Objective: To characterize methicillin-resistant Staphylococcus aureus (MRSA) strains responsible for nosocomial pneumonia collected during an inpatient cohort and investigate the role of SCCmec.

Methods: 435 MRSA baseline isolates were collected from subjects with NP in the USA (n = 265), Europe (n = 55), Latin America (n = 45), Asia (n = 101), and Australia (n = 22). Only one isolate per subject was included. PVL genes and SCCmec types were determined. Antimicrobial susceptibility testing results were performed by CLSI and EUCAST. MLST was performed to assign the strains to specific lineages. Results: The majority of isolates included in this study were CCC-MRSA-II/IV (56.1%), followed by CCC-MRSA-V (11.3%), and 34% were not assigned to specific categories. The rate of USA300 (21.1%) appears high, with significant rates of USA500 (56.1%) and USA100 (41.9%) also identified. The rate of USA300 (21.1%) appears high, with significant rates of USA500 (56.1%) and USA100 (41.9%) also identified. The rate of USA300 (21.1%) appears high, with significant rates of USA500 (56.1%) and USA100 (41.9%) also identified. The rate of USA300 (21.1%) appears high, with significant rates of USA500 (56.1%) and USA100 (41.9%) also identified. The rate of USA300 (21.1%) appears high, with significant rates of USA500 (56.1%) and USA100 (41.9%) also identified. The rate of USA300 (21.1%) appears high, with significant rates of USA500 (56.1%) and USA100 (41.9%) also identified. The rate of USA300 (21.1%) appears high, with significant rates of USA500 (56.1%) and USA100 (41.9%) also identified. Calling an isolate USA300 corresponded with increased rates of invasive disease as previously documented. Conclusions: USA300 is the most prevalent MRSA clone worldwide, with significant reporting from USA and Europe. It was associated with USA500 in Asia and Latin America. These large-scale genotypic and phenotypic characterization studies provide essential global insights into the MRSA population and support public health strategies targeting invasive disease.