Objective. To determine molecular epidemiology of methicillin-resistant S. aureus in Tanzania using whole genome sequencing. Methods. DNA from 33 Staphylococcus species was recovered from subcultured archived Staphylococcus isolates. Whole genome sequencing was performed on IlluminaMiseq using paired-end 2x250 bp protocol. Raw sequence data were analyzed using online tools. Results. Full susceptibility to vancomycin and chloramphenicol was observed. Thirteen isolates (43.3%) resisted cefoxitin and other antimicrobials tested. Multilocus sequence typing revealed 13 different sequence types among the 30 S. aureus isolates, with ST-8 (n = seven, 23%) being the most common. Gene detection in S. aureus stains were as follows: mecA, 10 (33.3%); pvl, 5 (16.7%); tst, 2 (6.7%). The SNP difference among the six Tanzanian ST-8MRSA isolates ranged from 24 to 196 SNPs and from 16 to 446 SNPs when using the USA300_FPR3757 or the USA500 2395 as a reference, respectively. The mutation rate was 1.38 x 10^{-11} SNPs/site/year or 1.4 x 10^{-6} SNPs/site/year as estimated by USA300 FPR3757 or the USA500 2395, respectively. Conclusion. S. aureus isolates causing infections in hospitalized patients in Moshi are highly diverse and epidemiologically unrelated. Temporal phylogenetic analysis provided better resolution on transmission and introduction of MRSA and it may be important to include this in future routines.