Genomic markers for athletic performance and trainability: What little we know

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The concept of individual differences in the response to exercise training, or trainability, has been proposed for the last three decades. For example, Bouchard *et al.* (1999) have shown that changes in aerobic capacity, vary markedly in a group of sedentary adults performing similar training. Recently, we have also shown large individual variability for changes in mitochondrial function (respiration) in response to exercise training (Bishop *et al.*, 2014). While environmental factors, such as training and diet, contribute to individual differences in the training response, twin and family studies suggest that ~50% of the variance can be explained by genetic factors.

Numerous reports of genetic associations with performance-related phenotypes have been published over the past few years (Wang *et al.*, 2013; Eynon *et al.*, 2011) but there has been limited progress in discovering and characterizing the genetic contribution to elite performance and adaptation to exercise training. This has mainly occurred due to few coordinated research efforts involving major funding initiatives/consortia, the use primarily of the candidate gene analysis approach, and limited number of training studies to identify the molecular mechanisms underlying the effects of gene variants on skeletal muscle physiology and athletic performance.

Recently, more and more physiologists are using genomic results to generate novel hypotheses concerning genes, pathways and systems involved in the ability to respond to training. Thus far, the *ACTN3* R577X variant has served as an excellent model as it is the only gene variant that shows a genotype and performance association across multiple cohorts (Eynon *et al.*, 2013), and this association is strongly supported by physiological insights gained from an Actn3 knockout (KO) mouse model (MacArthur *et al.*, 2007). Identifying more genetic variants that influence skeletal muscle physiology and performance, primarily using Genome-Wide approaches, and strictly controlled training studies, is of interest, and will be possible due to coordinated initiatives such as the **SpeedGene** study. It is believed that incorporating genomic data, arising from Genome-Wide studies, with other cost-effective OMIC (*i.e.* transcriptomics, metabolomics and proteomics) techniques, together with detailed individual physiological characterization will enable the development of individualised exercise training programs.

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