Original Article

Structure Based Computational Exploration of *Beilschmiedia* Compounds with Selected Targets against Multidrug-Resistant *Mycobacterium tuberculosis*

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ABSTRACT

Aim/Background: Tuberculosis is a serious health issue across the world. Various bioactive molecules show the affects against Multidrug-resistant tuberculosis (MDR-TB). There are various standard drugs developed against *Mycobacterium* for its treatment. But, the pathogen of tuberculosis is developing resistance towards the various standard. The present study was aimed to determine the effect of *Beilschmiedia* phytoconstituents against different protein targets of *Mycobacterium tuberculosis* (MTB). **Materials and Methods:** Proteins and ligands were retrieved from RCSB PDB and Knapsack 3D database. Data of active site of proteins were taken from Protein Data Bank Japan (PDBj) (https://pdbj.org/) and computed atlas of surface topography of proteins (CASTp) (http://sts.bioe.uic.edu/castp/index.html). Molecular docking was performed by AutoDock tool 4.0. **Results:** The Beilschmie flavonoid A and Beilschmie flavonoid B, Beilschmiedic Acid A and B were virtually screened for their free binding energy against various protein targets of MTB. Flavonoids showed binding with target proteins and exhibited well promising inhibition of MTB target proteins. There were some specific targets to which particular ligand binds strongly. **Conclusion:** We found that compounds of *Beilschmiedia* act in fatty acid degradation pathway at their various steps.

Key words: *Mycobacterium tuberculosis*, Multi-Drug Resistant Tuberculosis, *Beilschmiedia zenkeri, Beilschmiedia anacardioides*, Molecular Docking.

INTRODUCTION

Tuberculosis (TB) is a serious health issue across the world. It is an infectious disease caused by the bacillus *Mycobacterium tuberculosis* (MTB). Disease called "Consumption" in past because the way it would consume from within anyone who became infected.[1] About 64% TB patients are from countries like India, Indonesia, China, Philippines, Pakistan, Nigeria and South Africa and India tops the highest number of TB cases followed by the other six countries respectively.[2] MTB that causes tuberculosis develops resistance to antimicrobial drugs used to cure disease this condition is known as drug-resistance TB.[3] There are two main types of drug-resistant TB i.e., Multidrug-resistant TB (MDR-TB) and Extensively drug-resistant TB (XDR-TB). Multidrug-resistant TB (MDR-TB) is a type of TB that does not respond to at least isoniazid and rifampicin, which is the most powerful anti-TB drugs.[4] Drug resistance may be because of inadequate treatment or direct transmission of drug-resistant bacillus from one person to another.[5] The major health problem threatens the progress made in TB control worldwide. There is an urgent need to develop novel anti-tuberculosis agents, adjunct treatments and to improve immunity. In addition, most of the anti-TB drugs

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currently target metabolic reactions and proteins that are critical for the proliferation of *M. tuberculosis*.[6]

In recent years, there has been an increasing interest in natural product based medicines from plant origin.[7] These plants are an important source of bioactive secondary metabolites, which have enormous therapeutic potential.[8] Therefore, to overcome the serious issue of MDR-TB, plant metabolites can used. In this context, we will study the plant metabolites of two different species of *Beilschmiedia* i.e., *Beilschmiedia anacardioides* and *Beilschmiedia zenkeri*. *Beilschmiedia anacardioides* and *Beilschmiedia zenkeri* is an evergreen tree, distributed throughout Central Africa. The fruits of *Beilschmiedia zenkeri* are appetite stimulants.[9] *Beilschmiedia anacardioides* stem bark cure uterine tumours, rubella, female genital infections and rheumatisms.[10] The stem bark of *B. zenkeri* consists of four new methoxylated flavonoid derivatives, (2S, 4R)-5, 6, 7-trimethoxyflavan-4-ol, (2S, 4R)-4, 5, 6, 7-tetramethoxyflavan, beilschmie flavonoid A and beilschmie flavonoid B and with seven known compounds. They showed antibacterial effect against three strains of bacteria, *Pseudomonas agarici*, *Bacillus subtilis* and *Streptococcus minor* and for their antiplasmodial activity against *Plasmodium falciparum*, *chloroquine-resistant strain W2*.[11] Molecular docking is a computer simulation procedure to predict the conformation of a receptor-ligand complex, where the receptor is usually a protein or a nucleic acid molecule (DNA or RNA) and the ligand is either a small molecule or another protein. Objective of current study is to find the potential protein targets of MTB form docking.

MATERIALS AND METHODS

Retrieval of 3D Structure of Protein and Ligands

Molecular docking was performed using AutoDock 4.0 software.[12] Different target sites were selected by getting locus information of organism from target databases; 27 different targeted proteins were selected for docking Table 1. Their 3D structure were retrieved from RCSB PDB in pdb (PDB (TEXT)) file format.[13] Active sites of proteins were identified from Protein Data Bank Japan (PDBj) (https://pdbj.org/)[14] and Computed Atlas of Surface Topography of proteins (CASTp) (http://sts.bioe.uic.edu/castp/index.html).[15] The ligands retrieved from KNApSAcK-3D (http://knapsack3d.sakura.ne.jp/). The Ligand 3-D structures saved in 'mol' file. Files are converted in.pdb format, using Open babel Software version 2.3.2a[16] Table 2, Figure 1.

Protein Ligand Interaction with AutoDock 4.0

The crystal structure of proteins retrieved from the Protein Data Bank. All polar hydrogen atoms are added and partial charges are placed. Default values of atomic solvation parameters were used throughout the calculations. The grid maps of the protein calculated using the Auto Grid program. Docking simulations done with AutoDock 4.0 using Lamarckian genetic algorithm. The standard docking procedure used for rigid protein and flexible ligand whose torsion angles identified. A grid of 100, 100 and 100 points in x, y and z directions was built centered on the catalytic site of the protein. The default settings were used for all other parameters. All calculations were carried out on PC based machines running UBUNTU as operating systems. The results were analyzed using AutoDock Tools.

RESULTS

Docking of MTB targets with beilschmie flavonoid A

In silico molecular docking studies was performed using MTB protein targets with beilschmie flavonoid A (*B. zenkeri*). 13 target proteins shows interaction with beilschmie flavonoid A. All interactions with their binding energy are shown in Table 3. The docked ligands had binding energy ranging between -0.45 Kcal/mol to -2.77 Kcal/mol. The protein Zinc-substituted rubredoxin B exhibit excellent binding against beilschmie flavonoid A with binding energy -2.77 Kcal/mol Figure 2a.

Docking of MTB Targets with beilschmie flavonoid B

Only 13 target proteins of MTB were docked with the ligand beilschmie flavonoid B. All the interactions with their binding energy are showed in Table 4. The results showed that all the docked ligands had binding energy ranging between -0.01 Kcal/mol to -3.50 Kcal/mol. The protein enoyl-CoA hydratase echA6 exhibit best binding against beilschmie flavonoid B with binding energy -3.50 Kcal/mol Figure 2b.

Docking of MTB Targets with Beilschmiedic acid A

Beilschmiedic acid A and beilschmiedic acid B was obtained from stem bark of *B. anacardioides* plant. 23 target proteins of MTB interact with beilschmiedic acid. All the interactions with binding energy are shown in Table 5. The results showed that all the docked ligands had binding energy ranging between -1.71 Kcal/mol

Table 1: Selected target proteins of MTB for docking and their function.

Protein Name (PDB-ID)	Classification	Function
Antigen 85C **(1dqz)**	Immune system	Facilitates attachment of MTB to murine alveolar macrophages (AMs). Maintain the integrity of the cell wall.
Cytochrome P450 14 alpha-sterol demethylase (CYP51) **(1e9x)**	oxidoreductase	Essential enzyme in sterol biosynthesis in eukaryotes
Crystal structure of 3-bromopyruvate modified isocitrate lyase (icl) **(1f8m)**	Lyase	Catalyzes reversible formation of succinate and glyoxylate a key step of the glyoxylate cycle, which replenish the tricarboxylic acid cycle during growth on fatty acid substrates.
Mycolic acid cyclopropane synthase CmaA2 **(1kpi)**	Transferase	Major components of the cell wall.
Mycolic acid cyclopropane synthase PcaA **(1l1e)**	Transferase	Important for pathogenesis and PcaA catalyze cyclopropanation at the proximal position of the meromycolate chain.
Peptidyl-prolyl cis-trans isomerase A, PpiA **(1w74)**	Isomerase	Important for protein folding and also participate in signalling, cell surface recognition, chaperoning and heat-shock response.
Shikimate kinase **(1zyu)**	Signaling protein transferase	Catalyzes the reaction of phosphoryl transfer from ATP to shikimic acid (SA).
Transcriptional regulatory protein EmbR **(2ff4)**	Transcription	Positively regulates the transcription of the embCAB operon. Exhibits ATPase and GTPase activities.
Hydroxymycolate synthase MmaA4 **(2fk7)**	Transferase	Catalyze introduction of methyl branch together with an adjacent hydroxyl group essential for the formation of both keto- and methoxymycolates.
Zinc-substituted rubredoxin B **(2kn9)**	Electron transport	Play as electron carrier in ω-Hydroxylation of fatty acids.
Cell division protein FtsZ **(2q1x)**	Cell cycle signaling protein	Essential cell division protein that forms a contractile ring structure (Z ring) at the future cell division site and The regulation of the ring assembly controls the timing and the location of cell division.
CFP10 (Culture filtrate protein)-ESAT6 (Early secreted antigen target) **(3fav)**	Viral protein	Acts as a strong host (human) T-cell antigen and Involved in translocation of bacteria from the host (human) phagolysosome to the host cytoplasm.
DNA gyrase reaction core **(3ig0)**	Isomerase	Involved in the regulation of DNA topology.
DNA gyrase reaction core **(3m4i)**	Isomerase	Involved in the regulation of DNA topology.
Serine/threonine-protein kinase PknB **(3ori)**	Transferase	PknB, plays a key role in regulating growth and division.
Phosphothreonine-dependent FHA domain **(3po8)**	Peptide binding protein	FHA domains are well established as phospho-dependent binding modules mediating signal transduction in Ser/Thr kinase signaling networks in both eukaryotic and prokaryotic species.
3-hydroxyacyl-thioester dehydratase HtdX **(3wew)**	Lyase	3-hydroxyacyl-[acyl-carrier-protein] dehydratase activity, 3-hydroxyacyl-CoA dehydratase activity and fatty acid synthase activity.
Lipoamide channel-binding sulfonamides **(4m52)**	Oxidoreductase	It is a metabolic and detoxifying enzyme.
Ribosomal protein S1 **(4nni)**	Ribosomal protein	It plays a role in trans-translation; binds tmRNA (the product of the ssrA gene).
3-hydroxyacyl-thioester dehydratase HtdX **(4oob)**	Oxidoreductase	It is involved in synthesis of fatty acid synthase (FAS II), which is involved in synthesis of mycolic acid present in cell wall.
S/T (Serine – Threonine) protein kinase PknG **(4y12)**	Transferase	A soluble enzyme that controls central metabolism in Actinobacteria and has been linked to MTB infectivity.
Lipoarabinomannan carrier protein LprG **(4zra)**	Lipid binding protein	Regulate Triacylglyceride Levels, growth rate and virulence in *Mycobacterium tuberculosis*.
enoyl-CoA hydratase echA6 **(5duf)**	Lipid binding protein	It is essential for β-oxidation in fatty acid metabolism.
Serine/threonine-protein kinase PknI **(5m06)**	Signaling protein	It Plays an important role in slowing down the growth of mycobacteria within the infected host.

Table 1: Con'		
HTH-type transcriptional regulator EthR **(5mxv)**	Transcription	Involved in the repression of the monooxygenase EthA which is responsible of the formation of the active metabolite of ethionamide (ETH).
Beta›MTBSI of MTB RNA polymerase **(5uh7)**	Transcription	DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as substrates.
PE family protein PE8 **(5xfs)**	Protein transport	It is a family of proteins, which is unique to mycobacteria and essential for infection, antigenic variation and host-pathogen interactions.

Table 2: Selected ligands for docking with their representative source and molecular formula.

Name of Metabolite	Source	Molecular formula
Beilschmieflavonoid A	*B. zenkeri*	$C_{36}H_{38}O_9$
Beilschmieflavonoid B	*B. zenkeri*	$C_{35}H_{36}O_9$
Beilschmiedic acid A	*B. anacardiolides*	$C_{22}H_{32}O_3$
Beilschmiedic acid B	*B. anacardiolides*	$C_{22}H_{32}O_4$

to -5.12 Kcal/mol. The protein 3-hydroxyacyl-thioester dehydratase HtdX exhibit good binding against beilschmiedic acid A with binding energy -5.12 Kcal/mol Figure 2c.

Docking of MTB Targets with beilschmiedic acid B

17 target proteins of MTB were docked with the ligand beilschmiedic acid B. All interactions with their binding energy are shown in Table 6. The binding energy ranging between -1.33 Kcal/mol to -6.35 Kcal/mol. The protein 3-hydroxyacyl-thioester dehydratase HtdX exhibited highest binding against beilschmiedic acid B with binding energy -6.35 Kcal/mol Figure 2d.

DISCUSSION

In silico screening methods are extensively used to reduce cost and time of drug discovery. It has been clearly demonstrated that *in-silico* approach utilized in this study is successful for finding novel natural drugs like 1. Beilschmie flavonoid A, 2. Beilschmie flavonoid B, 3. Beilschmiedic Acid A and 4. Beilschmiedic Acid B which according to literature are present in stem bark of *Beilschmiedia zenkeri* (1 and 2) and *Beilschmiedia anacardioides*. These compounds have showed efficient binding with different protein targets of *Mycobacterium tuberculosis*.

Chen *et al*.[17] investigated the *in vitro* antitubercular effects of compounds isolated from *Beilschmiedia* plants. In another study *Beilschmiedia obscura* is reported to fight

Table 3: Docking results of Beilschmieflavonoid A with different Mtb drug target proteins.

Protein Name	PDB-ID	Binding Energy (Kcal/mol)
Antigen 85C	1dqz	-0.32
Cytochrome P450 14 alpha-sterol demethylase (CYP51)	1e9x	-
Crystal structure of 3-bromopyruvate modified isocitrate lyase (ICL)	1f8m	-
Mycolic acid cyclopropane synthase CmaA2	1kpi	-1.35
Mycolic acid cyclopropane synthase PcaA	1l1e	-1.29
Peptidyl-prolyl cis-trans isomerase A, PpiA	1w74	-
Shikimate kinase	1zyu	-2.54
Transcriptional regulatory protein EmbR	2ff4	-2.32
Hydroxymycolate synthase MmaA4	2fk7	-
Zinc-substituted rubredoxin B	**2kn9**	**-2.77**
Cell division protein FtsZ	2q1x	-0.45
CFP10 (Culture filtrate protein)-ESAT6 (Early secreted antigen target)	3fav	-
DNA gyrase reaction core	3ig0	-2.75
DNA gyrase reaction core	3m4i	-
Serine/threonine-protein kinase PknB	3ori	-
Phosphothreonine-dependent FHA domain	3po8	-
3-hydroxyacyl-thioester dehydratase HtdX	3wew	-
Lipoamide channel-binding sulfonamides	4m52	-
Ribosomal protein S1	4nni	-1.40
3-hydroxyacyl-thioester dehydratase HtdX	4oob	-2.69
S/T (Serine – Threonine) protein kinase PknG	4y12	-1.56
Lipoarabinomannan carrier protein LprG	4zra	-2.49
enoyl-CoA hydratase echA6	5duf	-
Serine/threonine-protein kinase PknI	5m06	-
HTH-type transcriptional regulator EthR	5mxv	-
Beta'MtbSI of Mtb RNA polymerase	5uh7	-1.42
PE family protein PE8	5xfs	-

Table 4: Docking results of Beilschmieflavonoid B with different Mtb drug target proteins.

Protein Name	PDB-ID	Binding Energy (kcal/mol)
Antigen 85C	1dqz	-3.35
Cytochrome P450 14 alpha-sterol demethylase (CYP51)	1e9x	-
Crystal structure of 3-bromopyruvate modified isocitrate lyase (ICL)	1f8m	-
Mycolic acid cyclopropane synthase PcaA	1kpi	-3.01
Mycolic Acid Cyclopropane SynthasePcaA	1l1e	-1.03
Peptidyl-prolyl cis-trans isomerase A, PpiA	1w74	-
Shikimate kinase	1zyu	-1.93
Transcriptional regulatory protein EmbR	2ff4	-1.29
Hydroxymycolate synthase MmaA4	2fk7	-
Zinc-substituted rubredoxin B	2kn9	-3.09
Cell division protein FtsZ	2q1x	-
CFP10 (Culture filtrate protein)-ESAT6 (Early secreted antigen target)	3fav	-
DNA gyrase reaction core	3ig0	-2.12
DNA gyrase reaction core	3m4i	-
Serine/threonine-protein kinase PknB	3ori	-
Phosphothreonine-dependent FHA domain	3po8	-
3-hydroxyacyl-thioester dehydratase HtdX	3wew	-1.33
Lipoamide channel-binding sulfonamides	4m52	-1.24
Ribosomal protein S1	4nni	-0.01
3-hydroxyacyl-thioester dehydratase HtdX	4oob	-
S/T (Serine – Threonine) protein kinase PknG	4y12	-
Lipoarabinomannan carrier protein LprG	4zra	-
enoyl-CoA hydratase echA6	**5duf**	**-3.50**
Serine/threonine-protein kinase PknI	5m06	-2.25
HTH-type transcriptional regulator EthR	5mxv	-
Beta'MtbSI of Mtb RNA polymerase	5uh7	-0.76
PE family protein PE8	5xfs	-

Table 5: Docking results of Beilschmiedic acid A with different Mtb drug target proteins.

Protein Name	PDB-ID	Binding Energy (Kcal/mol)
ANTIGEN 85C	1dqz	-4.31
Cytochrome P450 14 alpha-sterol demethylase (CYP51)	1e9x	-2.79
Crystal structure of 3-bromopyruvate modified isocitrate lyase (icl)	1f8m	-
Mycolic acid cyclopropane synthase CmaA2	1kpi	-2.12
Mycolic Acid Cyclopropane Synthase PcaA	1l1e	-2.16
Peptidyl-prolyl cis-trans isomerase A, PpiA	1w74	-4.62
Shikimate kinase	1zyu	-2.92
Transcriptional regulatory protein EmbR	2ff4	-3.76
Hydroxymycolate synthase MmaA4	2fk7	-2.36
Zinc-substituted rubredoxin B	2kn9	-3.51
Cell division protein FtsZ	2q1x	-2.55
CFP10 (Culture filtrate protein)-ESAT6 (Early secreted antigen target)	3fav	-
DNA gyrase reaction core	3ig0	-2.84
DNA gyrase reaction core	3m4i	-3.82
Serine/threonine-protein kinase PknB	3ori	-3.12
Phosphothreonine-dependent FHA domain	3po8	-1.71
3-hydroxyacyl-thioester dehydratase HtdX	3wew	-
Lipoamide channel-binding sulfonamides	4m52	-4.03
Ribosomal protein S1	4nni	-3.0
3-hydroxyacyl-thioester dehydratase HtdX	**4oob**	**-5.12**
S/T (Serine – Threonine) protein kinase PknG	4y12	-3.49
Lipoarabinomannan carrier protein LprG	4zra	-
enoyl-CoA hydratase echA6	5duf	-4.06
Serine/threonine-protein kinase PknI	5m06	-4.52
HTH-type transcriptional regulator EthR	5mxv	-2.32
Beta'MtbSI of Mtb RNA polymerase	5uh7	-1.91
PE family protein PE8	5xfs	-1.79

against infectious diseases caused by gram-negative bacteria and MDR phenotypes.[18]

The conformations of the docked compounds of *Beilschmiedia zenkeri* and *Beilschmiedia anacardioides* fits exactly into the active site region of receptor.

To evaluate the mechanism of the compounds with their respective targeted proteins we constructed the predicted pathway for drug-target mechanism Figure 3. We found that all the compounds act in fatty acid degradation pathway at their various steps. Beilschmie flavonoid A acts on rubredoxin enzyme, which acts as electron carrier in ω-Hydroxylation of fatty acids, beilschmie flavonoid B acts on echA6 enzyme, involved in β-oxidation of fatty acid metabolism and beilschmiedic acid A and B acts on synthesis of fatty acid synthase (FAS II), which is involved in synthesis of mycolic acid present in cell

Table 6: Docking results of Beilschmiedic acid B with different Mtb drug target proteins.

Protein Name	PDB-ID	Binding Energy (kcal/mol)
Antigen 85C	1dqz	-3.34
Cytochrome P450 14 alpha-sterol demethylase (CYP51)	1e9x	-
Crystal structure of 3-bromopyruvate modified isocitrate lyase (icl)	1f8m	-2.09
Mycolic acid cyclopropane synthase CmaA2	1kpi	-3.26
Mycolic acid cyclopropane synthase PcaA	1l1e	-
Peptidyl-prolyl cis-trans isomerase A, PpiA	1w74	-2.52
Shikimate kinase	1zyu	-3.65
Transcriptional regulatory protein EmbR	2ff4	-4.38
Hydroxymycolate synthase MmaA4	2fk7	-
Zinc-substituted rubredoxin B	2kn9	-3.46
Cell division protein FtsZ	2q1x	-2.99
CFP10 (Culture filtrate protein)-ESAT6 (Early secreted antigen target)	3fav	-2.37
DNA gyrase reaction core	3ig0	-1.45
DNA gyrase reaction core	3m4i	-2.36
Serine/threonine-protein kinase PknB	3ori	-2.04
Phosphothreonine-dependent FHA domain	3po8	-
3-hydroxyacyl-thioester dehydratase HtdX	3wew	-
Lipoamide channel-binding sulfonamides	4m52	-2.6
Ribosomal protein S1	4nni	-1.33
3-hydroxyacyl-thioester dehydratase HtdX	**4oob**	**-6.35**
S/T (Serine – Threonine) protein kinase PknG	4y12	-
Lipoarabinomannan carrier protein LprG	4zra	-
enoyl-CoA hydratase echA6	5duf	-
Serine/threonine-protein kinase PknI	5m06	-4.01
HTH-type transcriptional regulator EthR	5mxv	-3.2
Beta'MtbSI of Mtb RNA polymerase	5uh7	-
PE family protein PE8	5xfs	-

wall of Mycobacterium. Finding suggest that *Beilschmiedia* species can act as multifaceted antibiotic as cell wall, provide structural integrity, permeability and pathogenicity, both structurally and biosynthetically.

This study indicates the importance of phytoconstituents of *Beilschmiedia* species i.e., *B. zenkeri and B.*

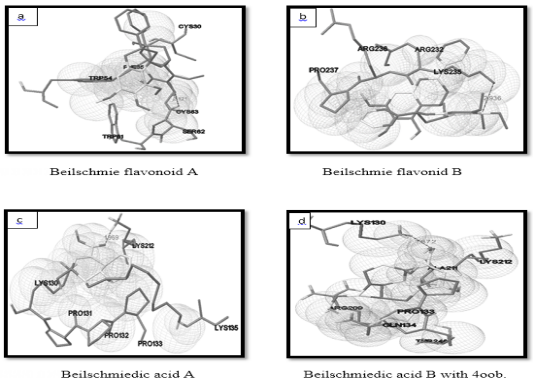

Figure 1: Structure of ligands used in docking.

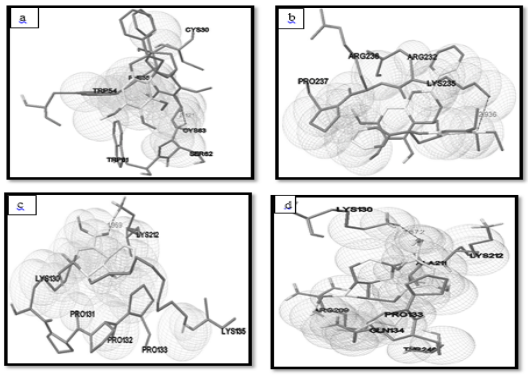

Figure 2: Docking pose of (a) Beilschmie flavonoid A with 2kn9, (b) Beilschmie flavonid B with 5duf, (c) Beilschmiedic acid A with 4oob, (d) Beilschmiedic acid B with 4oob.

anacardioides and their use as bioactive molecules. The findings suggest that in future these compounds could be developed as a lead compounds for designing of novel drugs against MDR-TB.

CONCLUSION

Structure based computational exploration have been applied to predict interaction of beilschmie flavonoid A, beilschmie flavonoid B, beilschmiedic acid A and beilschmiedic acid B with MDR-TB targets. Virtual screening strategies are time-saving, cost-effective and productive alternatives in the drug discovery process. *In silico* molecular docking studies clearly demonstrated binding activity of ligands with protein targets of *Mycobacterium tuberculosis* which warrants further studies for the development of potent inhibitors in the treatment of MDR-TB. Results clearly indicate that the phytochemicals from *Beilschmiedia* species as *Mycobacterium tuberculosis* inhibitors. Hence we conclude that secondary metabolites from *Beilschmiedia* species could be potential

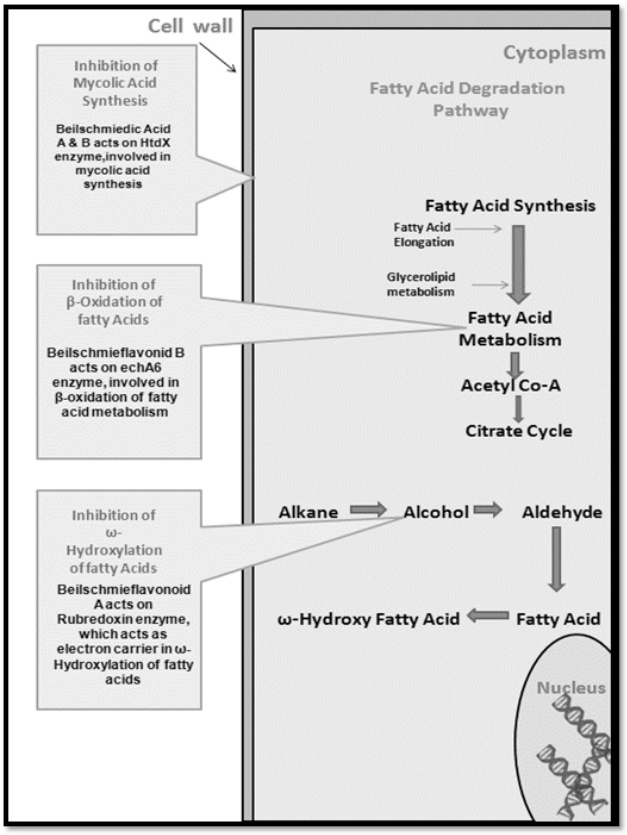

Figure 3: The predicted pathway for drug targets mechanism. Pathway showing that the Beilschmieflavonid A is inhibiting the ω-Hydroxylation of fatty acids; Beilschmieflavonid B is inhibiting β-oxidation of fatty acids Beilschmiedic Acid A and B is inhibiting mycolic acid synthesis, thus they can be used as drug for MDR-TB.

lead molecules against MDR-TB which can be further evaluated through *in vivo* studies.

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CONFLICT OF INTEREST

The authors declare no conflict of interest.

ABBREVIATIONS

CASTp: Computed Atlas of Surface Topography of Proteins; **DNA:** Deoxyribonucleic acid; **MTB:** *Mycobacterium tuberculosis*; **MDR-TB:** Multidrug-Resistant Tuberculosis; **PDBj:** Protein Data Bank Japan; **RNA:** Ribonucleic acid; **TB:** Tuberculosis; **XDR-TB:** Extensively drug-resistant TB.

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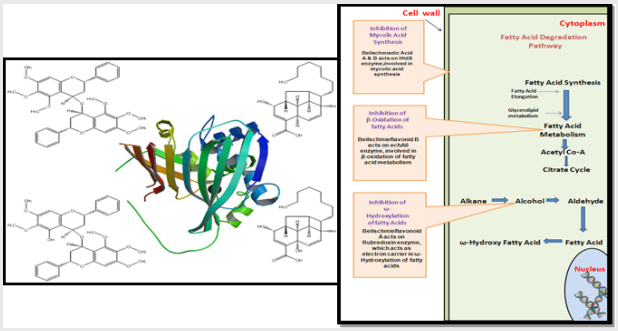
PICTORIAL ABSTRACT



SUMMARY

- There is a continuous need for the development of new drug molecules with newer targets and with an alternative mechanism of action due to increasing drug resistance of *Mycobacterium tuberculosis* to the currently used drugs. This study indicates the importance of phytoconstituents of *Beilschmiedia* species i.e., *B. zenkeri* and *B. anacardioides* and their use as bioactive molecules. The findings suggest that in future these compounds could be developed as a lead compounds for designing of novel drugs against MDR-TB.

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