"Small RNA transcriptome as novel approaches to detect autologous blood transfusion"

PROJECT REVIEW

Prof. J.T. Chi, Dr. J. Roback (Duke University, USA)

We will global characterize the transcriptional changes of red cell during storage and determine their ability to detect autologous blood transfusion. Red cells have abundant and diverse transcripts that undergo significant changes during in vitro storage. We have obtained compelling preliminary data of dramatic increase in miR-720 and other tRNA fragments during storage. These "storage signature" can be used to distinguish between fresh and stored red cells and detect autologous blood transfusion. We will develop and validate the utility of the storage signatures to detect autologous blood transfusion in vitro and in vivo in healthy volunteers.

RESULTS AND CONCLUSIONS

With the increased capacity to detect the drugs and chemicals used for doping to enhance performance, more instances of blood transfusion (allogeneic or autologous), termed “blood doping”, have been found in different athletic competitions. While blood doping methods were prohibited by the International Olympic Committee in the 1980s, there is a lack of direct and reliable methods to detect autologous blood transfusions (ABT). Therefore, there is an urgent need for the development of better and novel methods to detect ABT and other forms of blood doping. We have previously discovered the presence of large amount of microRNAs in the human mature RBC. These genetic materials offer an unique window into the development history and environmental exposure of the RBC, the main cell types used for blood doping. In our previous works, we have found that the genomic analysis of the RBC microRNAs in sickle cell diseases offer important insights into the heterogeneity of the anemia severity and malaria resistance that are caused by the elevated miR-144 and miR-451, respectively. In this project, we will perform global RNASeq analysis of the RBC during storage to identify a unique gene signature that is found only in the stored RBC. This signature can then be used to analyze the blood of athletes to detect the possibility of blood doping based on the presence of these signatures of stored RBC. To achieve this scientific goal, we first used the high throughput sequencing to comprehensively analyze all the long and short-sized RNAs in the fresh RBCs before placed under storage. In addition, we used a state-of-the-art profiling procedures to analyze the changes in the RBC microRNA during storages. We have identified and validated several microRNAs that are specifically found in the stored red cells that can be used for detecting blood doping. We will continue to seek support to further investigate the basis of this “storage gene signature” and validate their ability to detect blood doping.