosed with chronic skin lesions ($P = 0.015$). There were no significant differences in gender, mean age, or mean BMI in connection with urinary incontinence and mobility impairment.

Those colonized with *S. aureus* in the nasal mucosa were diagnosed with diabetes mellitus more frequently ($P = 0.006$) and treated with antibacterials more frequently ($P = 0.048$). They also registered more primary healthcare encounters ($P = 0.012$ when differentiated as more than one encounter vs less than one encounter every month). Those colonized with *S. aureus* in the pharyngeal mucosa were treated with antibacterials more frequently ($P = 0.028$ or $P = 0.001$ depending on the preparation and frequency of treatment). They also registered more primary healthcare encounters ($P = 0.021$ when differentiated as more than one encounter vs less than one encounter every month). Those colonized with *S. aureus* in the groin were diagnosed with diabetes mellitus to a greater extent ($P = 0.011$) and registered a more severe mobility impairment ($P = 0.024$).

Turning our attention to *E. coli*, those colonized with *E. coli* in the groin had more severe mobility impairment ($P = 0.006$)

Table IIb
Molecular diversity among all *Escherichia coli* isolates and the main subgroups as divided by accommodation[a]

Serial no.	Serogenotype	Frequency	Proportion of isolates within grouping	95% CI
All *Escherichia coli* isolates ($N = 136$)				
1	O-:H-	10		
2	O25:H01	10	15	9–22
3	O6:H01	7	5	2–11
4	O2:H06	6		
5	O18:H05	6		
6	O75:H05	6	13	8–20
7	O2:H01	5		
8	O4:H05	5		
9	O45:H06	5	11	6–18
10	O-:H04	4		
11	O1:H07	4		
12	O6:H-	4	9	5–15
13	O-:H16	3		
14	O-:H21	3		
15	O-:H28	3		
16	O-:H45	3		
17	O6:H05	3		
18	O7:H15	3		
19	O9:H30	3		
20	O15:H18	3		
21	O18:H07	3		
22	O24:H04	3	22	15–30
23	O-:H06	2		
24	O-:H07	2		
25	O-:H14	2		
26	O-:H38	2		
27	O7:H06	2		
28	O8:H04	2		
29	O8:H19	2		
30	O101:H37	2	12	7–19
31	O-:H08	1		
32	O-:H11	1		
33	O-:H33	1		
34	O2:H14	1		
35	O6:H04	1		
36	O8:H09	1		
37	O8:H26	1		
38	O9:H04	1		
39	O11:H43	1		
40	O21:H09	1		
41	O21:H12	1		
42	O25:H04	1		
43	O75:H07	1		
44	O104:H07	1		
45	O121:H07	1		
46	O148:H32	1		
47	ONT1:H18	1		
48	ONT2:H04	1	13	8–20
Total		136	100	
Isolates in the nursing home subgroup ($N = 69$)				
1	O75:H05	6	9	4–18
2	O6:H01	4		
3	O18:H05	4		
4	O45:H06	4	17	10–28

Table IIb (*continued*)

Serial no.	Serogenotype	Frequency	Proportion of isolates within grouping	95% CI
5	O-:H21	3		
6	O1:H07	3		
7	O4:H05	3		
8	O24:H04	3		
9	O25:H01	3	22	13–33
10	O-:H-	2		
11	O-:H06	2		
12	O-:H07	2		
13	O-:H14	2		
14	O-:H16	2		
15	O-:H28	2		
16	O-:H38	2		
17	O7:H06	2		
18	O15:H18	2		
19	O18:H07	2		
20	O101:H37	2	32	22–44
21	O-:H08	1		
22	O-:H11	1		
23	O2:H01	1		
24	O2:H06	1		
25	O6:H-	1		
26	O8:H09	1		
27	O8:H19	1		
28	O8:H26	1		
29	O9:H04	1		
30	O21:H09	1		
31	O21:H12	1		
32	O25:H04	1		
33	O104:H07	1		
34	O121:H07	1	20	12–32
Total		69	100	
Isolates in the unassisted living subgroup ($N = 61$)				
1	O-:H-	5		
2	O2:H06	5		
3	O25:H01	5	25	15–37
4	O-:H04	4		
5	O2:H01	4	13	6–24
6	O-:H45	3		
7	O6:H-	3		
8	O6:H01	3		
9	O6:H05	3		
10	O7:H15	3		
11	O9:H30	3	30	19–42
12	O4:H05	2		
13	O8:H04	2		
14	O18:H05	2	10	4–20
15	O-:H16	1		
16	O-:H28	1		
17	O-:H33	1		
18	O1:H07	1		
19	O2:H14	1		
20	O6:H04	1		
21	O8:H19	1		
22	O11:H43	1		
23	O15:H18	1		
24	O18:H07	1		
25	O45:H06	1		
26	O75:H07	1		
27	O148:H32	1		
28	ONT2:H04	1	23	14–35
Total		61	101	

CI confidence interval; ONT1, Non-Typeable 1 (O17 or O44 or O73 or O77 or O106); ONT2, Non-Typeable 2 (O13 or O129 or O135).

[a] The subgroup with indeterminate forms of accommodation has been removed due to its small size. The omission has left six *Escherichia coli* isolates unaccounted for.

and recorded more primary healthcare encounters ($P = 0.005$). Those colonized with *E. coli* in the urine were more likely to be female ($P = 0.002$), had a higher mean age ($P = 0.002$), and had a higher mean BMI ($P = 0.033$). For *S. aureus* and *E. coli* alike, no univariate associations involving hospitalization or antimicrobial resistance were found.

The multivariate analyses were based on the important univariate findings. Six logistic regressions were designed to explain colonization for each bacterial species and each body site using a six-item series of explanatory patient-level factors. Three results came back as being significant: (i) diabetes mellitus was associated with a higher degree of colonization with *S. aureus* in the nasal mucosa; (ii) mobility impairment was associated with a higher degree of colonization with *S. aureus* in the groin (Table III); (iii) mobility impairment was associated with a higher degree of colonization with *E. coli* in the groin (OR: 3.8, 95% CI: 1.2–12; the remaining results for *E. coli* are not shown).

Discussion

The low prevalence of multidrug-resistant organisms is an expected outcome of the study, bearing in mind the low prevalence of MRSA and ESBL in the Scandinavian countries. In Sweden, the estimated incidence of MRSA in 2015 was 39 per 100,000 inhabitants, and the parallel incidence of ESBL was 99 per 100,000 inhabitants [25]. The tendency towards a high degree of molecular diversity in colonizing strains of *S. aureus* is also an expected finding [26–28]. Hospital quality hygiene may well have affected the results as a considerable number of those in the nursing home group lived in a single room with a private bathroom. Even so, ecological niches that are closely related, yet physically separated, have not been investigated previously in this way.

We believe the strengths of our study were attributable to the close co-operation between investigators and participants. This resulted in a high degree of contextually correct inferences and a robust element of patient-level data that could not have been realized otherwise. Limitations of our study might be the small sample size, the non-random recruitment process, possible bias associated with a skewed age distribution, and the fact that testing a relatively small number of bacterial colonies from each culture plate may have meant that molecular diversity was sometimes missed.

There was some evidence of homogenization of the molecular diversity in the nursing home group. Herein, the proportion

Table III
Multivariate analyses (logistic regression) regarding the probability of colonization with *Staphylococcus aureus* in three different body sites as explained by a six-item series of patient-level factors

Explanatory variables	Nasal mucosa ($N = 73$)			Pharyngeal mucosa ($N = 73$)			Groin ($N = 73$)		
	OR	95% CI	*P*	OR	95% CI	*P*	OR	95% CI	*P*
Gender (female)	0.83	0.26–2.7	0.76	0.96	0.29–3.2	0.94	0.56	0.14–2.3	0.42
Age (years)	1.0	0.91–1.1	0.93	0.99	0.90–1.1	0.83	0.99	0.89–1.1	0.81
Body mass index (kg/m^2)	0.96	0.85–1.1	0.48	1.1	0.94–1.2	0.31	1.1	0.94–1.3	0.27
Diabetes mellitus	5.0	1.6–16	0.01	1.8	0.57–5.9	0.31	3.9	0.99–16	0.05
Mobility impairment	2.0	0.63–6.5	0.24	1.7	0.52–5.5	0.38	4.7	1.10–20	0.04
Antibacterials	1.3	0.35–5.1	0.68	2.0	0.48–8.1	0.34	1.5	0.29–7.9	0.63

OR, adjusted odds ratio within the explanatory variables; CI, confidence interval.

of *S. aureus* isolates, as represented in their *spa* types, was lower in one specific instance. In this context, however, there is a gap in the professionally agreed-upon methods for determining the expected yield of specific categories, and for analysing diversity among additional categories [29,30]. Interestingly, diabetes mellitus emerged as one of the few significant explanatory variables in the multivariate analyses. How this association was related to temporal aspects of colonization could not, on the other hand, be articulated by way of a cross-sectional study.

A recent review listed co-morbidities known to be associated with MRSA: congestive heart failure, diabetes mellitus, pulmonary disease, immunosuppression, and renal failure [31]. However, the obvious dissimilarities between these co-morbidities regarding patient selection make it difficult to suggest a single mechanism by which these associations are upheld. In the present study, the association between diabetes mellitus and bacterial colonization might indicate that diabetes mellitus has a more direct effect on the host–pathogen interaction than was previously thought, at least in a patient selection characterized by advanced age. Further, more evidence is emerging on the association between diabetes mellitus and infections, and their treatment with antibacterials [32–35].

In conclusion, active microbial surveillance of the residents of a nursing home and those in unassisted living situations yielded few notable differences regarding colonization with two common bacteria. In terms of a working model and proxy for infection transmission, the colonization pressure in a nursing home was not sufficient to create a homogenization of the molecular diversity. Further, in a selection of typical primary healthcare patients, there were few connections apparent between bacterial colonization and patient-level factors, e.g. treatment with antibacterials and hospitalization.

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Conflict of interest statement
None declared.

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