

In my opinion, this is a well-written, updated, and clear work. dealing with comprehensively investigating the bacterial microbiome across the three root-associated compartments in four different mangrove species by high-throughput amplicon sequencing. The significant overlap in key community members of the same rhizocompartment among distinct mangrove species was found at the phylum level. Furthermore, this is the first report of Acidothermus found in mangrove environments.

■ A Clear, unambiguous, professional English language is used throughout the whole manuscript a few language and punctuation problems in the whole text need editing which were listed below:

Line 47: remove the comma.

Line 108: add missing verb (the samples **were** divided).

Line 111: Fix the agreement mistake (The soils**s**) and add the missing verb (**is** attached)

Line 120: remove the verb (**were**) in were used for DNA isolation

Line 136: correct article usage base-calling to be **a** base-calling

Line 150: add the passive form Simpson and Shannon's

Line 160: correct article usage **The** FAPROTAX

Line 172: add a comma (**,** and the soil)

Line 173: correct article usage (of **the** other)

Line 174: correct the quantifier than to be (**more** than)

Line 177: change the capitalization shannon to be (**S**hannon)

Line 199: add an article proportion to be (**the** proportion)

line 216: correct article usage root to be **the** root

line 240: change the capitalization simpson to be **S**impson

line 241: change the verb form two compartments was to be (two compartments **were**)

line 250: correct article usage Figure (**the** Figure)

line 271 : change the preposition on to be(**in** different compartments)

line 284, 289,290,291, 292 and 312: add an article uncultured to be (**an** uncultured)

line 305: change the verb form compartments was to be **were**

line 337: correct your spelling i.e Chloroflexi to be (i.e. **C**hloroflexi)

line 352: correct subject-verb agreement is to be (**are** still poor) and remove the preposition **for**

line 374: change the verb form was to be **were**

line 395: change the preposition in to be **of**

line 399: correct article usage genus of Actinobacteria to be (genus of **the** Actinobacteria)

line 428: add an articles coastal slope to be (**the** coastal slope)

line 453 : add comma and then exploring to be (, and then exploring)

■ **Abstract:** need to write more detail about high-throughput sequencing and clarify the type of PCR used to detect the results whether it is conventional or nested or real-time.

■ **The intro & background** are well-referenced, and relevant, and covers the subject of the publication.

■ **The structure** conforms to PeerJ standards, discipline norm

■ **Figures** are relevant, high quality, well labeled & described.

■ **Raw data** supplied according to Peer J policy

■ **Experimental design** Original primary research within the Scope of the journal (applicability to the core areas of Biological, Environmental) and included Bioinformatics Software analysis).

■ **The research question** is well defined, relevant & meaningful.

■ **Rigorous investigation** performed to a high technical & ethical standard.

■ **Methods** described with sufficient detail & information to replicate.

■ **Discussion:** This section is well presented.

■ **References:** is well presented and follows a consistent pattern.

■ **Decision:** Accepted after minor revision.