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***Interactive comment on* “The shift of microbial population composition accompanying the injected water flowing in the water-flooding petroleum reservoirs” by P. Gao et al.**

Anonymous Referee #1

Received and published: 3 January 2015

The manuscript entitled “The shift of microbial population composition accompanying the injected water flowing in the water-flooding petroleum reservoirs”, by P.K. Gao and colleagues, describes the fluctuation of microbial communities along with injected water flowing into reservoir strata and production wells. Although there are some interesting findings in this manuscript, it is not acceptable in its present form. I think that experimental design needs to be further improved, some of the interpretations should be better qualified and perhaps even modified. Occasionally, the text may be misleading, since the usage of English is sometimes not adequate. Hence, the manuscript should be carefully revised.

Major comments:

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1. English should be significantly improved. This manuscript suffers from grammar errors and poor writing, particularly, in the Results and Discussion section. The Title should be reconsidered so that it can directly present the novel findings to the readers.

2. Experimental design: the authors chose a sandstone reservoir and a conglomerate reservoir in a Chinese typical oilfield, and analyzed the microbial population composition in injected water and produced water samples by using high-throughput sequencing technology, in order to test whether microbial populations in injected water could pass through oil-bearing strata. Overall the approach is straightforward. However, there are three major shortcomings in this study:

(i) The lack of control: These two kind of old well groups have water flooded for 13- and 30-years. The negative controls are missing. The indigenous microbial community in the same oil-bearing strata cannot be overlooked. A better way is to determine oilfield water samples from newly drilled well for comparison in the same oil-bearing block.

(ii) Some important geological parameters are missing: In this manuscript, by comparison of Lu and Liu field block reservoirs, the authors concluded that injected water can pass through reservoir strata, but the reservoir heterogeneity, sieve effect of strata and dissolved oxygen affect the microbial migration. However, geological parameters such as source rocks and oil sources of Lu and Liu field, the characteristics of crude oil (heavy oil or light oil), reservoir pressures, the depths of Lu and Liu oil-bearing strata are missing. If there are great differences between Lu and Liu field block in these parameters, the comparison does not make sense.

(iii) Environmental parameters such as dissolved oxygen (DO) or oxidation-reduction potential (ORP), subsurface temperature, and the composition of organic matter of crude oil (as substrate for fermentative bacteria and methanogenic archaea) have not determined in this study. These parameters are crucial for the fluctuation of microbial communities besides injected water. Therefore, it is also necessary to include these parameters in PCoA analysis. Without these information, the conclusion was unten-

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able.

3. Materials and methods: Amplicon sequencing was performed on two kinds of high-throughput sequencing platform (GS FLX+ and Miseq). Apparently, the outcomes must be different. Did the authors want to make a comparison? I cannot find any clue in this manuscript.

4. Discussion: There is no “going home” feeling in this part. Too many hypotheses were demonstrated. In situ DO in injected and production water and the composition of crude oil should be determined firstly. Then, the content of the true part of the “Discussion” should be carefully revised accompanying with more related new references.

5. The conclusion is too long and should be carefully rewritten.

Minor comments:

1. Page 16774 Line 5-8: “The results indicated that the injected water. . . in this reservoir.” This sentence needs to be rephrased.

2. Page 16777 Line 10-12: “All the injected and produced water samples were all collected from the wellhead of injection and production wells by the field personnel of PetroChina.” Once the samples were collected, how long would be the genomic DNA extracted?

3. Page 16779 Line 13-14: why do not quantitate archaeal populations? It would be helpful for the interpretation of methanogenic community later.

4. Page 16780 Line 3-4; Page 16781 Line 2-3: The diversity of the microorganisms in the sandstone reservoir (249-538) is much lower than it in the conglomerate reservoir (51273-128980). Why? In this respect, the geological and environmental condition of Lu and Liu field might be very different from each other.

5. Page 16781 Line 17: The word of “botained” should be revised to “obtained”.

6. Page 16784 Line 17: “LR, 2010” should be revised to “Brown, 2010”.

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7. Page 16791 Table 1: I guess the temperature was the surface temperature. The temperature of oil-bearing strata should also be given.

8. Page 16793 Figure 2: The color representing a designated microbial class should be consistent so that it is easy for comparison. (e.g. The color of Methanococci is blue in Fig. 2aII but red in Fig. 2bII.)

Interactive comment on Biogeosciences Discuss., 11, 16773, 2014.

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