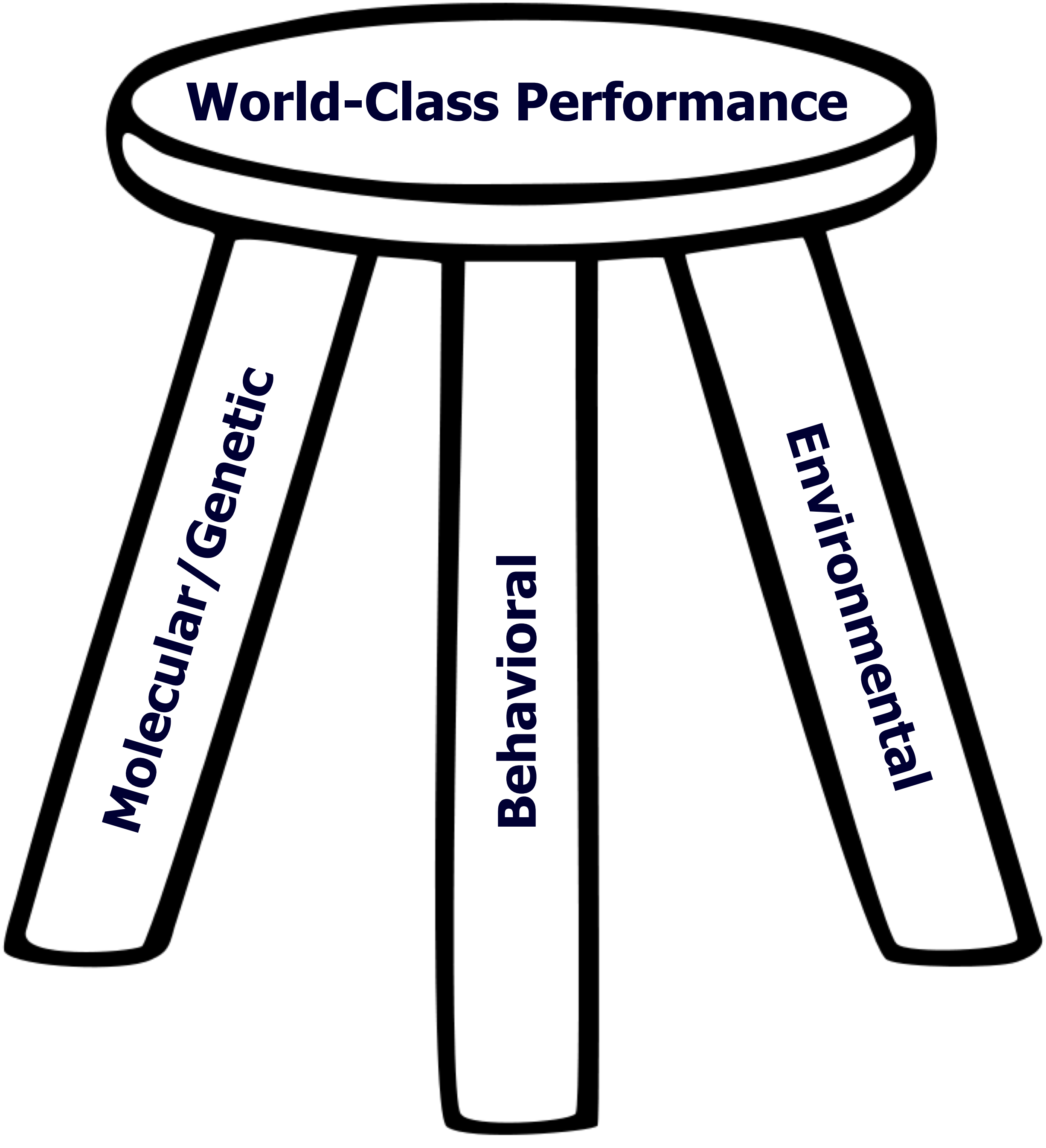
2018 world rowing
Sports Medicine and Science Conference
Berlin, Germany

Understand training? Integrating molecular, behavioral and environmental aspects

Yannis Pitsiladis, MMedSci., PhD, FACSM

Professor of Sport and Exercise Science
University of Brighton and University of Rome “Foro Italico”

The Scientific Basis of Training



World-Class Performance

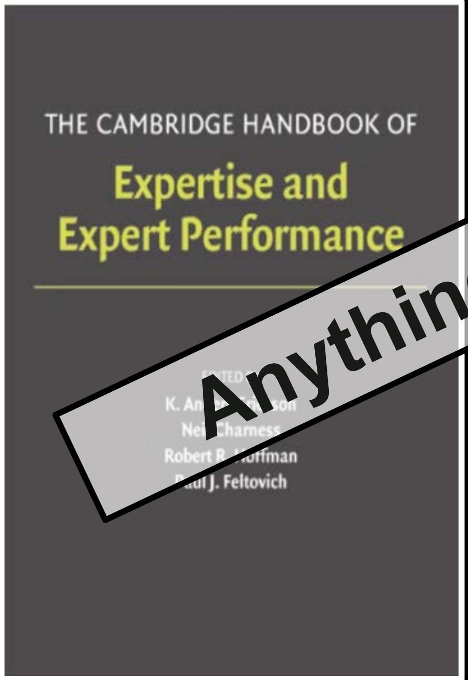
Molecular/Genetic

Behavioral

Environmental

“The genetic talent myth and the power of practice”

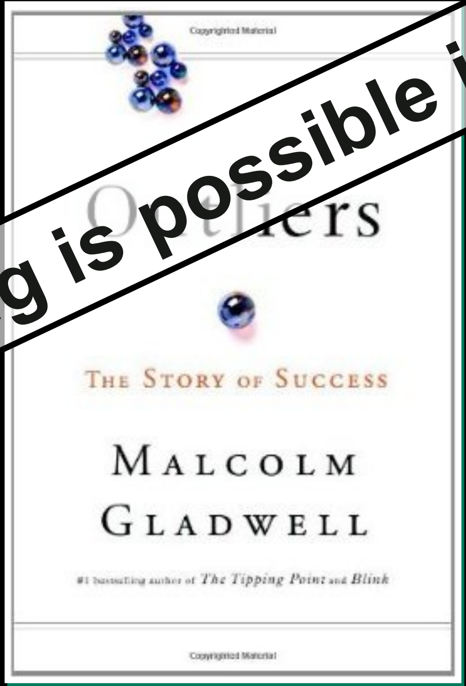

2006


THE CAMBRIDGE HANDBOOK OF

Expertise and Expert Performance

EDITED BY
K. Anders Ericsson
Neil Charness
Robert R. Hoffman
Paul J. Feltovich


2008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Outliers

The Story of Success

Malcolm Gladwell

#1 bestselling author of *The Tipping Point* and *Blink*

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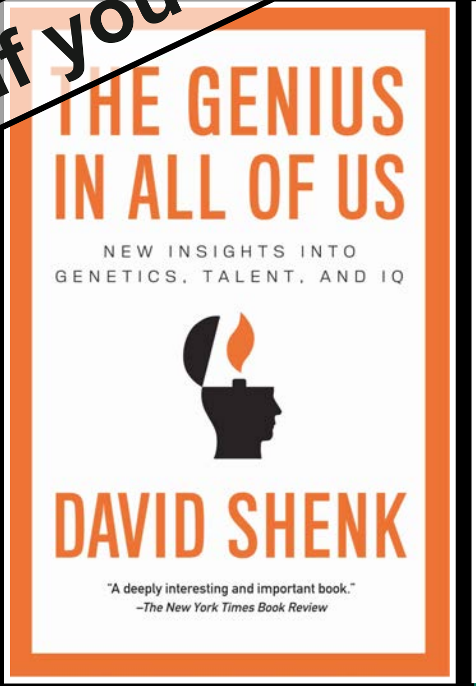
2010

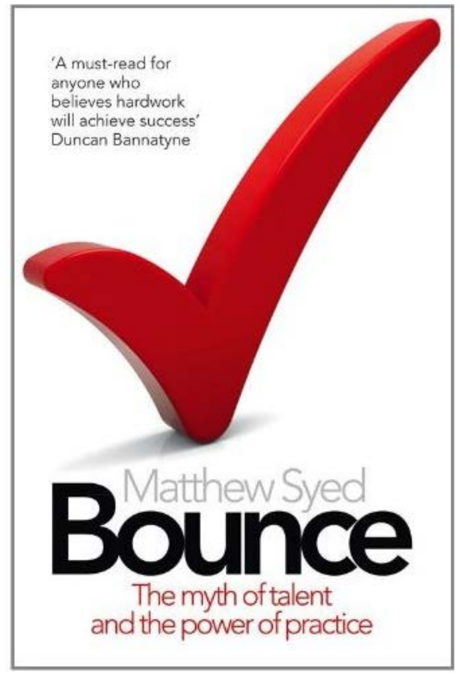

THE GENIUS IN ALL OF US

NEW INSIGHTS INTO GENETICS, TALENT, AND IQ

DAVID SHENK

“A deeply interesting and important book.”
–*The New York Times Book Review*


2010

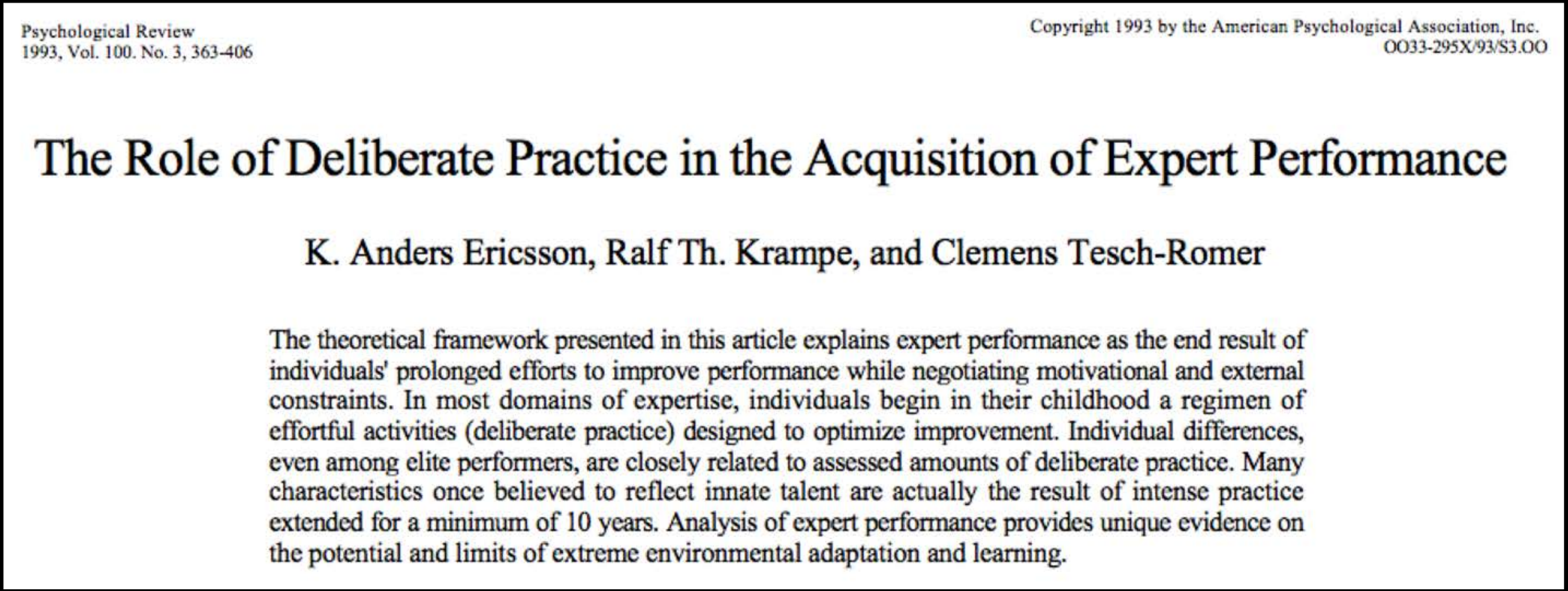

‘A must-read for anyone who believes hardwork will achieve success’
Duncan Bannatyne

Matthew Syed

Bounce

The myth of talent and the power of practice

Anything is possible if you work at it…



Psychological Review
1993, Vol. 100. No. 3, 363-406

The Role of Deliberate Practice in the Acquisition of Expert Performance

K. Anders Ericsson, Ralf Th. Krampe, and Clemens Tesch-Romer

The theoretical framework presented in this article explains expert performance as the end result of individuals' prolonged efforts to improve performance while negotiating motivational and external constraints. In most domains of expertise, individuals begin in their childhood a regimen of effortful activities (deliberate practice) designed to optimize improvement. Individual differences, even among elite performers, are closely related to assessed amounts of deliberate practice. Many characteristics once believed to reflect innate talent are actually the result of intense practice extended for a minimum of 10 years. Analysis of expert performance provides unique evidence on the potential and limits of extreme environmental adaptation and learning.

“….practice is both necessary and sufficient for the attainment of deliberate performance, and is effective because it selectively activates dormant genes that are contained within all healthy individuals’ DNA”.

Genetic Talent & The Myth of The 10,000 Hour Rule

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American College of Sports Medicine
59th Annual Meeting and
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May 29-June 2, 2012
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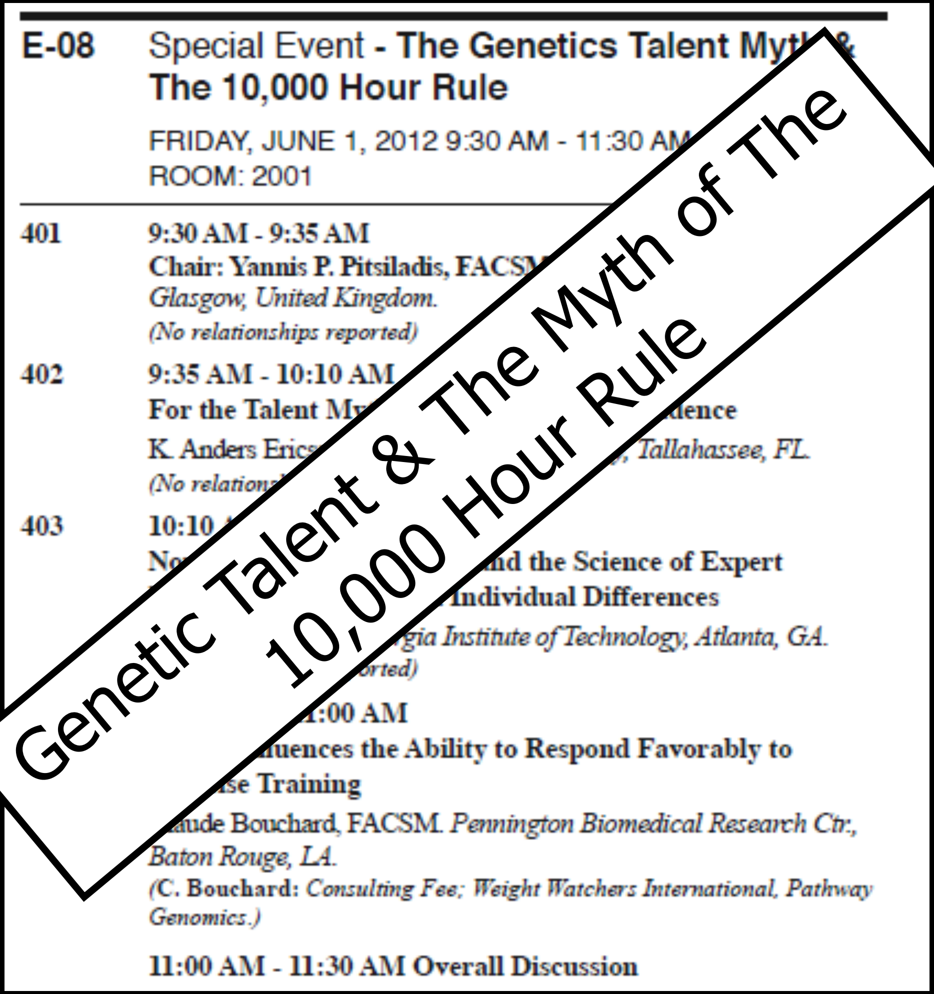


E-08 Special Event - **The Genetics Talent Myt &**
The 10,000 Hour Rule

FRIDAY, JUNE 1, 2012 9:30 AM - 11:30 AM
ROOM: 2001

401 **9:30 AM - 9:35 AM**
Chair: Yannis P. Pitsiladis, FACSM
Glasgow, United Kingdom.
(No relationships reported)

402 **9:35 AM - 10:10 AM**
For the Talent My ence
K. Anders Erics *, Tallahassee, FL.*
(No relation

403 **10:10**
No nd the Science of Expert
Individual Differences
gia Institute of Technology, Atlanta, GA.
orted)

1:00 AM
uences the Ability to Respond Favorably to
se Training
aude Bouchard, FACSM. *Pennington Biomedical Research Ctr., Baton Rouge, LA.*
(**C. Bouchard:** *Consulting Fee; Weight Watchers International, Pathway Genomics.*)

11:00 AM - 11:30 AM Overall Discussion

The Author(s) *BMC Genomics* 2017, **18**(Suppl 8):835
DOI 10.1186/s12864-017-4190-8

BMC Genomics

COMMENTARY Open Access

Why nature prevails over nurture in the making of the elite athlete

Evelina Georgiades[1], Vassilis Klissouras[2], Jamie Baulch[3], Guan Wang[1] and Yannis Pitsiladis[4,5*]

From 34th FIMS World Sports Medicine Congress
Ljubljana, Slovenia. 29th September – 2nd October 2016

Abstract

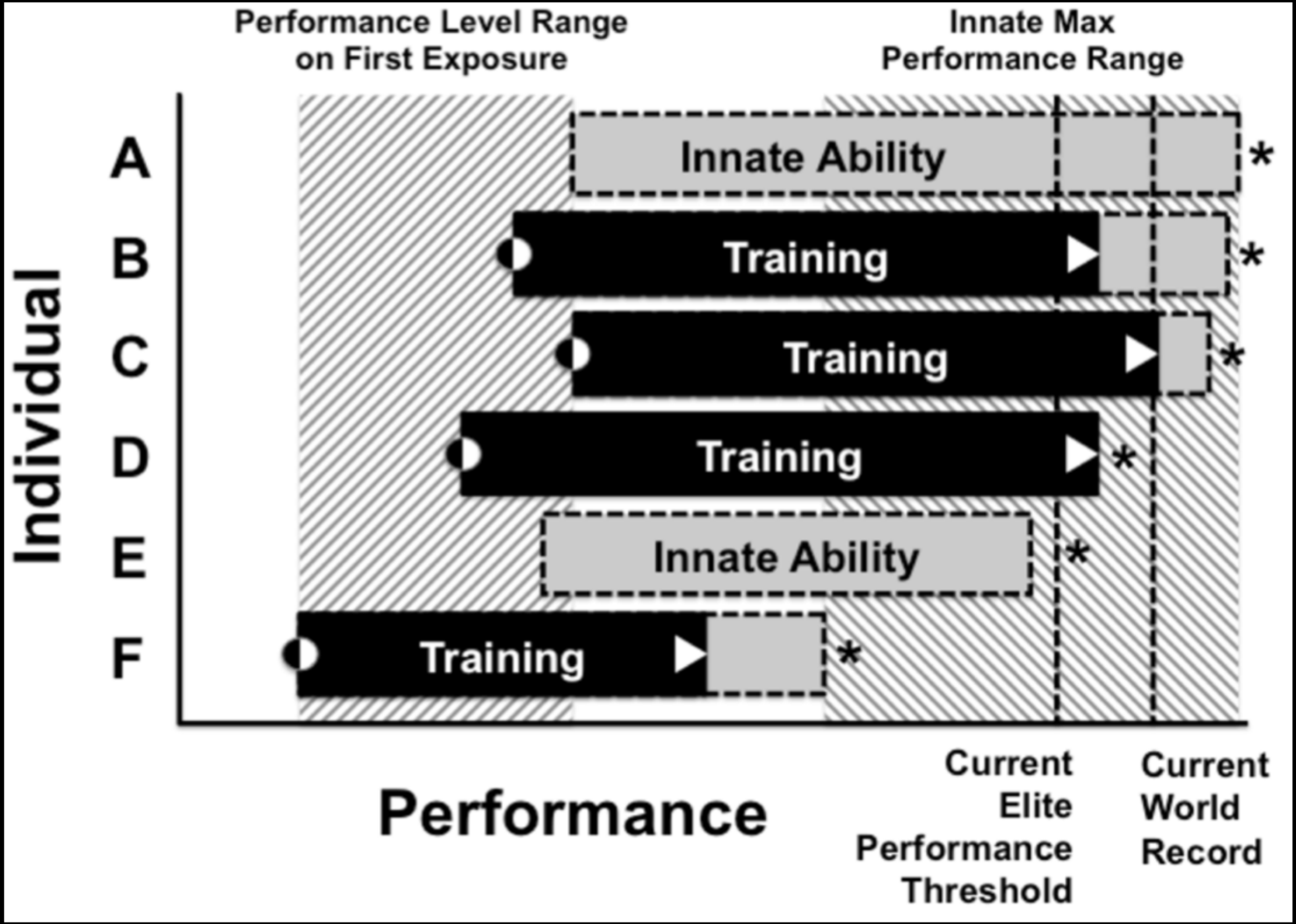
While the influence of nature (genes) and nurture (environment) on elite sporting performance remains difficult to precisely determine, the dismissal of either as a contributing factor to performance is unwarranted. It is accepted that a complex interaction of a combination of innumerable factors may mold a talented athlete into a champion. The prevailing view today is that understanding elite human performance will require the deciphering of two major sources of individual differences, genes and the environment. It is widely accepted that superior performers are endowed with a high genetic potential actualised through hard and prodigious effort. Heritability studies using the twin model have provided the basis to disentangle genetic and environmental factors that contribute to complex human traits and have paved the way to the detection of specific genes for elite sport performance. Yet, the heritability for most phenotypes essential to elite human performance is above 50% but below 100%, meaning that the environment is also important. Furthermore, individual differences can potentially also be explained not only by the impact of DNA sequence variation on biology and behaviour, but also by the effects of epigenetic changes which affect phenotype by modifying gene expression. Despite this complexity, the overwhelming and accumulating evidence, amounted through experimental research spanning almost two centuries, tips the balance in favour of nature in the "nature" and "nurture" debate. In other words, truly elite-level athletes are built – but only from those born with innate ability.

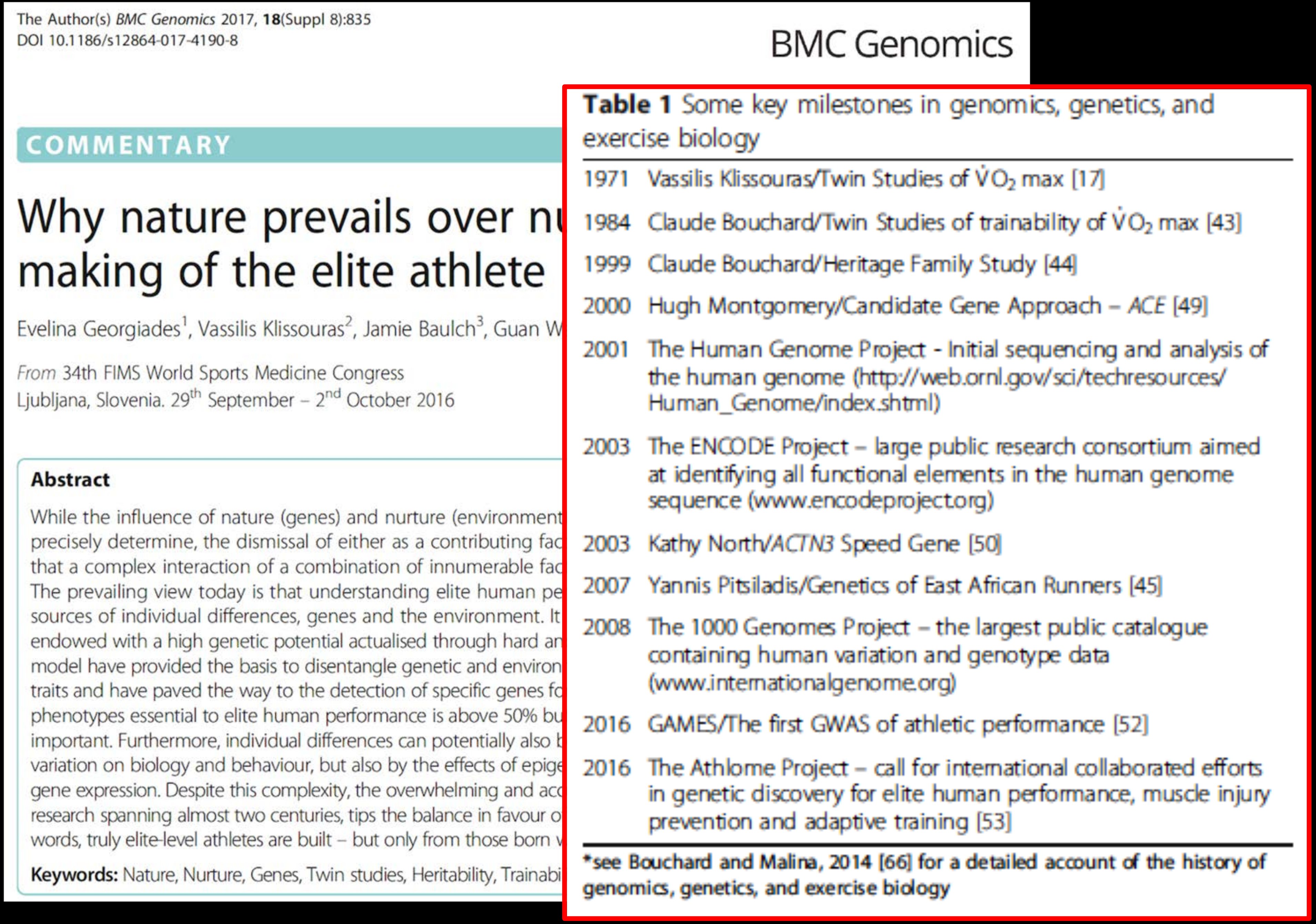
Keywords: Nature, Nurture, Genes, Twin studies, Heritability, Trainability, Sport performance

∴ truly elite-level athletes are built – but only from those born with innate ability

What makes champions? A review of the relative contribution of genes and training to sporting success

Tucker R, Collins M. *Br J Sports Med* (2012). doi:10.1136/bjsports-2011-090548





The Author(s) *BMC Genomics* 2017, **18**(Suppl 8):835
DOI 10.1186/s12864-017-4190-8

BMC Genomics

COMMENTARY

Why nature prevails over nu
making of the elite athlete

Evelina Georgiades[1], Vassilis Klissouras[2], Jamie Baulch[3], Guan W

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Abstract

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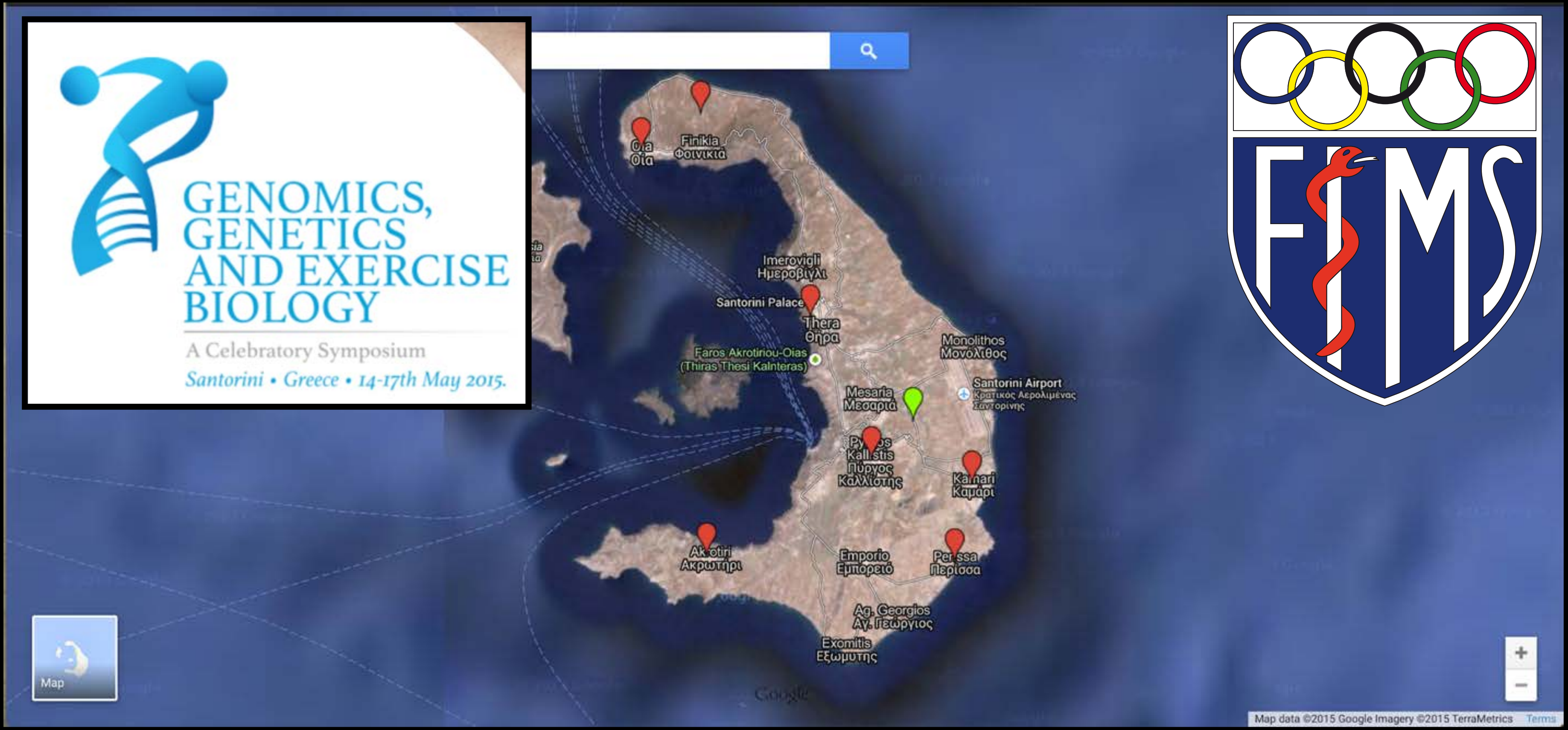
Keywords: Nature, Nurture, Genes, Twin studies, Heritability, Trainabi

Table 1 Some key milestones in genomics, genetics, and exercise biology

1971	Vassilis Klissouras/Twin Studies of $\dot{V}O_2$ max [17]
1984	Claude Bouchard/Twin Studies of trainability of $\dot{V}O_2$ max [43]
1999	Claude Bouchard/Heritage Family Study [44]
2000	Hugh Montgomery/Candidate Gene Approach – *ACE* [49]
2001	The Human Genome Project - Initial sequencing and analysis of the human genome (http://web.ornl.gov/sci/techresources/Human_Genome/index.shtml)
2003	The ENCODE Project – large public research consortium aimed at identifying all functional elements in the human genome sequence (www.encodeproject.org)
2003	Kathy North/*ACTN3* Speed Gene [50]
2007	Yannis Pitsiladis/Genetics of East African Runners [45]
2008	The 1000 Genomes Project – the largest public catalogue containing human variation and genotype data (www.internationalgenome.org)
2016	GAMES/The first GWAS of athletic performance [52]
2016	The Athlome Project – call for international collaborated efforts in genetic discovery for elite human performance, muscle injury prevention and adaptive training [53]

*see Bouchard and Malina, 2014 [66] for a detailed account of the history of genomics, genetics, and exercise biology

Athlome Project



GENOMICS, GENETICS AND EXERCISE BIOLOGY

A Celebratory Symposium

Santorini • Greece • 14-17th May 2015.

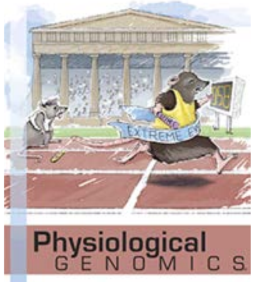
www.athlomeconsortium.org

Consensus statement

OPEN ACCESS

Direct-to-consumer genetic testing for predicting sports performance and talent identification: Consensus statement

Nick Webborn,[1] Alun Williams,[2] Mike McNamee,[3] Claude Bouchard,[4] Yannis Pitsiladis,[5] Ildus Ahmetov,[6] Euan Ashley,[7] Nuala Byrne,[8] Silvia Camporesi,[9] Malcolm Collins,[10] Paul Dijkstra,[11] Nir Eynon,[12] Noriyuki Fuku,[13] Fleur C Garton,[14] Nils Hoppe,[15] Søren Holm,[16] Jane Kaye,[17] Vassilis Klissouras,[18] Alejandro Lucia,[19] Kamiel Maase,[20] Colin Moran,[21] Kathryn N North, Fabio Pigozzi,[22] Guan Wang[5]



Current genetic testing has zero predictive power on talent identification and should not be used by athletes, coaches or parents

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British Journal of Sports Medicine

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International Federation of Sports Medicine

FIMS'16

34th WORLD CONGRESS OF SPORTS MEDICINE

From Theory to Practice...

Featuring

II. GENOMICS, GENETICS AND EXERCISE BIOLOGY

29 SEPTEMBER - 2 OCTOBER 2016
LJUBLJANA / SLOVENIA

www.fims2016.org

REVIEW

Open Access

CrossMark

Genetic testing for exercise prescription and injury prevention: AIS-Athlome consortium-FIMS joint statement

Nicole Vlahovich[1], David C. Hughes[1,8], Lyn R. Griffiths[2], Guan Wang[3], Yannis P. Pitsiladis[4,5], Fabio Pigozzi[4,5], Nobert Bachl[5,6] and Nir Eynon[7*]

From 34th FIMS World Sports Medicine Congress
Ljubljana, Slovenia. 29th September – 2nd October 2016

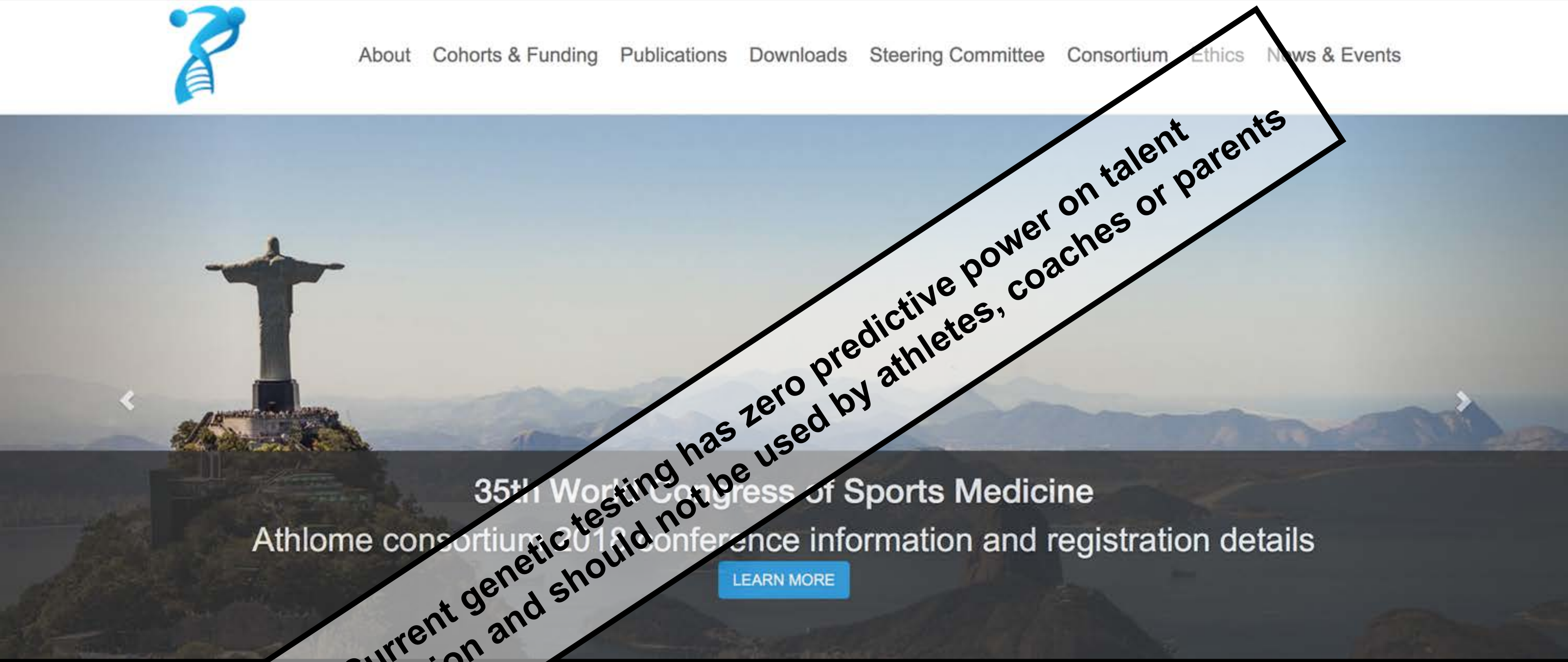
Abstract

Background: There has been considerable growth in basic knowledge and understanding of how genes are influencing response to exercise training and predisposition to injuries and chronic diseases. On the basis of this knowledge, clinical genetic testing may in the future allow the personalisation and optimisation of physical activity, thus providing an avenue for increased efficiency of exercise prescription for health and disease.

Results: This review provides an overview of the current status of genetic testing for the purposes of exercise prescription and injury prevention. As such there are a variety of potential uses for genetic testing, including identification of risks associated with participation in sport and understanding individual response to particular types of exercise. However, there are many challenges remaining before genetic testing has evidence-based practical applications, including adoption of international standards for genomics research, as well as resistance against the agendas driven by direct-to-consumer genetic testing companies. Here we propose a way forward to develop an evidence-based approach to support genetic testing for exercise prescription and injury prevention.

Conclusion: Based on current knowledge, there is no current clinical application for genetic testing in the area of exercise prescription and injury prevention, however the necessary steps are outlined for the development of evidence-based clinical applications involving genetic testing.

Current genetic testing has zero predictive power on talent identification and should not be used by athletes, coaches or parents



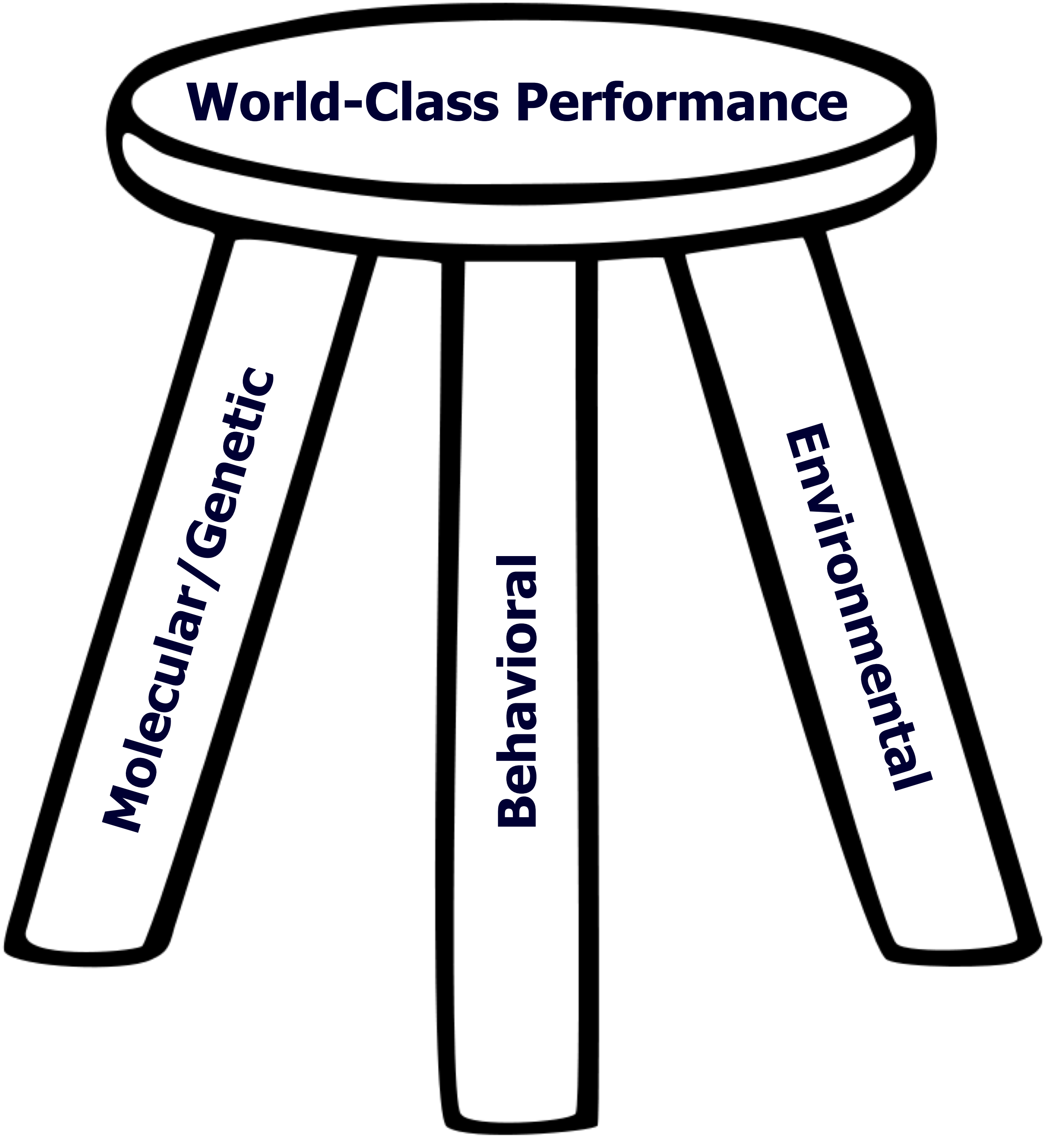
35th World Congress of Sports Medicine

Athlome consortium 2018 conference information and registration details

Current genetic testing has zero predictive power on talent identification and should not be used by athletes, coaches or parents

biogenetika
INDIVIDUALIZED MEDICINE

FIMS



World-Class Performance

Molecular/Genetic

Behavioral

Environmental

Which ℞ program is best?

How to individualize training?

“personalised medicine”

“stratified medicine”

“personalised prescription”

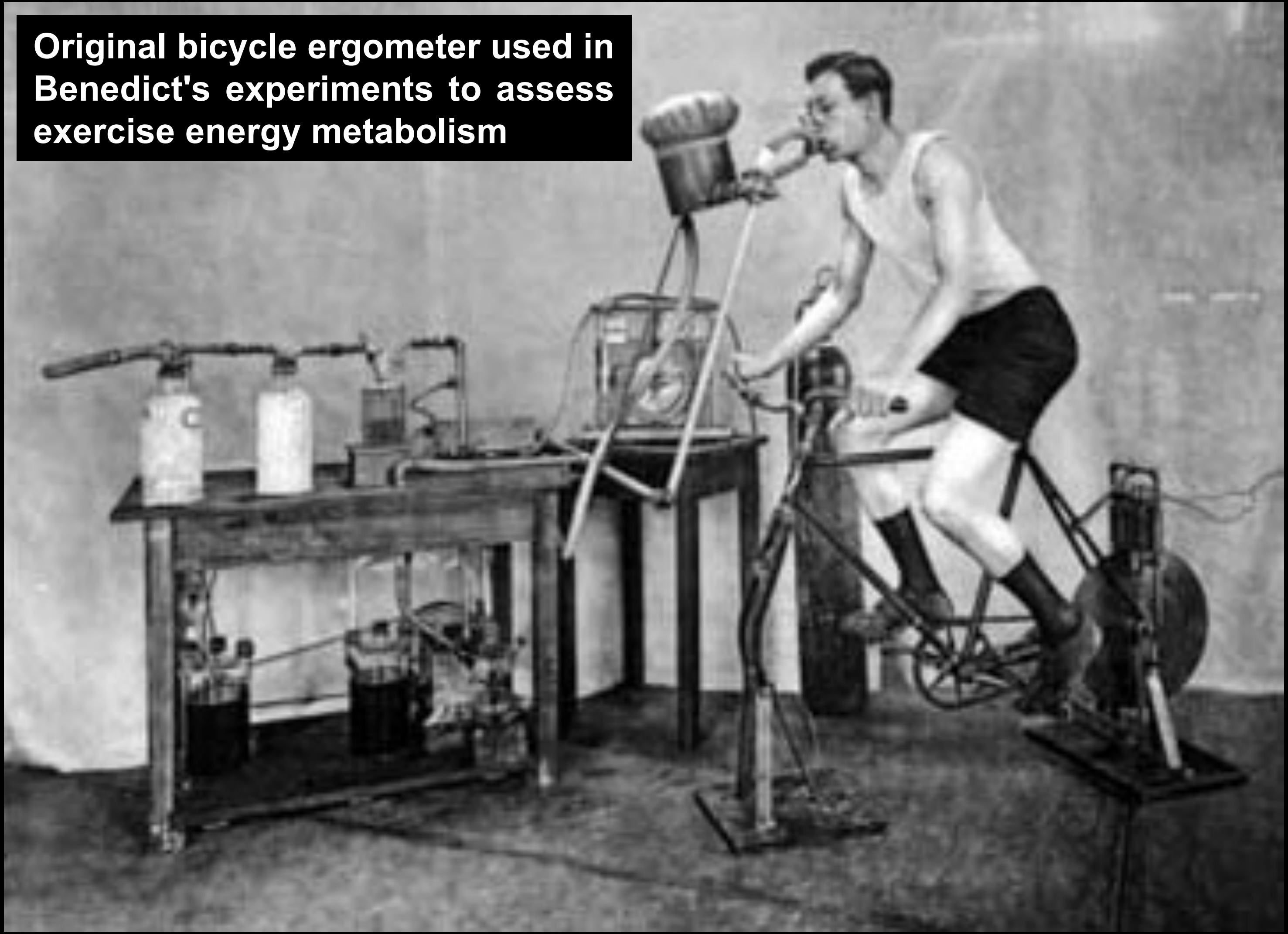
Poor Responders

Intermediate Responders

Good Responders

Very High Responders

Laboratory 1900s



Original bicycle ergometer used in Benedict's experiments to assess exercise energy metabolism

AV Hill and Otto Meyerhof (1922)

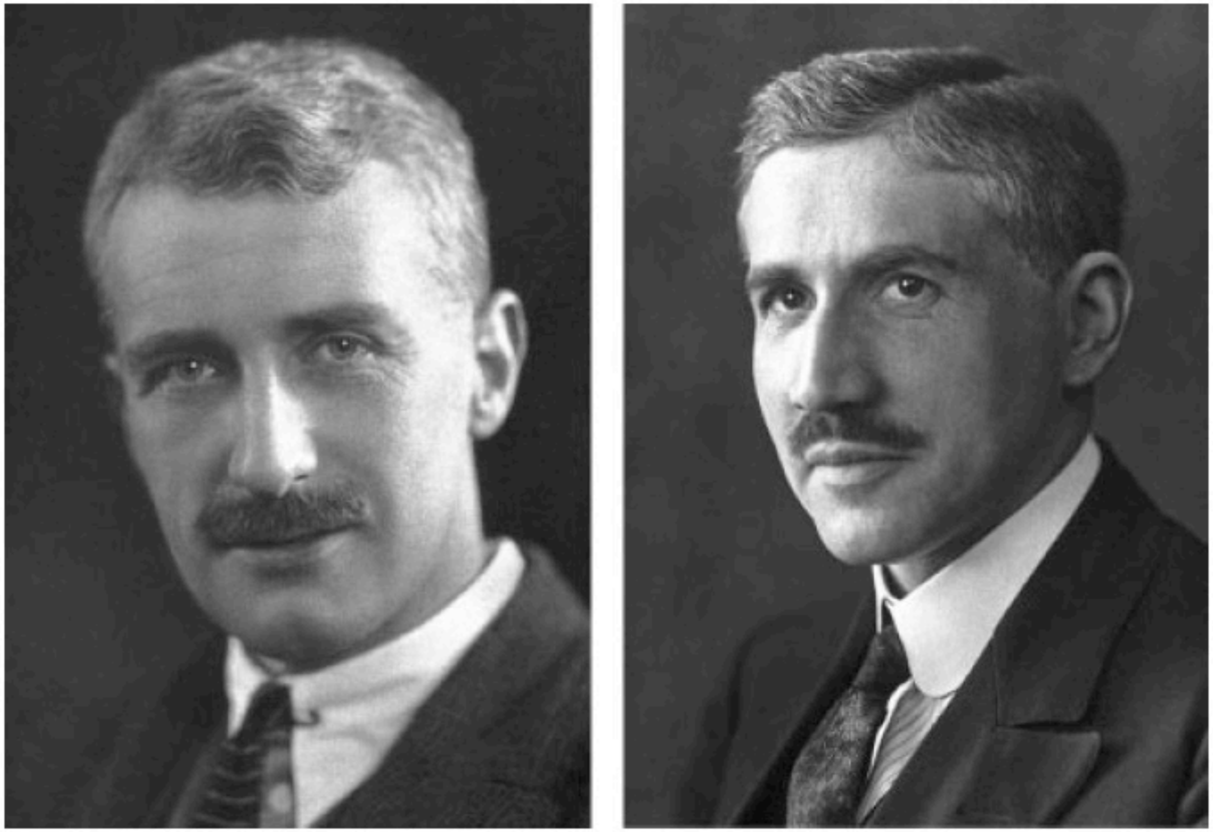
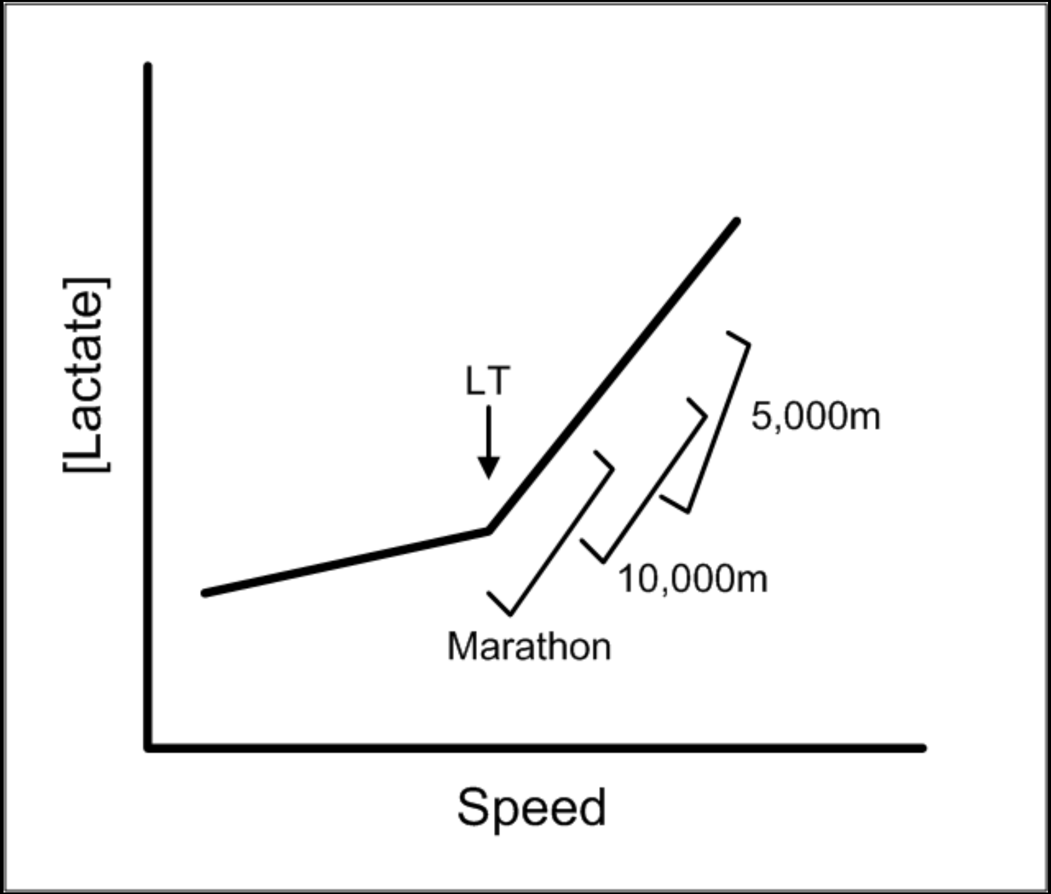


Fig. 2. Archibald V. Hill (*left*) and Otto Meyerhof (*right*). Figures borrowed with permission of the Nobel Foundation.

Lactate: Friend not foe and implications for training and performance

Measure of fatigue but NOT the cause of fatigue and … a measure of training intensity



Indoor testing

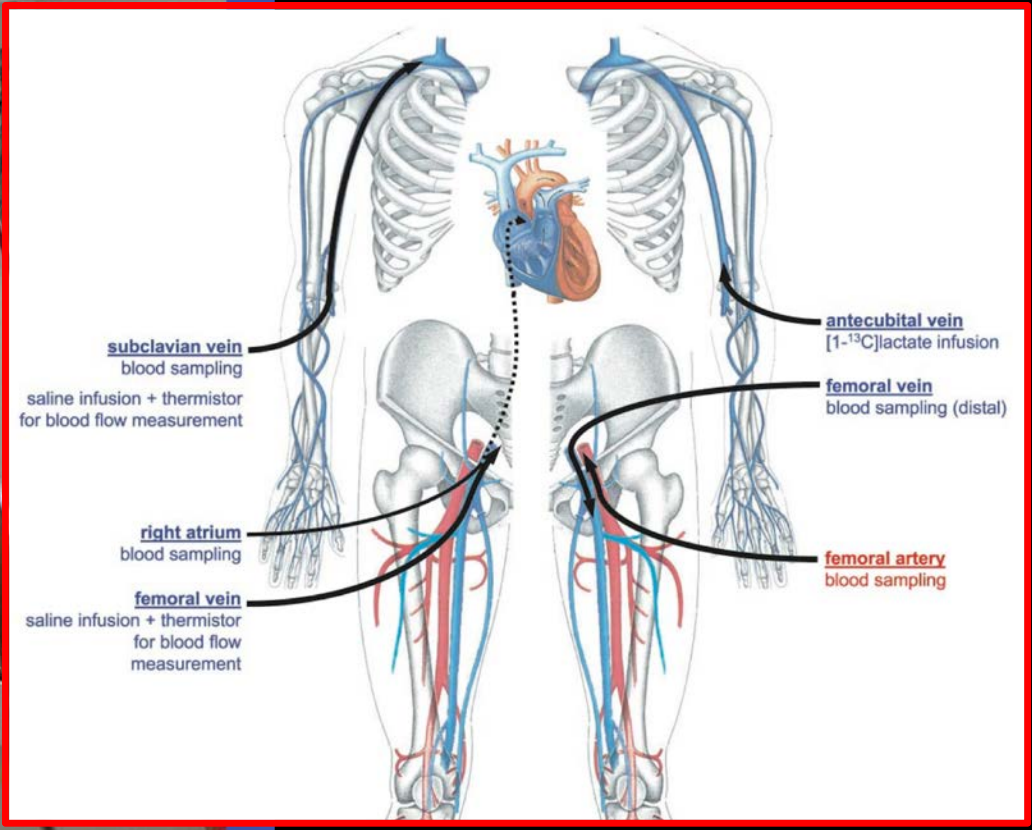
(Slide courtesy of Jamie Pringle, EIS)

(Slide courtesy of Jamie Pringle, EIS)

(Slide courtesy of Jamie Pringle, EIS)

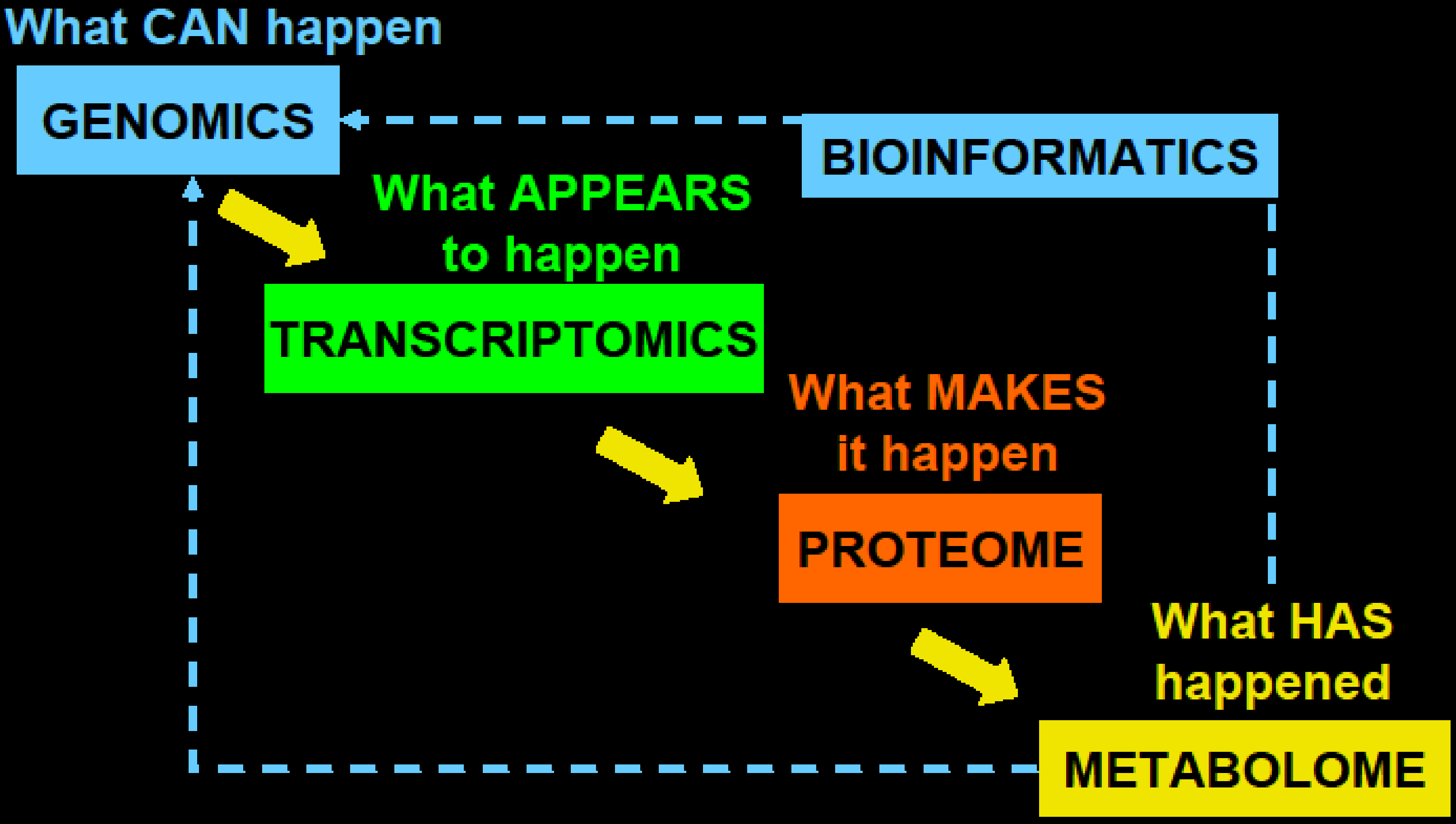
Modern (Research) Laboratory

Cross country skiing; classical



e.g. Culbet et al. 2004

The “Omics” Cascade



What CAN happen

GENOMICS

BIOINFORMATICS

What APPEARS to happen

TRANSCRIPTOMICS

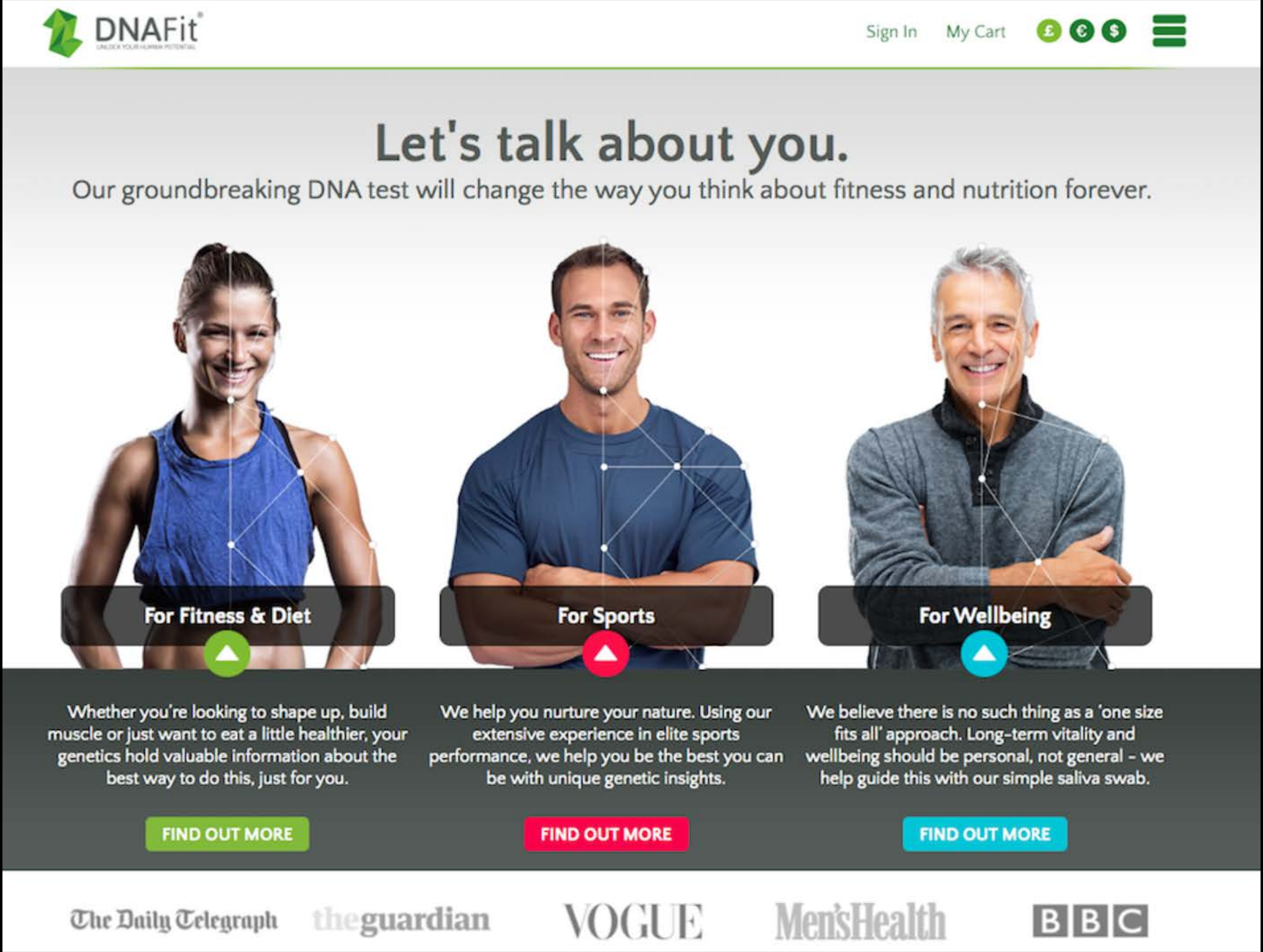
What MAKES it happen

PROTEOME

What HAS happened

METABOLOME

PHENOTYPE



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For Fitness & Diet

Whether you're looking to shape up, build muscle or just want to eat a little healthier, your genetics hold valuable information about the best way to do this, just for you.

For Sports

We help you nurture your nature. Using our extensive experience in elite sports performance, we help you be the best you can be with unique genetic insights.

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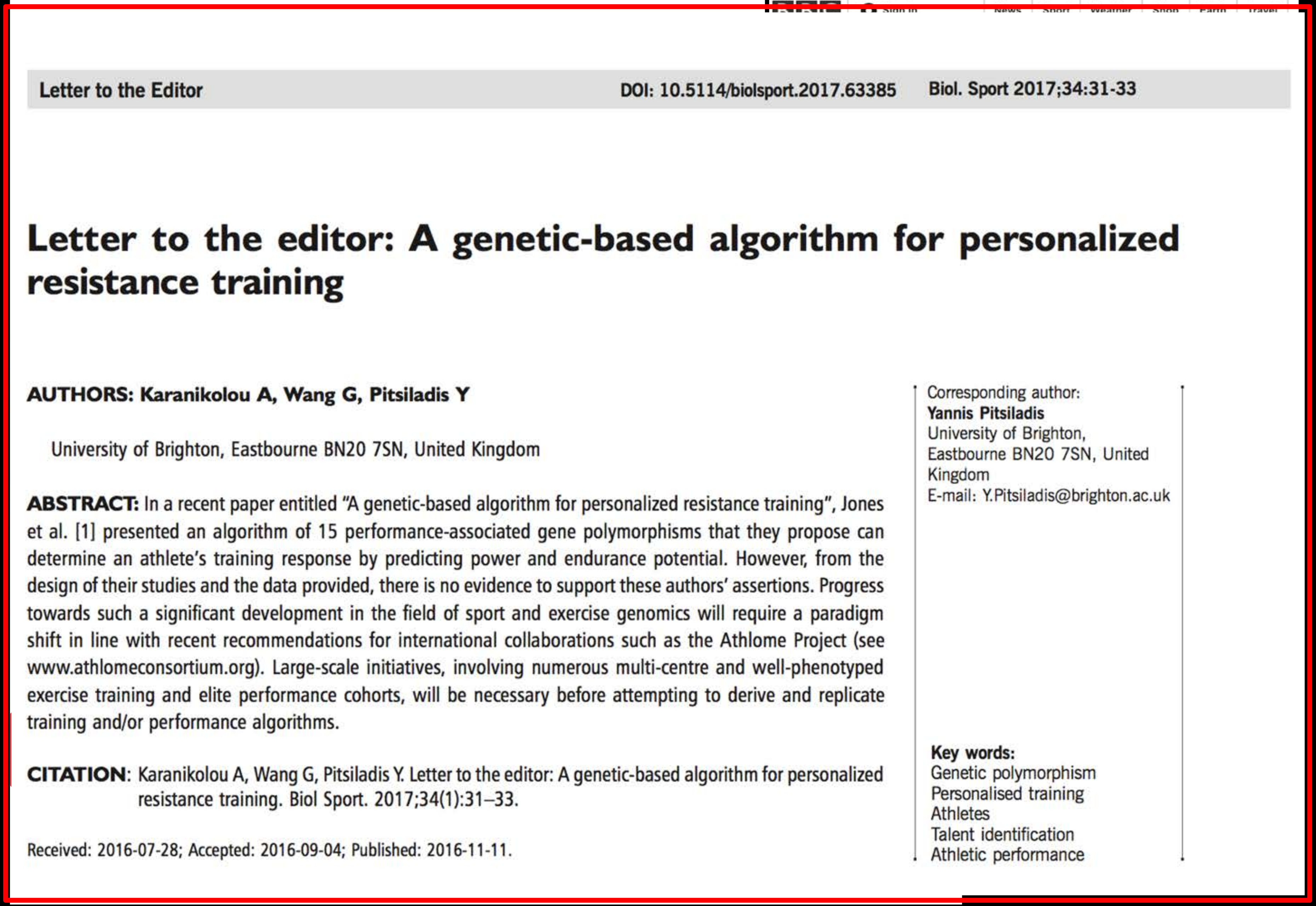
We believe there is no such thing as a 'one size fits all' approach. Long-term vitality and wellbeing should be personal, not general – we help guide this with our simple saliva swab.

A genetic-based algorithm for personalized resistance training



Letter to the Editor DOI: 10.5114/biolsport.2017.63385 Biol. Sport 2017;34:31-33

Letter to the editor: A genetic-based algorithm for personalized resistance training

AUTHORS: Karanikolou A, Wang G, Pitsiladis Y

University of Brighton, Eastbourne BN20 7SN, United Kingdom

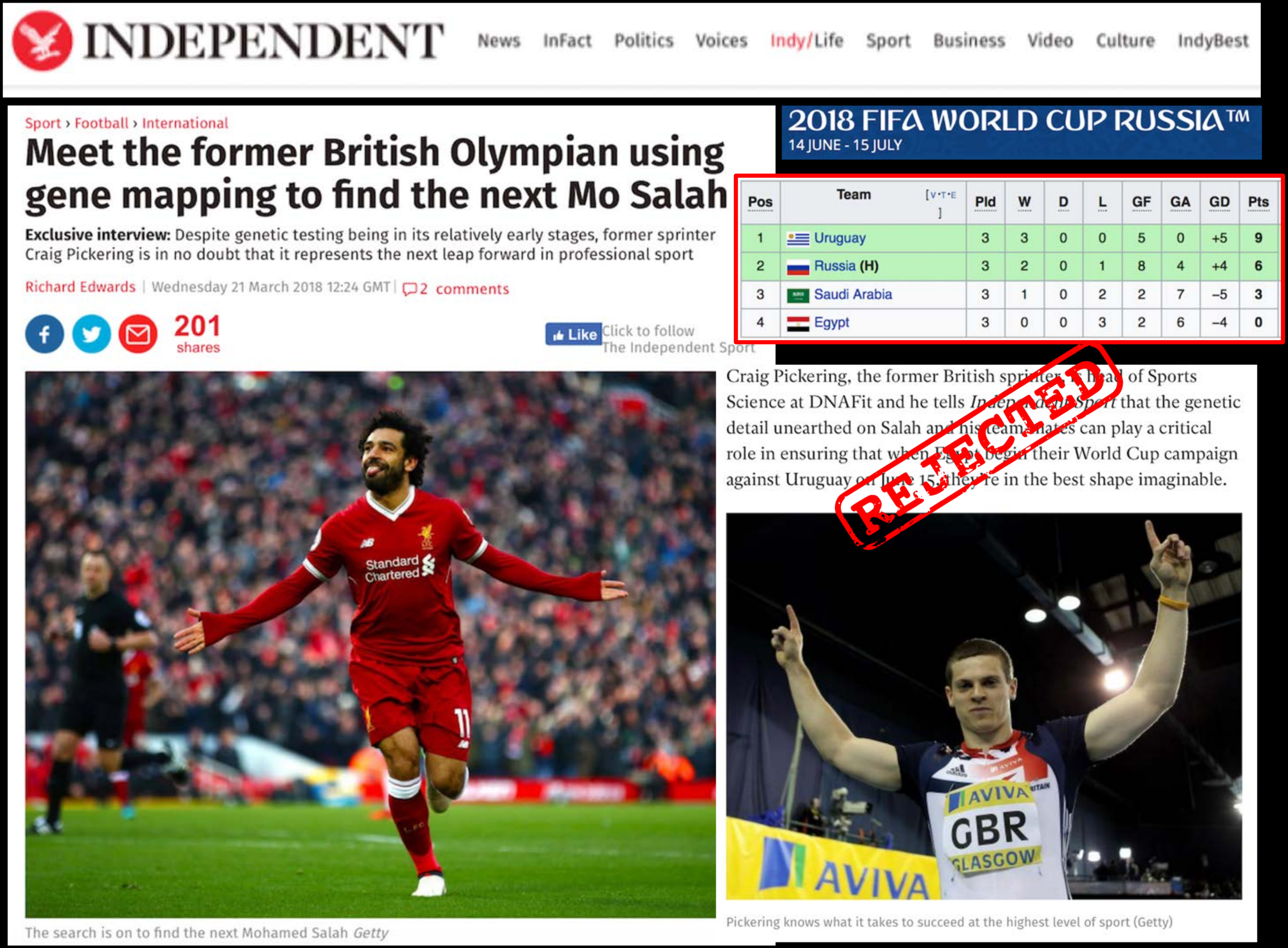
Corresponding author:
Yannis Pitsiladis
University of Brighton,
Eastbourne BN20 7SN, United Kingdom
E-mail: Y.Pitsiladis@brighton.ac.uk

ABSTRACT: In a recent paper entitled "A genetic-based algorithm for personalized resistance training", Jones et al. [1] presented an algorithm of 15 performance-associated gene polymorphisms that they propose can determine an athlete's training response by predicting power and endurance potential. However, from the design of their studies and the data provided, there is no evidence to support these authors' assertions. Progress towards such a significant development in the field of sport and exercise genomics will require a paradigm shift in line with recent recommendations for international collaborations such as the Athlome Project (see www.athlomeconsortium.org). Large-scale initiatives, involving numerous multi-centre and well-phenotyped exercise training and elite performance cohorts, will be necessary before attempting to derive and replicate training and/or performance algorithms.

CITATION: Karanikolou A, Wang G, Pitsiladis Y. Letter to the editor: A genetic-based algorithm for personalized resistance training. Biol Sport. 2017;34(1):31–33.

Received: 2016-07-28; Accepted: 2016-09-04; Published: 2016-11-11.

Key words:
Genetic polymorphism
Personalised training
Athletes
Talent identification
Athletic performance



INDEPENDENT

Sport › Football › International

Meet the former British Olympian using gene mapping to find the next Mo Salah

Exclusive interview: Despite genetic testing being in its relatively early stages, former sprinter Craig Pickering is in no doubt that it represents the next leap forward in professional sport

Richard Edwards | Wednesday 21 March 2018 12:24 GMT | 2 comments

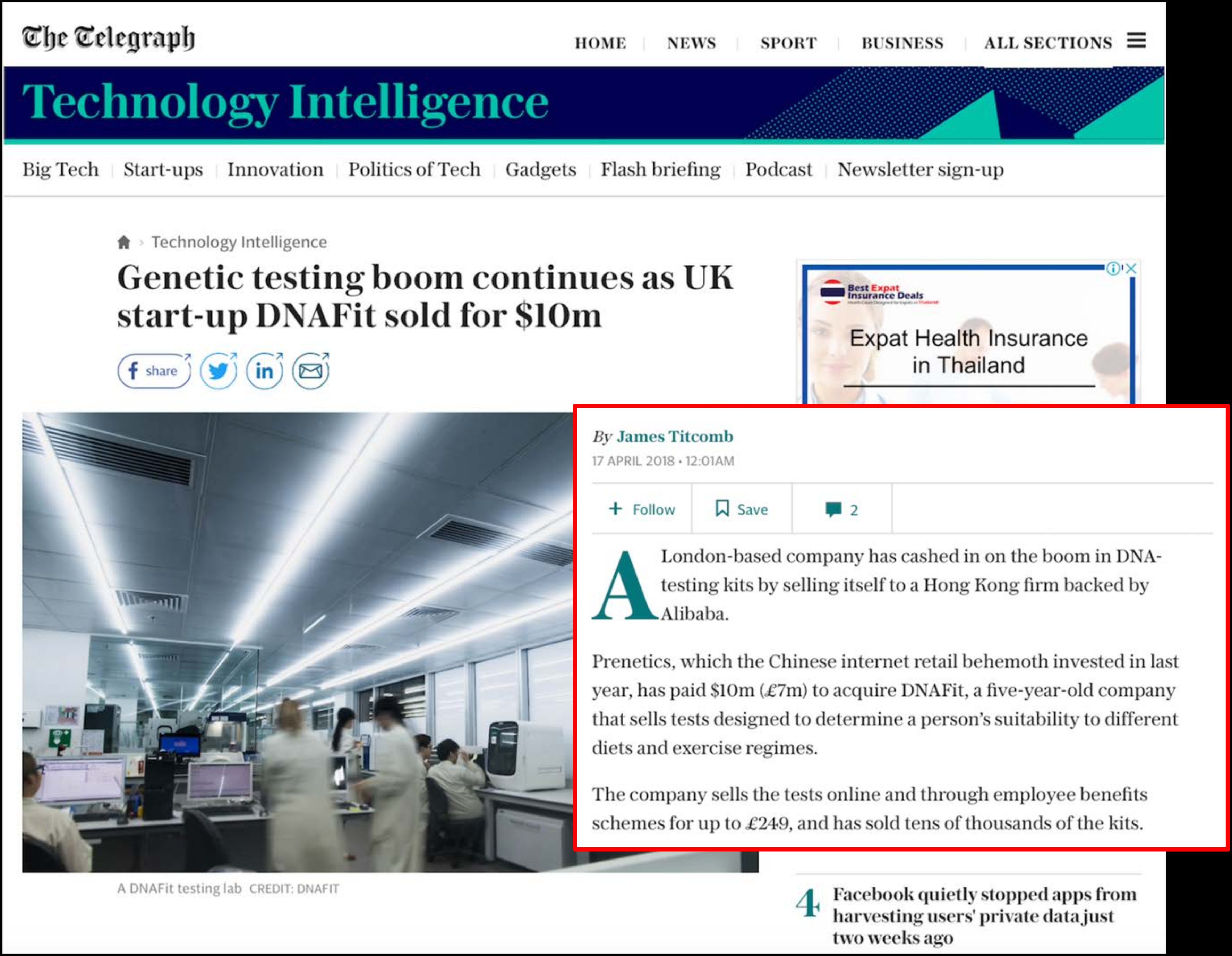
The search is on to find the next Mohamed Salah *Getty*

2018 FIFA WORLD CUP RUSSIA™
14 JUNE - 15 JULY

Pos	Team [v·t·e]	Pld	W	D	L	GF	GA	GD	Pts
1	Uruguay	3	3	0	0	5	0	+5	**9**
2	Russia **(H)**	3	2	0	1	8	4	+4	**6**
3	Saudi Arabia	3	1	0	2	2	7	−5	**3**
4	Egypt	3	0	0	3	2	6	−4	**0**

Craig Pickering, the former British sprinter, is head of Sports Science at DNAFit and he tells *Independent Sport* that the genetic detail unearthed on Salah and his teammates can play a critical role in ensuring that when Egypt begin their World Cup campaign against Uruguay on June 15 they're in the best shape imaginable.

Pickering knows what it takes to succeed at the highest level of sport (Getty)



Genetic testing boom continues as UK start-up DNAFit sold for $10m

A DNAFit testing lab CREDIT: DNAFIT

By **James Titcomb**

17 APRIL 2018 • 12:01AM

A London-based company has cashed in on the boom in DNA-testing kits by selling itself to a Hong Kong firm backed by Alibaba.

Prenetics, which the Chinese internet retail behemoth invested in last year, has paid $10m (£7m) to acquire DNAFit, a five-year-old company that sells tests designed to determine a person's suitability to different diets and exercise regimes.

The company sells the tests online and through employee benefits schemes for up to £249, and has sold tens of thousands of the kits.

4 Facebook quietly stopped apps from harvesting users' private data just two weeks ago

Olympic Selection using NGS

South China Morning Post EDITION: HONG KONG ▾ **THU** SEP 13, 2018

SCIENCE

HK CHINA ASIA WORLD COMMENT BUSINESS TECH LIFE CULTURE SPORT WEEK IN ASIA POST MAG

News / China / Science

China science

Gattacca by 2022? China to select Winter Olympics athletes by their genes

Sporting hopefuls will have to undergo whole genome sequencing as part of preparations by the host nation

PUBLISHED : Friday, 31 August, 2018, 4:06pm
UPDATED : Tuesday, 04 September, 2018, 1:55pm

COMMENTS: 18

China's athletic hopefuls for the 2022 Winter Olympics will have to undergo genetic screening for a chance to represent the host nation.

Stephen Chen

INKSTONE: CHINA NEWS BRIEFING

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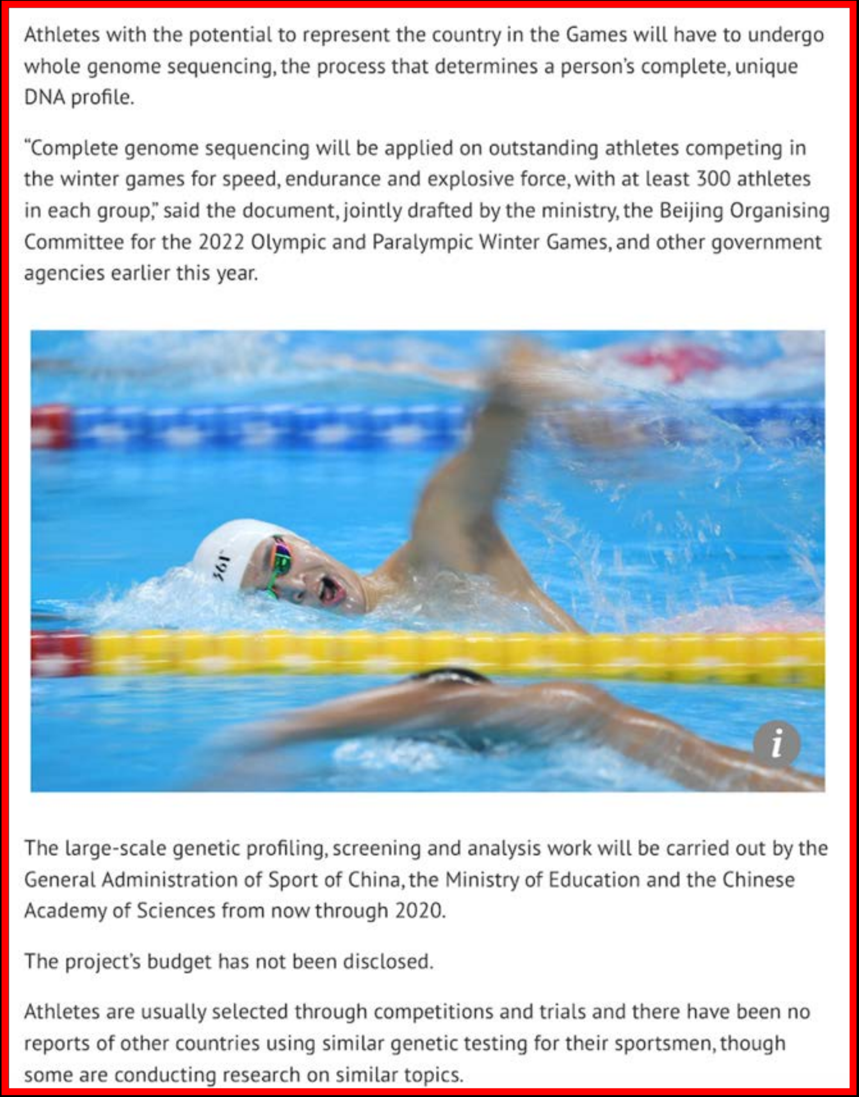


Athletes with the potential to represent the country in the Games will have to undergo whole genome sequencing, the process that determines a person's complete, unique DNA profile.

"Complete genome sequencing will be applied on outstanding athletes competing in the winter games for speed, endurance and explosive force, with at least 300 athletes in each group," said the document, jointly drafted by the ministry, the Beijing Organising Committee for the 2022 Olympic and Paralympic Winter Games, and other government agencies earlier this year.

The large-scale genetic profiling, screening and analysis work will be carried out by the General Administration of Sport of China, the Ministry of Education and the Chinese Academy of Sciences from now through 2020.

The project's budget has not been disclosed.

Athletes are usually selected through competitions and trials and there have been no reports of other countries using similar genetic testing for their sportsmen, though some are conducting research on similar topics.

Effective new technologies …

REVIEW

Nature (2017) | doi:10.1038/nature24286

Received 13 July 2017 | Accepted 21 September 2017 | Published online 11 October 2017

doi:10.1038/nature24286

DNA sequencing at 40: past, present and future

Jay Shendure[1,2], Shankar Balasubramanian[3,4], George M. Church[5], Walter Gilbert[6], Jane Rogers[7], Jeffery A. Schloss[8] & Robert H. Waterston[1]

This review commemorates the 40th anniversary of DNA sequencing, a period in which we have already witnessed multiple technological revolutions and a growth in scale from a few kilobases to the first human genome, and now to millions of human and a myriad of other genomes. DNA sequencing has been extensively and creatively repurposed, including as a 'counter' for a vast range of molecular phenomena. We predict that in the long view of history, the impact of DNA sequencing will be on a par with that of the microscope.

The Anti-Doping Crisis in Sport

Rio Olympics 2016: Anti-doping system needs complete reform - Thomas Bach

2 August 2016 | Olympics

Bach claimed a total ban went against "natural justice" for clean Russian athletes

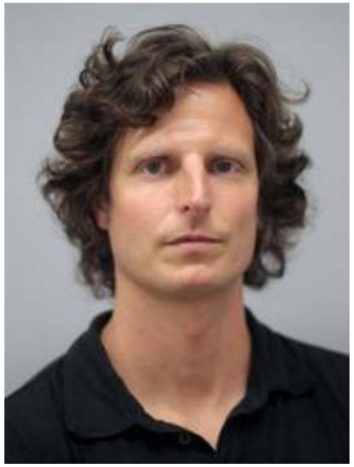
Sports Med (2018) 48:211–219
https://doi.org/10.1007/s40279-017-0765-4

CrossMark

ORIGINAL RESEARCH ARTICLE

Doping in Two Elite Athletics Competitions Assessed by Randomized-Response Surveys

Rolf Ulrich[1] · Harrison G. Pope Jr.[2,3] · Léa Cléret[4] · Andrea Petróczi[5,6] · Tamás Nepusz[5,7] · Jay Schaffer[8] · Gen Kanayama[2,3] · R. Dawn Comstock[9] · Perikles Simon[10]

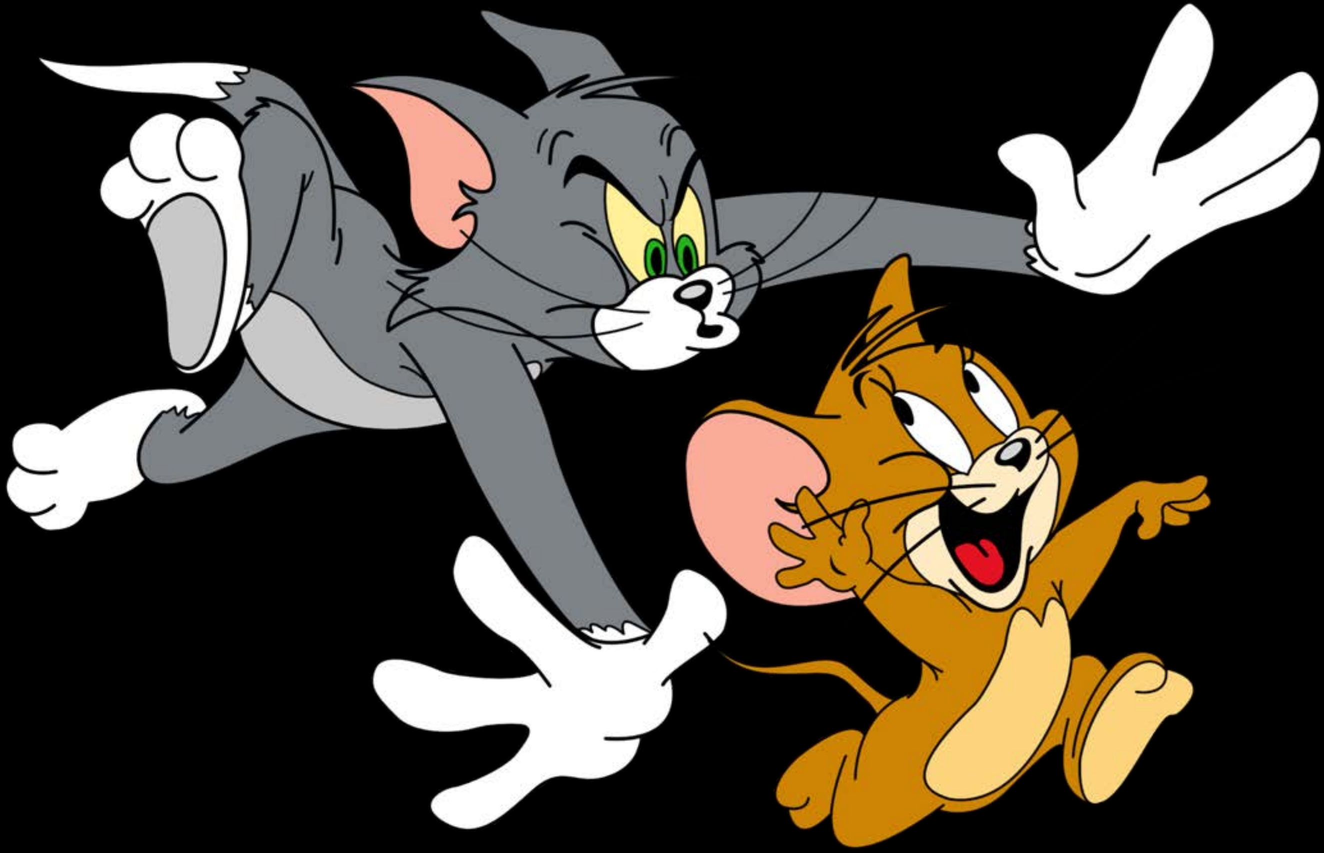


We utilized a "randomized response technique"—a method that guarantees anonymity for individuals when answering a sensitive question—to estimate the prevalence of past-year doping at two major international athletic events: the 13th International Association of Athletics Federations World Championships in Athletics (WCA) in Daegu, South Korea and the 12th Quadrennial Pan-Arab Games (PAG) in Doha, Qatar, both held in 2011.

After performing numerous sensitivity analyses, assessing the robustness of our estimates under various hypothetical scenarios of intentional or unintentional noncompliance by respondents, we found that the prevalence of past-year doping was at least 30% at WCA and 45% at PAG.

These findings suggest that biological testing greatly underestimates the true prevalence of doping in elite athletics, and indicate the need for future studies of the prevalence of doping in athletics using randomized response techniques.

A paradigm shift is needed



In sport, the cheats are usually a step ahead

Visit illumina

WORLD ANTI-DOPING AGENCY
play true

Physiol Genomics 48: 202–209, 2016.
First published January 12, 2016; doi:10.1152/physiolgenomics.00108.2015.

Blood transcriptional signature of recombinant human erythropoietin administration and implications for antidoping strategies

Jérôme Durussel,[1] Diresibachew W. Haile,[2] Kerli Mooses,[3] Evangelia Daskalaki,[4] Wendy Beattie,[1] Martin Mooses,[3] Wondyefraw Mekonen,[2] Neford Ongaro,[5] Edwin Anjila,[5] Rajan K. Patel,[1] Neal Padmanabhan,[1] Martin W. McBride,[1] John D. McClure,[1] and Yannis P. Pitsiladis[6]

[1]Institute of Cardiovascular and Medical Sciences, College of Medical, Veterinary and Life Sciences, University of Glasgow, Glasgow, United Kingdom; [2]Department of Medical Physiology, Addis Ababa University, Addis Ababa, Ethiopia; [3]Faculty of Sport and Exercise Sciences, University of Tartu, Tartu, Estonia; [4]Strathclyde Institute of Pharmacy and Biomedical Sciences, University of Strathclyde, Glasgow, United Kingdom; [5]Department of Medical Physiology, School of Medicine, College of Health Sciences, Moi University, Eldoret, Kenya; and [6]FIMS Reference Collaborating Centre of Sports Medicine for Anti-Doping Research, University of Brighton, Eastbourne, United Kingdom

Submitted 28 October 2015; accepted in final form 7 January 2016

SCO Group: 19 endurance trained males living and training at or near sea-level (Glasgow, Scotland)

KEN Group: 20 Kenyan endurance runners living and training at moderate altitude ~2150 m (Eldoret, Kenya)

INTERNATIONAL OLYMPIC COMMITTEE

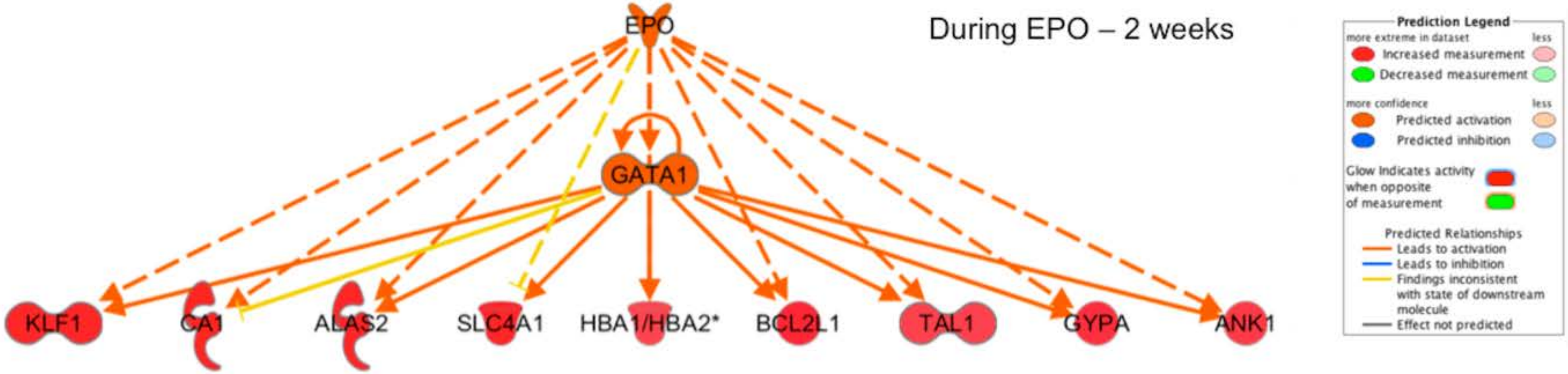
August, 2017

Next Generation Anti-Doping Tests

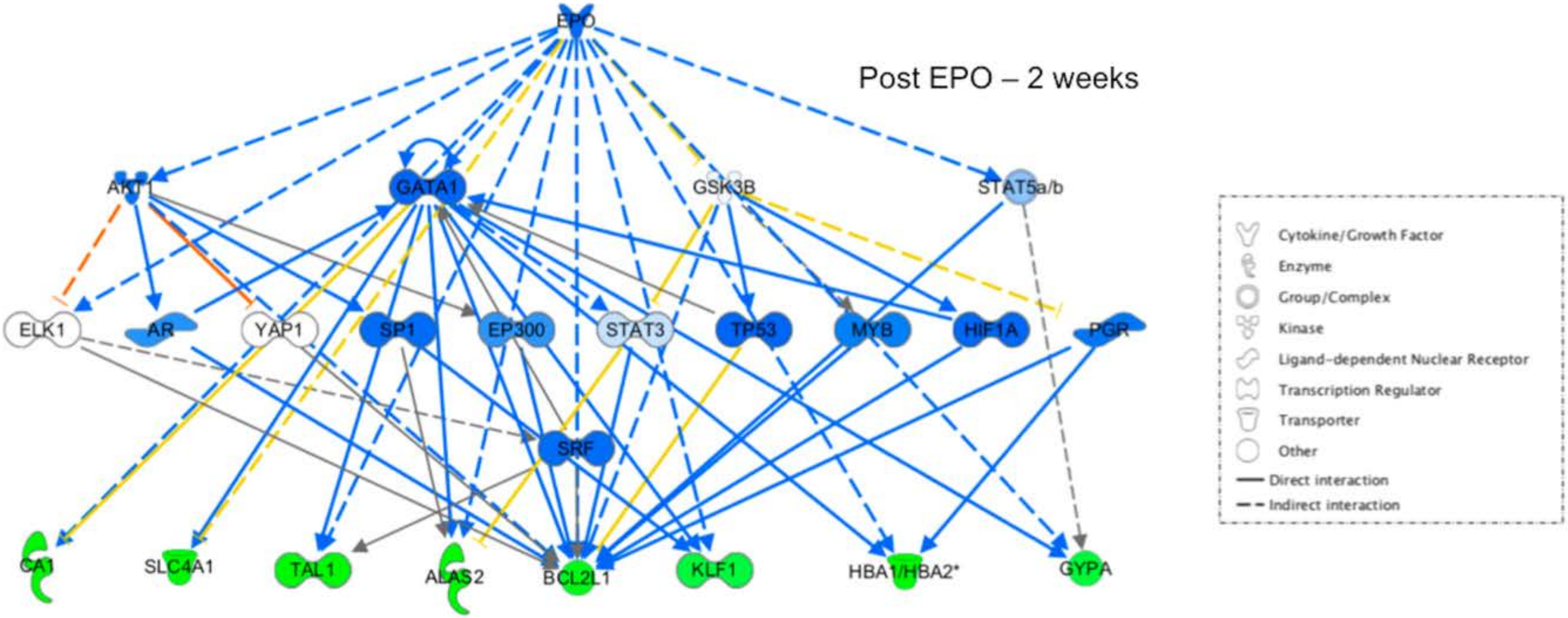
Application	Human Transcriptome Array 2.0, Thermo Fisher Scientific		
Biological replicates	N=10		
Comparison	2 days Epo	2 weeks Epo	2 weeks post Epo
Transcripts/ genes	67,528	67,528	67,528
Criteria	FDR<0.05	FDR<0.05	FDR<0.05
Significant transcripts/ genes	0	10,705 (3,764↓, 6,941↑)	18 (18↓)

Application	HumanHT-12 v4.0 Expression BeadChip, Illumina		
Biological replicates	N=10		
Comparison	2 days Epo	2 weeks Epo	2 weeks post Epo
Transcripts/ genes	28,007	28,007	28,007
Criteria	FDR<0.05	FDR<0.05	FDR<0.05
Significant transcripts/ genes	1↑	8,162 (4,942↓, 3,220↑)	960 (532↓, 428↑)

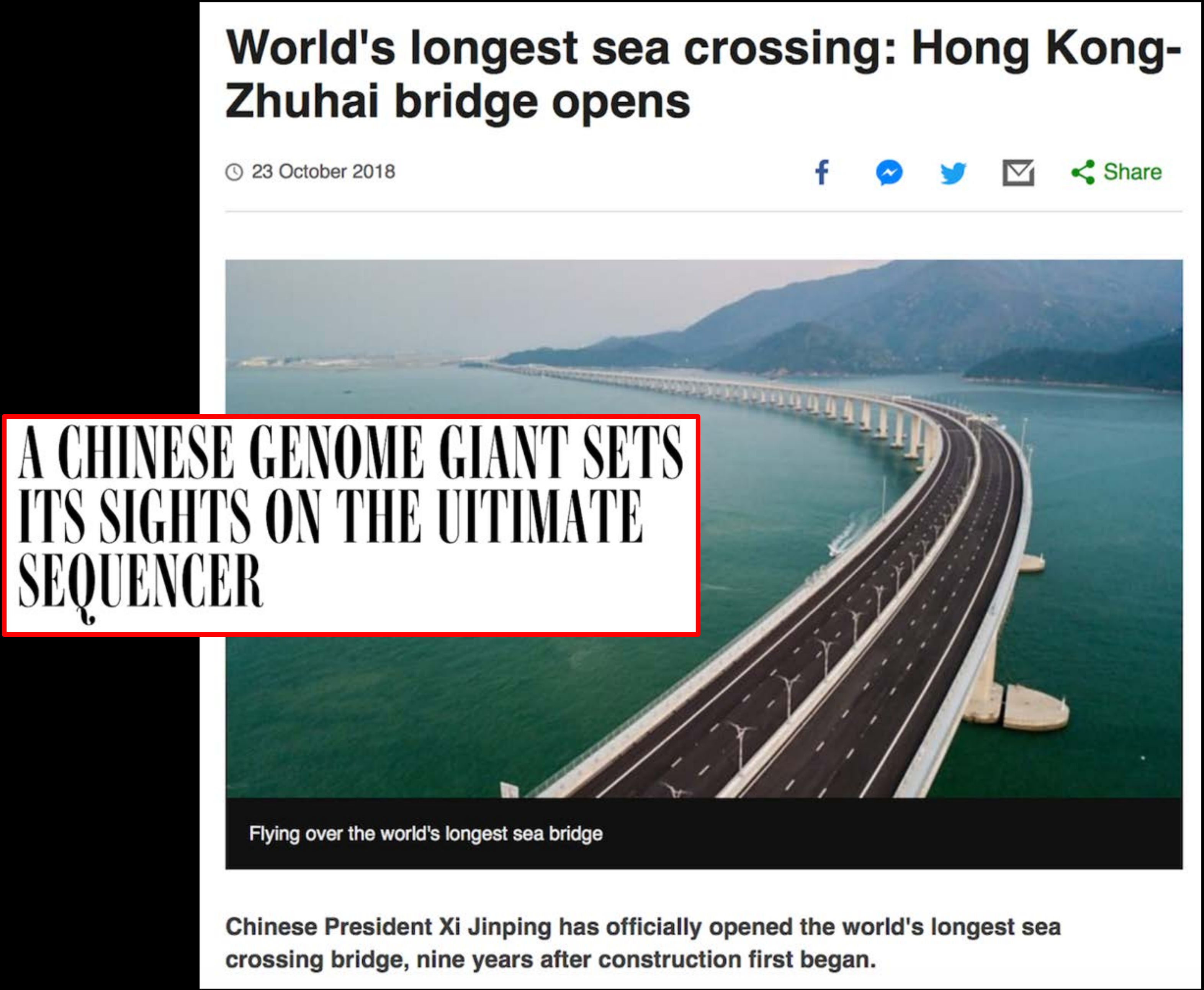
Application	RNA-Seq, Illumina		
Biological replicates	N=10		
Comparison	2 days Epo	2 weeks Epo	2 weeks post Epo
Transcripts/ genes	14,473	14,235	14,226
Criteria	FDR<0.05	FDR<0.05	FDR<0.05
Significant transcripts/ genes	4↑	4,831 (2,167↓, 2,664↑)	2,250 (1,414↓, 836↑)



During EPO – 2 weeks



Post EPO – 2 weeks



World's longest sea crossing: Hong Kong-Zhuhai bridge opens

23 October 2018

Flying over the world's longest sea bridge

Chinese President Xi Jinping has officially opened the world's longest sea crossing bridge, nine years after construction first began.

A CHINESE GENOME GIANT SETS ITS SIGHTS ON THE ULTIMATE SEQUENCER

华大基因
BGI

Industry	Genome sequencing
Founded	September 9, 1999 (Beijing)
Headquarters	Shenzhen, Guangdong, China
Number of locations	Shenzhen, Hong Kong, Wuhan, Hangzhou, Beijing, China; Boston, USA; Copenhagen, Denmark; Brisbane, Australia
Area served	Worldwide
Key people	Yang Huanming (Chairman) Wang Jian (President) Xun Xu (rotating CEO) Yang Shuang (COO)
Divisions	BGI China (Mainland) BGI Asia Pacific BGI Americas (North and South America) BGI Europe (Europe and Africa)
Subsidiaries	**List of subsidiaries:** [show]
Website	www.bgi.com/global/ www.genomics.cn

27th October, 2018

A CHINESE GENOME GIANT SETS ITS SIGHTS ON THE UITIMATE SEQUENCER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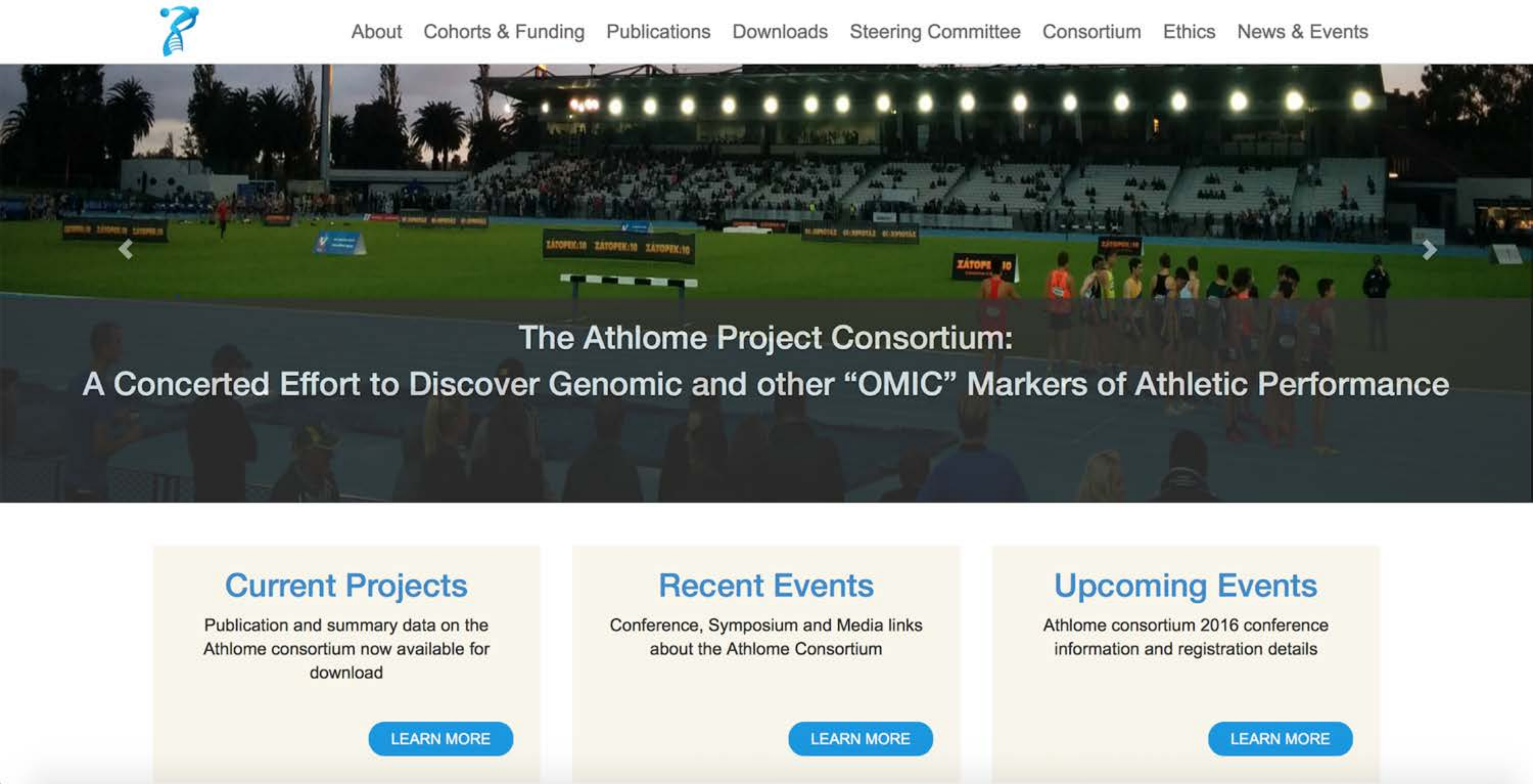
Application	RNA-Seq, BGI		
Biological replicates	N=10		
Comparison	2 days Epo	2 weeks Epo	2 weeks post Epo
Transcripts/ genes	-	-	-
Criteria	FDR<0.05	FDR<0.05	FDR<0.05
Significant transcripts/ genes	149 (145↑, 4↓)	4,168 (2,077↓, 2,091↑)	3,332 (1,917↓, 1,415↑)

Athlome Project



The Athlome Project Consortium:
A Concerted Effort to Discover Genomic and other "OMIC" Markers of Athletic Performance

Current Projects

Publication and summary data on the Athlome consortium now available for download

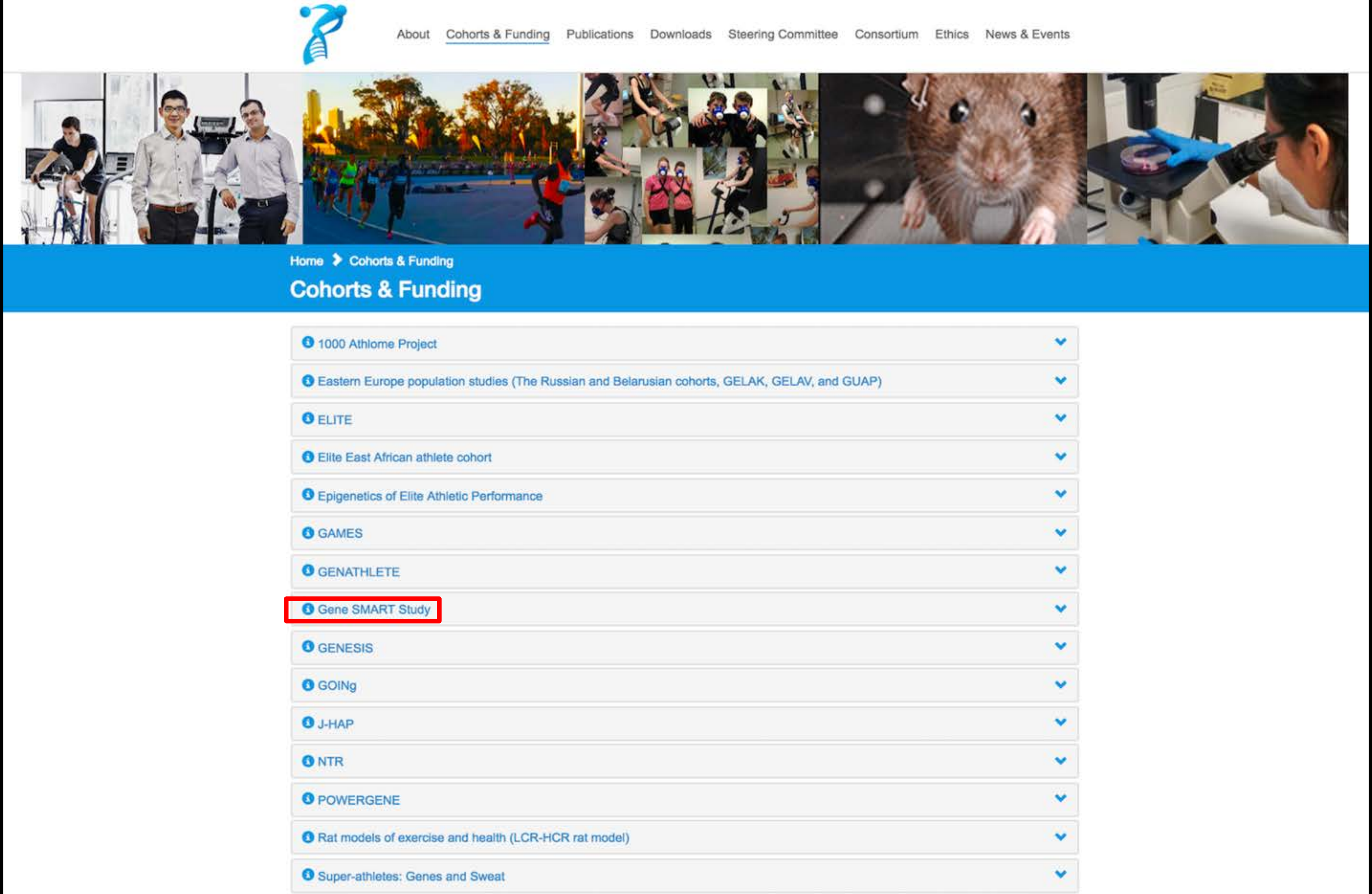
Recent Events

Conference, Symposium and Media links about the Athlome Consortium

Upcoming Events

Athlome consortium 2016 conference information and registration details

www.athlomeconsortium.org



Cohorts & Funding

- 1000 Athlome Project
- Eastern Europe population studies (The Russian and Belarusian cohorts, GELAK, GELAV, and GUAP)
- ELITE
- Elite East African athlete cohort
- Epigenetics of Elite Athletic Performance
- GAMES
- GENATHLETE
- Gene SMART Study
- GENESIS
- GOINg
- J-HAP
- NTR
- POWERGENE
- Rat models of exercise and health (LCR-HCR rat model)
- Super-athletes: Genes and Sweat

www.athlomeconsortium.org

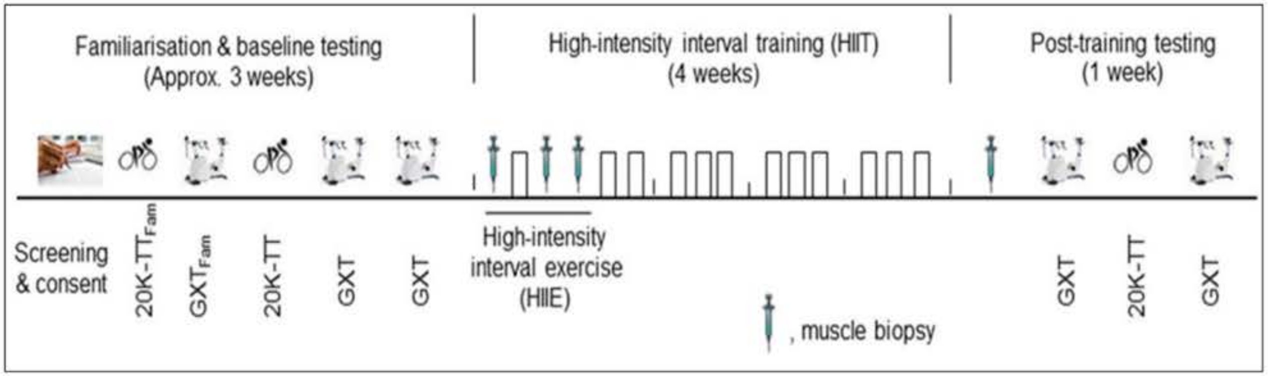
University of Brighton   Athlome PROJECT   VICTORIA UNIVERSITY   affymetrix

The use of whole-genome expression to predict exercise training response in the Gene SMART study: Preliminary results

Karanikolou A[1], Wang G[1], Papadimitriou ID[2], Yan X[2], Garnham A[2], Bishop DJ[2], Eynon N[2], Pitsiladis YP[1]
[1]FIMS Reference Collaborating Centre of Sports Medicine for Anti-Doping Research, University of Brighton, Eastbourne, UK; [2]Institute of Sport, Exercise and Active Living (ISEAL), Victoria University, Victoria, Australia

Study Design

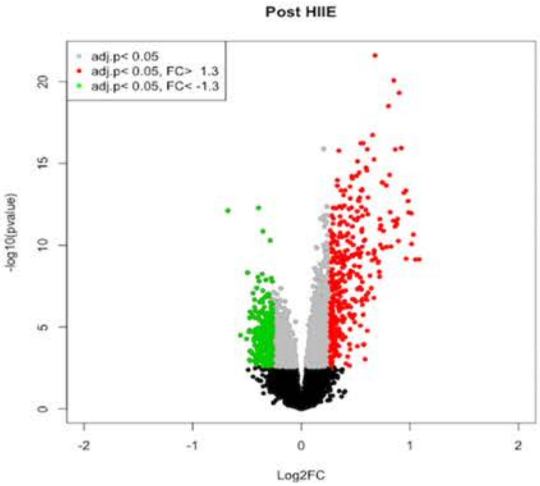
- 41 subjects, 4 time points (pre, post, 3hp, 4wp)

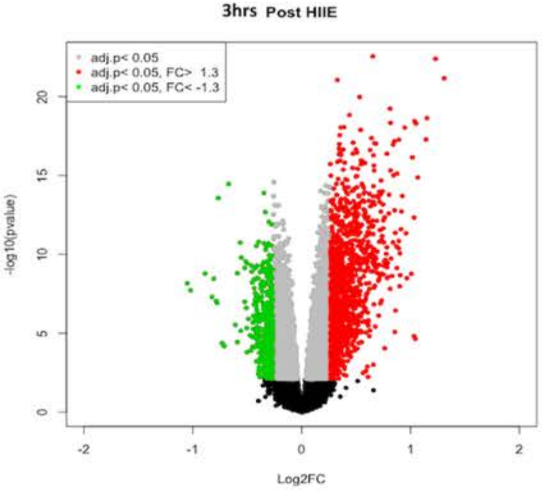


- Whole blood transcriptome analysis using GeneChip^{TM} HTA 2.0 (Affymetrix, Thermo Fisher Scientific; >285,000 full-length transcripts)
- Data analysis: Bioconductor “oligo” and “limma” packages
- Differentially expressed transcripts were reported at 5% false discovery rate (FDR)

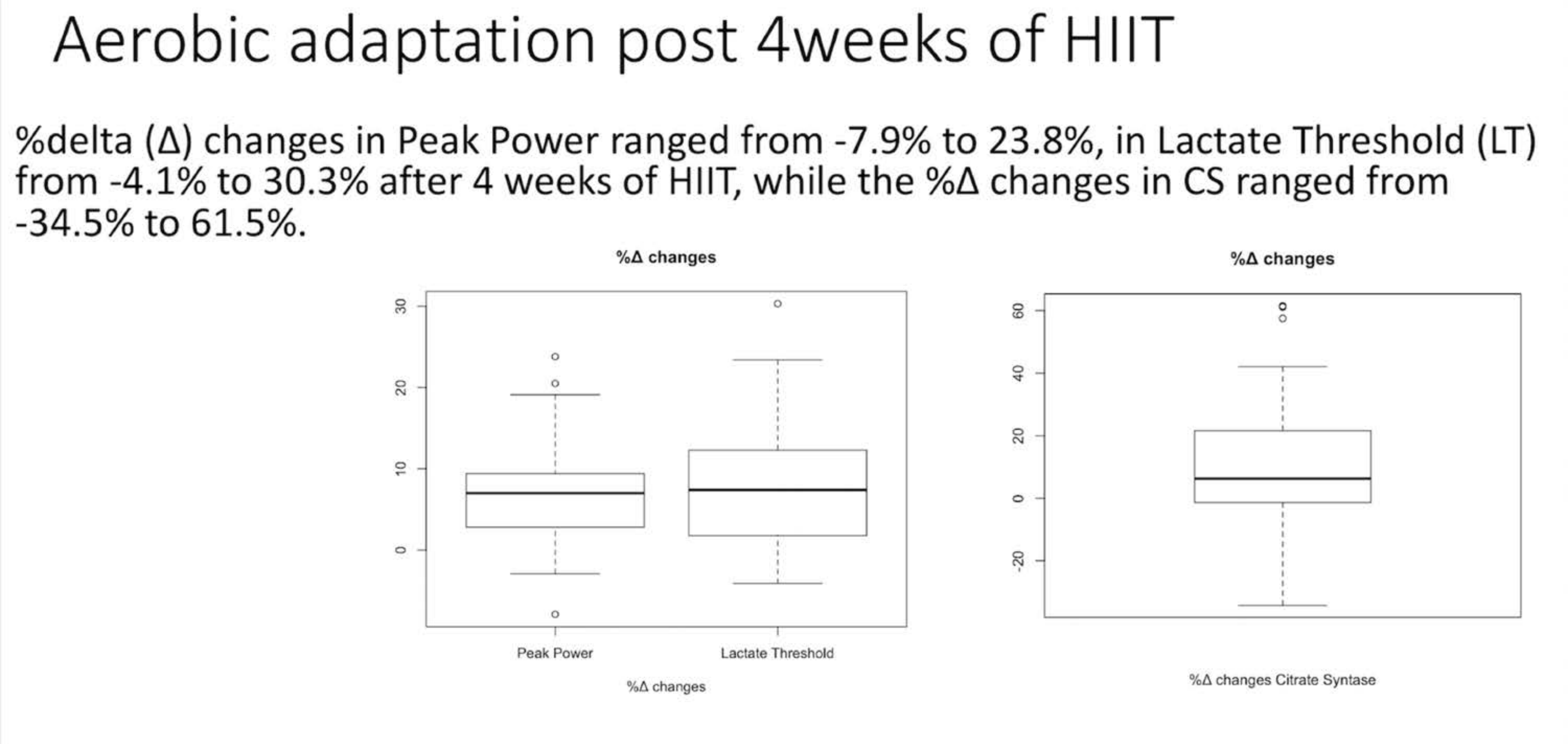
Differentially expressed transcripts

- 3,655 and 11,324 transcripts were differentially expressed immediately and 3hrs post HIIE (adj *p* value <0.05), respectively
- 1,417 were in common between the 2 time points
- No transcripts were differentially expressed after 4 weeks of HIIT





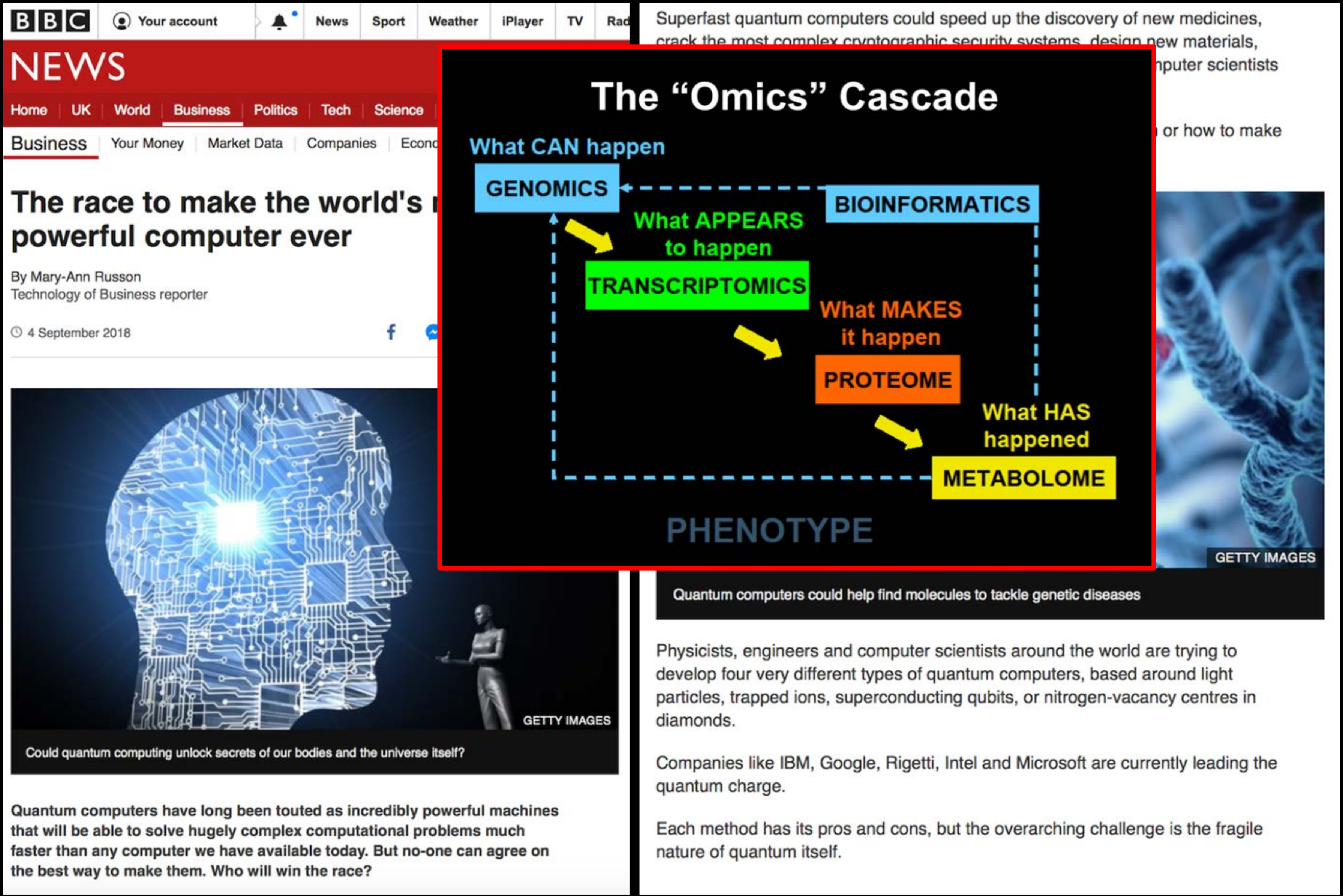
Gene SMART Study



Aerobic adaptation post 4weeks of HIIT

%delta (Δ) changes in Peak Power ranged from -7.9% to 23.8%, in Lactate Threshold (LT) from -4.1% to 30.3% after 4 weeks of HIIT, while the %Δ changes in CS ranged from -34.5% to 61.5%.

Machine Learning & Artificial Intellegence



The race to make the world's powerful computer ever

By Mary-Ann Russon
Technology of Business reporter

4 September 2018

Could quantum computing unlock secrets of our bodies and the universe itself?

Quantum computers have long been touted as incredibly powerful machines that will be able to solve hugely complex computational problems much faster than any computer we have available today. But no-one can agree on the best way to make them. Who will win the race?

The "Omics" Cascade

What CAN happen

GENOMICS

BIOINFORMATICS

What APPEARS to happen

TRANSCRIPTOMICS

What MAKES it happen

PROTEOME

What HAS happened

METABOLOME

PHENOTYPE

Superfast quantum computers could speed up the discovery of new medicines, crack the most complex cryptographic security systems, design new materials,

puter scientists

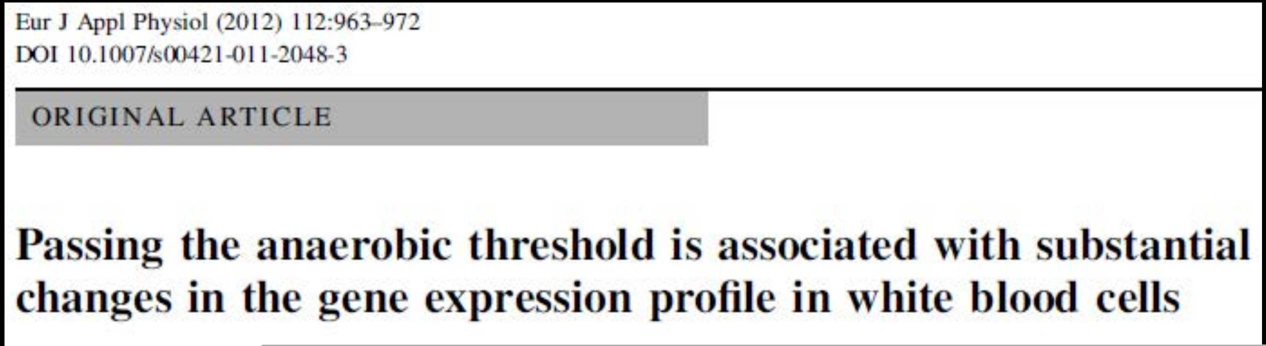
or how to make

Quantum computers could help find molecules to tackle genetic diseases

Physicists, engineers and computer scientists around the world are trying to develop four very different types of quantum computers, based around light particles, trapped ions, superconducting qubits, or nitrogen-vacancy centres in diamonds.

Companies like IBM, Google, Rigetti, Intel and Microsoft are currently leading the quantum charge.

Each method has its pros and cons, but the overarching challenge is the fragile nature of quantum itself.

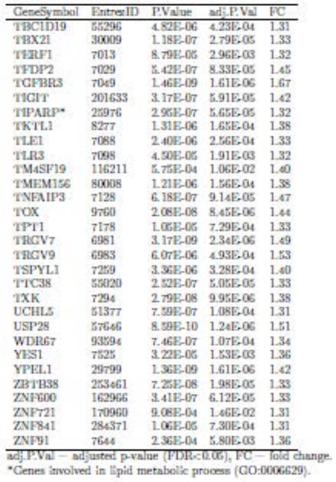


Eur J Appl Physiol (2012) 112:963–972
DOI 10.1007/s00421-011-2048-3

ORIGINAL ARTICLE

Passing the anaerobic threshold is associated with substantial changes in the gene expression profile in white blood cells

Dmitry A. Sakharo
Maxim U. Shkurnik
Anatoly I. Grigorie



GeneSymbol	EntrezID	P.Value	adj.P.Val	FC
TBC1D19	55296	4.82E-06	4.23E-04	1.31
TBX21	30009	1.18E-07	2.79E-05	1.33
TERF1	7013	8.79E-05	2.96E-03	1.32
TFDP2	7029	5.42E-07	8.33E-05	1.45
TGFBR3	7049	1.46E-09	1.61E-06	1.67
TIGIT	201633	3.17E-07	5.91E-05	1.42
TIPARP*	25976	2.95E-07	5.65E-05	1.32
TKTL1	8277	1.31E-06	1.65E-04	1.38
TLE1	7088	2.40E-06	2.56E-04	1.33
TLR3	7098	4.50E-05	1.91E-03	1.32
TM4SF19	116211	5.75E-04	1.06E-02	1.40
TMEM156	80008	1.21E-06	1.56E-04	1.38
TNFAIP3	7128	6.18E-07	9.14E-05	1.47
TOX	9760	2.08E-08	8.45E-06	1.44
TPT1	7178	1.05E-05	7.29E-04	1.33
TRGV7	6981	3.17E-09	2.34E-06	1.49
TRGV9	6983	6.07E-06	4.93E-04	1.53
TSPYL1	7259	3.36E-06	3.28E-04	1.40
TTC38	55020	2.52E-07	5.05E-05	1.33
TXK	7294	2.79E-08	9.95E-06	1.38
UCHL5	51377	7.59E-07	1.08E-04	1.31
USP28	57646	8.59E-10	1.24E-06	1.51
WDR67	93594	7.46E-07	1.07E-04	1.34
YES1	7525	3.22E-05	1.53E-03	1.36
YPEL1	29799	1.36E-09	1.61E-06	1.42
ZBTB38	253461	7.25E-08	1.98E-05	1.33
ZNF600	162966	3.41E-07	6.12E-05	1.33
ZNF721	170960	9.08E-04	1.46E-02	1.31
ZNF841	284371	1.06E-05	7.30E-04	1.31
ZNF91	7644	2.36E-04	5.80E-03	1.36

adj.P.Val – adjusted p-value (FDR<0.05), FC – fold change.
*Genes involved in lipid metabolic process (GO:0006629).

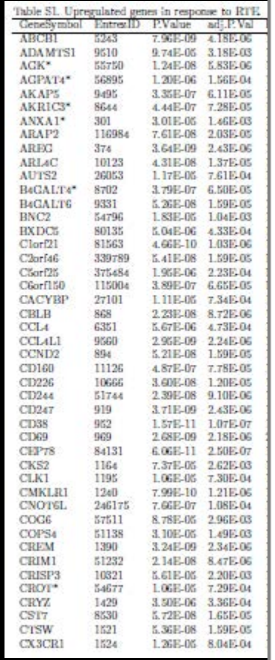
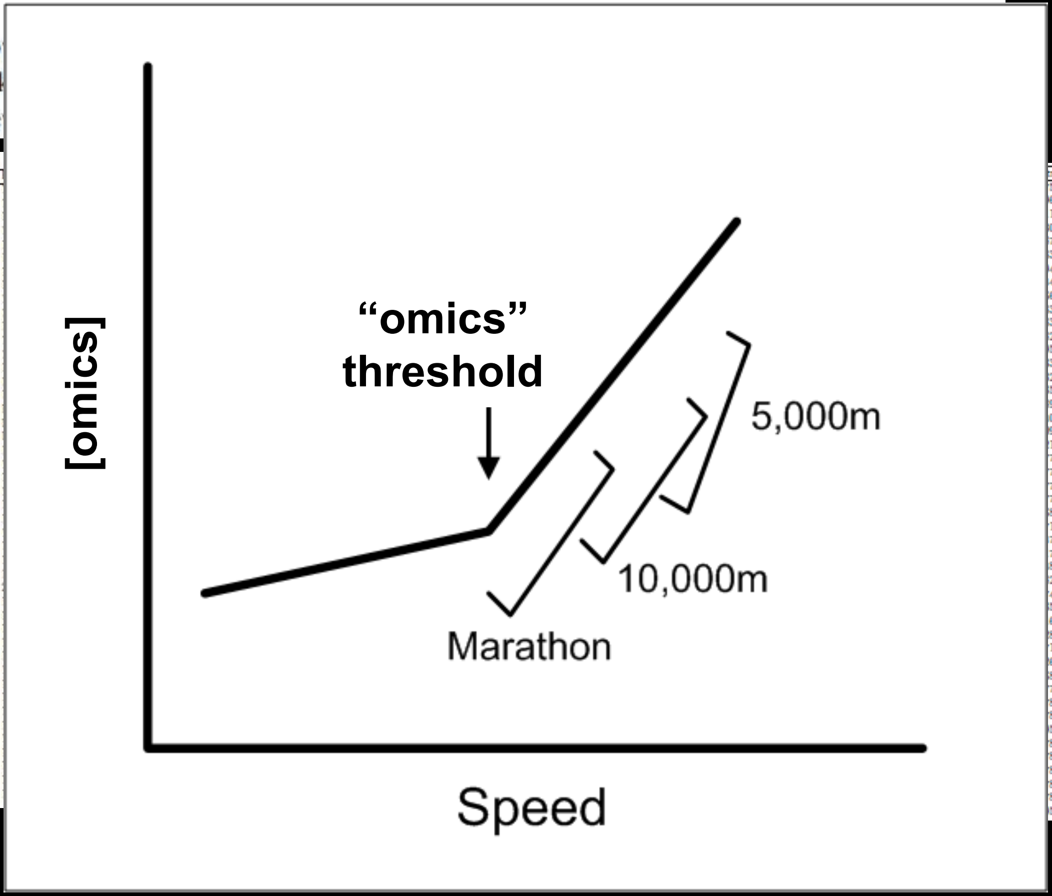
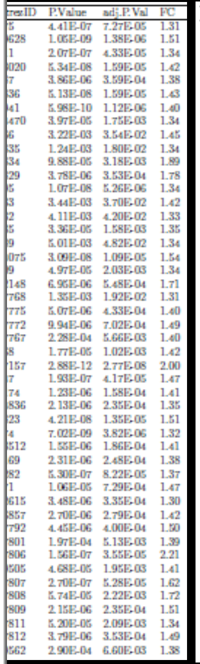


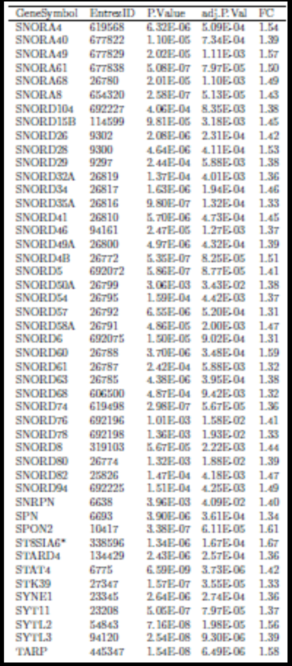
Table S1. Upregulated genes in response to RTE.

GeneSymbol	EntrezID	P.Value	adj.P.Val
ABCB1	5243	7.96E-09	4.18E-06
ADAMTS1	9510	9.74E-05	3.18E-03
AGK*	55750	1.24E-08	5.83E-06
AGPAT4*	56895	1.20E-06	1.56E-04
AKAP5	9495	3.35E-07	6.11E-05
AKR1C3*	8644	4.44E-07	7.28E-05
ANXA1*	301	3.01E-05	1.46E-03
ARAP2	116984	7.61E-08	2.03E-05
AREG	374	3.64E-09	2.43E-06
ARL4C	10123	4.31E-08	1.37E-05
AUTS2	26053	1.17E-05	7.61E-04
B4GALT4*	8702	3.79E-07	6.50E-05
B4GALT6	9331	5.26E-08	1.59E-05
BNC2	54796	1.83E-05	1.04E-03
BXDC5	80135	5.04E-06	4.33E-04
C1orf21	81563	4.66E-10	1.03E-06
C2orf46	339789	5.41E-08	1.59E-05
C5orf25	375484	1.95E-06	2.23E-04
C6orf150	115004	3.89E-07	6.65E-05
CACYBP	27101	1.11E-05	7.34E-04
CBLB	868	2.23E-08	8.72E-06
CCL4	6351	5.67E-06	4.73E-04
CCL4L1	9560	2.95E-09	2.24E-06
CCND2	894	5.21E-08	1.59E-05
CD160	11126	4.87E-07	7.78E-05
CD226	10666	3.60E-08	1.20E-05
CD244	51744	2.39E-08	9.10E-06
CD247	919	3.71E-09	2.43E-06
CD38	952	1.57E-11	1.07E-07
CD69	969	2.68E-09	2.18E-06
CEP78	84131	6.06E-11	2.50E-07
CKS2	1164	7.37E-05	2.62E-03
CLK1	1195	1.06E-05	7.30E-04
CMKLR1	1240	7.99E-10	1.21E-06
CNOT6L	246175	7.66E-07	1.08E-04
COG6	57511	8.78E-05	2.96E-03
COPS4	51138	3.10E-05	1.49E-03
CREM	1390	3.24E-09	2.34E-06
CRIM1	51232	2.14E-08	8.47E-06
CRISP3	10321	5.61E-05	2.20E-03
CROT*	54677	1.06E-05	7.29E-04
CRYZ	1429	3.50E-06	3.36E-04
CST7	8530	5.72E-08	1.65E-05
CTSW	1521	5.36E-08	1.59E-05
CX3CR1	1524	1.26E-05	8.04E-04

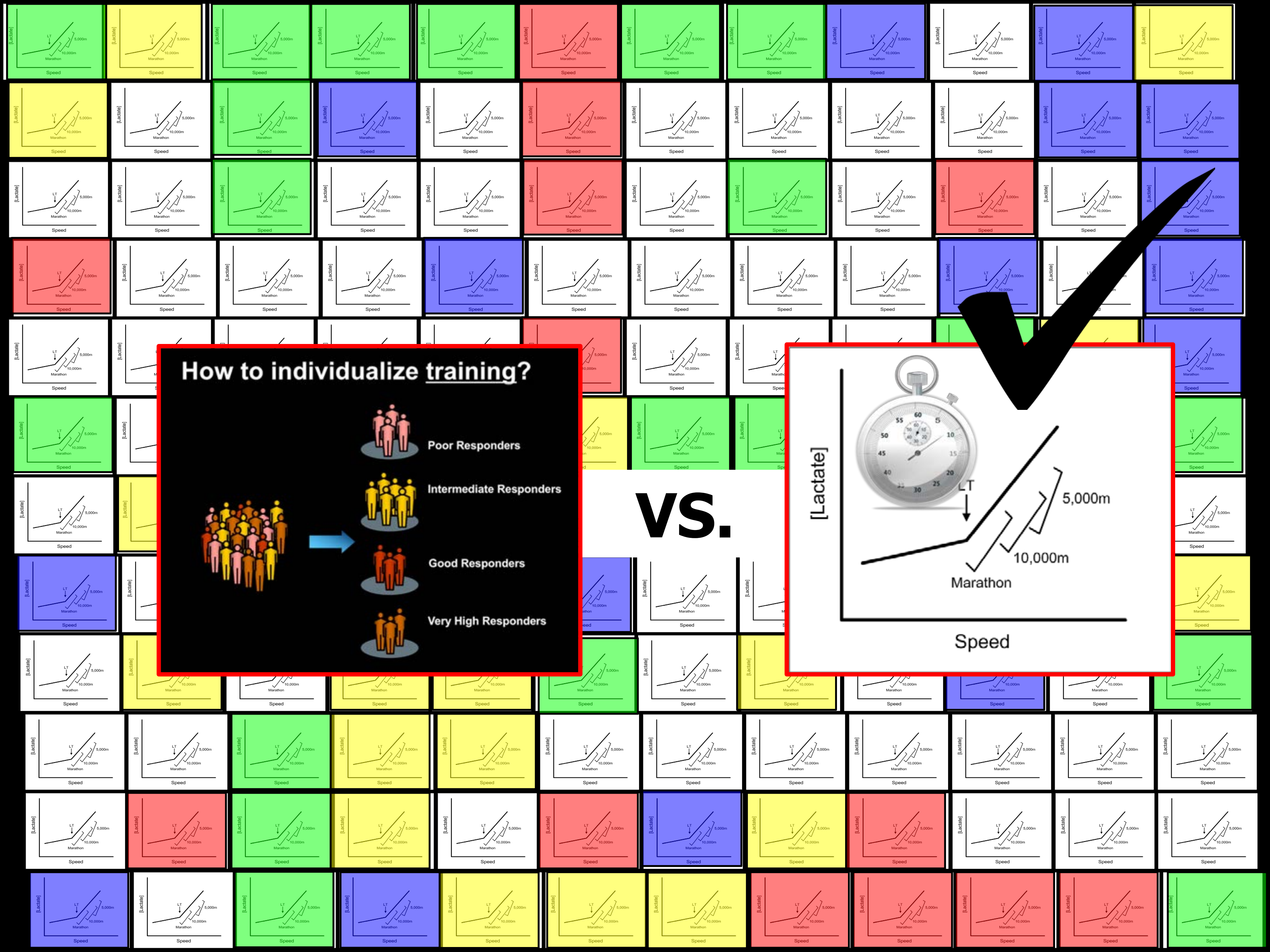




rezID	P.Value	adj.P.Val	FC
5	4.41E-07	7.27E-05	1.31
628	1.06E-09	1.38E-06	1.51
1	2.07E-07	4.33E-05	1.34
020	5.34E-08	1.59E-05	1.42
7	3.86E-06	3.59E-04	1.38
36	5.13E-08	1.59E-05	1.43
41	5.98E-10	1.12E-06	1.40
470	3.97E-05	1.75E-03	1.34
6	3.22E-03	3.54E-02	1.45
35	1.24E-03	1.80E-02	1.34
34	9.88E-05	3.18E-03	1.89
29	3.78E-06	3.53E-04	1.78
5	1.07E-08	5.26E-06	1.34
3	3.44E-03	3.70E-02	1.42
2	4.11E-03	4.20E-02	1.33
5	3.36E-05	1.58E-03	1.35
9	5.01E-03	4.82E-02	1.34
075	3.09E-08	1.09E-05	1.54
9	4.97E-05	2.03E-03	1.34
148	6.95E-06	5.48E-04	1.71
768	1.35E-03	1.92E-02	1.31
775	5.07E-06	4.33E-04	1.40
772	9.94E-06	7.02E-04	1.49
767	2.28E-04	5.66E-03	1.40
8	1.77E-05	1.02E-03	1.42
157	2.88E-12	2.77E-08	2.00
7	1.93E-07	4.17E-05	1.47
74	1.23E-06	1.58E-04	1.41
836	2.13E-06	2.35E-04	1.35
23	4.21E-08	1.35E-05	1.51
4	7.02E-09	3.82E-06	1.32
512	1.55E-06	1.86E-04	1.41
69	2.31E-06	2.48E-04	1.38
82	5.30E-07	8.22E-05	1.37
1	1.06E-05	7.29E-04	1.47
615	3.48E-06	3.35E-04	1.30
857	2.70E-06	2.79E-04	1.42
792	4.45E-06	4.00E-04	1.50
801	1.97E-04	5.13E-03	1.39
806	1.56E-07	3.55E-05	2.21
505	4.68E-05	1.95E-03	1.41
807	2.70E-07	5.28E-05	1.62
808	5.74E-05	2.22E-03	1.72
809	2.15E-06	2.35E-04	1.51
811	5.20E-05	2.09E-03	1.34
812	3.79E-06	3.53E-04	1.49
562	2.90E-04	6.60E-03	1.38



GeneSymbol	EntrezID	P.Value	adj.P.Val	FC
SNORA4	619568	6.32E-06	5.09E-04	1.54
SNORA40	677822	1.10E-05	7.34E-04	1.39
SNORA49	677829	2.02E-05	1.11E-03	1.57
SNORA61	677838	5.08E-07	7.97E-05	1.50
SNORA68	26780	2.01E-05	1.10E-03	1.49
SNORA8	654320	2.58E-07	5.13E-05	1.43
SNORD104	692227	4.06E-04	8.35E-03	1.38
SNORD15B	114599	9.81E-05	3.18E-03	1.45
SNORD26	9302	2.08E-06	2.31E-04	1.42
SNORD28	9300	4.64E-06	4.11E-04	1.53
SNORD29	9297	2.44E-04	5.88E-03	1.38
SNORD32A	26819	1.37E-04	4.01E-03	1.36
SNORD34	26817	1.63E-06	1.94E-04	1.46
SNORD35A	26816	9.80E-07	1.32E-04	1.33
SNORD41	26810	5.70E-06	4.73E-04	1.45
SNORD46	94161	2.47E-05	1.27E-03	1.37
SNORD49A	26800	4.97E-06	4.32E-04	1.39
SNORD4B	26772	5.35E-07	8.25E-05	1.51
SNORD5	692072	5.86E-07	8.77E-05	1.41
SNORD50A	26799	3.06E-03	3.43E-02	1.38
SNORD54	26795	1.59E-04	4.42E-03	1.37
SNORD57	26792	6.55E-06	5.20E-04	1.31
SNORD58A	26791	4.86E-05	2.00E-03	1.47
SNORD6	692075	1.50E-05	9.02E-04	1.31
SNORD60	26788	3.70E-06	3.48E-04	1.59
SNORD61	26787	2.42E-04	5.88E-03	1.32
SNORD63	26785	4.38E-06	3.95E-04	1.38
SNORD68	606500	4.87E-04	9.42E-03	1.32
SNORD74	619498	2.98E-07	5.67E-05	1.36
SNORD76	692196	1.01E-03	1.58E-02	1.41
SNORD78	692198	1.36E-03	1.93E-02	1.33
SNORD8	319103	5.67E-05	2.22E-03	1.44
SNORD80	26774	1.32E-03	1.88E-02	1.39
SNORD82	25826	1.47E-04	4.18E-03	1.47
SNORD94	692225	1.51E-04	4.25E-03	1.49
SNRPN	6638	3.96E-03	4.09E-02	1.40
SPN	6693	3.90E-06	3.61E-04	1.34
SPON2	10417	3.38E-07	6.11E-05	1.61
ST8SIA6*	338596	1.34E-06	1.67E-04	1.67
STARD4	134429	2.43E-06	2.57E-04	1.36
STAT4	6775	6.59E-09	3.73E-06	1.42
STK39	27347	1.57E-07	3.55E-05	1.33
SYNE1	23345	2.64E-06	2.74E-04	1.36
SYT11	23208	5.05E-07	7.97E-05	1.37
SYTL2	54843	7.16E-08	1.98E-05	1.56
SYTL3	94120	2.54E-08	9.30E-06	1.39
TARP	445347	1.54E-08	6.49E-06	1.58



How to individualize training?

Poor Responders

Intermediate Responders

Good Responders

Very High Responders

vs.

The Scientific Basis of Training

FIMS: International Perspectives

Current Sports Medicine Reports
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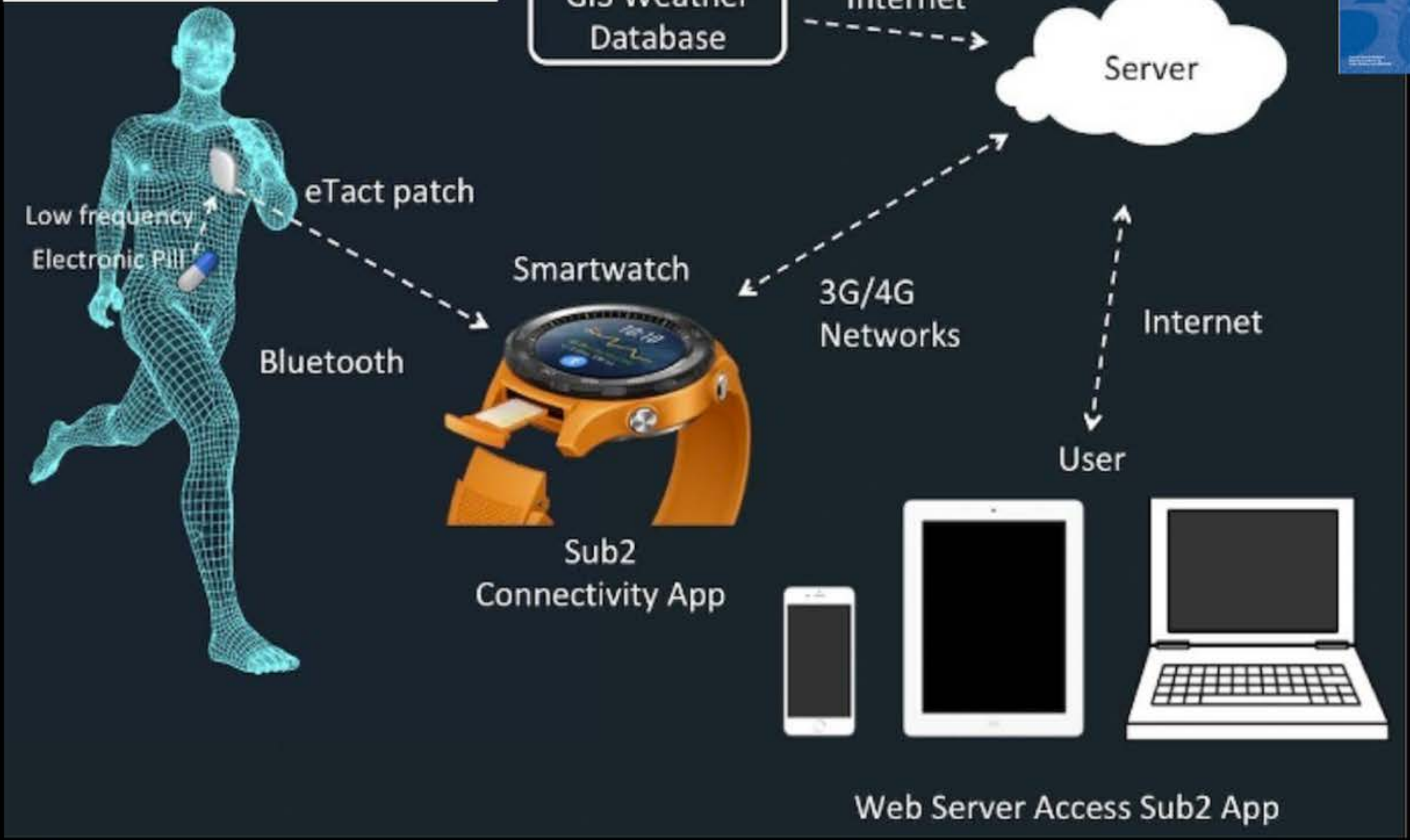
Volume 17 • Number 6 • June 2018

Necessary Steps to Accelerate the Integration of Wearable Sensors Into Recreation and Competitive Sports

Peter Düking, MSc[1,2]; Christian Stammel, MBA[2]; Billy Sperlich, PhD[1]; Shaun Sutehall, BSc[3]; Borja Muniz-Pardos, MSc[4]; Giscard Lima, BPhEd, MSc[5]; Liam Kilduff, BSc, PhD[6]; Iphigenia Keramitsoglou, MSc, PhD[7]; Guoping Li, MD[8,9]; Fabio Pigozzi, MD, PhD[5,9,10,11]; and Yannis P. Pitsiladis, MMedSci, PhD, FACSM[5,9,10]

“Intelligent” coaching

CURRENT SPORTS MEDICINE REPORTS



e-Celsius®

Performance

e-Celsius Performance®pill

Storage: Up to one year
Weight: 1.7g
Size: 17.7mm x 8.9 mm
Sampling: 30s
Accuracy: 0.2°C
Operational range: 25°C to 45°C
Records up to 2000 data
Wireless transmission (433 MHz)
Communication range: 1 m
Operational duration: 20 days

Monitor

3 pills per monitor
Multichannel: 7 monitors in parallel
Storage: 80 000 data per pill
Autonomy in charge: 24h
Size: 120mm x 70mm x 15mm

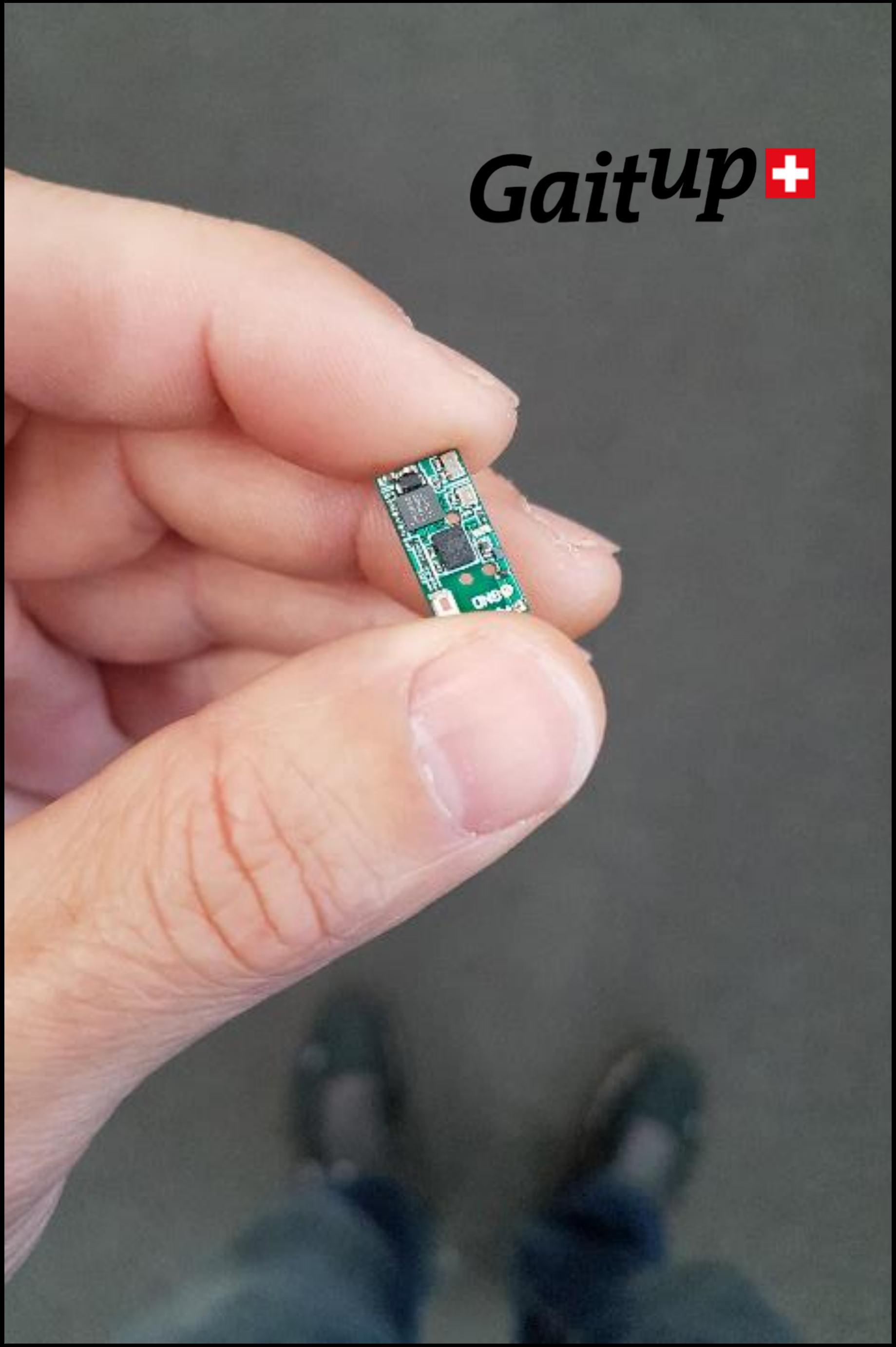
e-Celsius Performance®, is a miniaturised ingestible electronic pill that wirelessly transmits a continuous measurement of gastrointestinal temperature.

The data are stored on a monitor called e-Viewer Performance®. This device shows alerts if the measurement is outside the desired range. The activation box is used to turn the pill on from standby mode and connect with the monitor for data collection in either real time or by recovery from the internal memory of e-Celsius Performance®. Each monitor can be used with up to three pills at once to enable extended use. The monitor's interface allows the user to download data to a PC/ Mac for storage. The pill is safe, non-invasive and easy to use, leaving the gastric system after one or two days, depending on individual transit time.

Physilog®
NanoCore™

"A motion lab-on-chip"

- Hardware: IMU sensing, processing, memory, communication
- Know-how from medical applications and Swiss luxury watch industry
- Miniaturisation at its best:
  Start of project: 18g -> **Now: 0.2g**
- Weight on shoe requires more effort than anywhere else

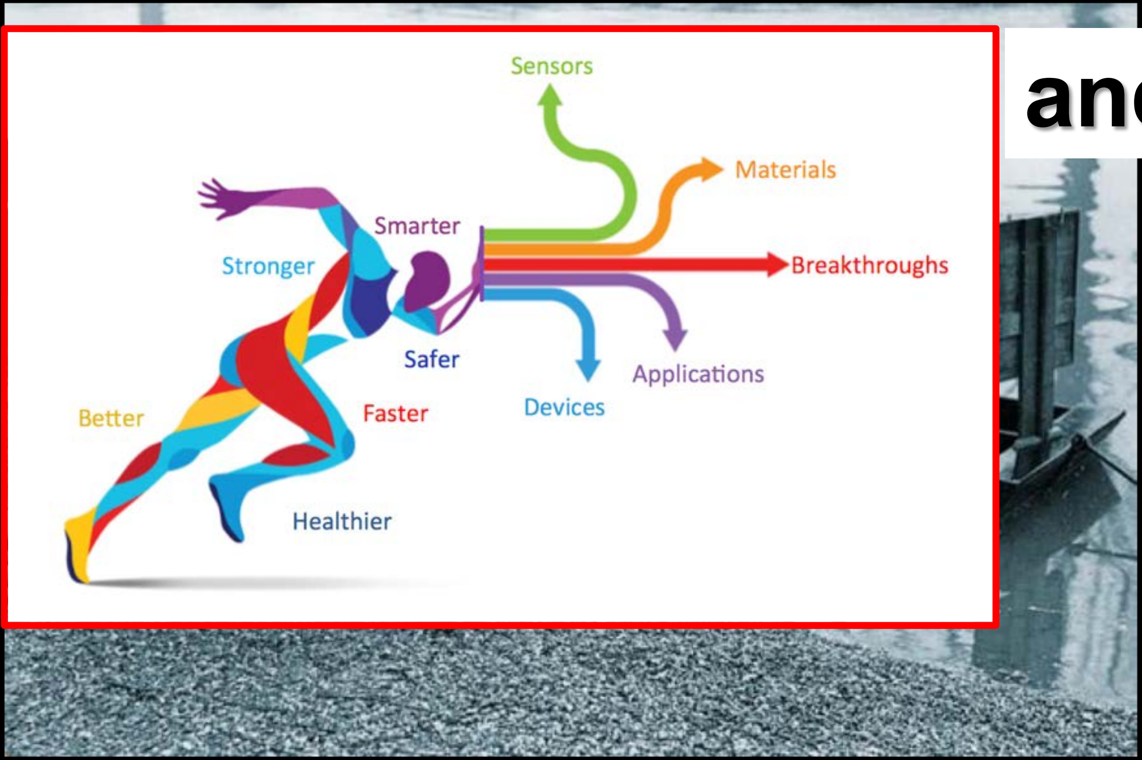


Wearable biomarker devices

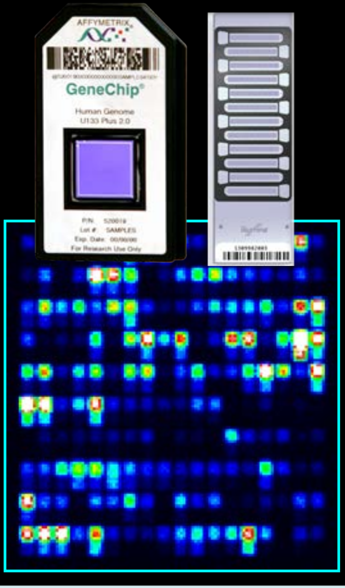
This Wearable Can Measure Your Stress Through Stress Hormones in Your Sweat

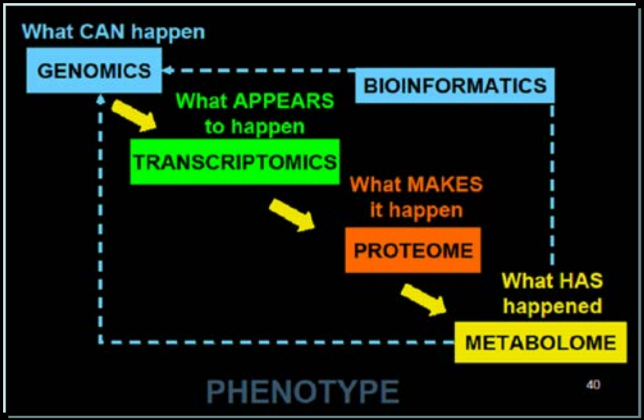
By **Cathy Russey**

The Scientific Basis of Training



and





What CAN happen

GENOMICS

BIOINFORMATICS

What APPEARS to happen

TRANSCRIPTOMICS

What MAKES it happen

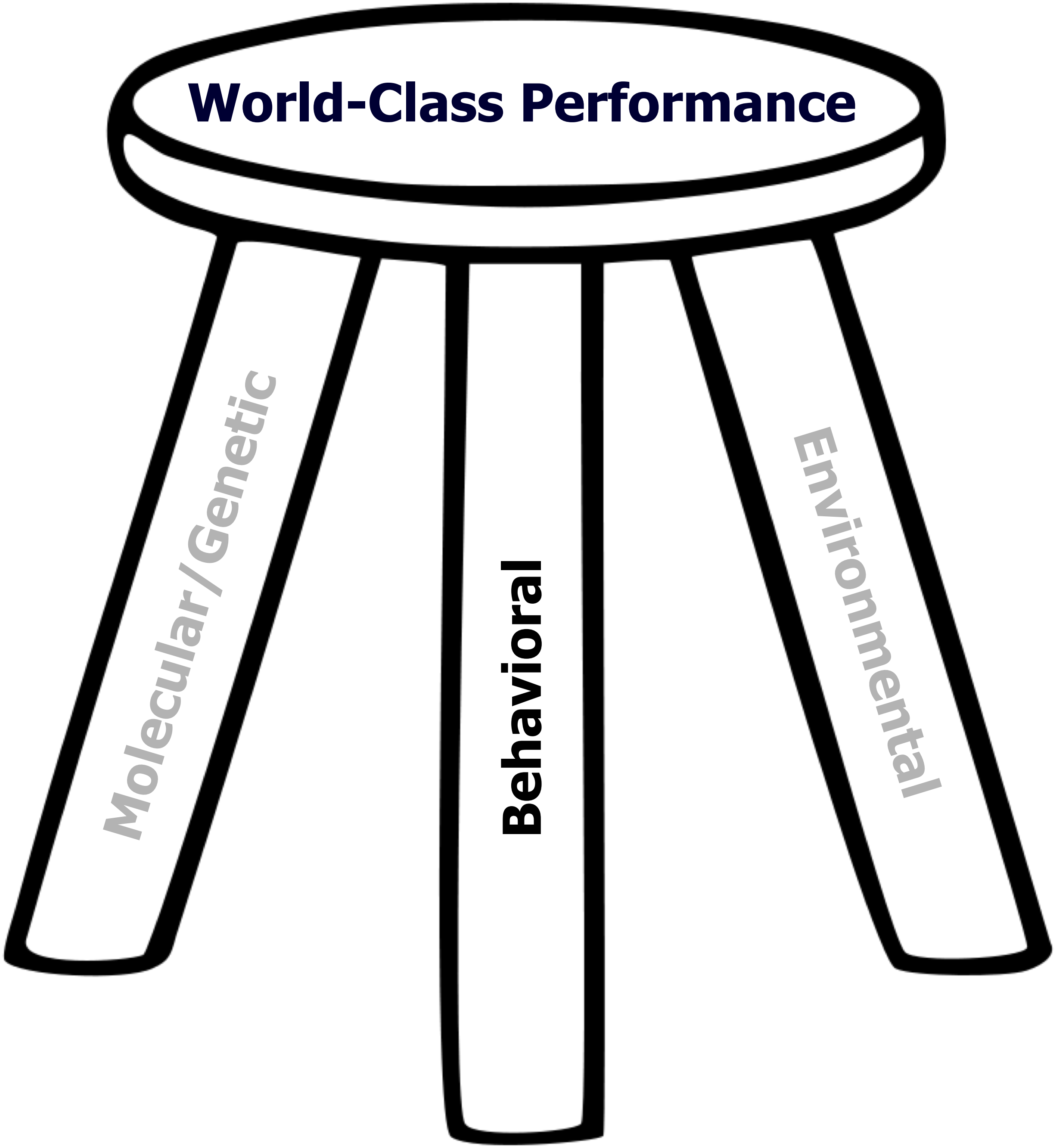
PROTEOME

What HAS happened

METABOLOME

PHENOTYPE

New bioinformatics methods will be needed



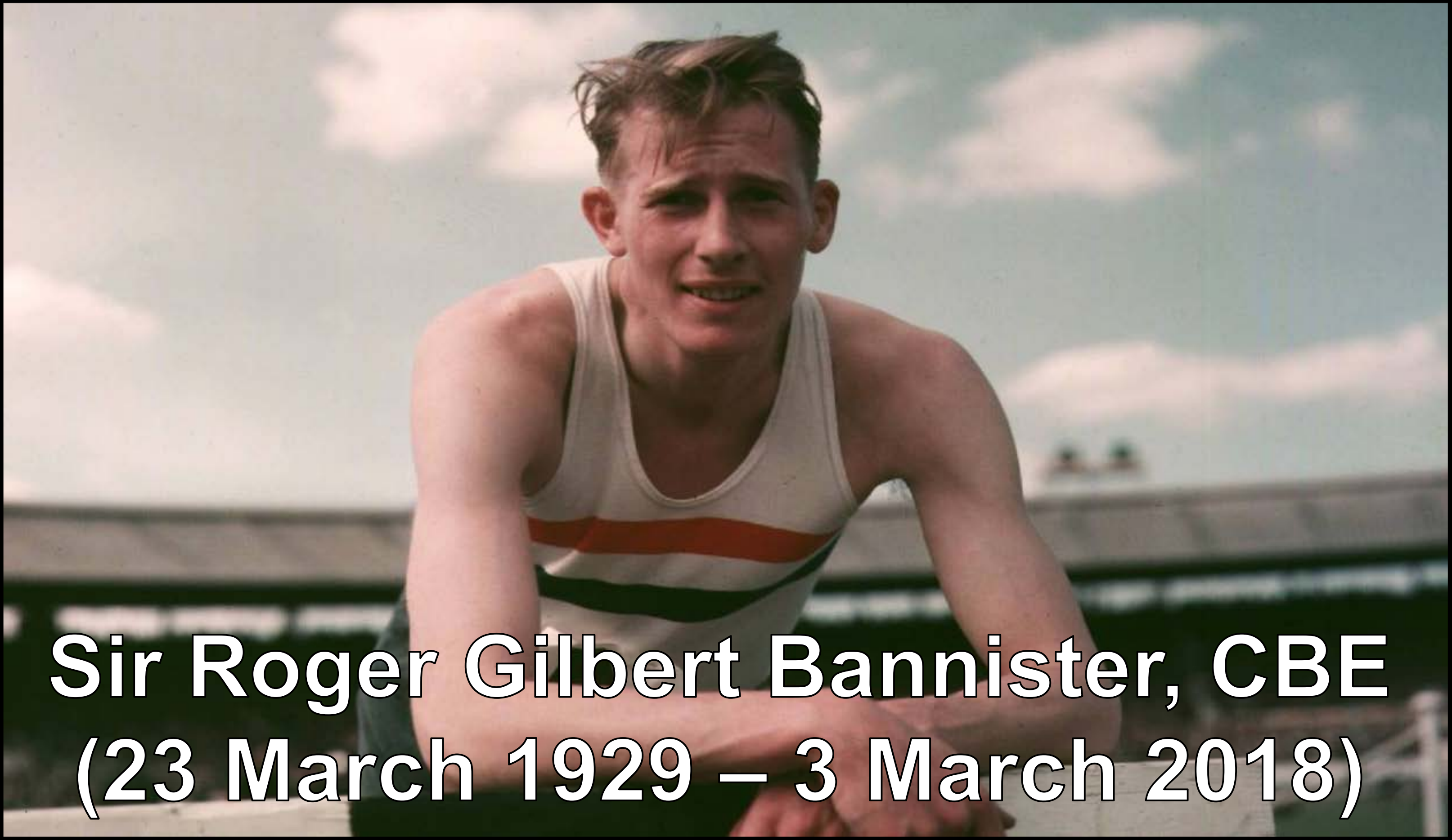
World-Class Performance

Molecular/Genetic

Behavioral

Environmental

The first sub-4-minute mile



Sir Roger Gilbert Bannister, CBE
(23 March 1929 – 3 March 2018)

John Landy
3:58.0
21st June 1954

3:58.8

Roger Bannister
3:59.4
6th May 1954

"Mile of the Century"
Vancouver Empire Games
Saturday 7th August 1954

Slides courtesy of Tim Noakes

Belief

(and have a good support team)

Bannister achieved what he believed his coach believed he could achieve.

Support team: By your actions you contribute to the perception each athlete has of her or his ultimate performance potential.

Slides courtesy of Tim Noakes

Belief

“The crucial thing that he (Stampfl) said was: ‘Well I think you can run a 3:56 mile’. If he believed that - I hope he did - it certainly was a helpful comment. And he said if you have the chance and you don’t take it you may regret it for the rest of your life”

Sir Roger Bannister May 6th 2004

Slides courtesy of Tim Noakes


RESEARCH
"White" men can't run:
Where is the scientific evidence?
Jamaica
With the recent Olympics in mind, BASES International Travel Grant
Yannis Pitsiladis and Robert Scott provide a timely report
THE MAKING OF ME
BBC
SUB2
BREAKING MARATHON BARRIERS...
The SUB2 Project (www.sub2hrs.com)
EAST AFRICAN RUNNING
TOWARDS A CROSS-DISCIPLINARY PERSPECTIVE
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Research news and discovery
In brief
Endurance running is in the genes of east Africans
the SPORTS GENE
DAVID EPSTEIN
Athlome PROJECT
Physiological GENOMICS
EXTREME EV
Matthew Syed
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The myth of talent and the power of practice
Inside the UVA Lacrosse Killing
Dallas Braden Is Perfect
The Genetic Makings Of an
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Can He Deliver a Ring to the King?
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SPEED
SPORT GENE
The Asahi Shimbun
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International Herald Tribune
AsahiWeekly
Peering Under the Ho
Different strokes
Genen kennen geen kleur
p2/3
aar een genetische schat
Essay The makings of the perfect athlete
An Everlasting Gender Gap?
desire succee
SHOES YOU LOSE
Athletic footwear is big business, fuelled by the unstoppable rise of running as a hobby. But could ditching your trainers give you better technique – and a happier body?
nature
MARTIAN METHANE An explosion of interest
MAKING MORE OF BIOMASS Bacterial production of biofuels
QUANTUM COMPUTING How, why and when
TREAD SOFTLY
How we ran in comfort before we started wearing shoes
affymetrix
part of Thermo Fisher Scientific

Thank you