PREDIKSI STRUKTUR 3 DIMENSI DAN ANALISIS *IN SILICO* PROTEIN MUTAN DELESI 3,7 KB GEN α-GLOBIN PADA α-THALASSEMIA

Yusfia Urwatul Wutsqa

17/421599/PBI/01527

INTISARI

Thalassemia merupakan kelainan yang bersifat herediter dengan pola pewarisan autosomal resesif. Thalassemia dapat disebabkan adanya mutasi pada gen penyandi rantai globin. Mutasi tersebut dapat mempengaruhi stabilitas dan fungsi dari hemoglobin yang terbentuk. Mutasi delesi satu gen α-globin yang paling umum terjadi adalah tipe 3,7 kb. Penelitian ini bertujuan untuk memprediksi struktur 3 dimensi protein hasil ekspresi dari gen yang mengalami mutasi delesi -$\alpha^{3,7}$ dengan metode *in silico*. Penelitian ini dilakukan dengan menggunakan data sekuens hasil deteksi mutasi delesi -$\alpha^{3,7}$ yang akan dibandingkan dengan sekuens α-globin normal. Kedua sekuens tersebut dilakukan proses alignment yang kemudian dianalisis mengenai proses translasi, struktur protein dan interaksinya menggunakan software EXPASY, CHIMERA, PYMOL, dan POLYVIEW-2D.

Hasil menunjukkan bahwa letak titik potong mutasi delesi -$\alpha^{3,7}$ pada gen α-globin dimulai dari basa nomor 173.030 pada kromosom 16. Struktur 3 dimensi protein mutan delesi -$\alpha^{3,7}$ memiliki struktur berbeda dengan protein α-globin normal yang ditandai dengan berkurangnya asam amino. Hal tersebut menyebabkan berubahnya kondisi ikatan penstabil protein seperti jembatan garam dan ikatan hidrogen. Interaksi protein AHSP dengan protein mutan delesi -$\alpha^{3,7}$ menunjukkan bahwa tidak adanya ikatan AHSP dengan protein HBA2 sedangkan dengan HBA1 ikatannya masih sama dengan protein α-globin normal. Dari kondisi tersebut, protein mutan delesi -$\alpha^{3,7}$ dapat kehilangan fungsi dan kemampuan untuk membentuk hemoglobin. Hal tersebut sesuai dengan kondisi hematologis sampel darah yang menunjukkan nilai MCV dan MCH yang rendah serta menunjukkan kondisi abnormalitas seperti mikrosit hipokromia.

Kata kunci : α-thalassemia, protein mutan, delesi -$\alpha^{3,7}$, *in silico*, *Alpha Globin Stabilizing Protein* (AHSP)

THREE DIMENSIONS STRUCTURE PREDICTION AND IN SILICO ANALYSIS OF MUTANT PROTEIN 3.7 KB DELETION α- GLOBIN GENES IN α-THALASSEMIA

Yusfia Urwatul Wutsqa

17/421599/PBI/01527

ABSTRACT

Thalassemia is a hereditary disorder with an autosomal recessive inheritance pattern. Thalassemia can be caused by mutations in the globin chain coding gene. These mutations can affect the stability and function of formed hemoglobin. The most common deletion mutation of the α-globin gene is type 3.7 kb. This study aims to predict the 3-dimensional structure of proteins resulting from expression of genes that have a -$\alpha^{3.7}$ deletion mutation with the in silico method. This research was conducted using sequence data of the detection result of -$\alpha^{3.7}$ deletion mutation which will be compared with normal α-globin sequence. The two sequences were aligned and then analyzed the translation process, protein structure and its interactions using EXPASY, CHIMERA, PYMOL, and POLYVIEW-2D software.

The results show that the break point of the -$\alpha^{3.7}$ deletion mutation in the α-globin gene starts from base number 173.030 on chromosome 16. The 3 dimensions structure of the mutation protein -$\alpha^{3.7}$ mutation has a different structure than the normal α-globin protein which is characterized by a decrease in amino acids . This causes changes the condition of protein stabilizing bonds such as salt bridges and hydrogen bonds. The interaction of AHSP protein with mutation protein -$\alpha^{3.7}$ shows that there is no AHSP bond with HBA2 protein, whereas with HBA1 the binding is still same as normal α-globin protein. From these conditions, the deletion mutant protein -$\alpha^{3.7}$ can lose the function and ability to form hemoglobin. This is in accordance with the haematological conditions of blood samples that show low MCV and MCH values and indicate abnormalities such as hypochromic microsites.

Keyword : α-thalassemia, mutant protein, deletion -$\alpha^{3.7}$, in silico, *Alpha Globin Stabilizing Protein* (AHSP)