Construction of a full-length cDNA library and preliminary analysis of expressed sequence tags from lymphocytes of half-pipe snowboarding athletes

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ABSTRACT. The genes of top athletes are a valuable genetic resource for the human race, and could be exploited to identify novel genes related to sports ability, as well as other functions. We analyzed the expressed sequence tags from top half-pipe snowboarding athletes using the SMART complementary DNA (cDNA) library construction method to elucidate the characteristics of the athlete genome and the differential expression of the genes it contains. Overall, we established a full-length cDNA library from the lymphocytes of half-pipe snowboarding athletes and analyzed the inserted gene fragments. We also classified those genes according to molecular function, biological characteristics, cellular composition, protein types, and signal paths. A total of 201 functional genes were noted, which were distributed in 27 pathways. *TXN*, *MDH1*, *ARL1*, *ARPC3*, *ACTG1*, and

other genes measured in sequence may be associated with physical ability. This suggests that the SMART cDNA library constructed from the genetic material from top athletes is an effective tool for preserving genetic sports resources and providing genetic markers of physical ability for athlete selection.

Key words: Half-pipe snowboarding; Full-length cDNA library; Lymphocyte; Expressed sequence tags