A collection of 101 clinical isolates of M. tuberculosis from pulmonary tuberculosis patients living in Okinawa, collected between 2003 and 2005, was studied by spoligotyping, a reverse-line-based hybridization assay that allows to study the genetic diversity of the Direct-Repeat locus, the infra-species classification of M. tuberculosis.

Results on all isolates were available. 72 clinical isolates (71.3%) belong to the Beijing type, the predominant clade in Okinawa. 5 clinical isolates belong the previously described East-African-Indian (EAI)-2-Manilla clade. A total of 18 clusters (from 2 to 69 isolates) and 4 unique spoligotypes are described. Comparison to the latest available international spoligotyping database (SpolDB4) allowed to detect two identical and one similar isolates between this study and previous studies performed in Okayama and Osaka, thereby characterizing the spoligotyping-international-type SIT627 as representative of a new genetic family of M. tuberculosis, which was baptised the Osaka-type family (T. Matsumoto). Further characterization of this genotype by an independent genotyping method, VNTR-MIRU-typing, provided classical 5-VNTR and 12 MIRU allelic values of 32423 and 215125113322 respectively (VNTR-MIRU international type, VIT310). VIT310 had previously been detected in Turkey, which raises interesting hypothesis about the genetic link between these two bacterial populations. The 72 clinical isolates of the Beijing type were further discriminated using QUB (Queen-University-Belfast) markers and a set of four epidemiologically-informative MIRU markers to search for epidemiological-linked clusters within the Beijing group of strains.