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Risk of shallow tube well water for drinking due to microbial contamination from pollution sources in rural Bangladesh: A challenge to SDGs

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Improving water quality by reducing pollution has been identified as an important target of Sustainable Development Goals (SDGs). This study area covered four hydrological regions of Bangladesh, aimed at determining the risk of selected shallow tube wells (STW; depth <30 m) used for drinking purpose. About 62% of sampled TWs were at medium to high risk according to WHOs' sanitary inspection guidelines, while the situation was worst in south-west region. Microbiological contamination was significantly higher in sampled category-1 STWs (≤10 m from latrine) compared to category-2 TWs (>10 m from latrine), while the number of contaminated TWs and level of contamination was higher during wet season. Analysis revealed that over 96% of household did not treat water before drinking. Over 20%, 54%, and 58% of water samples collected from category-1 TWs were contaminated by *E. coli*, FC, and TC, respectively during the wet season. The number of category-1 TWs having *E. coli* was highest in the north-west (n=8) and north-central (n=4) region during wet season and dry season respectively, while the level of *E. coli* contamination in TWs water was significantly higher in north-central region. However, the south-west region had the highest number of FC contaminated category-1 TWs and significantly a higher level of TC and FC in sampled Category-1 TWs than north-west, north-central and south-east region, mainly during wet season. Position of latrine and other pollution sources within 10m of TWs, and platform absent/broken were significantly associated with presence of microbial contaminants in STW water ($p<0.01$). Water should be treated before drinking.

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The relic legume *Oxytropis popoviana* forms symbiosis with rhizobial co-microsymbionts having complement sets of symbiotic genes

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The legume *Oxytropis popoviana* Peschkova belongs to the Miocene-Pliocene relic and grows in restricted habitats of the Baikal Lake region. Microsymbionts of this rare and endemic plant species have never been isolated, although the study of relict symbiotic systems is very important in the context of evolution of plant-rhizobia interactions. The aim of this work was to obtain root nodules of *O. popoviana* under laboratory conditions, to get and identify rhizobial isolates as well as to search their symbiotic genes. Pot experiment was conducted using soil and seeds collected in distribution area of this legume. Plants were cultivated for 60 days in the growth chamber and nodules were collected. Identification of bacterial isolates was performed by the 16S rRNA gene sequencing method. Genomes of two strains were sequenced by the Illumina MiSeq genome sequencer. Symbiotic genes were searched with CLC Genomics Workbench 7.5.1. Total of 18 strains belonging to 4 rhizobial genera (*Mesorhizobium, Bradyrhizobium, Rhizobium* and *Bosea*) were isolated from nodules obtained in the pot experiment. Some nodules contained a pair of different strains. Two strains isolated from the same nodule were most closely related to the species *Mesorhizobium erdmanii* and *Bradyrhizobium betae*. Analysis of whole genome sequences of these strains showed that they had different sets of symbiotic genes. Thus we hypothesize that the pair of strains isolated from root nodule of *O. popoviana* can be ancestral rhizobial co-microsymbionts and their simultaneous presence in roots is required for efficient nodulation of this relic legume.

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