

NutraHacker

Fitness Metabolism Report for Customer: 84adea33-9194-4753-925f-529a87656048

Instructions:

This report analyzes polymorphisms that have been found to influence activity related primarily to metabolism.

PEP - Performance Enhancing Polymorphism

When one PEP allele is written, each allele provides a benefit, when two are listed then both alleles have to be present for the benefit.

NOTICE: NutraHacker reports are for scientific, educational and nutritional information only and are not intended to diagnose, cure, treat or prevent any disease, disorder or condition. Consult your doctor before beginning any treatment.

Thank you for using NutraHacker. To your health!

Gender of customer: Male

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs16892496	TRHR	N/A	CC	N/A	N/A	power	Stimulates the release of thyroxine, which is important in developing skeletal muscle.
Compared to subjects carrying TT or GT genotypes at rs16892496, those carrying the GG genotype had 2.70 kg higher LBM, on average							
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2668008/							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs7832552	TRHR	N/A	TT	N/A	N/A	power	Stimulates the release of thyroxine, which is important in developing skeletal muscle.
subjects carrying the TT genotype at rs7832552 had 2.55 kg higher LBM compared to subjects with CC or CT genotypes							
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2668008/							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs9939609	FTO	N/A	T	AT	45.8076%	metabolism	Some variants of the FTO gene are widely recognized as being associated with a risk for being overweight. This gene affects the hypothalamus region of the brain, which regulates appetite, energy intake, and satiety. It also affects the rate at which fat cells accumulate.
Individuals with the AA genotype may tend to have an increased BMI and a higher body fat percentage. Depending on other factors, this effect may be reduced if the individual engages in higher levels of physical activity							
Evidence to date suggests that the association between SNPs in FTO and BMI is predominantly driven by increased energy intake. Subjects homozygous for the obesity-risk A allele of rs9939609 exhibit overall increased ad libitum food-intake (7–9), particularly fat consumption (7, 9–11), and impaired satiety							
It has been shown that adults who are homozygous for the A-allele weigh on average 1.5 to 3 kg more than those homozygous for the T allele.							
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3726147/							
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3616005/							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1050450	GPX1	pro198leu	A	AG	33.7827%	selenium metabolism	We hypothesize that the presence of genetic polymorphisms in selenoprotein genes may: (1) influence the gene expression of specific selenoproteins and (2) influence the pattern of global gene expression after Brazil nut supplementation.
Brazil nut supplementation significantly increased GPX1 mRNA expression only in subjects with CC genotype at rs1050450 ($p < 0.05$). SELENOP mRNA expression was significantly higher in A-carriers at rs7579 either before or after supplementation ($p < 0.05$).							
https://www.ncbi.nlm.nih.gov/pubmed/28696394							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs4988235	LCT	N/A	A	AG	42.0803%	lactose metabolism	Lactase non-persistence (leading to primary lactose intolerance) is a genetically dependent inability to digest lactose in adulthood. As part of the human adaptation to dairying, the human lactase LCT-13910C/T mutation (which propagates adult expression of lactase) developed, spread and participated in the adaptation to dairying. This variant is associated with lactase activity persistence, and its carriers are able to digest lactose.
T encodes lactase persistence (ability to digest lactose)							
https://www.ncbi.nlm.nih.gov/pubmed/28497837							
https://www.ncbi.nlm.nih.gov/pubmed/25505833							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs328	LPL	ser474stop	C	CC	78.4129%	sugar metabolism	The LPL gene is involved in triglyceride clearance and cholesterol metabolism.
Fasting glucose was reduced in rs328 CC homozygotes ($p=0.028$) but not G carriers ($p=0.686$) within the intervention group.							
Increased carbohydrate intakes were positively associated with homeostasis model assessment of insulin resistance and insulin in rs328 G carriers but not CC homozygotes (p for interaction was 0.025). These results indicate that diet high in carbohydrate may not be suitable for metabolic syndrome rs328 G carriers, calling for the development of personalized dietary intervention for metabolic syndrome subjects.							
https://www.ncbi.nlm.nih.gov/pubmed/26420199							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1801282	PPARG	pro12ala	G	CC	75.654%	sugar metabolism	Peroxisome proliferator-activated receptor gamma (PPAR-gamma; encoded by PPARG; location: 3p25) plays a critical physiological role as a central transcriptional regulator of adipogenic and lipogenic programs, insulin sensitivity and glucose homeostasis.
Compared with Pro/Pro individuals, PPARG Ala carriers experienced greater improvements in glucose and insulin metabolism in response to regular endurance training							
12Ala variant of the PPARG gene Pro12Ala polymorphism (rs1801282 C/G) was associated with decreased receptor activity (Deeb et al., 1998), improved insulin sensitivity (Deeb et al., 1998) and increased body mass index in humans (Ahmetov et al., 2007b; Masud and Ye, 2003). The carriers of the 12Ala allele show better glycaemic response to exercise training (Adamo et al., 2005), higher rates of skeletal muscle glucose uptake (Vänttinen et al., 2005b) and greater cross-sectional area of muscle fibres (Ahmetov et al., 2008d). In a study of Russian power-oriented athletes (n = 260), the higher frequency (23.8% vs. 15.1%, P < 0.0001) of the PPARG 12Ala allele compared to 1,073 controls has been reported (Ahmetov et al., 2008d).							
C encodes proline							
https://www.ncbi.nlm.nih.gov/pubmed/20043145							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs4880	SOD2	ala6val	G	AG	49.0786%	manganese metabolism	The SOD2 gene produces an enzyme that has antioxidant activity inside your cells. SOD2 is also known as the MnSOD gene.
Exercise-induced oxidative stress is a state that primarily occurs in athletes involved in high-intensity sports when pro-oxidants overwhelm the antioxidant defense system to oxidize proteins, lipids, and nucleic acids. During exercise, oxidative stress is linked to muscle metabolism and muscle damage, because exercise increases free radical production							
The T allele of the Ala16Val (rs4880 C/T) polymorphism in the mitochondrial superoxide dismutase 2 (SOD2) gene has been reported to reduce SOD2 efficiency against oxidative stress.							
The frequency of the SOD2 TT genotype (18.6%) was significantly lower in power/strength athletes (n = 524) compared to controls (25.0%, p = 0.0076) or athletes involved in low-intensity sports (n = 180; 33.9%, p < 0.0001). Furthermore, the SOD2 T allele was significantly associated with increased activity of CK (females: p = 0.0144) and creatinine level (females: p = 0.0276; males: p = 0.0135) in athletes. Our data show that the SOD2 TT genotype might be unfavorable for high-intensity athletic events.							
https://www.ncbi.nlm.nih.gov/pubmed/24865797							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs7903146	TCF7L2	N/A	C	CT	40.7113%	metabolism	Transcription factor 7-like 2 (TCF7L2) polymorphisms are strongly associated with type 2 diabetes, but controversially with plasma lipids and cardiovascular disease
Our novel results suggest that MedDiet (mediterranean diet) may not only reduce increased fasting glucose and lipids in TT individuals, but also stroke incidence.							
https://www.ncbi.nlm.nih.gov/pubmed/23942586							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs12255372	TCF7L2	N/A	G	GT	40.1644%	metabolism	TCF7L2 gene variants have been associated with increased risk of type 2 diabetes and higher adiposity
Individuals with the TCF7L2 rs12255372 risk genotype may reduce body adiposity by consuming a diet lower in total fat. These reductions may induce better glycemic control for such individuals predisposed to type 2 diabetes.							
https://www.ncbi.nlm.nih.gov/pubmed/23034957							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1544410	VDR	bsml	C	CT	46.8562%	power	Involved in sustaining normocalcemia by inhibiting the production of parathyroid hormone and has effects on bone and skeletal muscle biology.
https://www.ncbi.nlm.nih.gov/pubmed/27683185							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1801253	ADRB1	Arg389Gly	C	CG	36.3535%	endurance, vO2	- beta-adrenergic receptors 1/2/3: G-protein coupled receptors in cardiac and adipose tissue that regulate cardiac function and metabolism - cardiac tissue: activated receptor -> increased cardiac output - adipose tissue: activated receptor -> increased lipid mobilization for energy production
- C allele associates with increased VO2 max and exercise time/endurance (p=0.002) - G allele associates with decreased VO2 max (p=0.006)							
ADRB1 389Gly homozygotes had a greater training-induced increase in exercise tolerance than 389Arg homozygotes (P=0.04).							
An association of positive tilt table testing to a single nucleotide polymorphism with a Gly to Arg switch at position 389 of the beta(1)AR was found. This polymorphism may contribute to susceptibility to faint during orthostatic challenge.							
https://www.ncbi.nlm.nih.gov/pubmed/23065660							
https://www.ncbi.nlm.nih.gov/pubmed/17463065							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1042713	ADBR2	Arg16Gly	G	AG	47.2603%	endurance, vO2	- beta-adrenergic receptors 1/2/3: G-protein coupled receptors in cardiac and adipose tissue that regulate cardiac function and metabolism - cardiac tissue: activated receptor -> increased cardiac output - adipose tissue: activated receptor -> increased lipid mobilization for energy production
G allele associates with elite endurance performance in males (p=0.03) - A allele associates with increased BMI and decreased VO2 max (p<.001)							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1042714	ADBR2	Gln27Glu	C	CG	46.3545%	endurance, vO2	- beta-adrenergic receptors 1/2/3: G-protein coupled receptors in cardiac and adipose tissue that regulate cardiac function and metabolism - cardiac tissue: activated receptor -> increased cardiac output - adipose tissue: activated receptor -> increased lipid mobilization for energy production
- C allele associates with elite distance running in middle age women (p=0.05) - G allele associates with increased BMI and decreased VO2 max (p=0.0001)							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs5370	EDN1	Lys198Asn	G	GG	60.7866%	vo2	Endothelin 1: expressed in vascular endothelium; acts as a vasoconstrictor to regulate blood pressure
G allele associates with increased cardiorespiratory fitness (OR=1.95; p=0.00025) - T allele associates with increased hypertension (p=.0003) - for Caucasians only and not African Americans - T allele decreases the VO2 max and pulse pressure response to training							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs7515322	DIO1	D1a	A	N/A	N/A	brassica (broccoli, cabbage) metabolism	People in New Zealand with Crohn's disease and low selenium levels and with this SNP rs7515322 may have also a heightened adverse response to Broccoli.
Those people with CD having this SNP rs7515322 may with the ingestion of broccoli experience a greater degree of deficiency in iodine.							
https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3875924/							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1800849	UCP3	C-55T	A	AG	34.1415%	homocysteine metabolism, lean body mass	The expression of UCP3 mainly in skeletal muscle mitochondria made UCP3 an attractive target for studies toward manipulation of energy expenditure to fight disorders such as obesity and type 2 diabetes. Overexpressing human UCP3 in mice resulted in lean, hyperphagic mice (Clapham et al., 2000). In humans, acute exercise induces up-regulation of UCP3, most likely because of elevated plasma free fatty acid levels (Schrauwen et al., 2002; Pilegaard et al., 2000).
Youth homozygous or heterozygous for the T allele of the rs1800849 polymorphism had significantly higher levels of homocysteine than those carrying the CC genotype							
There was a significant interaction effect of fitnessxrs1800849 polymorphism (P=0.042). The effect of the rs1800849 polymorphism on homocysteine levels persisted in youth with low fitness, whereas it was abolished in those with moderate or high cardiorespiratory fitness (P>0.1).							
https://www.ncbi.nlm.nih.gov/pubmed/20031128							
Several polymorphisms in the UCP3 gene (location: 11q13.4) have been identified and related to markers of energy metabolism, aerobic capacity and obesity (Ahmetov et al., 2008e; Schrauwen and Hesselink, 2002; Halsall et al., 2001). One of the early detected observations was 5'UTR -55 C/T polymorphism (rs1800849), of which the T allele was reported to be associated with increased skeletal muscle UCP3 mRNA expression (Schrauwen et al., 1999), reduced BMI (Halsall et al., 2001) and increased aerobic capacity in Russian female rowers (Ahmetov et al., 2008e). The frequency of the UCP3 T allele was significantly higher in 694 Russian elite endurance athletes compared to 1,132 controls (Ahmetov et al., 2009b).							
https://www.ncbi.nlm.nih.gov/pubmed/19653005							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs2070744	NOS3	Glu298Asp	TT	N/A	N/A	power	Nitric oxide (NO) is involved in human skeletal muscle uptake during exercise (McConell and Kingwell, 2006) and modulation of oxygen consumption in skeletal muscles (Wilkerson et al., 2004). Dietary nitrate supplementation enhances muscle contractile efficiency during knee-extensor exercise and tolerance to high-intensity exercise in humans (Bailey et al., 2010; Bailey et al., 2009).
eNOS, the endothelial nitric oxide synthase gene, is the key promoter for the production of nitric oxide (NO). Nitric oxide plays a major role in regulating the vascular tone and facilitates vasodilation. Studies have shown that individuals with this genotype (TT) have an increased level of nitric oxide, which facilitates vasodilation and increased blood supply to muscles during exercise. These factors are associated with increased muscle performance and, depending on other factors, may increase performance in power sports such as weightlifting or sprinting.							
Indeed, Drozdovska et al. (2009) have found that the frequency of the NOS3 rs2070744 T (-786 T/C polymorphism) allele was significantly higher in 56 Ukrainian power-oriented athletes (jumpers, throwers, sprinters) compared to 147 controls (77.7% vs. 65.0%; P = 0.024).							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1049305	AQP1	N/A	C	N/A	N/A	Fluid loss	In a following study of 91 international 10 km runners, the same group of authors have demonstrated that carriers of the AQP1 rs1049305 C allele had a significantly greater body fluid loss (3.7 ± 0.9 kg) than non-carriers (1.5 ± 1.1 kg) ($P < 0.05$) (Rivera et al., 2011).
<p>However, triathletes who carry a C-allele were found to complete the 42.2-km run stage faster (mean 286, s = 49 min) than triathletes with a GG genotype (mean 296, s = 47 min; $P = 0.032$).</p> <p>https://www.ncbi.nlm.nih.gov/pubmed/25495276</p>							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs17602729	AMPD1	Gln12X	G	AG	20.6326%	endurance, vO2	Adenosine monophosphate deaminase 1 (AMPD1) catalyzes the deamination of adenosine monophosphate to inosine monophosphate in skeletal muscle. Deficiency of the AMPD1 is apparently a common cause of exercise-induced myopathy and probably the most common cause of metabolic myopathy in the human.
<p>In the overwhelming majority of cases, AMPD1 deficiency is due to a 34C/T transition in exon 2 (rs1760272934 C/T) of the AMPD1 gene (location: 1p13), which creates a nonsense codon (Gln12X) that prematurely terminates translation. AMPD1 deficiency individuals exhibit a low AMP deaminase activity and reduced submaximal aerobic capacity (VO2 at the ventilatory threshold) (Rubio et al., 2008).</p> <p>In a study of Rico-Sanz et al. (2003), subjects with the AMPD1 XX genotype had diminished exercise capacity and cardiorespiratory responses to exercise in the sedentary state. Furthermore, the training response of ventilatory phenotypes during maximal exercise was more limited in XX (Rico-Sanz et al., 2003). In a study of 935 coronary artery disease patients the carriers of the X allele had a significantly lower relative increase in peakVO2 after three months of aerobic training (Thomaes et al., 2011). Finally, two studies reported low frequency of the mutant X allele in a group of top-level Spanish male endurance athletes (cyclists and runners, n = 104) (Rubio et al., 2005) and 127 Polish rowers (Cieszczyk et al., 2011c) compared with controls.</p>							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1799945	HFE	His63Asp	G	CC	71.2648%	iron metabolism	The HFE protein functions to regulate iron absorption by regulating the interaction of the transferrin receptor with transferrin.
<p>Most patients with the manifest of hereditary hemochromatosis are homozygous for the Cys282Tyr mutation, and a small proportion are heterozygous for both the Cys282Tyr and His63Asp (rs1799945 C/G or H63D) mutation of the HFE gene. The HFE gene His63Asp polymorphism was shown to be associated with blood iron indices (subjects with one or more mutations show higher blood iron concentrations and transferrin saturation than subjects without mutations) (Burt et al., 1998).</p> <p>Furthermore, Valenti et al. (2008) have demonstrated that HFE mutations reduce the amount of recombinant human erythropoietin and iron necessary to support erythropoiesis in hemodialysis. Interestingly, Deugnier et al. (2002) had shown an increased frequency of the 63Asp allele in 83 elite French road male cyclists when compared to controls (P = 0.04).</p> <p>Consistently, in a second study of 65 elite endurance-oriented Spanish athletes (50 professional road cyclists and 15 Olympic class endurance runners) Chicharro et al. (2004) had found that the frequency of the His/Asp genotype was significantly higher in athletes in comparison with 134 controls (41.5% vs. 24.6%; P = 0.01), suggesting that 63Asp allele may confer some advantage in endurance performance.</p>							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs5219	KCNJ11	Glu23Lys	C	CT	45.7066%	potassium metabolism, endurance, VO2	The encoded protein, which has a greater tendency to allow potassium to flow into a cell rather than out of a cell, is controlled by G-proteins (Smith et al., 2007). The KCNJ11 gene is expressed in several tissues, including cardiac and skeletal muscle, where it is involved in the coupling of cell metabolism to cell electrical activity.
<p>Yi et al. (2008) had shown that the Glu/Glu genotype was associated with the highest values of VO2max and maximal minute ventilation in women in untrained state than in Glu/Lys heterozygotes. Furthermore, two independent case-control studies have demonstrated that the KCNJ11 Glu23 was significantly over-represented in endurance-oriented athletes compared to controls in mixed Caucasian (184 male endurance-oriented athletes with VO2max > 75 ml/kg/min; 61.0% vs. 50.0%, P = 0.01) (González et al., 2003) and Spanish (98 marathon runners; 68.0% vs. 53.0%, P = 0.04) (Ortiz et al., 2005) cohorts.</p>							

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rs11959820	PGC1-beta	Arg292Ser	A	CC	92.4444%	endurance	The second polymorphism, Arg292Ser (rs11959820 C/A) seems to be functional as well. The frequency of the minor 292Ser allele was lower among type 2 diabetes mellitus patients and higher in elite male endurance athletes from the Genathlete study (n = 316) (Wolfarth et al., 2007a) compared to controls.
<p>(SNP; +102605C>A; Arg292Ser) in exon 5 showed marginal significant associations with the risk of T2DM. The allele frequency of the minor allele [A (= Ser) allele of +102605C>A] was lower among T2DM patients (frequency = 0.101) than among control subjects (frequency = 0.135) [P = 0.03, OR = 0.71 (95% CI: 0.51-0.94)]. Furthermore, serum triglyceride level was also associated with this non-synonymous SNP (+102605C>A; Arg292Ser) in exon 5 among controls (P = 0.03 in the dominant analysing model). Serum triglyceride levels [1.46 +/- 0.70 (log-transformed value; 0.12 +/- 0.18)] were lower in individuals who carry one or two copies of minor alleles than among others [1.60 +/- 0.85 (log-transformed value; 0.16 +/- 0.21)].</p> <p>https://www.ncbi.nlm.nih.gov/pubmed/?term=arg292ser</p>							

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rs660339	UCP2	Ala55Val	A	GG	33.7688%	vo2, endurance, power	Val/Val genotype has been reported to be associated with higher exercise efficiency (Bumann et al., 2001), enhanced metabolic efficiency and physical activity (Astrup et al., 1999) and higher VO2max in 27 male Russian rowers (Ahmetov et al., 2008e). Recently, it has been shown that the frequency of the 55Val allele was over-represented in 694 Russian elite endurance athletes (Ahmetov et al., 2009b) compared to 1,132 controls. On the other hand, Sessa et al. (2011) found an increased frequency of the Ala55 allele in 29 Italian power-oriented athletes.

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1801131	MTHFR	N/A	G	GG	10.75%	methylation	The frequencies of MTHFR rs1801131 C (37.0% vs. 19.8%), MTR rs1805087 G (20.7% vs. 10.8%) and MTRR rs1801394 G (42.7% vs. 17.0%) alleles (probably associated with a reduced DNA methylating capacity) were significantly higher in athletes compared with controls (Terruzzi et al., 2011). Taken together, these data indicate that elite athletes have a genetic predisposition to DNA hypomethylation and synthesis (factors leading to myogenic differentiation stimulation, muscle mass increase and induction of genes involved in energy metabolism).

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1805087	MTR	N/A	G	AA	65.1583%	methylation	The frequencies of MTHFR rs1801131 C (37.0% vs. 19.8%), MTR rs1805087 G (20.7% vs. 10.8%) and MTRR rs1801394 G (42.7% vs. 17.0%) alleles (probably associated with a reduced DNA methylating capacity) were significantly higher in athletes compared with controls (Terruzzi et al., 2011). Taken together, these data indicate that elite athletes have a genetic predisposition to DNA hypomethylation and synthesis (factors leading to myogenic differentiation stimulation, muscle mass increase and induction of genes involved in energy metabolism).

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1801394	MTRR	N/A	G	AG	49.3678%	methylation	The frequencies of MTHFR rs1801131 C (37.0% vs. 19.8%), MTR rs1805087 G (20.7% vs. 10.8%) and MTRR rs1801394 G (42.7% vs. 17.0%) alleles (probably associated with a reduced DNA methylating capacity) were significantly higher in athletes compared with controls (Terruzzi et al., 2011). Taken together, these data indicate that elite athletes have a genetic predisposition to DNA hypomethylation and synthesis (factors leading to myogenic differentiation stimulation, muscle mass increase and induction of genes involved in energy metabolism).

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rs8111989	CKM	N/A	TT	CT	39.9519%	VO2	The muscle isoform of creatine kinase (CKM) is a key enzyme of energy supply for muscle. In contracting muscles ADP formation triggers the creatine kinase mechanism of anaerobic ATP resynthesis which provides rephosphorylation between creatine phosphate and ADP.
Muscle-specific creatine kinase is thought to play an integral role in maintaining energy homeostasis by providing a supply of creatine phosphate. The genetic variant, rs8111989, contributes to individual differences in physical performance, and thus the purpose of this study was to determine if rs8111989 variant is predictive of Physical Fitness Test (PFT) scores in male, military infantry recruits							
Participants with 2 copies of the T allele for rs8111989 variant had higher PFT scores for run time, pull-ups, and total PFT score. Specifically, participants with 2 copies of the TT allele (variant) (n = 97) demonstrated an overall higher total PFT score as compared with those with one copy of the C allele (n = 79) (TT: 250 ± 31 vs.							
A significantly lower VO2max response to endurance training program was detected in parents and offspring with CKM GG genotype. In a following study, Rivera et al. (1999) have confirmed these results in 277 full sib pairs from 98 Caucasian families. The association study of 102 male volunteers from northern China revealed significant association between the A/G CKM gene polymorphism and running economy response to endurance training (Zhou et al., 2006). AG genotype carriers showed larger running economy response than those with AA and GG genotypes. Furthermore, Heled et al. (2007) have demonstrated association between the A/G CKM gene polymorphism and susceptibility to exertional rhabdomyolysis.							
Furthermore, the CKM AA genotype was associated with higher values of VO2max (n = 85, P = 0.0097) in a group of rowers (Fedotovskaya et al., 2012b).							
https://www.ncbi.nlm.nih.gov/pubmed/26327553							

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rs5443	GNB3	C825T	T	CC	45.3757%	VO2	Heterotrimeric guanine nucleotide-binding proteins (G proteins) transduce binding of numerous ligands such as hormones, neurotransmitters, chemokines, local mediators, and sensory stimuli to G protein-coupled receptors into intracellular responses, which underlie physiological responses of tissues
The T allele was associated with the occurrence of a biologically active GNB3 splice variant with deleted nucleotides 498?620 of exon 9, which causes loss of 41 amino acids in beta subunit of G protein and enhances G protein activation (Siffert et al., 1998). In a study of 95 healthy African American university students significant association of the rs5443 T allele with peak oxygen consumption was observed (Faruque et al., 2009). The GNB3 C825T polymorphism plays a role in the heart rate and body fatness regulation in African Americans and in responsiveness of resting blood pressure to endurance training in African American women (Rankinen et al., 2002).							
Recently, Eynon et al. (2009c) have determined the frequencies of GNB3 C825T genotypes among 155 elite Israeli athletes (119 men and 36 women; 74 long-distance runners and 81 sprinters) and 234 healthy non-athletic controls. There was a significant difference in GNB3 genotype frequencies between endurance athletes and sprinters (P = 0.045) as well as between endurance athletes and controls (P = 0.046). The proportion of the TT genotype was significantly higher in the group of endurance athletes (18.9%) than in sprinters (4.9%, P = 0.014) and controls (8.5%, P = 0.026).							

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rs7732671	PPARGC1 B	Ala203Pro	C	GG	78.9877%	endurance	The rare 203Pro allele of the Ala203Pro (rs7732671 G/C) polymorphism has been reported to be associated with reduced risk of obesity (Andersen et al., 2005), enhanced insulin-stimulated glucose metabolism and protection against an age-related decline in PGC1-beta expression in muscle (Ling et al., 2007). In a study of Russian elite endurance athletes (n = 578), the frequency of the 203Pro allele has been shown higher than in controls (n = 1,132) (Ahmetov et al., 2009b).

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs2267668	PPARD	N/A	A	AA	68.6313%	metabolism, vo2 peak	Peroxisome proliferator-activated receptor (PPAR)-delta (gene PPARD) and PPARGgamma coactivator 1alpha (gene PPARGC1A) are determinants of mitochondrial function in animals and in vitro.
After 9 months of intervention, the minor G allele of SNP rs2267668 in PPARD and the minor serine-encoding allele of the common Gly482Ser SNP in PPARGC1A were independently associated with less increase in individual anaerobic threshold (n = 136, P = 0.002 and P = 0.005), a precise measurement of aerobic physical fitness							
In addition, low skeletal muscle mitochondrial function in vitro was detected in young carriers of the G allele of the SNP rs2267668 in PPARD (n = 19, P = 0.02).							
https://www.ncbi.nlm.nih.gov/pubmed/17327385							

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rs17099207	HIF1A	pro582ser	A	N/A	N/A	VO2	Hypoxia-inducible factor-1alpha (HIF1A) is a transcription factor regulating several genes in response to hypoxic stimuli. HIF1A target genes code for proteins involved in oxygen transport, glycolytic enzymes, and glucose transporters
A common HIF1A haplotype (frequency: 15%), including the rs11549465 Pro allele and the minor A allele of rs17099207 in the 3' flanking region of the gene, showed a significant association with EEA (elite endurance athlete) status (OR: 2.37, 95% CI: 1.21-4.66, P=0.012)							
https://www.ncbi.nlm.nih.gov/pubmed/?term=rs17099207							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs2287019	GIPR	N/A	T	CC	65.2106%	glucose metabolism	GIPR is the acronym for the glucose-dependent insulinotropic polypeptide receptor gene. GIPR encodes for a protein which plays an important role in the release of insulin after ingestion of glucose and fat.
Glucose-dependent insulinotropic polypeptide [also known as gastric inhibitory polypeptide (GIP)] and its receptor (GIPR) may link overnutrition to obesity, insulin resistance, and type 2 diabetes. A GIPR variant rs2287019 was recently associated with obesity and glucose metabolism.							
The T allele of GIPR rs2287019 is associated with greater improvement of glucose homeostasis in individuals who choose a low-fat, high-carbohydrate, and high-fiber diet							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1522813	IRS1	N/A	A	N/A	N/A	glucose metabolism	The IRS1 gene codes for an important mediator protein in the insulin signaling pathway and is important in generating energy from dietary carbohydrates. Other variants of the IRS1 gene may contribute to blood glucose remaining in circulation longer and ending up stored as fat.
high-fat weight-loss diets might be more effective in the management of the MetS compared with low-fat diets among individuals with the A-allele of the rs1522813 variant near IRS1.							
https://www.ncbi.nlm.nih.gov/pubmed/24009303							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs2070895	LIPC	N/A	A	AG	34.347%	cholesterol metabolism	LIPC, the hepatic lipase gene, is involved in the hydrolysis of triglycerides and phospholipids in LDL and HDL particles.
Hepatic lipase (HL) plays a pivotal role in the metabolism of HDL and LDL.							
At 2 y of intervention, dietary fat modified effects of the variant on changes in serum TC, LDL cholesterol, and HDL cholesterol (P-interaction: 0.0008, 0.004, and 0.03, respectively). In the low-fat group, as compared to the G allele, the A allele tended to be related to the decrease in TC and LDL cholesterol concentrations [TC (beta ± SE): -5.5 ± 3.0, P = 0.07; LDL cholesterol: -4.8 ± 2.5, P = 0.06] and a lower increase in HDL cholesterol concentrations (beta ± SE: -1.37 ± 0.69, P = 0.048), whereas an opposite effect in the high-fat diet group was evident [TC (beta ± SE): 7.3 ± 2.7, P = 0.008; LDL cholesterol: 4.1 ± 2.3, P = 0.07], and there was no genetic effect on changes in HDL cholesterol concentrations (P = 0.54).							
https://www.ncbi.nlm.nih.gov/pubmed/25926410							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs1800588	LIPC	C-514T	CC	CT	34.8103%	cholesterol metabolism	LIPC, the hepatic lipase gene, is involved in the hydrolysis of triglycerides and phospholipids in LDL and HDL particles.
A high carbohydrate diet induces the beneficial effect of the CC genotype of hepatic lipase C-514T polymorphism on the apoB100/apoAI ratio only in young Chinese males.							
https://www.ncbi.nlm.nih.gov/pubmed/22935046							

rsID	Gene	Variant	PEP	Your Genotype	Genotype Freq	Category	Publication Highlights
rs4343	ACE	N/A	A	AG	49.6778%	fat metabolism	Angiotensin-converting enzyme (ACE) plays a major role in blood pressure regulation and cardiovascular homeostasis. Contrary to the assumption that ACE levels are stable, circulating ACE has been shown to be altered in obesity and weight loss
The GG genotype of the ACE rs4343 polymorphism represents a robust nutrigenetic marker for an unfavorable response to high-saturated-fat diets.							
https://www.ncbi.nlm.nih.gov/pubmed/28096099							