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Structural Studies of a Circularly Permuted Human Hemoglobin Containing Low O₂-affinity Mutations

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Structural Studies of a Circularly Permuted Human Hemoglobin Containing Low O₂-affinity Mutations

Rachel Hubbard, P. Clint Spiegel and Spencer Anthony-Cahill **Department of Chemistry, Western Washington University**

Abstract

Our research is focused on the production of a hemoglobin-based oxygen carrier (HBOC) which can be used as a therapeutic in the event of acute blood loss. The administration of cell-free hemoglobin is associated with severe adverse effects due to dissociation of the tetrameric $\alpha_2\beta_2$ complex into $\alpha\beta$ heterodimers. Our approach to designing an effective HBOC is based on a recombinant circularly permuted human hemoglobin in which all of the subunits are linked in a singlechain fashion. This design would prevent the dissociation of the tetramer and allow for the biosynthesis of polymeric hemoglobins of defined mass. Preliminary ligand binding data with our permuted hemoglobins indicates that they prefer the high O₂-affinity R-state conformation over the low O₂-affinity T state. The β N108K and α V96W mutations were introduced to restore T state stability. Preliminary studies of the mutants have shown that while the βN108K mutation improved T-state stability, the α V96W mutation displays an unexpected destabilizing effect on the T state. We would like to understand the molecular basis for these surprising results. We intend to determine the X-ray crystal structure of the α V96W mutant as well as the β N108K mutant and the α V96W + β N108K double mutant to gain an atomic-level picture of protein structural differences that could explain these results.

Why sc-Hb?







Protein Purification

Marguardt, D.A., Doyle, M.P., Davidson, J.S., Epp, J.K., Aitken, J.F., Lemon, D.D. and Anthony-Cahill, S.J. Monodisperse 130 kDa and 260 kDa recombinant human hemoglobin polymers as scaffolds for protein engineering of hemoglobin-based oxygen carriers. J. Funct. Biomater. 2013 2, 1-24.

Hemoglobin States



Circular Permutation



Flash Photolysis







(Strong Anion Exchanger)



(Size Exclusion Chromatography)





| | • | | |
|------|-------|-------|--|
| Prot | ein Y | leids | |
| | | | |

| 4 sm | HUG |
|--------|---|
| (mg/L) | (mg/L) |
| 10.7 | - |
| 21.9 | _ |
| 2.7 | 2.5 |
| .583 | .883 |
| .133 | .120 |
| | 4 sm (mg/L) 10.7 21.9 2.7 .583 .133 |

Ligand Binding Studies

Metal Ion Affinity

Chromatography)



Structural Determination of Permuted Hbs

X-ray Crystallography

Functional characterization of the permutiens show a significant reduction in protein stability. Structural models are essential to guide protein engineering efforts aimed at increasing stability and optimizing function. X-ray crystallography was employed to obtain atomic resolution electron density maps of α cp β and sc α -cp β which were then used to refine models of the proteins and reveal structural changes due to the modifications.

HbA Ligand binding data shows distinct ACPB stabilization of the the R-state. Several ACPR 6MT ACPB N108K point mutations have been made to ACPB V96W enhance T-state stability. Ligand binding data shows that the βN108K mutation improved T state stability however the α V96W mutation further destabilized the T state.



Maillett, David H.; Simplaceanu, Virgil; Shen, Tong-Jian; Ho, Nancy T.; Olson, John S.; Ho, Chien. Interfacial and Distal-Heme Pocket Mutations Exhibit Additive Effects on the Structure and Function of Hemoglobin. Biochemistry, 2008, 47(40), 10551-10563





Post Nono Q

Sec

Post

PostIMAC

adder

kDa

~260 ~140 ~100

~70

~35

~25

~15





sc-α-cpβ



Future Work/ Research Goals

0.008

• Obtain crystal structures of

0.002

0.004

Time (sec)

0.006

- αcpβ + V96W + N108K
- αcpβ + V96W

436 rm

0.25

0.000

- αcpβ + N108K
- Gain understanding of anomalous effects of V96W on T state structure
- Establish reliable bioreactor fermentation protocol to increase yields

Acknowledgments









