**INTRODUCTION**

Meticillin-resistant *Staphylococcus aureus* (MRSA) is a major pathogen that causes surgical site infections, pneumonia and bloodstream infections in hospitalized patients. Since the late 1990s, however, MRSA has been rapidly emerging in communities with no MRSA risk factors. Community-associated MRSA (CA-MRSA) is now established in many countries including South Korea (Kim et al., 2007).

In the USA, the most representative CA-MRSA clone is USA300, which is sequence type (ST) 8 and staphylococcal cassette chromosome mec (SCCmec) type IV (King et al., 2006; Moran et al., 2006). However, several studies have reported that the major CA-MRSA clone in South Korea is ST72 (Kim et al., 2007; Ko et al., 2008; Park et al., 2009). Although ST72 MRSA in Korea possesses SCCmec type IVA, it lacks the Panton–Valentine leukocidin (pvl) gene, unlike the USA300 clone. Recently, ST72 MRSA isolates were also found in raw meat in South Korea (Lim et al., 2010). In this study, we compared ST72 MRSA isolates from humans, raw meat and soil in South Korea.

**METHODS**

A total of 12 ST72 *S. aureus* isolates from South Korea were analysed (Table 1). Four ST72 MRSA isolates from hospitalized patients were selected randomly from 84 isolates collected in four surveillance studies, which were carried out by the Asia Pacific Foundation for Infectious Diseases in South Korea. Three ST72 meticillin-susceptible *S. aureus* (MSSA) isolates from humans were selected from five ST72 MSSA isolates collected in the same studies. Four MRSA isolates were from beef and pork (Lim et al., 2010), and one MRSA strain was isolated from soil unrelated to a slaughterhouse. Antimicrobial susceptibility testing was performed using a broth microdilution method according to the Clinical and Laboratory Standards Institute (CLSI, 2009). Multilocus sequence typing, SCCmec typing, spa typing and PFGE were performed as described previously elsewhere (Enright et al., 2001; Oliveira & de Lencastre, 2002). Enterotoxin genes (sea, seb, sec, sed, see, seg, seh, sei, sek and tst) and the pvl gene were also screened using PCR methods (Jarraud et al., 2002). To compare the genetic backgrounds of the ST72 *S. aureus* isolates, the nucleotide sequences of 12 chromosomal regions, all of which flank essential housekeeping genes, were determined: SA004 (*recF*), SA124 (a gene encoding a hypothetical protein similar to glycosyltransferase TuaA), SA342 (*yqiL*), SA560 (a gene encoding a hypothetical protein), SA729 (*spi*), SA1052 (*gmk*), SA1244 (*odlB*), SA1792 (a gene encoding a ssDNA-binding protein), SA2020 (a gene encoding a hypothetical protein similar to the ABC transporter), SA2414 (a gene encoding a hypothetical protein similar to glutathione peroxidase), SA2425 (*arcC*) and SA2499 (*gidB*). These genes were identified as essential genes for growth in our previous knockout study (Ko et al., 2006).
We determined the nucleotide sequences of 15,986 bp from 12 chromosomal regions, and 76 variable sites were obtained. Based on these nucleotide sequences, the phylogenic tree of the ST72 \(S. \) aureus isolates was reconstructed (Fig. 2). The phylogenic tree showed three distinct clusters, supported by bootstrap analysis. Two clusters were homogeneous: the first was composed of two MRSA isolates from animals (05-B-52 and 05-B-60) and the second consisted of the three MSSA isolates (K01-799, K07-006 and K07-561). However, the third cluster was heterogeneous, including four MRSA isolates from humans (K01-140, K07-016, K07-204 and K07-322), two MRSA isolates from raw meat (08-B-93 and 08-P-236) and the MRSA isolate from soil (4-009). Thus, two MRSA isolates from raw meat clustered with MRSA isolates from humans and soil, but the other two MRSA isolates from raw meat formed an independent and divergent clade. The two MRSA isolates forming the divergent clade (05-B-52 and 05-B-60) co-diverged from other isolates in two loci, SA004, encoding recF and its flanking regions, and SA1792, encoding a ssDNA-binding protein. In addition, the three ST72 MSSA isolates co-diverged from MRSA isolates in SA1792.

**DISCUSSION**

To date, ST72 MRSA isolates have rarely been reported in countries other than South Korea. Those ST72 MRSA isolates reported in other countries were sporadic and not disseminated (Ghebremedhin et al., 2009; Schuenck et al., 2009). Thus, we assume that ST72-MRSA-IVA is an MRSA clone specific to South Korea. The relationships among ST72 \(S. \) aureus isolates, the representative clone of CA-MRSA in South Korea, was investigated. It has been suggested that ST72 MRSA isolates first emerged in the community and disseminated into hospitals (Park et al., 2009). Now, ST72
MRSA isolates are frequently found as agents of nosocomial infections in South Korea (Bae et al., 2010). No ST72 S. aureus isolates included in this study possessed the pvl gene, in contrast to CA-MRSA from the USA (USA300 clone). This absence of the pvl gene in CA-MRSA isolates from South Korea has been reported repeatedly (Kim et al., 2007; Ko et al., 2008; Park et al., 2009).

It has been reported that the main clone of livestock-associated MRSA in Europe and North America is ST398. These ST398 MRSA isolates are of concern due to their transmissibility to humans (Golding et al., 2010). Although ST398 MRSA has not been reported so far in South Korea, ST72 MRSA has emerged as the main clone of raw meat-associated MRSA in South Korea (Lim et al., 2010). In the current study, ST72 S. aureus isolates, both MRSA and MSSA, showed very homogeneous features such as SCCmec type, spa type, distribution of virulence genes and PFGE types, which may indicate that these ST72 S. aureus isolates originated from a common ancestor. However, the

**Fig. 1.** PFGE results of the 12 ST72 S. aureus isolates. PFGE was performed as described previously (Mulvey et al., 2001). Agarose plugs containing genomic DNA were digested with Smal. Electrophoresis was performed with a CHEF Mapper apparatus (Bio-Rad Laboratories) at 6 V cm\(^{-1}\) for 22 h.

**Fig. 2.** Neighbour-joining tree of the 12 ST72 S. aureus isolates based on nucleotide sequences of 12 dispersed chromosomal loci. This midpoint-rooting tree was constructed using PAUP. Numbers at branching nodes are percentages of 1000 bootstrap replications. Only values >50% are shown.
nucleotide sequences of 12 chromosomal regions represented detectable divergence. Thus, the ST72 MRSA isolates from humans were closely related to some ST72 MRSA isolates from raw meat. In addition, an MRSA isolate from soil also showed a close relatedness to these other strains. In contrast, three ST72 MSSA isolates formed a group distinct from the MRSA isolates.

Our study also suggested that ST72 MRSA has not emerged repeatedly from ST72 MSSA. Judging from the clade of ST72 MSSA isolates distinct from the MRSA isolates, ST72 MRSA might have originated from ST72 MSSA, but the uptake of SCCmec type IVA is not recent and did not occur repeatedly. Further investigation including more ST72 MRSA and MSSA isolates could unveil the detailed evolution of ST72 MRSA in South Korea, although ST72 MSSA isolates have rarely been found in both hospital and community settings (Ko et al., 2008).

In summary, we showed that ST72 MRSA isolates from humans, raw meat and soil shared the same characteristics. Some ST72 MRSA isolates from meat and soil showed close relationships with ST72 MRSA isolates from humans, suggesting the possibility of transmission of ST72 MRSA among humans, animals and the environment.

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REFERENCES


