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Synthesis and antimicrobial, antiviral evaluation of novel derivatives heterocycles-tetrahydronaphthalene

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A new series of novel derivatives of tetrahydronaphthalene moiety conjugated with biologically active various side chains and heterocycles such as substituted pyrazole and/or substituted thiazole ring systems were synthesized and evaluated as antibacterial, antifungal and antiviral (H5N1) agents. The evaluation exhibited that analogue compound A and compound B produced the highest broad spectrum antibacterial activity against the tested Gram positive and Gram negative bacteria comparing to reference Clotrimazole drug. Antiviral evaluation of the novel derivatives exhibited moderate activity. More structural modifications are required to improve their antimicrobial potency.

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The genome and the proteome landscapes of the genus *Bacillus*- A perfect harmony between purine asymmetry, taxonomic traits and ecological adaptation

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The genus of *Bacillus* is known for the metabolic diversity, ecological ubiquity, clinical significance and commercial potential of its members. Co-existence of three conspicuous genome features an explicit Purine Asymmetry (PAS), extremely high Strand bias in Gene Distribution (SGD) and the presence of PolC (DNA polymerase III, α subunit) has differentiated *Bacillus* and some other members of *Firmicutes*, *Fusobacteria* and *Tenericutes* from the rest of the bacterial world. The primary objective of the present study was to examine whether these features, especially PAS, could impart any influence on protein evolution in these organisms and the genus of *Bacillus* has been selected as a case study. Analysis of various protein features in 21 *Bacillus* species of varied metabolic, pathogenic and ecological traits has revealed that all *Bacillus* species except the Se-respiring *Bacillus selenitireducens*, display distinct strand-specific biases in amino acid usage. This strand asymmetry is often reflected also in the pI profiles or surface charge distribution of *Bacillus* proteins with prevalence of acidic and basic residues in the leading and lagging strand proteins respectively. The dinucleotide relative abundance signatures of *Bacillus* genomes are however not affected by PAS. Distinct lineage-specific and/or niche-specific trends also prevail in the gene and protein features of the members of this genus. Divergence in synonymous codon usage patterns between two strands of replication is quite apparent in the cereus group but not in the non-cereus group of *Bacillus*. Higher occurrences of Cys or Asp in halophilic/alkaliphilic members or abundance of basic residues in thermo-tolerant species corroborate earlier reports on hypersaline and thermal adaptation of bacteria. The study, therefore suggests that protein evolution in *Bacillus* may be an outcome of a perfect harmony between three distinct factors, purine asymmetry, taxonomic heritage and niche specialization.

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