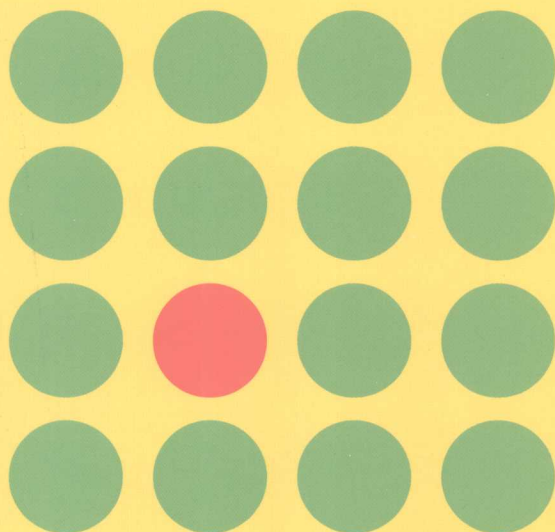


中国体育博士文丛

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——论华东地区汉族耐力运动员 ACE 基因和 mtDNA
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中文摘要

研究目的: 为探寻与人类运动能力相关的遗传标记, 本文对上海市部分重点项目(游泳、赛艇)汉族优秀运动员的 ACE 基因 I/D 多态性和 mtDNA 高变区 I 序列多态性的分布特点进行研究, 并与运动员有氧工作能力进行了关联分析, 从而为解决耐力性项目优秀运动员耐力素质的诊断和早期选材等问题提供帮助, 并为从分子水平揭示人类运动能力的遗传生物学机制进行了一些前期的探索性研究工作。

研究方法: 本研究主要以华东地区(主要为上海地区) 89 名优秀游泳运动员、87 名优秀赛艇运动员、40 名国家男子柔道队优秀柔道运动员、23 名国家男子水球队优秀水球运动员和 85 名上海籍的普通人为研究对象(不同研究部分研究对象数量有所不同)。采用 PCR 方法对 ACE 基因 I/D 多态性进行检测; 采用 PCR 产物测序的方法进行 mtDNA 高变区序列多态性的测试, 并选用 DNASTAR 软件进行序列分析; 采用力竭性递增负荷模式和一口气接一口气法(Breath by breath)测试方法, 游泳和柔道运动员采用功率自行车(Monark 839)递增负荷的运动方式, 赛艇运动员采用 CONCEPT II 型划船测功仪(美国产)递增负荷的运动方式, 对运动员的最大摄氧量(VO_{2max})、相对最大摄氧量(VO_{2max}/BW)、最大二氧化碳排出量(VCO_{2max})、最大呼吸商(RQ_{max})、最大通气量(VE_{max})、最大氧脉搏($O_2 - pluse_{max}$)、最大呼吸频率(BF_{max})、最大心率(HR_{max})、最大功率(P_{max})、最大运动时间(T_{max})、最大负荷阶段的工作时间($W_{max} - T$)等指标进行测定; 并对不同项目运动员 ACE 基因 I/D 多态性和 mtDNA 高变区 I 序列多态性的分布特点与运动员有氧工作能力进行关联分析。

主要研究结果:

(1) 华东地区汉族游泳、赛艇运动员和我国优秀男子柔道、水球运动员以及我国不同地区汉族普通人的 ACE 基因 II 基因型和 I 等位基

因频率均显著的高于我国新疆维吾尔族人群、Caucasian 人和西班牙人群 ($P < 0.05 \sim 0.001$), 而 DD 基因型和 D 等位基因频率显著的低于他们 ($P < 0.01 \sim 0.001$), ACE 基因 I/D 多态性表现出明显的差异。

(2) 与我国其它地区汉族人群比较, 华东地区游泳和赛艇运动员的基因型和等位基因频率分布与河南地区汉族普通人差异明显 ($P < 0.05 \sim 0.01$), 柔道运动员与广东、黑龙江和河南地区汉族普通人的基因型和等位基因频率分布比较, 表现出显著或非常显著的差异 ($P < 0.05 \sim 0.001$)。

(3) 85 名游泳运动员中有国际健将 7 名, 全部为 II 型; 87 名赛艇运动员有国际健将 4 名, 其中 3 名为 II 型, 1 名为 DD 型, 在总数不多的国际健将中以 II 型占主体, 表现出较高的一致性。

(4) 游泳、赛艇和水球三个项目运动员的 ACE 三种基因型分布频率的变化趋势依次为: II 型 > ID 型 > DD 型; 而柔道运动员与上海普通人相同, 表现为: ID 型 > II 型 > DD 型。不同项目间等位基因 I 的分布频率依次为: 水球 > 赛艇 > 游泳 > 普通人 > 柔道, 等位基因 D 的分布频率正好与 I 相反。

(5) 游泳、赛艇和柔道等项目不同等级运动员间 ACE 基因 I/D 多态性分布频率存在着明显差异 ($P < 0.05 \sim 0.001$)。游泳健将 II 基因型频率明显高于一级运动员 ($P < 0.05$), D 等位基因频率明显低于一级 ($P < 0.05$); 赛艇健将的 ID 基因型和 D 等位基因频率明显高于一级运动员 ($P < 0.05$); 柔道健将的基因型和等位基因频率一级运动员和上海普通人均不存在显著性差异 ($P > 0.05$)。

(6) 华东地区游泳和赛艇运动员与欧美、英国和澳大利亚等同项目运动员在 ACE 基因 I/D 多态性上存在较大差异 ($P < 0.05 \sim 0.001$), 但赛艇运动员的差异程度要小于游泳; 我国男子优秀柔道运动员与英国同项群项目比较无明显差异 ($P > 0.05$)。

(7) 不同 ACE 基因型游泳运动员的 $VO_{2\max}$ 、 $VO_{2\max}/BW$ 、 $VCO_{2\max}$ 、 VE_{\max} 、 $O_2 - pluse_{\max}$ 、 W_{\max} 和 T_{\max} 等指标均表现为 II 型 > DD 型 > ID 型, II 型明显优于 ID 型 ($P < 0.05 \sim 0.01$), 而赛艇运动员则表现为 ID 型 > II 型 > DD 型, ID 明显优于 DD 型 ($P < 0.05 \sim 0.01$); 柔道运动员不同基因型间 $VO_{2\max}$ 等指标无明显差异 ($P > 0.05$); 表现出明显的项目差别。

(8) 具有 II 基因型的游泳健将、具有 ID 基因型的赛艇健将运动员



的 $VO_{2\max}$ 、 $VO_{2\max}/BW$ 、 $VCO_{2\max}$ 、 VE_{\max} 、 $O_2 - pluse_{\max}$ 、 W_{\max} 和 T_{\max} 等指标均表现为 II 型 > DD 型 > ID 型, II 型明显优于 ID 型 ($P < 0.05 \sim 0.01$), 而赛艇运动员则表现为 ID 型 > II 型 > DD 型, ID 明显优于 DD 型 ($P < 0.05 \sim 0.01$); 柔道运动员不同基因型间 $VO_{2\max}$ 等指标无明显差异 ($P > 0.05$); 表现出明显的项目差别。

(9) 不同项目、不同基因型、不同等级运动员间的有氧工作能力表现出较明显差异 ($P < 0.05 \sim 0.01$)。游泳项目中 II 基因型的差异程度大于其它两种基因型的运动员; 赛艇项目中三种基因型不同等级的运动员间均存在较大差异 ($P < 0.05 \sim 0.01$), 但 ID 基因型的差异小于其它两种基因型; 柔道项目中, 不同基因型不同等级运动员间无明显差异 ($P > 0.05$)。

(10) 华东地区汉族游泳、赛艇运动员和普通人 mtDNA 高变区 I 的多态位点分别为 84、86、91 个, 碱基变异数分别为 475、487 和 421 个; 其中替换类位点分别为 75、80、83 个, 碱基变异数分别为 450、464 和 405 个; 插入或缺失类位点分别为 9、6、8 个, 碱基变异数分别为 25、23 和 16 个。替换类多态位点包括单碱基替换和多点碱基替换, 单碱基替换主要以 T→C 和 C→T 最为常见, 多点碱基替换以 CC→TT 和 TT→CC 最为常见; 插入或缺失类中, 插入的碱基为 A、C、T 和 G。缺失只有 A 和 C 两种。

(11) 华东地区游泳、赛艇运动员和普通人 mtDNA 高变区 I 多态位点和碱基数变异率的变化趋势表现为: 普通人 > 总体运动员 > 一级 > 健将; 同时, 普通人明显高于游泳和赛艇健将运动员 ($P < 0.05 \sim 0.01$)。

(12) 华东地区游泳和赛艇运动员 mtDNA 高变区 I 独有的多态位点分别为 22 和 28 个, 要高于普通人 (16 个), 但这些位点在本群体中的频率分布都很低, 均低于 mtDNA 高变区 I 总体多态的 5%。

(13) 华东地区游泳、赛艇运动员和普通人 mtDNA 高变区 I 序列多态性主要表现为碱基的转换、颠换、插入和缺失四种类型; 在各项目和普通人中, 碱基变异的发生频率依次为转换 > 颠换 > 插入 > 缺失。碱基转换多态性发生频率普通人显著的高于游泳健将、一级和赛艇健将与一级的运动员 ($P < 0.05 \sim 0.001$), 表现为运动员水平越高, 发生频率就越高; 碱基颠换的发生频率普通人明显低于运动员 ($P < 0.05$); 游泳、赛艇运动员和普通人碱基插入和缺失多态发生频率均低于 10%, 运动员和普通人、不同等级运动员均无明显差异 ($P > 0.05$)。

(14) 华东地区汉族游泳和赛艇运动员 mtDNA 高变区 I SNPs 在其群体中分布频率高于 10% 的位点分别为 15 个和 12 个; SNPs 频率大于 20% 位点有各有 6 个, 除位点 C16167A 外, 其它均为常见 SNPs; 上海汉族普通人 SNPs 频率大于 10% 位点共有 13 个, 大于 20% 位点有 7 个, 其中位点 C16168A 为普通人所独有。

(15) 华东地区游泳和赛艇运动员位点 C16167A 频率显著高于普通人 ($P < 0.05 \sim 0.001$), 也高于我国优秀皮划艇运动员。提示我们该位点可能成为运动能力相关的基因标记。

(16) 游泳运动员独有插入位点 (I - C16188), 其频率为 11.2%, 同时, 健将和一级运动员的频率也都大于 10%, 目前还未见到类似的报道。

(17) 华东地区优秀游泳和赛艇运动员运动员、我国优秀皮划艇运动员以及中国不同地区汉族人与亚洲人 mtDNA 的多态性无明显差异 ($P > 0.05$), 但与欧美和非洲人群和存在明显差异 ($P < 0.05 \sim 0.001$)。

(18) 游泳运动员有 3 个 SNPs 位点 (T16362C、T16304C、C16167A)、赛艇运动员有 2 个 SNPs 位点 (T16362C、T16223C), 非剑桥序列组的 VO_{2max}/BW 、 VE_{max} 、 $O_2 - pluse_{max}$ 、 W_{max} 或 T_{max} 等指标显著高于剑桥序列组运动员 ($P < 0.05 \sim 0.01$)。

主要结论:

(1) 我国不同地区汉族人群与上海地区汉族的 ACE 基因 I/D 多态性基本相同, 基因型以 II 型为主, 等位基因以 I 为主, 具有相对稳定的遗传性。

(2) 不同人群间, 不同种族间, ACE 基因 I/D 多态表现出明显差异, 这可能主要是由于不同民族或人种间的不同遗传变异导致。

(3) 华东地区游泳、赛艇优秀运动员和我国男子柔道、水球运动员的 ACE 基因 I/D 多态性的特点与其项目特征和多年专项化训练存在一定关系。

(4) 具有 ACE 基因 II 基因型或 I 等位基因、特别是 II 基因型的游泳和水球运动员成为优秀运动员的可能性更大; 赛艇和柔道项目具有 ID 基因型的运动员成为优秀运动员的可能更大。

(5) 华东地区游泳和赛艇运动员与欧美和澳大利亚等国家同项目优秀运动员的 ACE 基因 I/D 多态性存在明显差异, 表现出较为明显的种族和项目特征, 表明不同种族间 ACE 基因 I/D 多态与运动能力和对

训练的适应存在一定差异。

(6) 华东地区游泳运动员中 ACE - II 基因型和 I 等位基因与其有氧工作能力存在关联; 赛艇运动员 ID 基因型和 I 等位基因与运动员的有氧能力存在关联, 具有这种基因型或等位基因的运动员可能属于运动训练敏感的高反应群体。

(7) 华东地区游泳和赛艇项目中不同等级、不同 ACE 基因型运动员的多态性差异程度与该项目对有氧能力的需求程度密切相关。

(8) ACE 基因 I/D 多态性可作为运动训练和选材中高敏感的、非常重要的遗传标记之一。

(9) 华东地区汉族耐力运动员水平越高, mtDNA 高变区 I 序列的突变率就越低, 表现出的稳定性就越高。

(10) 游泳和赛艇运动员 mtDNA 高变区 I 独有的多态位点数高于普通人, 但在本群体中的频率分布均低于总体多态的 5%, 表明这些位点能否作为该项目运动员运动能力相关的基因标记, 还有待于进一步的深入研究。

(11) 游泳和赛艇运动员水平越高, mtDNA 高变区 I 的碱基转换发生频率就越低, 颠换的发生频率就越高, 表现出较为明显的运动项目和人群特征; 碱基的插入和缺失的发生率在运动员和普通人中都很低 (低于 5%), 且无明显不同, 表现出较强的稳定性。

(12) 位点 C16167A 可能是华东地区游泳和赛艇运动员运动能力相关的基因标记, 但还需要进一步与运动员不同身体素质 and 运动能力表型进行关联研究后才能做出更为确定的结论。

(13) 插入位点 (I - C16188) 可能成为新的标记上海汉族游泳运动员运动能力的 SNPs 位点。

(14) 不同种族间 mtDNA 高变区 I 的多态性存在差异, 从而相关的基因标记也可能不同。

(15) 游泳运动员的 3 个 SNPs 位点 (T16362C、T16304C、C16167A)、赛艇运动员的 2 个 SNPs 位点 (T16362C、T16223C) 与其有氧工作能力存在关联, 但不同项目间存在一定差异; 可作为对运动训练有高敏感性的遗传标记, 对人类有氧能力和不同个体有氧能力以及运动能力的预测、评定、及其在选材中的应用均有重要意义。

(16) 研究样本量在 50 ~ 100 名之间, 对 ACE 基因 I/D 多态性分布频率和 mtDNA 高变区 I 多态位点频率大于 10% SNPs 影响不明显。

(17) 本次研究选择的研究对象无论是运动员还是普通人,主要来自上海地区,具有较单一的遗传背景;同时,在研究和分析过程中以各运动项目为主体进行比较分析,所以运动员具有基本相同的训练模式,其多年运动刺激内容也基本相同。因此,本次研究结果具有一定探索和实践意义。

本研究创新点:

(1) 首次对华东地区(以上海为主)汉族优秀耐力运动员(游泳和赛艇)的 ACE 基因 I/D 多态性和 mtDNA 高变区序列多态性的分布特点进行了全面的分析,同时对不同基因多态性与身体素质进行关联分析,为上海重点项目寻找遗传标记将提供有效帮助。目前还未见到相关的研究报道

(2) 首次发现华东地区汉族优秀游泳和赛艇两项目运动员在 ACE 基因和 mtDNA 高变区的多态性分布特点及与有氧工作能力的关联度方面存在一定差异,在某些方面表现出较为明显的项目特征。

(3) 首次发现位点 C16167A 可能成为华东地区游泳和赛艇运动员运动能力相关的基因标记。

(4) 首次发现上海游泳运动员独有插入位点(I-C16188),该位点可能成为新的标记上海汉族游泳运动员新的 SNPs 位点,目前还未见到类似的报道。

(5) 选择的研究对象具有较单一的遗传背景,并以各运动项目为主体进行比较分析,因此,本次研究结果具有一定可靠性和实践意义。

关键词: 运动能力; 最大摄氧量; 基因多态性; 血管紧张素转换酶; 线粒体 DNA 高变区 I; 序列多态性、单核苷酸多态性

Abstract

Objective: The purpose of these experiments is to detect some genetic markers related to the human athletic capacity. Therefore, we have studied insert/delete (I/D) polymorphism of angiotensin converting enzyme (ACE) gene and hypervariable regions I (HVRI) sequence polymorphism of mitochondrial DNA (mtDNA) in the Han nationality elite athletes of partial major events (swimming and rowing) in East China (mainly in Shanghai). And we have analyzed the association between these polymorphism and the maximal aerobic capacity ($VO_2\max$) of these athletes. So, what we have done would be beneficial to diagnose the endurance performance and to select material initially in elite athletes of some endurance events. And it would also become the initial exploring research to introduce the physiological mechanism of human physical performance at the molecule level.

Methods: 89 elite swimmers, 87 elite rowers, 40 elite judokas from the national judo team, 23 elite water polo members from the national male water polo team and 85 normal subjects from Shanghai as the controls, (different numbers of subjects in different research sections). We investigated I/D polymorphism of ACE gene by using polymerase chain reaction (PCR) and HVRI sequence polymorphism of mtDNA by sequencing of PCR production. DNASTAR software was correspondingly applied to the sequence analysis. Otherwise, Maximal O_2 consumption ($VO_2\max$), relative maximal O_2 consumption ($VO_2\max/kg$), maximal CO_2 consumption ($VCO_2\max$), maximal respiratory quotient ($RQ\max$), maximal exercise ventilation ($VE\max$), O_2 - pulse_{max}, maximal breath frequency ($BF\max$), maximal heart rate ($HR\max$), maximal power ($P\max$), maximal exercise time ($T\max$) and maximal watt exercise time ($W\max - T$) etc. were investigated by a

maximal test with graded increase and a test with breath by breath. Finally, we have performed a relative analysis between the distribution of I/D polymorphism of ACE and HVRI sequence polymorphism of mtDNA and maximal athletes' aerobic capacity.

Main Research Results:

1. II genotype, and I allele frequency are all remarkably higher in the Han nationality swimmers, the rowers, the judokas from the national judo team, the water polo members from the national male water polo team in East China and the normal subjects from different areas in China than the Sinkiang Uigur, Caucasian, and Spanish ($P < 0.05 \sim 0.001$). However, DD genotype, and I allele frequency are lower significantly in the former ($P < 0.01 \sim 0.001$) and I/D polymorphism of ACE gene manifests the obvious differences.

2. Compared to the Han nationality normal subjects from Henan, the swimmers and rowers' genotype and allele distributions frequency from East China are remarkably different ($P < 0.05 \sim 0.01$). In addition, the judokas' genotype and allele distributions frequency manifest obvious or very obvious difference compared to the Han nationality normal subjects from Guangdong, Heilongjiang and Henan ($P < 0.05 \sim 0.001$).

3. There are 7 master swimmers in 85 swimmers and these 7 swimmers all are II genotype. Otherwise, there are 4 master rowers in 87 rowers and 3 master rowers are II genotype and the other one is DD genotype. Therefore, the main genotype is II genotype in the small group of master athletes, which shows relative consistency.

4. The variational trends of three ACE genotype distribution frequency in swimmers, rowers and water polo members ordinarily are: II genotype > ID genotype > DD genotype. But in judokas the trends are ID genotype > II genotype > DD genotype, which is the same of Shanghai normal subjects. I allele distribution frequency in various events ordinarily are: water polo > row > swim and D allele is the contrary to the I allele.

5. I/D polymorphism of ACE gene varies significantly among different grade of swimmers, rowers and judokas ($P < 0.05 \sim 0.001$). The frequency of II genotype is obviously higher in master swimmers than first - degree



athletes ($P < 0.05$) and D allele is lower significantly. ID genotype and D allele frequency are higher markedly in master rowers than first – degree athletes ($P < 0.05$). There are no significant difference of the frequency of genotype and allele between the master judokas and the first – degree athletes and the normal subjects in Shanghai ($P > 0.05$).

6. I/D polymorphism of ACE gene differs significantly between the East China rowers and swimmers and the Euramerican, British and Australian athletes ($P < 0.05 \sim 0.001$). But this difference is less in the rowers than in the swimmers. In addition, our elite judokas are not significantly different compared to British'.

7. VO_{2max} , VO_{2max}/kg , VCO_{2max} , VE_{max} , $O_2 - pluse_{max}$, W_{max} and T_{max} etc. in the different ACE genotype of the swimmers show II genotype being obviously higher than DD genotype and DD genotype being higher than ID genotype. These indexes in the various ACE genotype of the judokas show no significant difference. It thus indicates obvious difference in various events

8. VO_{2max} , VO_{2max}/kg , VCO_{2max} , VE_{max} , $O_2 - pluse_{max}$, W_{max} and T_{max} etc. in the II genotype of the master swimmers and ID genotype rowers show II genotype being obviously higher than DD genotype and DD genotype being higher than ID genotype ($P < 0.05 \sim 0.01$). ID genotype being obviously higher than II genotype and II genotype being than DD genotype in rowers ($P < 0.05 \sim 0.01$). There are no significant difference about VO_{2max} etc. in various genotype judokas ($P > 0.05$). So it manifests obviously different in various events.

9. The aerobic capacity shows relatively obvious different in various event, genotype and degree athletes ($P < 0.05 \sim 0.01$). The degree of difference is higher in II than other two genotype swimmers. There exists obvious difference in the different degree of the three genotype rowers ($P < 0.05 \sim 0.01$) and the difference degree is lower in ID genotype than others. In addition, there are no significant differences of genotype in different degree judokas.

10. There are respectively 84, 86 and 91 site of polymorphism of mtDNA HVRI in the Han nationality swimmers, the rowers and the normal group



from East china and the amount of base variance are respectively 475, 487 and 421. The sites of replacement are 75, 80 and 83 and the amounts of base variance are respectively 450, 464 and 405. The sites of insertence or absence are 9, 6 and 8 and the amounts of base variance are respectively 25, 23 and 16. The replacement site of polymorphism includes single base and multi - base replacement. The main replacements are T→C and C→T in the single base but CC→TT and TT→CC in multi - base. Otherwise, the insertence or absence base are respectively A, C, T, G and A, C.

11. The site of polymorphism of mtDNA HVRI and the variance rate of base in the swimmers, the rowers and the normal group from East china show the normal subjects being obviously higher than the athletes and the athletes being higher than the first - degree athletes and the first - degree athletes being higher than the master athletes. In addition, the normal subjects is significant higher than the mater swimmers and the rowers ($P < 0.05 \sim 0.01$).

12. The amount of the particular site polymorphism of mtDNA HVRI are 22 and 28 respectively in the swimmers and rowers from East china, which are higher than the normal group. These sites' distribution frequency is very low in the nations groups.

13. The frequency polymorphism site of mtDNA HVRI have four kinds including conversion, reversal, insertence and absence in the swimmers and the rowers from East china. The frequencies of variance of base ordinally are conversion, reversal, insertence and absence in all events and the normal group. The frequency of polymorphism of base conversion is obviously higher than the master and the first - degree swimmers and rowers ($P < 0.05 \sim 0.001$). It suggests that more better of the athletes more high of the frequency. Otherwise, the frequency of base reversal is lower in the normal group than the athletes ($P < 0.05$). The frequency polymorphism of insertence and absence are all below 10% in the swimmers, ther rowers and the normal subjects and no significant difference exist between the athletes and the normal group and among all the degree athletes ($P > 0.05$).

14. The sites that distribution frequency of SNPs in the swimmers and the rowers' mtDNA HVRI are over 10% are respectively 15 and 12. The sites over 15% are both 6. Except C16167A, others are all familiar SNPs. The sites that

distribution frequency of SNPs in Shanghai normal subjects are over 10% is 13. The sites over 20% is 7 and C16168A is monopolized by the normal subjects.

15. The frequency of the site of I – C16167A in the swimmers and the rowers from East china are significantly higher than the normal subjects and the elite canoeists ($P < 0.05 \sim 0.001$). It indicates that this site may become the genetic marker about sports performance.

16. The distribution frequency of individual insert site I – C16188 in the swimmers is 11.2%. While, the frequency in the master athletes and the first – degree athletes are both more than 10%. This site is likely to be a new single nucleotide polymorphisms (SNPs) site of genetic marker in the Han nationality swimmers in Shanghai. And the alike result has not so far been reported yet.

17. mtDNA polymorphism shows no different between the elite swimmers and the rowers from East China and the elite canoeists and the Han nationality normal groups in various areas in China and Asian ($P > 0.05$). But obvious difference exists between them and the Euramerican and African.

18. There are 3 SNPs sites (T16362C、T16304C、C16167A) in the swimmers and 2 SNPs sites (T16362C、T16223C) in the rowers. And $VO_2\max/kg$, VE_{\max} , $O_2 - pluse_{\max}$, W_{\max} or T_{\max} etc. in non Cambridge reference sequence (CRS) group are higher than CRS group ($P < 0.05 \sim 0.001$).

Conclusions:

1. I/D polymorphism of ACE gene are almost same between the Han nationality normal groups in various areas in China and in Shanghai. The main genotype is II genotype and the main allele is I genotype. They are relatively stable in transmissibility.

2. Probably due to the genetic variation in various nations and ethnic groups, the distribution frequency of I/D polymorphism of ACE gene varies from nation to nation.

3. It suggests that I/D polymorphism of ACE in the elite athletes of various events has certain relations with the event characteristics and the long – term professional training.



4. The distribution frequency of I/D polymorphism of ACE gene is significantly different among the athletes at different levels and various events. It accordingly indicates that the swimmers and the water polo members with II genotype and I allele are possible to become elite athletes after the long-term professional training. And it is highly possible that athletes with II genotype as well as the rowers and the judokas with ID genotype can become elite athletes.

5. I/D polymorphism of ACE gene differs significantly between the East china rowers and the swimmers and the Euramerican and the Australian athletes. The obvious characteristic of nations and events tells us that in various nations I/D polymorphism of ACE gene, sports performance and adaptation to training are different.

6. ACE - II genotype and I allele are associate with aerobic capacity in the East china swimmers. ID genotype and I allele are associate with aerobic capacity in the East china rowers. Probably these athletes with these genotype and allele are more sensitive to training.

7. The variance degree of polymorphism of ACE gene is closely correlative with aerobic capacity needed in the different degree and genotype athletes from the East china rowers and swimmers.

8. I/D polymorphism of ACE gene can be the great sensitive and very important index in the training and selecting practice.

9. More better of the East china endurance athletes, more low of the break rate in mtDNA HVRI and then the stability is also higher.

10. The amount of particular polymorphism site of mtDNA HVRI sequence is higher in the East china rowers and the swimmers than the normal group and the distribution frequency in their groups are all below 5% of the total. This indicates that whether these site can be the genetic markers of sports performance needs to explore more deeply.

11. The better the East China swimmers and the rowers, the lower the frequency of base conversion in mtDNA HVRI and more high of reversal. It manifests the obvious characteristic of nations and events. The frequency of insertence and absence are both low in the athletes and the normal group (< 5%). No significant different exists in them and they are stable.

12. C16167A may be the genetic marker related to the sports performance in the East china rowers and the swimmers, but making out a better conclusion must be deeply investigate the correlation between different body conditions and sports performance.

13. I – C16188 may become the new SNPs sites to mark the sports performance in the Han nationality swimmers in Shanghai.

14. Polymorphism of mtDNA I appear different in various ethnic groups, therefore relational genetic markers probably are different.

15. There are 3 SNPs sites (T16362C、T16304C、C16167A) in the swimmers and 2 SNPs sites (T16362C、T16223C) in the rowers correlate to the aerobic capacity. And different events have different characteristic, so it is meaningful to use the sensitive genetic marker for predicting, assessing the human and individual's aerobic capacity and selection material in athletes.

16. Samples in the experiments are 50 to 100. It doesn't influence greatly the distribution frequency of HVRI sequence polymorphism site of mtDNA HVRI which are more than 10% SNPs site.

17. No matter the athletes or the normal group, the subjects who were tested in our experiments are mainly from Shanghai; therefore, they possess the single genetic background. At the same time, the research was conducted with the focus on the comparative analysis of various events, so the athletic groups possess basically the same training mode and the alike physical stimulus in the long term. To sum up, this research is significant and meaningful in its practicability and its exploratory value.

Innovations:

1. It is the first time to roundly analyze the I/D polymorphism of ACE gene and polymorphism of mtDNA HVRI sequence. Otherwise, we study the correlation between body additions and different polymorphism. Therefore it will give help to find out genetic marker for important events. Correlative reports are not found heretofore yet.

2. We firstly find different characteristic of the distribution frequency of I/D polymorphism of ACE gene, polymorphism of mtDNA and correlation to the aerobic capacity. In some aspects event's characteristics are obvious.

3. Firstly find the site (C16167A) may probably be the genetic marker



about sports performance in the East China swimmers and rowers.

4. We firstly find the particular insertence site (I - C16188) of swimmers from Shanghai, which may probably be the new SNPs sites to mark the sports performance in the Han nationality swimmers in Shanghai. Similar reports are not found yet.

5. The subjects who were tested in our experiments possess the single genetic background and the research was conducted with the focus on the comparative analysis of various events, so this research is significant and reliable.

Keywords: Athletic Capacity; Maximal O₂ consumption; Gene Polymorphism; Angiotensin Converting Enzyme; Hypervariable Regions I Sequence of mitochondrial DNA; Sequence Polymorphism; Single Nuclotide Polymorphisms

