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Divergences in gene repertoire among the reference *Prevotella* genomes derived from distinct body sites of human

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In a human body, the distinct body-sites form unique niches for the resident microbiota. There has been an increasing amount of literature on the habitat-specific variations in the microbiome composition at the phylum, genus or species levels not much information is available on the variations at the genome/sub-genome levels of a specific microbial community across different niches. This report aims to explore as a case study the habitat-driven changes in the gene repertoire of 28 *Prevotella* reference genomes derived from different body-sites. Pan-genome analysis of *Prevotella* has yielded 24885 distinct gene families. Among these 456 form the conserved core, 7263 are accessory genes and 17166 are singletons. The study reveals exclusive presence of 11798, 3673, 3348 and 934 gene families and exclusive absence of 17, 221, 115 and 645 gene families in *Prevotella* genomes derived from oral cavity, gut, urogenital-tract and skin respectively. Distribution of functional COG categories differs appreciably among the niche-specific genes. Accessory and singletons show high frequencies of Signal transduction mechanisms category in skin and gut isolates while Defense mechanisms category is over represented among singletons of the urogenital-tract and some oral isolates. These observations clearly point towards the niche-specific modulation in genetic make-ups of microbiome components. Plausible metabolic/physiological implications of such niche-specific gene repertoire are now being investigated in an attempt to have an insight into the host-microbiome interactions at different body-sites. A novel computational pipeline for pan-genome analysis of microbial organisms has also been developed in course of this study.

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Heavy metal mercury phytotoxicity on germination, seedling growth and biochemical changes in crop plants

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Heavy metal toxicity, such as due to mercury in our environment, is seriously dangerous because these metals persist in the environment for years together. Though, Lead is a ubiquitous poison known to man from biblical times Mercury became notorious in the recent past as a result of Minamata disease in Japan and has been found guilty as a harmful environmental pollutant. What worries us now and causes considerable concern is that this and other toxic metals are being found in an increasing amount in the human environment, in the air we breathe, in the water we drink and in the food we consume. The present investigation contains the results of the comparative studies made on seed germination, seedling growth fresh and dry weights and seedling metabolism showing physiological and biochemical parameters (chlorophyll a and b, carbohydrate and protein contents and anti-oxidative enzymes peroxidase superoxide dismutase and catalase) in four major crops (Legumes – Vicia and Mustard; Cereals – Barley and Wheat) under heavy metal (Hg) stress conditions. Their relative heavy metal tolerance was found to be Mustard > Vicia > Wheat > Barley. Thus, mercury treatment at early seedling stage caused more inhibition in wheat and barley as compared to mustard and vicia. These observations clearly show that the crops mustard and vicia suffered lesser than the crops wheat and barley, i.e., the former two crops are more tolerant than the later crops. This basic finding into the growth and physiological parameters associated with heavy metal-tolerance can in turn be expected to advance the applied work which may lead to the finding of structural and/or physiological and biochemical features associated with the development of heavy metal-tolerance. On reviewing the overall results and considering the performance of the crops it seems that tolerance is due to the total plant response.

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