

Groundwater Resource Management of Rampurbaghelan Area, Satna District, Madhya Pradesh India

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The paper deals with management of groundwater resource of Rampurbaghelan area Satna district, Madhya Pradesh. Geologically, the area is a part of Bhandar Group of Vindhyan Supergroup. The limestone and shale are the main aquifers of the area. For the assessment of groundwater resource, groundwater recharge, groundwater development stage, water table trends, water table fluctuation etc. have been studied. The Pre and Post monsoon water tables are falling. The calculated stage of groundwater development suggests that the area falls in semicritical category. However due to decline in water level, quality and quantity of groundwater have been adversely affected. For scientific management, utilization and augmentation of groundwater resource, the following suggestions have been recommended:

Artificial recharge structures like percolation pond, check dam and contour trenches should be preferred at suitable sites with the help of geological and geomorphological data.

The area having moderate slope can be utilise for contour bunding. The soil taken from the trenches may be placed down the hill in the form of bund. The soil erosion and vegetal. cover can be controlled by growing such seeds of grasses and shrubs on the bunds which are suitable to the area.

Recharge augmentation is positive may, while pumpage control is negative way of management. In extreme cases, when pumpage control is to be observed in the area, the best way of monitoring is at the level of Gram Panchayat.

The groundwater management policies and practices should transcend from academic echelon to actual field implementation. All the related departments publics, stake holders and research institution should be jointly initiate the sustainable action plan with short term and long term plan strategy. Besides these, NGO's may play vital role to conserve the groundwater resource of the area.

The awareness programme is honestly and urgently needed.

Proteogenomic insights into completely oxidizing sulphate reducers (*Desulfobacteriaceae*)

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Sulfate-reducing bacteria are pivotal to carbon turnover in marine sediments, as Jørgensen (1982) demonstrated in his seminal work on organic carbon rich shelf sediments. The observed high in situ activities could concurrently be explained best by the key properties of newly discovered sulphate reducers belonging to the family *Desulfobacteriaceae* (Widdel 1988): (i) capacity to completely oxidize organic carbon to CO₂, and (ii) broad nutritional versatility spanning from simple fermentation end-products to less well degradable substrates such as aromatic compounds. These early findings and concepts motivated more recent genomic and proteomic investigations to further our molecular understanding of this group's physiological capacity. The first published genome of a *Desulfobacteriaceae* member was that of *Desulfobacterium autotrophicum* HRM2 (Strittmatter *et al.* 2009), which degrades long-chained fatty acids and is capable of chemolithoautotrophy (with H₂ and CO₂). The 5.6 Mbp genome displayed an unusually high degree of plasticity and contains a large suite of genes for regulation and electron transport. The recently completed genome of *Desulfobacula toluolica* Tol2 (Wöhlbrand *et al.* 2012) in combination with sub-proteomics and metabolite analysis allowed a detailed reconstruction of the catabolic network for aromatic-compound utilization and discovery of new degradative capacities. Taken together first genome-based insights are emerging that causally explain the ecosystems function of *Desulfobacteriaceae*.

[1] Jørgensen BB (1982) *Nature* **296**: 643-645 [2] Strittmatter AW *et al.* (2009) *Environ Microbiol* **11**: 1038-1055. [3] Widdel F (1988) In *Biology of Anaerobic Microorganisms*. Munich, Germany: Carl Hanser Verlag, pp. 469-585 [4] Wöhlbrand L *et al.* (2012) *Environ Microbiol* doi:10.1111/j.1462-2920.2012.02885.x