Project Review

"Genomic, Proteomic and Informatic Analysis of Doping"

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This proposal is an extension of a current WADA research project in this laboratory aimed at determining the changes in genes and proteins caused by doping agents and to use such information to identify a set of changes that can represent definitive tests of "signatures" of exposure to doping agents. WADA is supporting many studies in many laboratories to determine how drugs and doping agents affect the expression of genes and proteins, but because this technology looks at changes in all of the 25,000 genes and even larger numbers of protein variants in the body and because the different laboratories use a large number of different methods, drugs and analytical methods, they generate huge amounts of complex new information that require extensive comparison by methods not generally available to most individual laboratories. We have completed a pilot study for WADA to determine the feasibility of establishing a central internet-based data analysis or "informatics" core facility (www://wadainformatics.org) that will serve all of the participating WADA research laboratories worldwide, and with follow-up 1-year WADA funding we are now working with several WADA laboratories to acquire their results and analyze them for genetic changes that are common to the different laboratories, thereby identifying the gene signatures most likely to represent changes that rigorously reflect exposure to a doping agent.

We now propose an additional 2-year extension consisting of two components – 1) molecular tests of genetic and proteomic changes caused in vitro and in vivo by exposure to specific doping agents such as growth hormone, insulin-like growth factor and similar muscle growth factors, and 2) continued development of the central WADA informatics facility to coordinate the analysis of research studies from a number of WADA laboratories on genetic and proteomic effects of growth factors, steroids and other agents.

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Results and Conclusions

Our studies give support to the idea that the detection of doping may become possible through an analysis of the ways in which doped tissues show defects or changes in the ways in which their genes are expressed. Our studies have identified some changes that may be characteristic of exposure to reduced oxygen conditions and the resulting increase in blood production. We think that these kinds of analyses could be equally applicable to the detection of exposure to other agents such as growth factors and growth hormones and even to anabolic steroids. If that is the case, this approach would add a very powerful new approach to the detection of doping, that traditionally relies on the detection of the doping agent itself rather than on the detection of its effects on the body.

Publications

a. King C.C., Bouic K., Friedmann T. “A fractionation method to identify quantitative changes in protein expression mediated by IGF-1 on the proteome of murine C2C12 myoblasts.” Proteome Sci. 2009 Aug 11;7:28.

b. Friedmann T., Rabin O., Frankel M.S. “Ethics. Gene doping and sport.” Science. 2010 Feb 5;327(5966):647-8.

c. Friedmann, T. Invited Speaker, AAAS Annual Meeting, San Diego, 2010.

d. Invited Speaker, SAIC Conference on Enhancement, Washington, D.C. 2009.