There have been increasing reports of blaOXA-23-carrying strains of carbapenem-resistant Acinetobacter baumannii (CRAB), which has become a significant public health concern in Taiwan. To determine the origin of these CRAB strains, the prevalence of CRAB and blaOXA-23-carrying CRAB in a regional hospital was analysed retrospectively. The genome of A. baumannii TYTH-1 was completely sequenced and annotated. Multiple comparative genomics studies, including phylogenetic analysis, functional comparison via the Clusters of Orthologous Groups (COGs) database, and determination of variance in GC profiles in the whole genome and gene arrangements in resistance islands, were performed using 11 completely sequenced A. baumannii genomes. blaOXA-23-carrying CRAB isolates became dominant clones in 2007. A comparative genomics analysis revealed a common strain lineage between Taiwanese strains (TYTH-1 and TCDC-AB0715) and Chinese strains (MDR-TJ and MDR-ZJ06). Phylogenetic studies and GC profiles showed that the genome of TYTH-1 was closest to MDR-ZJ06. However, the resistance island of TYTH-1 (RITYTH-1) was nearly identical to that of RIMDT-TJ. The functional category for COGs was similar in the tested genomes. The results reveal that dissemination of blaOXA-23-carrying CRAB in Taiwan may have been mediated by the transfer of people between Taiwan and China during 2007. The global spread of CRAB is now a worldwide public health problem. In Taiwan, the government needs to focus more attention on the importance of identifying and tracing resistant pathogens and issuing notifications of CRAB infections.