

Antimicrobial Investigation and Docking Analysis of Quinoline Compounds

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Abstract

Keywords: Quinoline-8-ol, quinol, quinhydrone, zone of inhibition, biological activity, auto dock and binding energy. The organic compounds quinoline-8-ol, quinol and quinhydrone were subjected to antimicrobial studies against few Gram positive and Gram negative bacteria and fungi. The zone of inhibition towards the microbes was investigated by agar well diffusion method and the compound quinoline-8-ol exhibited lethal zone for the species *Streptococcus* (43 mmml), *Trichophyton* (42 mm/ml), quinol is more resistant towards the organisms like *Bacillus subtilis* (38 mm/ml), *Enterococcus faecalis* (40 mm/ml), *Mucor* (42 mm/ml), *Aspergillus niger* (40 mm/ml) and quinhydrone *Staphylococcus aureus* (40 mm/ml), *Pseudomonas aeruginosa* (38 mm/ml), *Trichophyton* (36 mm/ml) at higher concentrations. Auto dock 4.2.6 was used to perform docking analysis for tiny ligand interactions with macromolecules and the least binding energy; hydrogen atom interactions were reported.

INTRODUCTION

The compound guinol is originated in the plant food as glucose or its conjugate called as arbutin widely found in fruit pears, beverages, onion and it is hydrolyzed to free benzene-1,4-diol or quinol and absorbed by the intestinal gland¹. They are active against few bacteria, weed, pests and fungus ²⁻⁵. The multidrug resistance is also shown by few pathogenic strains like Enterococcus faecium, Streptococcus pneumonia and Staphylococcus aureus⁶. Various heterocyclic compounds have antitumour^{7, 8}, analgesic activities⁹, anti-inflammatory¹⁰ and antiallergic activity¹¹. The derivatives of 1-hydroxy 4aminoanthraguinones and 9, 10- hydrazones possess antimicrobial activity¹²⁻¹⁵ and sedative action¹⁶. The cigarette smoke is rich in quinol and injuring respiratory tract^{17, 18}. Quinhydrone shows antifungal potential against yeast Saccharomyces cerevisiae¹⁹. Quinhydrone is employed as redox electrodes and it is used as an alternative for the glass electrode. Naturally it is found in humic substances comprising of sea water, coal and soil particles. Quinoline-8-ol has extensive biological activities due to its molecular structure.Quinoline-8-ol and the derivatives²⁰ have extensive antibacterial action against neurodegenerative diseases, inhibitor of tuberculosis, antimalarial agents, Parkinson disease, anti-Human Immuno deficiency virus. The antibacterial and antifungal behavior of the prepared compounds quinol, quinoline-8-ol and quinhydrone are evaluated against few bacteria and fungi like Streptococcs, Micrococcus, E.coli, Vibrio chlorae, Candida albicans, A. flavus, Trichophyton, Fusarium, Enterococcus faecalis, Salmonella typhi, A. niger, Mucor, Trichoderma and Klebsiella pneumonia. The hydrogen bond interactions, pi-alkyl interactions, aromaticity and many ligand interactions are predicted using docking method. The prepared compounds are employed as the ligand interacts with the macromolecule and the binding sites, binding energy are determined from auto dock tools²¹ and Discovery studio visualizer software.

EXPERIMENTAL:

Materials and Methods

The organic compounds quinoline-8-ol, quinol and quinhydrone (Figure 1) were purchased from Sigma Aldrich of AnalaR grade. The bacteria and fungus were acquired from Eumic analytical Laboratory and Research Institute, Tiruchirappalli. The Hi media nutrient agar slant at 4^o C was employed to uphold the bacterial strains.



Fig-1: Structure of a. Quinoline-8-ol b. Quinol c. Quinhydrone

Spectral Data

Quinoline-8-ol: The carbon hydrogen stretching frequency (3050 cm⁻¹), aromatic (-C=C-) stretching at 1572 cm⁻¹, 1500cm⁻¹, 1460 cm⁻¹, -C-O-stretching vibration was observed at 1105 cm⁻¹, hydroxy group (phenolic) at 3600 to 2600 cm⁻¹, -CH₂- assymmetric bending at 1450 cm⁻¹, stretching at 2910 cm⁻¹, carbon - nitrogen bending vibrations at 1220 and 1020 cm⁻¹ and stretching between 1660 cm⁻¹.

Benzene-1, 4-diol: Benzene-1,4-diol (quinol) proved to have stretching frequency (O-H) at 3300 - 3500 cm⁻¹, aromatic carbon-hydrogen stretching at 3025cm⁻¹, double bonded carbon-carbon stretching of alkene at 1660 cm⁻¹ and aromatic -C-C- double bond stretching frequency at 1450 and 1502 cm⁻¹.

Quinhydrone: Strong peak at 3034 cm⁻¹ (-C-H), -OH (stretching) group at 3852cm⁻¹, -C=O stretching frequency at 1700cm⁻¹, bending frequency for -C-H- at 3100 to 3000 cm⁻¹, 3640 to 3610 cm⁻¹, =C=O at 1760 to 1665 cm⁻¹, benzene ring at 3100 to 300 cm⁻¹.

Selection of Ligand and Macromolecules

The structures of the protein macromolecule were obtained from the website of protein data bank resource. The protein with ID 7BRA and 5AF1 were collected for studying the bio interaction of ligand and the protein molecules. The compound quinoline-8-ol, quinol and quinhydrone were the ligands. The ligand structures were downloaded from NCBI-PubChem database and the molecule in the SDF mode was converted into charged PDBQT form and saved for docking, using open bable software²².

General procedure

Anti-bacterial Assay : Standard agar well diffusion method²³⁻²⁵ was employed for anti-bacterial assay. On Nutrient agar plates, 0.5 ml (10⁵ CFU/ml) of diluted inoculums of the test organism was distributed. Different concentrations of plant extracts were filled inside the well (8mm diameter) perforated into the agar medium and incubated at 37°C. The zone of inhibition against the test organism was used to assess the antibacterial activities. The diameter of the zone of inhibition is measured and compared to the standard antibiotics, with the results interpreted. The ingredients used for preparing the culture media includes peptone (5g/l), beef extract (3g/l), agar (15g/l), NaCl (5g/l), yeast extract (1.5g/l) and maintained at neutral pH seven.

Auto docking Analysis

The extensive structure and activity of the ligands like quinolin-8-ol, quinol and quinhydrone auto docking was performed for the selected bacteria (*E. coli* and *Candida albicans*) macromolecules in the binding sites using AUTO DOCK 4.2.6 models. All the necessary extension files like autogrid.exe, auto dock.exe, AD4-parameter file, AD 4.1 bound data files were kept in the same folder for docking. The polar hydrogen and the charges were added using Kollman United atom and Gasteiger charges. The AUTOGRID be employed to generate auxiliary programme. The text files were used to save the data regarding the macromolecule, ligand, grid size. The docking results were further analyzed using the Discovery Studio Visualizer of version 3.5, to view the various docked pose of the ligand interactions, aromaticity, hydrogen bonds, charges, ionisability, and hydrophobicity. The runs were repeated to get various docked structures and minimum Root Mean Square Deviations. The strong hydrogen bonding between the ligand the receptor is evaluated. The least binding energy shows that the interactions are instantaneous, rigid and constant.

RESULTS AND DISCUSSION:

Zone of Inhibition of quinoline-8-ol, quinol and quinhydrone

The antibacterial and antifungal activity of organic compounds dissolved in Dimethyl Sulphoxide $(CH_3)_2SO$ extract on various species is shown in the table1. It is clear from the data that all of the fungus and bacteria are efficient against the antibiotic Gentamicin. The activity is measured by the diameter of a reduce zone that forms around each well, measuring the degree of inhibition. The table 1 data show that the degree of inhibition varies based on the species. The inhibitory zone diameter produced in DMSO extract was determined to be less than, higher than, or equivalent to that of conventional antibiotics against each species.

	(CH ₃) ₂ SO Extract 100 μ l added and Zone of inhibition (mm/ml)								
Quinoline-8-ol	Microorganisms	25 µl	50 µl	75 µl	100 µl	Control			
						Gentamicin			
						antibiotic disc			
	Streptococcus	36	38	40	43	20			
	Micrococcus	34	36	38	42	20			
	E.coli	30	34	36	38	18			
	Vibrio cholerae	30	34	36	38	18			
	Candida albicans	34	36	38	40	20			
	A.flavus	34	36	38	40	20			
	Trichophyton	36	38	40	42	20			
	Fusarium	36	38	40	42	20			
Quinol	Bacillus subtilis	25	30	34	38	20			
	Enterococcus faecalis	28	34	36	40	18			
	E.coli	25	30	34	38	18			
	Salmonella typhi	20	22	24	26	20			
	Candida albicans	30	34	37	40	20			

Table-1: Inhibition zone of the organic compounds

	A.niger	30	34	36	40	20
	Mucor	30	35	38	42	20
	Trichoderma	20	22	25	28	20
Quinhydrone	Staphylococcus aureus	26	26	36	40	20
	Streptococcus	22	25	28	32	20
	Pseudomonas aeruginosa	28	32	36	38	20
	Klebsiella pneumoniae	22	25	29	32	23
	Candida albicans	20	24	28	30	22
	A.flavus	23	26	30	34	20
	Trichophyton	24	28	32	36	20
	Fusarium	22	26	30	32	20

The compound quinoline-8-ol or 8-hydroxyquinoline showed lethal zone for the species Streptococcus (43 mmml), Trichophyton (42 mm/ml) at higher concentrations. For the species, Bacillus subtilis (38 mm/ml), E.coli (38 mm/ml), Salmonella typhi (26 mm/ml), Candida albicans (40 mm/ml), A.niger(40 mm/ml), Mucor (42 mm/ml), Trichoderma (28 mm/ml) was observed for the compound quinol. The bacteria Staphylococcus aureus (40 mm/ml), Klebsiella pneumoniae (32 mm/ml), A.flavus (34 mm/ml), Trichophyton (36 mm/ml), Fusarium (32 mm/ml) showed activity against the compound quinhydrone. The external membrane of cell walls of gram-negative bacteria consist of lipoprotein lipid bilaver, and

The external membrane of cell walls of gram-negative bacteria consist of lipoprotein, lipid bilayer, and lipopolysaccharide. The cell membrane is comparable to the lipid (bilayer).

Furthermore, gram-negative bacteria have periplasmic space, which contains a range of enzymes such as protease, nuclease, and detoxifying enzymes, all of which are important in bacterial antidrug resistance. The chemical compounds were more active to extinguish the progress of the microorganisms and hence proved to be more resistant.



Fig-2: Inhibition of quinoline-8-ol



Fig-3: Inhibition of quinol



Fig-4: Inhibition of quinydrone

Molecular Docking

The docking result of quinoline-8-ol depicts the interactions between the aminoacid chain GLY319, GLN347, TYR326, PRO350, HIS343, GLU342, SER346 (Figure 5). The hydrogen bond interaction is between GLY338, -C-H bond interactions in ILE268, GLY319, conventional hydrogen bond interactions in LEU339, attractive charge between ARG283, alkyl interactions in LYS416. The minimum binding energy is -6.35 Kcal/mol, torsional energy and internal energy is 0.3 and -0.32Kcal/mol. The docking results of quinoline-8-ol with 7BRA macromolecule represent the interactions between the amino acid chain VAL447, ALA58, LEU448, PRO441. The hydrogen bond between PRO441, LEU339, (Figure 6) the binding energy is -7.53 Kcal/mol.



Fig-5 : The wire structure of interactions of ligand with 7BRA macromolecule



Fig-6 : The 3D and 2D pictures of interactions of ligand with 7BRA macromolecule



Fig-7: Two Hydrogen atom bonds for the 5AF1 macro molecule

The ligand quinol bind with the macromolecule 5AF1 exhibits two hydrogen atoms in bonds through the residue HIS57, LEU61, SER60 (Figure 7). The binding energy is -5.17 Kcal/mol, intermolecular energy is - 5.77 Kcal/mol, torsional energy 0.6 Kcal/mol respectively. The protein 7BRA exhibits hydrogen bond contact with GLN347, SER345 residue, binding energy is -6.34 Kcal/mol, intermolecular and internal energy is -6.94 Kcal/mol, 0.41 Kcal/mol, torsional energy is 0.41 respectively.

The quinhydrone ligand bind with the 5AF1 macro molecule and exhibits pi donor hydrogen bond through HIS220, SER60, conventional hydrogen bond with LEW59, LEU61, LYS55, HIS57, SER50, pi alkyl interaction with HIS220, HIS57 as shown in the figure 8. The same ligand has the bonded with the residue with energy -4.87 Kcal/mole, intermolecular energy -5.46 Kcal/mol and torsional energy 0.6 Kcal/mol.



Fig-8: The Quinhydrone ligand interaction with 5AF1 macromolecule

CONCLUSION

The current investigation provides a basis for the treatment of pathogenic microorganisms using quinol, quinoline-8-ol and quinhydrone. They hydroxyl groups, hetero cyclic nitrogen atom imparts more potential towards Gram-positive, Gram-negative bacteria and few fungi. The computer assisted molecular docking predicts the ligand interactions, the hydrogen bond interactions at various poses of macromolecule and the natural activities of quinoline compounds are efficiently determined.

ACKNOWLEDGEMENT:

The authors are grateful to the President of Nehru Memorial College and all the people for supporting to carry the work in a successful manner. The authors are also grateful for the free software providers of AUTO DOCK, Discovery Studio Visualizer and PyMOL.

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