

Allicin and propolisbenzofuran B: Interaction pattern with ATP-binding cassette B1 (ABCB1) transporter

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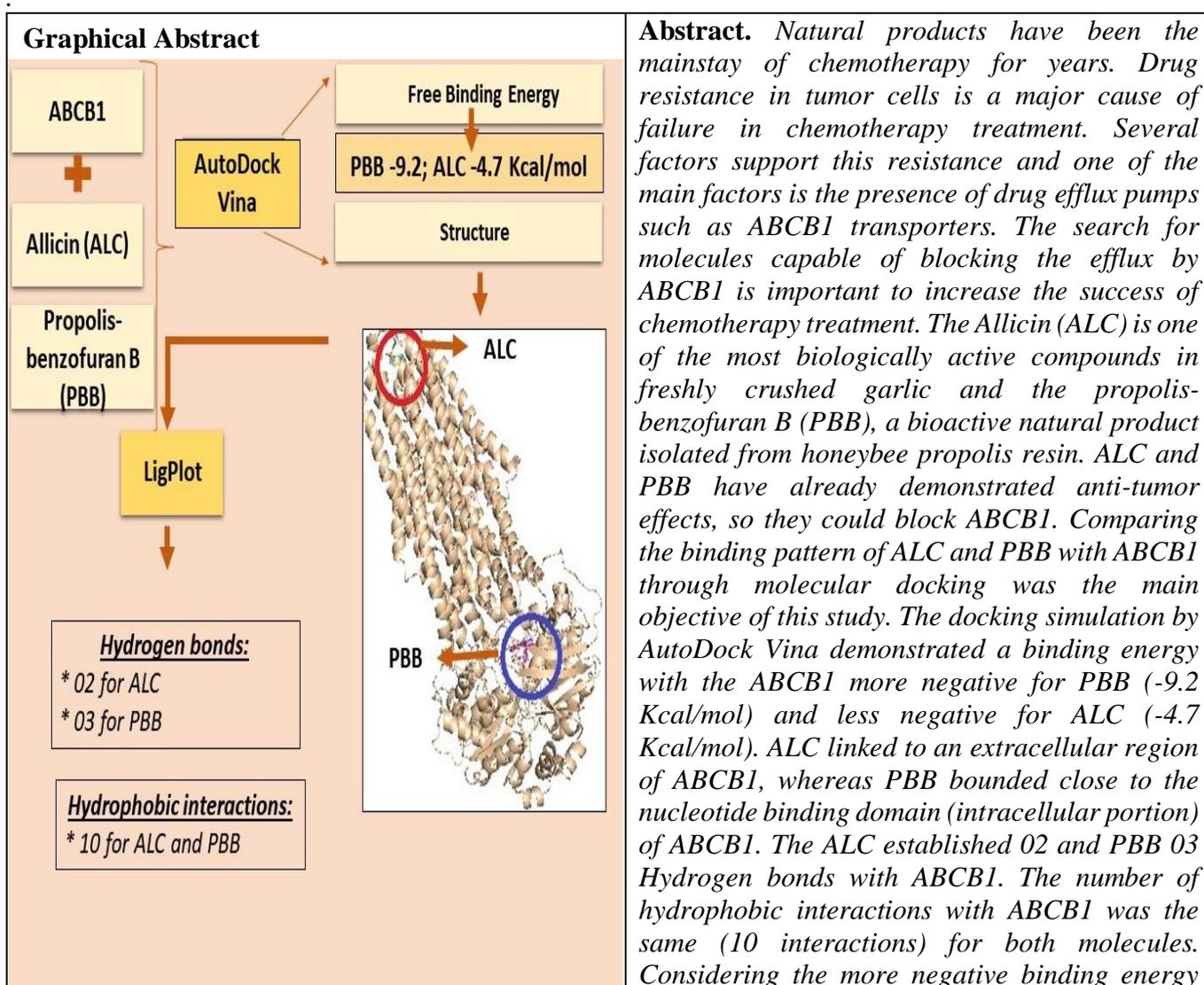
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Introduction

Drug resistance in tumor cells is a major cause of failure in cancer chemotherapy treatment. Several factors support this resistance and one of the main factors is the presence of drug efflux pumps such as ABCB1 transporters (1). Natural products have been the basis of cancer chemotherapy for the last 30 years (2). The Allicin (ALC) is one of the most biologically active compounds in freshly crushed garlic (3) and the (PBB), a bioactive natural product isolated from honeybee propolis resin (4). ALC and PBB have already demonstrated anti-tumor effects (3,5), so they could block ABCB1. The search for molecules capable of blocking the efflux by ABCB1 is important to increase the success of chemotherapy treatment. Comparing the binding pattern of ALC and PBB with ABCB1 through molecular docking was the main objective of this study.

Materials and Methods

The ABCB1 structure (receptor) was obtained from Protein Data Bank PDB (PDB ID: 6C0V) (6) and ligands ALC and PBB were obtained from Pubchem (PubChem ID: 65036 for ALC and 10455788 for PBB) (7). Firstly, using the UCSF chimera (available to download at <http://www.cgl.ucsf.edu/chimera/download.html>) we remove heteroatoms from the ABCB1. Then, we prepare receptor and ligand input files using AutoDockTools software for AutoDockVina (8). To perform docking simulations, we configure grid box as: size $x = 62 \text{ \AA}$; size $y = 90 \text{ \AA}$; and size $z = 126 \text{ \AA}$; and center box coordinates are $x = 162.664 \text{ \AA}$ center; $y = 167.261 \text{ \AA}$ center; $z = 149.020 \text{ \AA}$; considering exhaustiveness as 500. Molecular docking simulations were performed with AutoDock Vina (8). The more negative FEB indicates the greater stability of ligand-receptor complex. Visual analysis of docking results was performed with PyMol (available for download <https://pymol.org/2/>) and for check the types of connections between molecules we used the LigPlot (9).

Results and Discussion

The docking simulation by AutoDock Vina demonstrated a binding energy with the ABCB1 more negative for PBB (-9.2 Kcal/mol) and less negative for ALC (-4.7 Kcal/mol). ALC linked to an extracellular region of ABCB1, whereas PBB bounded close to the nucleotide binding domain (intracellular portion) of ABCB1 (Fig. 1A). The ALC established 02 (Fig 1B) and PBB 03 Hydrogen bonds with ABCB1 (Fig 1C). The number of hydrophobic interactions with ABCB1 was the same (10 interactions) for both molecules (Fig 1B and C).

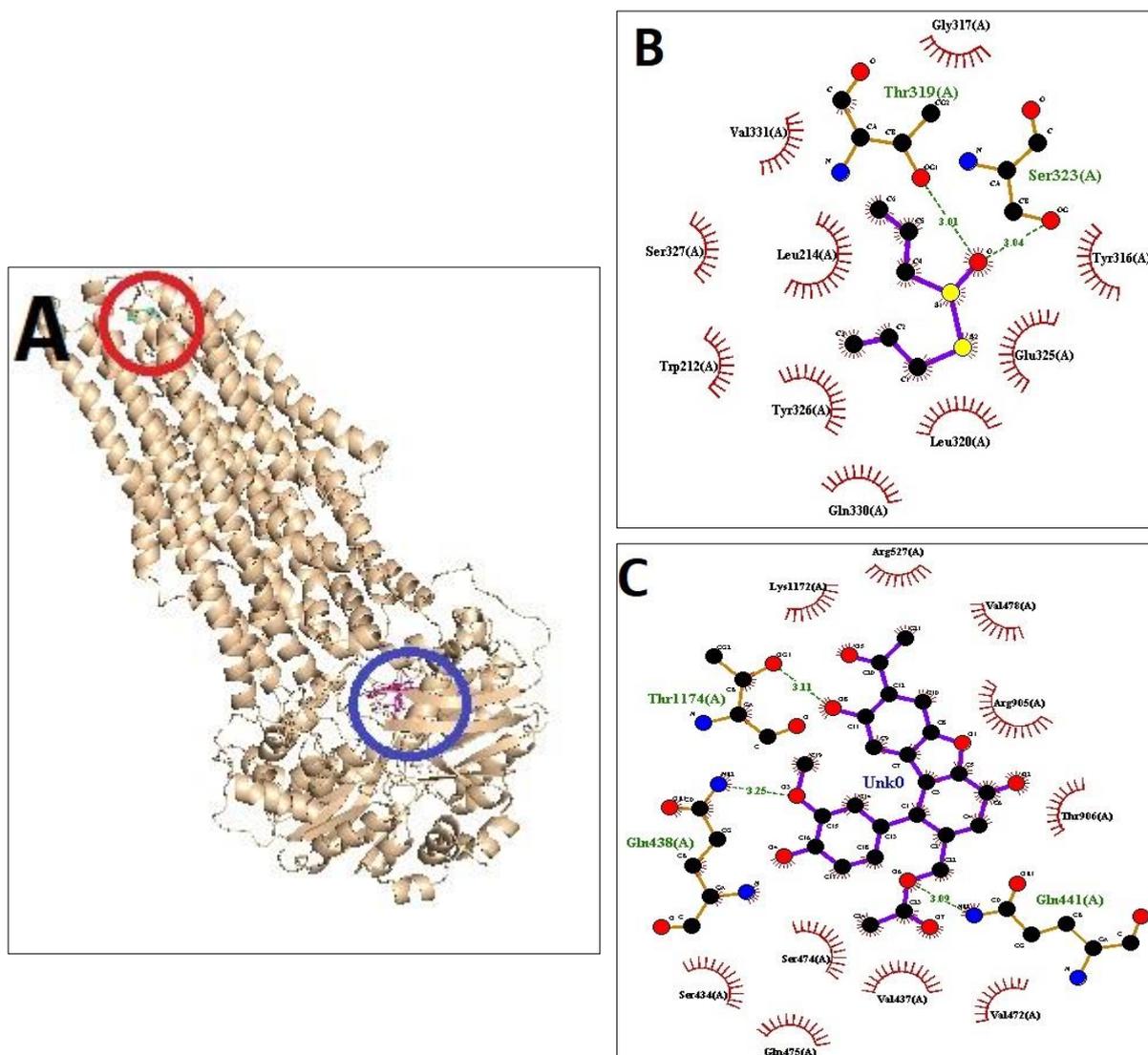


Figure 1: ABCB1 (wheat color), Allicin (cyan strokes with red circle around) and Propolis-benzofuran B (violet strokes with blue circle around) (A). ABCB1 and Allicin interaction (B). ABCB1 and PBB interaction (C). For B and C: Black, blue, red or yellow circles – ABCB1 or Allicin or Propolis-benzofuran B atoms; Purple strokes – bonds between the atoms of Allicin or Propolis-benzofuran B; Orange strokes – bonds between the atoms of Abcb1; Dotted green lines – Hydrogen bonds with distances (numbers) between ABCB1 and Allicin (B) or Propolis-benzofuran B (C); Red semi-circles with lines - hydrophobic interactions.

Conclusions

Considering the more negative binding energy and the higher number of hydrogen bonds (evidence of greater affinity and stability) PBB appears to be a better ABCB1 inhibitor. However, it is necessary to continue *in vitro* and *in vivo* studies.

References

1. Kathawala RJ, Gupta P, Ashby CR, Chen ZS. The modulation of ABC transporter-mediated multidrug resistance in cancer: A review of the past decade. *Drug Resistance Updates*. 2015.
2. Fernandes e Silva E, Figueira F da S, Lettnin AP, Carrett-Dias M, Filgueira D de MVB, Kalil S, et al. C-Phycocyanin: Cellular targets, mechanisms of action and multi drug resistance in cancer. *Pharmacological Reports*. 2018.
3. Chen H, Zhu B, Zhao L, Liu Y, Zhao F, Feng J, et al. Allicin Inhibits Proliferation and Invasion *In Vitro* and *In Vivo* via SHP-1-Mediated STAT3 Signaling in Cholangiocarcinoma. *Cell Physiol Biochem*. 2018;

4. Brian T. Jones CTA and RJT. Total synthesis of propolisbenzofuran B. *Chem Sci.* 2014;5:1794–8.
5. Ramana KS and C V. Total Synthesis of Propolisbenzofuran B. *Org Lett.* 2017;19:6466–6469.
6. Berman HM, Westbrook J, Feng Z, Gilliland G, Bhat TN, Weissig H, et al. The Protein Data Bank (www.rcsb.org). *Nucleic Acids Res.* 2000;
7. Bolton EE, Wang Y, Thiessen PA, Bryant SH. Chapter 12 PubChem: Integrated Platform of Small Molecules and Biological Activities. In: *Annual Reports in Computational Chemistry.* 2008.
8. Trott O, Olson AJ. AutoDock Vina: Improving the speed and accuracy of docking with a new scoring function, efficient optimization, and multithreading. *J Comput Chem.* 2009;
9. Wallace AC, Laskowski RA, Thornton JM. Ligplot: A program to generate schematic diagrams of protein-ligand interactions. *Protein Eng Des Sel.* 1995;