Article

Bacterial Community Changes Associated with Land Use Type in the Forest Montane Region of Northeast China

Shi-Jun Wu1#, Jiao-Jiao Deng1,2#, You Yin2,3, Sheng-Jin Qin2,3, Wen-Xu Zhu2,3, Yong-Bin Zhou1,2, Bing Wang1\*，Honghua Ruan4 and Long Jin 4\*

1College of Land and Environment, Shenyang Agricultural University, Shenyang 110866, China;

2 College of Forestry, Shenyang Agricultural University, Shenyang 110161, China;

3 Research Station of Liaohe-River Plain Forest Ecosystem, Chinese Forest Ecosystem Research Network, Changtu 112500, Shenyang, China;

4College of Biology and the Environments, Nanjing Forestry University, Nanjing, 210037, China

**#** The authors contributed equally to this work.

**\***To whom correspondence should be addressed. E-mail: [isacckim@kaist.ac.kr](mailto:isacckim@kaist.ac.kr) E-mail: [wangbing@caf.ac.cn](mailto:wangbing@caf.ac.cn)

Received: date; Accepted: date; Published: date

**Keywords:** Forest; Land use type; High-throughput sequence

**Figure S1.** Relative abundances of soil bacteria at the genus level under different land use types. Relative abundances are based on the proportional frequencies of bacterial DNA sequences that could be defined at the genus level. QM; *Quercus mongolica*; LG: *Larix* *gmelinii*; PK: *Pinus* *koraiensis*; SL: Shrubland; ZM: *Zea* *mays*.

D:\博士\微生物测序\草河口\细菌\数据分析\Venn_5set_pretty.tiff

**Figure S2.** Venn diagrams of OTU richness. QM: *Quercus mongolica*; LG: *Larix gmelinii*; PK: *Pinus koraiensis*; SL: Shrubland; ZM: *Zea mays*.