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Short communication

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Regulation Role of Thyroxin and Triiodothyronine towards Drug-Metabolizing Enzymes (DMEs) Involved in the Metabolism of Drugs to Treat *Klebsiella pneumoniae*

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***SUMMARY*. Polymyxins were efficient drugs to treat bacteria with multiple drug resistence (MDR) properties, and drug-metabolizing enzymes (DMEs) UDP-glucuronosyltransferases (UGTs) might participate in the metabolic elimination of polymyxins. This study aims to determine the inhibition of thyroxin and triiodothyronine on the activity of UGT1A3 using *in silico* docking method. Homology modeling was firstly used to construct the crystal structure of UGT1A3, and thyroxin and triiodothyronine were docked into the activity cavity of UGT1A3 using Autodock program. The active site of UGT1A3 binding with thyroxin and triiodothyronine was composed of amino acids residues Asp37, Gly38, Ser39, His40, Phe111, Arg112, Ser113, Met116, Leu117, Met120, Arg174, Asn175, Phe239, Gly309, Ser310, Val312, Ser313, His373, Gly375, Ser376, His377, Gly378, Phe395, Gly396, Asp397, Gln398, Asn401. The hydrogen bonds and hydrophobic interactions contributed the interaction of thyroxin and triiodothyronine with UGT1A3. In conclusion, this study added the new information for the inhibitors of UGTs through demonstrating that thyroxine and triiodothyroxine showed the inhibition on the activity of UGT1A3 using *in silico* docking method.**

RESUMEN. Las polimixinas fueron fármacos eficaces para tratar bacterias resistentes a fármacos múltiples (MDR) y las UDP-glucuronosiltransferasas (UGTs) podrían participar en la eliminación metabólica de polimixinas. Este estudio tiene como objetivo determinar la inhibición de la tiroxina y la triyodotironina sobre la actividad de la UGT1A3 utilizando el método de acoplamiento *in silico*. La homología de modelado se utilizó en primer lugar para construir la estructura cristalina de UGT1A3, en tanto que tiroxina y triyodotironina fueron acopladas en la cavidad activa de UGT1A3 utilizando el programa Autodock. El sitio activo de unión a UGT1A3 de tiroxina y triyodotironina estaba compuesto por los residuos de aminoácidos Asp37, Gly38, Ser39, His40, Phe111, Arg112, Ser113, Met116, Leu117, Met120, Arg174, Asn175, Phe239, Gly309, Ser310, Val312, Ser313, His373, Gly375, Ser376, His377, Gly378, Phe395, Gly396, Asp397, Gln398 y Asn401. Los enlaces de hidrógeno y las interacciones hidrofóbicas contribuyeron a la interacción de tiroxina y triyodotironina con UGT1A3. En conclusión, este estudio agregó nueva información para los inhibidores de las UGTs a través de demostrar que la tiroxina y la triyodotiroxina inhibieron la actividad de la UGT1A3 utilizando el método de acoplamiento *in silico*.

KEY WORDS: Klebsiella pneumoniae, UDP-glucuronosyltransferase (UGT) 1A3, thyroxin, triiodothyronine.

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