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Title of the Presentation

Chaired by **Dr. Alfredo Berzal-Herranz** and **Prof. Dr. Maria Emília Sousa**





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Computational Analysis of Phosphodiesterase-5 antagonists from *Aframomum melegueta* against Erectile Dysfunction





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Abstract

Erectile dysfunction is a condition of insufficient ability of man to maintain erection for sexual performance.

Active molecules from *Aframomum melegueta* were docked against the target via maestro suite, 2017-1. The hit molecules in comparison with sildenafil were validated by MD-simulation at 100 ns with Desmond tool.

The result of this study revealed nine (9) hit molecules as potent antagonists of PDE-5 with 1,7-bis(3,4-dihyroxy-5-methoxyphenyl)heptane-3,5-diyldiacetate (-11.522 kcal/mol) having the best binding affinity comparable with standard drug (sildenafil = -11.872 Kcal/mol).

The result of the QSAR and pharmacophore models validation confirmed the hit molecules as inhibitors of the target with pIC50 range of 3.835 to 7.976 μ M and fitness score of 0.754 to 2.605 respectively.

The hit molecules obeyed Lipinski's rule of five with good pharmacokinetic profile. The stability of the hit molecule complex with PDE-5 was confirmed by MD-simulation analysis which was comparable with sildenafil-PDE-5 complex.

Overall, this study predicted phytochemicals from *A. melegueta* as inhibitors of PDE-5 for further experimentally validation for erectile dysfunction management.

Keywords: Sildenafil; Erection; Schrodinger; Phosphodiesterase-5; Inhibitors





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Introduction



Fig. 1: Signaling mechanism of erectile process with inhibitors





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Results and discussion



Fig. 2: Crystal structure of PDE-5 and Ramachandran plot of residues distribution



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Figure 3: Superimposition of sildenafil at the active site of PDE-5







ASP 764



Fig. 4: Binding affinity and Binding Energies of the hit compound

Fig. 5: presentation of extra precision binding of all hit compounds







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Fig. 5: Pharmacophore Hypothesis Generation

Fig. 7: Scatter plot from AutoQSAR modeling





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Compound Name	Fitness Score	Predicted pIC50 (µM)
Sildenafil	2.605	7.976
1,7-bis(3,4-dihydroxy-5- methoxyphenyl)heptane-3,5-diyldiacetate	1.187	5.592
1-(3,4-dihydroxy-5-methoxyphenyl)-7-(3,4- dihdroxyphenyl)heptane-3,5-diyldiacetate	0.754	3.835
Apigenin	1.908	4.765
quercetin-3,7,3,4-tetramethylether	1.904	6.536
letestuianin A	1.483	6.167
kaempferol-3,7,4-trimethylether	1.355	5.742
Buplerol	1.247	5.706
Letestuianin C	1.312	5.727
5-hydroxy-7-methoxyflavone	1.986	5.459







Compound Name	MW	HBD	HBA	TPSA	RO5
Sildenafil	474.58	1.00	11.75	119.09	0
1,7-bis(3,4-dihydroxy-5-	492.52	4.00	8.50	169.85	0
methoxyphenyl)heptane-3,5-					
diyldiacetate					
1-(3,4-dihydroxy-5-	462.50	6.00	7.75	190.70	1
methoxyphenyl)-7-(3,4-					
dihdroxyphenyl)heptane-3,5-					
diyldiacetate					
Apigenin	270.24	2.00	3.75	100.03	0
quercetin-3,7,3,4-	296.28	0.00	4.75	89.04	0
tetramethylether					
letestuianin A	324.38	2.00	3.25	87.36	0
kaempferol-3,7,4-	324.38	0.00	2.75	28.35	0
trimethylether					
Buplerol	372.42	1.00	6.00	85.35	0
Letestuianin C	312.37	2.00	5.50	95.15	0
5-hydroxy-7-methoxyflavone	268.27	0.00	3.00	63.25	0

Molecular weight (MW), Hydrogen bond donor (HBD), Hydrogen bond acceptor (HBA), topological surface area (TPSA), Rule of five (RO5)



Fig. 8: Evaluation of RMSD of protein-ligand complex for 100 ns



Sildenafil

Fig. 9: Representation of the Root mean square fluctuation (RMSF) of complex over 100 ns simulation





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Fig. 10: Complex protein-Ligand interaction mapping







Conclusions

Overall, this study predicted phytochemicals from *A. melegueta* as inhibitors of PDE-5 for further experimentally validation for erectile dysfunction management.





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