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Determination of minimum inhibitory concentration of *Chrysobacterium indolegenes* HMT 47 isolated from Zawar mines, Udaipur, Rajasthan, India

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Heavy metal pollution is an environmental problem of worldwide concern because most of them can be toxic even at low concentrations. Industrialized societies are responsible for increasing environmental contamination by trace metals produced as wastes from industrial and agricultural processes and household activities. In the present study isolation, identification and determination of the minimum inhibitory concentration (MIC) of *Chrysobacterium indolegenes* HMT 47 was done. The strain was isolated from rhizospheric soil of plants growing in mine spoil of Zawar mines, Udaipur, Rajasthan, India. Isolation was done on nutrient agar supplementated with 0.5 mM of Lead Nitrate by standard Pour Plate Method. The isolate was then identified on the basis of morphological and biochemical characteristics which was further confirmed by 16S rRNA gene sequencing. The amplification reaction was proformed using 16S rRNA gene specific universal primers namely 27F and 1492R. The minimum inhibitory concentration of *Chrysobacterium indolegenes* HMT 47 against lead was determined on nutrient agar supplementated with varying concentrations of lead nitrate ranging from 100 to 1100 µg/ml. The MIC of the isolate against lead nitrate was found to be 1000 µg/ml. The lead tolerant bacterium can proved to be a potential bioremediation tool for *in situ* stabilization and remediation of Lead contamination sites.

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SOCS5 in malaria vector: Annotation, domain organization and phylogenetic analysis in 18 *Anopheles species*

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Insects are amongst the most primitive creature and their encounter with varied groups of pathogen has led to the enormous diversity in their genome. Such diversity is seen to be more pronounced in Anopheles, a deadly vector of Malaria. With the advent of unannotated genome sequence of 18 *Anopheles* species, it will be feasible to understand the intricacy of this diverged genome. Here we identify and annotate SOCS gene, which known to be involved in immunity, growth and development of mosquitoes. SOCS gene from *An. culicifacies* was cloned and sequenced and was used to retrieved SOCS gene from unannotated genome of other anopheles species. Sequence analysis of all *Anopheles* genome database confirmed the presence of three exons separated by two introns (~500 bp in the N terminal region and ~70-80 bp in the SH2 domain).SOCS in all *Anopheles* share a similar domain organization, with a central SH2 domain and a conserved C-terminal SOCS box, the N-terminal domains of SOCS proteins vary in length and amino acid sequence. The SH2 and SOCS box domains showed 99-100% similarity with each other and 80-85% similarity while comparing the whole SOCS protein of *Anopheles*. It indicates that SH2 and SOCS box domains are highly conserved during evolution due to their important role in receptor signaling. These observations indicate that SOCS N-terminal amino acids identity is solely similar, rather limited to, *Anopheles* SOCSs. This variability may indicate that all the domains of AcSOCS experienced differential selection pressures and it provides the evidence that N-terminal domain is under least selection pressure. Phylogeneticanalysis of SOCS gene of all *Anopheles* mosquito species revels that SOCS of same subgenus are similar to each other but diverged from other subgenus mosquitoes. This suggested that SOCS follows the same taxonomical pattern in which Anopheles are classified.

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