
**Figure S1.** Nucleotide sequence comparison of *orf46* (bright purple), *orf51* (pale purple), and both recombined *orf*s after excision of the UCS in KM45013 (*orf* located in the UCS and the one on the chromosomal DNA). Their 120-bp upstream- and 84/86-bp downstream regions are also depicted and colored in blue or green, respectively. The start and stop codons of *orf46*, *orf51* and both recombined *orfs* are boxed. The expected sites (5'-TTACAG-3') involved in *orf46* and *orf51* recombination are shown in black. The nucleotide positions with double peaks in the sequence chromatograms (Sanger sequencing) of both recombined CDS are indicated as K (T or G), Y (T or C), R (G or A), W (A or T) or M (A or C) and colored in yellow. Divergent nucleotides in *orf46* and *orf51* with respect to those of the recombined *orfs* are underlined.

**Table S1.** Oligonucleotide primers used in this study and description of regions amplified.

| Description | Gene/region amplified | Primer designation | Sequence (5'→3')[a] | Amplicon size (bp) |
|---|---|---|---|---|
| *ccrAm2/Bm2* of SCC*mec*$_{KM45013}$ | *ccrAm2* | ccrAm2-fw<br>ccrAm2-rv | TTCKTCCAGAACCGATATCA<br>GGCAGCGTTCATTTAAWCSY | 797[b] |
| | *ccrBm2* | ccrBm2-fw<br>ccrBm2-rv | GACGGCAAGCATACTCCAAT<br>GCAGTGCTTCCTCTGGTTSK | 808[b] |
| *mec* complex of SCC*mec*$_{KM45013}$ | *mecB* | mecB-fw<br>mecB-rv | TGTTCGGCATTTCCGACGAA<br>TCTCCCTGGCCATATCCTGA | 469[b] |
| | *mecIm* | mecIm-fw<br>mecIm-rv | TGAGGCATTGAGTGCTAAACA<br>TTCGGTCAATTCTTCAGGTG | 265[b] |
| | *mecR1m* | mecRm-fw<br>mecRm-rv | CAGCTTGTGACATGGAAGTGA<br>TACCAGTTTTTCCCCACAKC | 861[b] |
| | *blaZm* | blaZm-fw<br>blaZm-rv | AAGTACAATATTCAAGCGGGTGT<br>AATTAGCTCCCTGCCCACTT | 586[b] |
| *orfX* of strain KM45013 | *orfX* | orfX_KM-fw<br>orfX_KM-rv | GAAGCGGAGCGCATACTATC<br>GCATAGTTTGAGCGGTCCAT | 197[b] |
| Transposase gene of Tn*6045* | *tnp* | tnp-rv_096<br>tnp-fw_096 | CGCCACAGGCGTTAAATAAT<br>GCTCCGAAAATTGCGTAAAG | 906[b] |
| MCCL_0033 | MCCL_0033 | MCCL_0033_096-fw<br>MCCL_0033_096-rv | GCTGGAAACGAAAGAAGCTG<br>ACCCATAGCTCGCACAAAAT | 413[b] |
| MCCL_0034 | MCCL_0034 | MCCL_0034_096-fw<br>MCCL_0034_096-rv | AAAATGGATGCTGAGGGTGA<br>TCCACCAATTTCTTGTGCTG | 339[b] |
| Restriction analysis of SCC*mec*$_{KM45013}$ | Joining region 3 (J3) | orfX_KM-fw<br>ccrAm2-fw | GAAGCGGAGCGCATACTATC<br>TTCKTCCAGAACCGATATCA | 10,740[c] |
| | 5' end J2 | ccrAm2-rv<br>C16_ISP2 | GGCAGCGTTCATTTAAWCSY<br>ACAGGTACGCCTGCTTCTGT | 11,777[c] |
| | 3' end J2 + *mec* operon | C16_ISP3<br>blaZm-rv | AGCAGGCGTACCTGTTGAGT<br>AATTAGCTCCCTGCCCACTT | 17,074[c] |
| SCC*mec*$_{KM45013}$ CIs and UCS | SCC*mec*$_{KM45013}$ | SCCmec5'_inv (1)<br>SCCmec3'_inv (4, C) | TCCCACTGATTCTGCCTTTT<br>GGTGATAAAAGTGGGCAAGG | 688[c] |
| | SCC$_{KM45013}$ | SCCmec5'_inv (1)<br>ISS2-up (2) | TCCCACTGATTCTGCCTTTT<br>CCCACTAGAAAAAGCGGATG | 989[c] |
| | ψSCC*mec*$_{KM45013}$ | ISS2-dn (3)<br>SCCmec3'_inv (4, C) | AACCCAAATTCAACCATATGATAA<br>GGTGATAAAAGTGGGCAAGG | 547[c] |
| | UCS | mecIm-fw (B)<br>SCCmec3'_inv (4, C) | TGAGGCATTGAGTGCTAAACA<br>GGTGATAAAAGTGGGCAAGG | 1,702[c] |
| Detection of chromosomal regions after excision | SCCmec$_{KM45013}$ | orfX-fw2 (0)<br>orf52_inv (5, D) | CGCTCAAACTATGCCCTCTC<br>GTTTGGCCTTTATGGGCTTT | 1,744[c] / 40,405[c] |
| | SCC$_{KM45013}$ | orfX-fw2 (0)<br>ISS2-dn (3) | CGCTCAAACTATGCCCTCTC<br>AACCCAAATTCAACCATATGATAA | 369[c] / 27,245[c] |
| | ψSCC*mec*$_{KM45013}$ | ISS2-up (2)<br>orf52_inv (5, D) | CCCACTAGAAAAAGCGGATG<br>GTTTGGCCTTTATGGGCTTT | 2,029[c] / 14,087[c] |
| | UCS | orf45_inv (A)<br>orf52_inv (5, D) | CACTGAATCAGCATGATGTCCT<br>GTTTGGCCTTTATGGGCTTT | 1,535[d] / 7,814[c] |

[a] Specifications for degenerate primer: K (T or G), Y (T or C), R (G or A), W (A or T), S (G or C), or M (A or C).
[b] Taq DNA polymerase was used following the manufacturer's recommendations (Solis BioDyne).
[c] GoTaq DNA polymerase was used following the manufacturer's recommendations (Promega).
[d] HOT FIREPol DNA polymerase was used following the manufacturer's recommendations (Solis BioDyne).