CONCISE COMMUNICATION

Prevalence of MRSA ST398 Carriage in Nursing Home Residents in an Area of Spain With a High Density of Pig Farming

Esteban Reynaga, MD;[1,2] Carmen Torres, PhD;[3] Marian Garcia-Nuñez, PhD;[4,5] Marian Navarro, MD;[6] Anna Vilamala, MD;[6] Emma Puigoriol, MS;[7] Gianni Enrico Lucchetti, MD;[1] Daniella Nunes, MD;[1] Adriana Silva, MD;[1] Miquel Sabrià, PhD[2,4,5]

MRSA nasal carriage was detected in 15.7% of 204 residents from 6 nursing homes (NHs) in the Osona region (Barcelona, Spain), and the MRSA-ST398 lineage was identified in 15.6% of MRSA-positive residents and in 2.5% of all NH residents evaluated. Most MRSA-ST398 carriers (4 of 5) had direct or indirect contact with pig farms.

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Elderly people who reside in nursing homes (NHs) for long-term care represent an important reservoir for *Staphylococcus aureus*, and residence in a NH is a well-established risk factor for *S. aureus* carriage and infection.[1] A new livestock-associated MRSA clone (ST398), which is mostly linked to pig farms and people in contact with them but is also found in other animals, is spreading in many countries.[2] There have been few reports of transmission of MRSA ST398 in NH healthcare settings.[3]

Previous studies have established that tetracycline resistance (Tet^R) is a good marker for rapid identification of ST398 strains.[4] The county of Osona (Barcelona, Catalonia, Spain) is an area with a high density of pig farms, and a high nasal carriage rate of MRSA ST398 (all Tet^R) has been recently detected in pig-farm workers and farm animals in the Osona region.[5] The aim of our study was to determine the prevalences of MRSA and MRSA-ST398 nasal carriage in NH residents in the Osona region.

MATERIAL AND METHODS

A prospective study was performed during January–July 2015 in 6 NHs in the county of Osona (Barcelona, Spain). Nursing homes 1, 2 and 3 are located in in urban areas and NHs 4, 5, and 6 are located in rural areas.

A questionnaire with the epidemiological details of each resident was completed during a personal interview with them or their family or legal representative. Residents who were colonized with MRSA were divided into 2 groups depending on whether the strains were tetracycline sensitive or resistant (Tet^S or Tet^R, respectively), and these groups were compared. Permission for the study was obtained from the Hospital Universitari de Vic (HUV) Ethics Committee.

Sample Processing and MRSA Detection and Characterization

Nasal samples were processed for culture and bacterial identification in the Microbiology Department of HUV. One strain per person was studied. Detailed microbiological methods can be found in the Supplementary material. All MRSA-Tet^R strains were analyzed using multilocus sequence typing (MLST) and *spa* typing.[6,7]

Statistical Analysis

Statistical analysis was performed using SPSS software version 23.0 (IBM, Armonk, NY).

Categorical variables were expressed as frequency (%) and continuous variables as mean ± standard deviation (SD). The prevalence of positive results in MRSA was estimated with a 95% confidence interval (CI). Statistical significance for intergroup differences was assessed by the Pearson χ^2 or the Fisher exact test for categorical variables and the Student t test for continuous variables. A P value < 0.05 was considered statistically significant.

RESULTS

Of the 204 NH residents analyzed in this study, 32 were MRSA carriers (15.7%; 95% CI, 10.7%–20.7%). Of the 32 MRSA-positive residents, 8 (25%; 95% CI, 10.0%–40.0%) carried MRSA-Tet^R. Of these, 5 (15.6%; 95% CI, 3.0–28.0) carried MRSA-ST398.

Table 1 shows the epidemiological differences between residents colonized versus not colonized with MRSA and those colonized with MRSA-Tet^S versus those with MRSA-Tet^R (Table 1). Of the MRSA-Tet^S–positive residents, 87% were identified in urban NHs and 55% were identified in rural NHs ($P = .023$). A total of 26 (12.7%) residents had had contact with relatives of farm workers in the previous 12 months, all of them working on pig farms and none on cow or chicken farms. Of these residents, 7 (26.9%) were colonized with MRSA and 4 (57.1%) were colonized with MRSA-Tet^R-ST398 ($P = .026$). Furthermore, only 2 residents had direct contact with pig farms, and both were positive for MRSA-ST398 ($P = .018$).

A rural NH showed the highest prevalence of MRSA-Tet^R (3 of 3 residents, 100%; 2 carried ST398), and an urban NH had the lowest prevalence (1 of 13 residents, 7.7%; typed as ST398).

Table 2 shows the characteristics for residents colonized with MRSA Tet^R as well as the antibiotic resistance phenotype of the isolates. Of 8 isolates, 5 were typed as ST398-t011, although the lineages ST1, ST9, and ST146 were also detected.

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TABLE 1. Epidemiological Differences for the Residents Colonized With MRSA Versus Not Colonized and MRSA-Tet^R Versus MRSA-Tet^S in the 6 Nursing Homes Studied.

Characteristics	MRSA (n = 32) No. (%)	Non-MRSA (n = 172) No. (%)	*P* Value[a]	MRSA-Tet^R (n = 8) No. (%)	MRSA-Tet^S (n = 24) No. (%)	*P* Value[a]
Urban NHs	23 (71.9)	98 (57.0)	.115	3 (37.5)	20 (83.3)	**.023**
Rural NHs	9 (28.1)	74 (43.0)		5 (62.5)	4 (16.7)	
Age, mean y ± SD	89.0 ± 6.2	85.9 ± 12.0	.161	91.2 ± 3.6	88.2 5 ± 6.8	**.044**
Female	27 (84.4)	134 (77.9)	.410	7 (87.5)	20 (83.3)	.779
Leaves the nursing home	7 (21.9)	57 (34.1)	.174	3 (37.5)	4 (16.7)	.217
Years in the NH, mean ± SD	7.2 ± 4.1	5.8 ± 3.8	.069	9.0 ± 4.6	6.6 ± 3.9	.176
Hospital admissions in previous 12 mo	15 (46.9)	44 (25.6)	**.015**	4 (50.0)	11 (45.8)	.838
Pig Farmer relatives in previous 12 mo	7 (21.9)	19 (11.0)	.092	4 (50.0)	3 (12.5)	**.026**
Contact with pig farm in previous 12 mo	2 (6.3)	0 (0.0)	**.004**	2 (25.0)	0 (0.0)	**.018**
>4 comorbidities[a]	21 (15.1)	118 (84.9)	.740	4 (19.0)	17 (81.0)	.283
<4 comorbidities[a]	11 (16.9)	54 (81.1)		4 (36.4)	7 (63.6)	
Antibiotic treatment in previous 12 mo	22 (68.8)	90 (52.3)	.086	7 (87.5)	15 (62.5)	.186
BI ≥ 90	10 (31.3)	47 (27.3)	.865	2 (25.0)	8 (33.3)	.782
BI = 85–25	13 (40.6)	78 (45.3)		3 (37.5)	10 (41.7)	
BI ≤ 20	9 (28.1)	47 (27.3)		3 (37.5)	6 (25.0)	
No CI	6 (18.8)	44 (25.6)	.129	1 (12.5)	5 (20.8)	.348
Mild–moderate CI[b]	9 (28.1)	69 (40.1)		1 (12.5)	8 (33.3)	
Severe CI	17 (53.1)	59 (34.3)		6 (75)	11 (45.8)	

NOTE. MRSA, methicillin-resistant *Staphyloccus aureus*; Tet^R tetracycline resistant; Tet^S tetracycline susceptible; NH, nursing home; BI, Barthel index; CI, cognitive impairment.
[a]Bold *P* values indicate statistical significance.
[b]Comorbidity includes cerebrovascular disease, chronic cardiovascular disease, liver disease, chronic lung disease, chronic renal disease, auto-immune disease, neurological comorbidity, diabetes, and malignancy.

TABLE 2. Molecular Typing and Resistance Phenotypes for the 8 MRSA-Tet^R Strains Recovered From the Residents of the 6 Nursing Homes Analyzed

Resident With MRSA Patient No. (NH No.)[a]	MRSA CC/ST	Spa Type	Leaves the NH	Pig Farmer Relatives Contact[b]	Pig Farm Contact[b]	Hospital Admission[b]	Antibiotic Resistance Phenotype for Non–β-Lactams
1 (1)	1/1	t768	No	No	No	No	TET, CIP
2 (2)	398/398	t011	Yes	Yes	Yes	Yes	TET, CIP, ERY
3 (3)	398/398	t011	No	Yes	No	Yes	TET, GEN, TOB, CIP, LEV, CLI, SXT
4 (4)	398/398	t011	No	No	No	No	TET, CIP, LEV
5 (5)	146/146	t002	No	No	No	No	TET, GEN, CIP, LEV
6 (6)	398/398	t011	Yes	Yes	No	Yes	TET, CIP, ERY, CLI, SXT,
7 (6)	398/398	t011	Yes	Yes	Yes	Yes	TET, GEN, TOB, ERY, CLI, SXT
8 (6)	9/9	t3446	No	No	No	No	TET, GEN, CIP, ERY, CLI, SXT

NOTE. MRSA, methicillin-resistant *Staphylococcus aureus*; Tet^R tetracycline resistant; CC, Clonal Complex; ST, Sequence Type; NH, nursing home; TET, tetracycline; ERY, erythromycin; CLI, clindamycin; GEN, gentamicin; TOB, tobramycin; CIP, ciprofloxacin; SXT, trimethoprim-sulfamethoxazole; LEV, levofloxacin.
[a]Nursing homes 1, 2, and 3 are in urban areas and nursing homes 4, 5, and 6 are in rural areas.
[b]In the previous 12 months.

DISCUSSION

In our study, the prevalence of MRSA in NHs (15.7%) was similar to that described in other studies carried out in Spain.[8] The prevalence rate of MRSA-ST398 detected in our study in NHs in the region of Osona is significant (15.6% among MRSA-colonized residents and 2.5% of all NH residents). This is the first study to describe the presence of MRSA-ST398 in NHs in Catalonia and in Spain.

The NH with the highest prevalence of MRSA-Tet^R was in a rural area, and the NH with the lowest prevalence was in an urban area. This difference may be due to the rural character of

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NH-6, which generally admits people straight from their homes, whereas urban NH-3 regularly admits patients referred from hospital.

In our study, 4 of the 5 residents colonized with MRSA-ST398 had direct or indirect contact with pig farms. This finding suggests that acquisition of MRSA-ST398 could be from relatives and not the nursing home itself. It is well known that nursing homes are a reservoir for MRSA, and they could also be reservoir for MRSA-ST398. Two residents in the same NH were identified as carriers of MRSA-ST398 with the same *spa*-type (t011) and a similar though not identical resistance phenotype (Table 2). Both had contact with relatives of farm workers but not directly with the farms. We ascertained that the residents and the farm workers' relatives were not related and that they only had occasional contact at mealtimes. Even though this could have constituted an outbreak, it was not possible to confirm this hypothesis because neither the relatives nor the health workers were screened.

The first outbreak of MRSA-ST398 in a NH was described in the Netherlands, in which 1 of 7 residents and 2 of 4 healthcare workers were MRSA-ST398 carriers. They had contact either with pig farms or with relatives of pig-farm workers.[3] Another study performed in China detected MRSA-ST398 carriage in 21 of 491 residents from 7 NHs, although no information about potential contact with farmers or the type of transmission was included.[9]

The county of Osona has one of the highest pig densities in Spain.[5] In a recent study in this same area of Osona, 57.8% of pig-farm workers were carriers of MRSA-ST398[5], and approximately 45% of patients diagnosed with MRSA in the hospital of this county in 2015 had the ST398 lineage.[10] These data suggest that the MRSA-ST398 clone plays a significant role both in colonization and in infections in the population of the Osona region.

Although the current prevalence of MRSA-ST398 in our study is moderate compared to other MRSA lineages, the characteristics of the region (with a high density of pigs) suggest that MRSA-ST398 might have greater prevalence in the future. Consequently, surveillance should be maintained to track the development of MRSA-ST398.

The present study has several limitations. We only looked at residents in NHs and not at the relatives of the residents and healthcare NH workers, who might be a cause of MRSA-ST398 transmission. In addition, extra-nasal colonization was not assessed in our study. The MRSA-Tet^R carrier group vs the MRSA-Tet^S carrier group were analyzed, and the results must be interpreted with caution because these groups were too small to allow firm conclusions to be drawn.

In conclusion, the prevalence of MRSA-ST398 colonization in NHs in Osona county is 15.6% of MRSA carriers and 2.5% of the total of residents studied. The prevalence of MRSA in the NHs studied was similar to that found in previous studies. Nursing homes are a well-known reservoir for MRSA, and in the region where this study was conducted, they could also be a reservoir for MRSA-ST398.

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Affiliations: 1. Department of Internal Medicine, Hospital Universitari de Vic, Barcelona, Spain; 2. Department of Medicine, Universitat Autònoma de Barcelona, Barcelona, Spain; 3. Area de Bioquímica y Biología Molecular, Universidad de La Rioja, Logroño, Spain; 4. Infectious Diseases Unit, Health Sciences Research Institute of the Germans Trias i Pujol Foundation, Badalona, Barcelona, Spain; 5. CIBER de Enfermedades Respiratorias, Madrid, Spain; 6. Microbiology Department, Hospital Universitari de Vic, Barcelona, Spain; 7. Epidemiology Department, Hospital Universitari de Vic, Barcelona, Spain

Address correspondence to Esteban Reynaga, Department of Internal Medicine, Hospital Universitari de Vic, Francesc Pla El Vigatà 1, Vic (08500), Barcelona, Spain (eareynaga@chv.cat).

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SUPPLEMENTARY MATERIAL

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REFERENCES

1. Yoshikawa T, Bradley SF. *Staphylococcus* infections and antibiotic resistance in older adults. *Clin Infect Dis* 2002;34:211–216.
2. Becker K, Ballhausen B, Kahl BC, Köck R. The clinical impact of livestock-associated methicillin-resistant *Staphylococcus aureus* of the clonal complex 398 for humans. *Vet Microbiol* 2017;200:33–38.
3. Verkade E, Bosch T, Hendriks Y, Kluytmans J. Outbreak of methicillin-resistant *Staphylococcus aureus* ST398 in a Dutch nursing home. *Infect Control Hosp Epidemiol* 2012;33:624–626.
4. Lozano C, Rezusta A, Gómez P, et al. High prevalence of spa types associated with the clonal lineage CC398 among tetracycline-resistant methicillin-resistant *Staphylococcus aureus* strains in a Spanish hospital. *J Antimicrob Chemother* 2012;67:330–334.
5. Reynaga E, Navarro M, Vilamala A, et al. Prevalence of colonization by methicillin-resistant *Staphylococcus aureus* ST398 in pigs and pig farm workers in an area of Catalonia, Spain. *BMC Infect Dis* 2016;16:716.
6 Lozano C, Aspiroz C, Charlez L, et al. Skin lesion by methicillin-resistant *Staphylococcus aureus* ST398-t1451 in a Spanish pig farmer: possible transmission from animals to humans. *Vector Borne Zoonotic Dis* 2011;11:605–607.
7. Harmsen D, Claus H, Witte W, et al. Typing of methicillin-resistant *Staphylococcus aureus* in a university hospital setting by using novel software for *spa* repeat determination and database management. *J Clin Microbiol* 2003;41:5442–5448.

8 Manzur A, Gavalda L, Ruiz De Gopegui E, et al. Prevalence of methicillin-resistant *Staphylococcus aureus* and factors associated with colonization among residents in community long-term-care facilities in Spain. *Clin Microbiol Infect* 2008;14: 867–872.
9. Zhang J, Gu FF, Zhao SY, et al. Prevalence and molecular epidemiology of *Staphylococcus aureus* among residents of seven nursing homes in Shanghai. *PLoS ONE* 2015;10(9): e0137593.
10. Reynaga E, Torres C, Garcia-Nuñez M, et al. Clinical impact and prevalence of MRSA CC398 and differences between MRSA-Tet^{R} and MRSA-Tet^{S} in an area of Spain with a high density of pig farming: a prospective cohort study. *Clin Microbiol Infect* 2017;23:678.e1–678.e4.

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