

Prediction of ADME and Toxicity of Anti-Fungal drugs by InSilico methods

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ABSTRACT

The research paper is about the Computer Aided Drug Design is a modern computational technique used in the drug discovery process to identify and develop a potential lead. The recent introduction of a new generation of anti-fungal drugs promises to alter significantly therapy for both systematic and superficial mycoses. The article present in depth view of the Azoles (Ketoconazole, Fluconazole, Clotrimazole), Polyenes (nystatin), Heterocyclic benzofuran (Griseofulvin). At the conclusion of the learning activity, discuss the selected approaches for the prediction of ADME/TOX properties of the drugs by In silico methods.

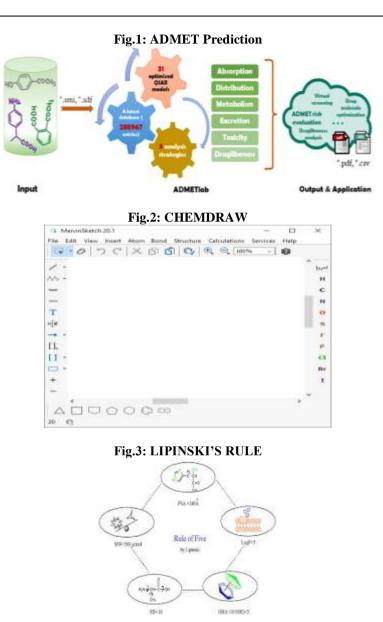
KEYWORDS: Anti-fungal, CADD, ADME/ TOX prediction, Target prediction.

I. INTRODUCTION (1-5)

Computer aided drug design is a computer technology that design the product. Main efforts to increasing efficacy of development of drugs are directed to stage of discovery and optimization of leads. In silico method can help in identifying grid targets via bio informative tools. They are also used to analyse the target structure for possible binding sites, generate candidate molecule, dock these molecules with target according to binding affinities of structure-based drug design and ligand based drug design.Toxicity is the measure of any undesirable or unwanted effect of chemicals. Specific types of these adverse effects are called toxicity end points, such as carcinogenicity, mutagenicity, cytotoxicity, and can be quantitative (e.g., LD 50; toxicity test aimed to identify harmful effects caused by substances on human, animals, or the environment through single dose or multiple dose.

ADME properties of adsorption, distribution, metabolism, excretion. Animal models have been used for a long time for toxicity testing. However, in-vitro toxicity tests become plausible due to the advance in high throughput screening. In silico toxicology is one type of toxicity assessment computational that uses resources to organize, analyse, models, stimulate, visualize, or predict toxicity of chemicals. It is intertwined with in silico pharmacology which is information from computational tool to analyse beneficial or adverse effects of drugs therapeutic for purposes.Computational methods aim to complement in vitro or in vivo toxicity test to potentially minimize the need for animal testing, reduce the cost and time of toxicity tests and improve toxicity prediction and safety assessment.Marvin sketch features an extensive set to enable the fast and accurate drawing of chemical compounds, reactions, Markush structures and query molecules (Fig 1-3).





II. METERIALS AND METHODS^(6,7) I).ADME Prediction

Drug development involves assessment of absorption, distribution, metabolism and excretion (ADME) increasingly earlier in the discovery process, at a stage when considered compounds are numerous but access to the physical samples is limited. Swiss ADME web tool that gives free access to a pool of fast yet robust predictive models for physicochemical properties, pharmacokinetics, drug-likeness and medicinal chemistry friendliness, among which in-house proficient methods such as the BOILED-Egg, iLOGP and Bioavailability Radar. The prediction results for the acute toxicity and toxicity targets are generated instantly. The result page will show the predicted median lethal dose (LD_{50}) in mg/kg weight, toxicity class, and prediction accuracy as well as average similarity alongwith three most similar toxic compounds from the dataset with the known rodent oral toxicity value. A novelty of the ProTox-II webserver is that the prediction scheme is classified into different levels of toxicity such oral toxicity, organ toxicity (hepatotoxicity), toxicological endpoints (such as mutagenicity, carcinogenecity, cytotoxicity and immunotoxicity) and toxicity targets thereby providing insights into the possible molecular mechanism behind such toxic response.

II). Toxicity Prediction

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III. RESULT

I). ADMEStudies

The ADMES tudies proven that Ny statin could not crosstheBBB(Bloodbrainbarrier)(Table.1)andproveditas an inhibitorofcytochromeP450CYP3A4substrate. It is notfollowed the lipinskisruleoffive.

Table.1:ADMEPrediction							
	NYSTATIN	GRESIOFULVIN	KETOCONA ZOLE	FLUCONAZ OLE	CLOTRIMAZ OLE		
TPSA	319.61A2	71.06A2	69.06A2	81.65A	17.82A		
LOGPo/w (iLOGP)	4.30	2.95	3.96	0.41	3.07		
LOGPo/w (XLOGP3)	-0.20	2.18	4.34	0.35	5.41		
LOGPo/w (WLOGP)	0.94	2.81	3.34	1.47	5.38		
LOGPo/w(M LOGP)	-1.67	0.71	2.47	1.47	4.38		
LOG P o/w(SILICO S-IT)	-4.26	3.39	3.69	0.71	4.98		
LOGS(ESO L)	-5.26	-3.39	-5.69	-2.17	-5.80		
LOGS(Ali)	-6.06	-3.31	-5.51	-1.63	-5.54		
LOG S(SILICOS)- IT	2.54	-4.71	-7.20	-3.54	-8.59		
GIABSORP TION	LOW	HIGH	HIGH	HIGH	HIGH		
BBBPERME ANT	NO	YES	YES	NO	YES		
P- GPSUBSTR ATE	YES	NO	NO	NO	YES		
CYP1A2INH IBITOR	NO	YES	NO	NO	YES		
CYP2CI9IN HIBITOR	NO	NO	YES	YES	YES		
CYP2C9INH IBITOR	NO	YES	YES	NO	YES		
CYP2D6INH IBITOR	NO	NO	YES	NO	YES		

II). Toxicitystudies

Thetoxicity studies revealed that the drug hastoxicity of immunotoxicity with active0.99 probability of lethaldose100 mg/kg (Table 2-7).

S.NO	DRUG	TARG	LD ₅₀	PREDICTED	PREDICTI	PROBABLITY
		ЕТ		ACCCURACY	ON	
1.	Nystatin		100mg/kg	72.9%	Inactive	0.97
2.	Clotrimazole		708mg/kg	100%	Inactive	0.67
3.	Fluconazole		1271mg/kg	100%	Active	0.84

Table 2. Han atotoxisity Dradiction Table

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4.	Ketoconazole	Hepatot	166mg/kg	100%	Active	0.76
5.	Griseofulvin	oxicity	10000mg/kg	100%	Active	0.77

Table.3: Carcinogenicity Prediction Table							
S.NO	DRUG	TARG	LD ₅₀	PREDICTED	PREDICTION	PROBAB	
		ET		ACCCURACY		LITY	
1.	Nystatin		100mg/kg	72.9%	Inactive	0.73	
2.	Clotrimazole		708mg/kg	100%	Inactive	0.53	
3.	Fluconazole		1271mg/kg	100%	Inactive	0.62	
4.	Ketoconazole	Carcin	166mg/kg	100%	Inactive	0.51	
5.	Griseofulvin	ogenici	10000mg/kg	100%	Active	0.76	
		ty					

T-11. 2 igity Prodiction Tabl

Table.4: Immunogenicity Prediction Table

S.N	DRUG	TARGET	LD ₅₀	PREDICTED	PREDICTIO	PROBA
0				ACCCURAC	Ν	BLITY
				Y		
1.	Nystatin		100mg/kg	72.9%	Active	0.99
2.	Clotrimazole	Immunotoxicit	708mg/kg	100%	Inactive	0.99
3.	Fluconazole	у	1271mg/kg	100%	Inactive	0.83
4.	Ketoconazol		166mg/kg	100%	Active	0.98
	e					
5.	Griseofulvin		10000mg/k	100%	Active	0.85
			g			

Table.5: Mutagenicity Prediction Table

S.NO	DRUG	TA RG ET	LD ₅₀	PREDICTED ACCCURACY	PREDICTION	PROBAB LITY
1.	Nystatin		100mg/kg	72.9%	Inactive	0.89
2.	Clotrimazole		708mg/kg	100%	Inactive	0.65
3.	Fluconazole	Mut	1271mg/kg	100%	Inactive	0.52
4.	Ketoconazole	agen	166mg/kg	100%	Inactive	0.69
5.	Griseofulvin	icity	10000mg/kg	100%	Inactive	0.87

Table.6: Cytotoxicity Prediction Table

S.NO	DRUG	TARGET	LD_{50}	PREDICTED	PREDICTION	PROBABLITY		
			50	ACCCURACY				
1.	Nystatin		100mg/kg	72.9%	Inactive	0.83		
2.	Clotrimazole		708mg/kg	100%	Inactive	0.87		
3.	Fluconazole	Cytotoxicity	1271mg/kg	100%	Inactive	0.76		
4.	Ketoconazole		166mg/kg	100%	Inactive	0.69		
5.	Griseofulvin		10000mg/kg	100%	Inactive	0.58		

Table.7: Toxicity Prediction Table

G NO								
S.NO	TARGET	DRUG	LD_{50}	PREDICTION	PROBABLITY			
1.	Hepatotoxicity			Inactive	0.97			
2.	Carcinogenicity			Inactive	0.73			
3.	Immunotoxicity	NYSTATIN	100mg/kg	Active	0.99			
4.	Mutagenecity			Inactive	0.89			
5.	Cytotoxicity			Inactive	0.83			



Toxicity prediction of the compounds Nystatin, Griseofulvin, Ketoconazole Fluconazole, Clotrimazolewere predicted by using PRO TOX II. The toxicity was compared by LD50 values. The lowest compared valueindicates the highest toxicity compound. The highest toxicity of the compared

compound is NYSTATIN. In theprediction nystatin with toxicity of immunotoxicity with active toxicity of probability 0.99. The target predictionwhichofnystatin with thekinaseenzymewiththe46.7 percentage.

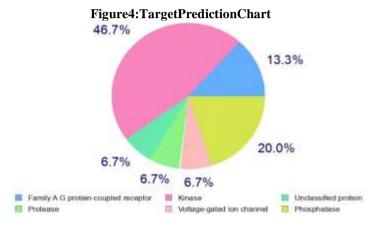


Table8:TargetPredictionTable

			i i culcuoli i ubic		
TARGET	Commonname	UniprotID	ChEMBLID	TargetClass	Probability*
Alpha-1aadrenergic	ADRA1A	P35348	CHEMBL229	Family A	0.0642387798076
receptor				Gprotein	
(byhomology)				coupledreceptor	
Vascularendothelial	KDR	P35968	CHEMBL279	Kinase	0.0642387798076
growthfactorreceptor2					
Proteinkinase Cdelta	PRKCD	Q05655	CHEMBL2996	Kinase	0.0642387798076
Proteinkinase Calpha	PRKCA	P17252	CHEMBL299	Kinase	0.0642387798076
Motilinreceptor	MLNR	O43193	CHEMBL2203	Family A	0.0642387798076
				Gprotein	
				coupledreceptor	

IV. DISCUSSION⁽⁸⁻¹¹⁾

Pharmacokineticsisthestudyofadrug'sabsor ption,distribution,metabolismandexcretionovertime .Topredictpharmaceuticalpartitioningbetweentheblo odandthebrain,thelogBBvalueis

employed.Compoundsthatarelipophilicaredispersed through the blood-brain barrier (BBB). Highlipophilic substances flow through the BBB due

todiffusion, whereas low lipophilic molecules pass thro ughduetospecificcarriers.Inordertobesuccessful,CN Stherapeuticdrugsmustbeabletopenetrate the BBB. Compounds with a log BB valuemore than 0.3 have ahigh absorption to the CNS, those with a log BB value between 0.3 and 1.0 have amediumabsorptiontotheCNS, and those with a log BB valueless than -1.0have alow absorptiontotheCNS.Humanintestinalabsorption is

the process by which drugs are absorbed from the into the bloodstream (HIA). gut Compounds with absorption rates of 0-20percentarepoorlyabsorbed, those with absorption rates of 20-70 percentaremoderatelyabsorbed, and those with absorp ratesof70-100percentarewelltion absorbed.Proteinbindinghasanimpactonadrug'seffec tiveness. Drugs bind to albumin and other plasmaproteins. Medicines' half-lives are influenced by theirinteractionswithplasmaproteins. Amedication's plasmaproteinbindingshouldbeminimisedfordiffusi onanddistributionacrossthebody.Drugprotein complexes are too large to pass through theplasmamembrane. The difference in pharmaceutical binding to plasmaproteins might be anything from 11 and 82 percent. The drug's

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efficacy is influenced by plasma proteinbindingoverathresholdof80-85percent.Theoctanol-

waterpartitioncoefficient(logP)andmolecular

weight are thought to have an impact on theexcretion process that eliminates the molecule from human body. The log P scale is used to determinelipophilicity. In the membrane permeability equation, it is a critical variable. The greater the lipophilicity of a chemical, the slower its metabolism and absorption. It's also more prone to bind to undesired hydrophobicmacromolecules, perhaps causing toxicit y.Thehydrophobicity of medication increases, making it lesssolubleinthestomachandmoresolubleinfatglobul es.The Cytochrome P450 enzymesare incharge of drug metabolism in the liver. The enzymesCYP3A4,CYP2D6,CYP2C9,andCYP2C19 help

withdrugmetabolism.Eachdrughasadifferentinteract ion with CY450. Drugs can either inhibit orincrease the cytochrome P450 enzymes. Drugs may

ormaynotinhibitorstimulateallkindsofCYP450enzy mes. One CYP450 is adequate for metabolism ToxicityandPharmacodynamicStudies.

Anti- fungal agents are the agents used to treat fungal infections by the microbes. The compounds of Nystatin, Griseofulvin, Fluconazole, Ketoconazole, Clotrimazole. It works on the mechanism of inhibition of cell wall synthesis, depletion of ergosterols, inhibit DNA transcription, cell death by depolarization.

The toxicity is the study of the drug toxicity by which produce by the drug, it includes to the drug which are more toxic effects with they are compared with lethal dose. The low value of Lethal Dose 50 value indicates the high toxicity compound.In which we compared, Nystatin, Ketoconazole, Griseofulvin, Fluconazole, Clotrimazole that the nystatin is high toxicity compound compared by the Lethal Dose 50 value of 100 mg/kg, The nystatin which has Immunotoxicity with probability of 0.99% with active toxicity. The immunotoxicity caused by the nystatin is predicted by the target prediction chart given in the fig.4, the Family A G Protein coupled receptor with the 46.7%.

V. CONCLUSION

In this study, we designed 5 derivatives of 5 drugs and evaluate their ADME and toxicity study of antifungal drugs through Insilico studies. The comparison study showed Nystatin has no effective pharmacokinetics, not cross the BBB decreased absorption, not obey the Lipinski's rule and has high toxicity of immunotoxicity. According to this study, Nystatindoes not gives to the person with low immuneresponse accor ding to the Insilicoprediction.

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