"Detecting autologous blood doping through the analysis of erythrocyte transcriptome"

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Project description

With the increased capacity to detect the drugs and chemicals used for doping to enhancing performance, more instances of blood transfusion (allogeneic or autologous), termed "blood doping", have been found in different athletic competition. While blood doping methods was prohibited by the International Olympic Committee in the 1980s, there is a lack of direct and reliable methods to detect blood doping, especially from their own blood (autologous blood transfusion (ABT)). Therefore, there is an urgent need for the development of better and novel methods to detect ABT and other blood doping. These blood doping efforts are to increase the number of red blood cells (RBC) to better the oxygen-carrying capacity and athletic performance. We have discovered and characterized the large amount of genetic information in the red blood cells (RBC) that are usually used for the blood doping. We plan to apply genomic technology and advanced bioinformatics to global analyze the changes of the genetic materials of RBC during in vitro storage to identify "gene signatures" of blood storages. These gene signatures will be validated and used to identify individuals who may have received their own stored blood to enhance their athletic performance.

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 microRNA 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 in additional samples and real volunteers who have received ABT.