Termites are dominant decomposers of organic matter in tropical and subtropical terrestrial ecosystems and this is partly due to their association with gut microbes. Termites have acquired the capacity to digest wood and sustain themselves on this nutrient poor diet as gut fauna provides help in digestion of cellulose and nutrients acquisition. Here, we intend to document the evolution of gut microbial communities in related termite species inhabiting distinct ecosystems and geographical regions. To do so, we selected 13 termite colonies belonging to nine species of *Coptotermes* and two species of *Heterotermes*, that we sampled in lowland tropical forests, peat swamp forests and in man-made habitats. We used a meta-genomic approach and sequenced two fragments of the 16S rRNA gene of the termite gut microbiota for each colony using Ion Torrent. Altogether, we obtained 325,000 and 310,000 sequences for both fragments. Both 16S fragments provided comparatively similar results, although they suggested different species diversity. Microbial communities were dominated by *Candidatus Azobacteroides* (Bacteroidetes) and *Treponema* (Spirochaetes). These two genera are involved in nitrogen fixation and made up between 70% and 90% of the microbial abundance. Microbiota species diversity was higher for colonies collected in peat swamp and lower for colonies collected in man-made habitats. No correlations were found between species composition and phylogeny or habitat. Overall, our results show that the taxonomic composition of termite gut fauna is relatively similar among *Coptotermes* and *Heterotermes* species and is dominated by nitrogen fixating bacteria.