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Docking based 3D-QSAR studies applied at the B-RAF inhibitors to understand the binding mechanism

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B-RAF is a member of the RAF protein kinase family involved in the regulation of cell growth, differentiation, and proliferation. **B**It forms a part of conserved apoptosis signals through the RAS-RAF-MAPK pathway. V600EB-RAF protein has much potential for scientific research as therapeutic target due to its involvement in human melanoma cancer. In the current work, molecular modeling study was carried out for the first time with 3D-QSAR studies by following the docking protocol on three different datasets of V600EB-RAF inhibitors. Based on the co-crystallized compound (PDB ID: 1UWJ), a receptor-guided alignment method was utilized to derive reliable CoMFA and CoMSIA models. The selected CoMFA model gives the best statistical values (q²=0.753, r²=0.890). With the same alignment protocol, a statistically reliable CoMSIA model out of fourteen different combinations was also derived (q²=0.807, r²=0.961). Actual predictive powers of both models were rigorously validated with an external test set, which gave satisfactory predictive r² values for CoMFA and CoMSIA models, 0.89 and 0.88, respectively. Additionally, y-randomization test was also performed to validate our 3D-QSAR models. Contour maps from CoMFA and CoMSIA models supported statistical results, revealed important structural features responsible for biological activity within the active site and explained the correlation between biological activity and receptor-ligand interactions. Based on the developed models few new structures were designed. The newly predicted structure (IIIa) showed higher inhibitory potency (pIC50 of 6.826) than that of the most active compound of the series.

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Research on safety and efficacy of traditional medicine: Antimycobacterial activity of five plant spp. on multi drug resistant tuberculosis

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Introduction: Tuberculosis (TB) is one of the leading causes of death among infectious diseases with a third of the world's population being infected and 9.2 million new cases recorded each year (WHO 2007). This devastating situation has steadily worsened, exacerbated by the emergence of drug-resistant strains (MDR and XDR) and HIV co-infection. Available treatment regimens are lengthy and complex, inviting problems of non-adherence, inadequate response and in the case of MDR TB, second line drugs used are more toxic and expensive. There is need for new leads that can be developed in to new drugs.

Objectives: (1) To document plant species commonly used by traditional medicine practitioners to treat TB and (2) To determine the minimum inhibitoryconcentration of selected plant species on MDR TB.

Methods: The method included use of a guided questionnaire for the first objective and then micro-titer Alamar Blue Assay (MABA) for the second objective.

Results: A total of 90 plant species, distributed within 43 families were documented in this study. TMPs had knowledge of how TB is transmitted and they admitted that it is closely associated with HIV. Five plants were tested for antimycobacterial activity on multidrug resistant strainsusing the Micro-titre Alamar Blue Assay. Of the five species tested, *Zanthoxylum* spp. and *Callistemon* spp. showed the highest activity with MICs of 0.128333 mg/ml and 0.195 mg/ml on the isoniazid resistant strain, respectively, while Callistemon spp. had an MIC of 0.158333 mg/ml on the rifampicin resistant strain. *Piptadenistrum africanum and Blighia unijugata* were not active on any of the strains.

Conclusion: The plant species that were mentioned most by the Traditional Medicine Practitioners showed activity not only on the pan sensitive strains of TB but also on the multidrug resistant strains. These could be developed into drugs for the treatment of MDR TB.

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