Recent studies have found that the Archaea domain is widespread and this group plays an important role in ecosystem functioning, especially in mangrove sediments where the extreme conditions imposed by daily tidal variations turn these ecosystems into hot spots for microbial diversity. However, studies on the archaeal communities in mangrove sediments are still scarce. Thus, the aim of this work was to investigate the archaeal diversity in 5 different mangroves in the State of Ceará, Northeast Brazil, with different types of impacts, i.e., shrimp farming (COR an ACA), urbanization (CEA), river damming (PAC) and also included a pristine mangrove as a control (TIM). Samples from the top 10 centimeters from bulk sediment and the root zones of *Rhizophora mangle* and *Avicennia shaueriana* were collected in 4 sampling expeditions, in the dry and wet seasons from two consecutive years and environmental variables such as pH, salinity, organic matter and silt-clay percentages were measured. In total 300 samples were collected, extracted and 16S rRNA V4 amplified according to the Earth Microbiome Project standard protocols. A total of 5,094,521 sequences were obtained and assigned to 115,360 OTUs, from which 3.4% belonged to the domain Archaea. Only two phyla were found, Crenarchaeota and Euryarchaeota, with the first being predominant in all the analyzed mangroves. A shrimp-farming (COR) mangrove had the highest number of sequences affiliated to Archaea, followed by the urbanized mangrove (CEA). Also, the urbanized mangrove presented exclusive genus, namely Halobacterium, Natrococcus and Thermogymnomonas and a highest number of Archaea in the bulk sediment samples. The pristine mangrove had the highest values of alpha diversity followed by the urbanized mangrove. Analyzing just the environmental variables of the samples by PCA it is possible to evidence three groups, one formed by COR, another by TIM and ACA and another one by PAC and CEA with high, intermediate and low values of organic matter and silt-clay, respectively. However, none of the variables correlated significantly with the genus-level composition according to RDA analyses. In summary, mangroves have high archaeal diversity that is possibly being affected by the distinct pressures caused by anthropogenic activities.

**Keywords**: mangrove, archaea, soil, 16S sequencing,