Staphylococcus aureus, a major food-poisoning pathogen, is a common contaminant in dairy industries worldwide, including in Brazil. We determined the occurrence of S. aureus in five dairies in Brazil over 8 months. Of 421 samples, 31 (7.4%) were positive for S. aureus and prevalence varied from 0 to 63.3% between dairies. Sixty-six isolates from the 31 samples were typed by Multi-Locus Sequence Typing to determine if these isolates were persistent or continuously reintroduced. Seven known sequence types (STs), ST1, ST5, ST30, ST97, ST126, ST188 and ST398, and four new ST were identified, ST3531, ST3540, ST3562 and ST3534. Clonal complex (CC) 1 (including the four new ST), known as an epidemic clone, was the dominant CC. However, there were no indications of persistence of particular ST. The resistance toward 11 antibiotic compounds was assessed. Twelve profiles were generated with 75.8% of strains being sensitive to all antibiotic classes and no Methicillin-resistant S. aureus (MRSA) strains were found. The enterotoxin-encoding genes involved in food-poisoning, e.g., sea, sed, see, and seg were targeted by PCR. The two toxin-encoding genes, sed and see, were not detected. Only three strains (4.5%) harbored seg and two of these also harbored sea. Despite the isolates being Methicillin-sensitive S. aureus (MSSA), the presence of CC1 clones in the processing environment, including some harboring enterotoxin encoding genes, is of concern and hygiene must have high priority to reduce contamination.