

Prevalence of *HOXB13* G84E germline mutation and prostate cancer risk in the UK

Christos Mikropoulos¹, Zsofia Kote-Jarai¹, Tokhir Dadaev¹, Daniel A. Leongamornlert¹, Malgorzata Tymrakiewicz¹, Edward J. Saunders¹, Michael Jones¹, Sarah Jugurnauth-Little¹, Koveela Govindasami¹, Michelle Guy¹, , Freddy Hamdy³, Jenny Donovan⁴, David Neal², J. Athene Lane², David Dearnaley¹, Rosemary A. Wilkinson¹, Emma J. Sawyer¹, Angela Morgan¹, The UK Genetic Prostate Cancer Study Collaborators, and the ProtecT Study Group Antonis C. Antoniou⁵, Rosalind A. Eeles^{1, 6}

Disclosure slide

- Research funded by CRUK
- The Ronald and Rita McAulay Foundation

- The *HOX* genes are a subfamily of the homeobox superfamily of transcription factors
- There are *HOX* clusters on chromosomes 7 (**HOXA**), 17 (**HOXB**), 12 (**HOXC**), and 2 (**HOXD**)
- The genes within each *HOX* cluster are essential for the pattern formation of the human body
- *HOX* genes in paralogue group 13 are involved in the developing of the urogenital system in vertebrates
- *HOXB13* maintains a high expression level into adulthood in normal prostate

Germline Mutations in *HOXB13* and Prostate-Cancer Risk

Charles M. Ewing, M.S., Anna M. Ray, M.S., Ethan M. Lange, Ph.D., Kimberly A. Zuhlke, B.A., Christiane M. Robbins, M.S., Waibhav D. Tembe, Ph.D., Kathleen E. Wiley, M.S., Sarah D. Isaacs, M.S., Dorhyun Johng, B.A., Yunfei Wang, M.S., Chris Bizon, Ph.D., Guifang Yan, B.S., Marta Gielzak, B.A., Alan W. Partin, M.D., Ph.D., Vijayalakshmi Shanmugam, Ph.D., Tyler Izatt, M.S., Shripad Sinari, M.S., David W. Craig, Ph.D., S. Lilly Zheng, M.D., Patrick C. Walsh, M.D., James E. Montie, M.D., Jianfeng Xu, M.D., Dr.P.H. John D. Carpten, Ph.D., William B. Isaacs, Ph.D., and Kathleen A. Cooney, M.D.

- Prostate cancer region of linkage17q21-22
- Non-synonymous mutation in *HOXB13*, a change of **adenosine** for **guanine** (transition, c.251G→A) in the second position of codon 84 (GGA→GAA) resulting in a non-conservative substitution of glycine for glutamic acid (G84E).
- European men with prostate cancer more likely to carry the *HOXB13* G84E allele (**carrier frequency, 1.4%**) than healthy controls (carrier frequency, 0.1%) (**odds ratio in families, 20.1; 95% CI 3.5 to 803.3**)
- Carrier frequency in men with **early-onset prostate cancer (3.1%)**

International Consortium for Prostate Cancer Genetics (ICPCG)

HOXB13 is a susceptibility gene for prostate cancer: results from the International Consortium for Prostate Cancer Genetics (ICPCG)

Jianfeng Xu · Ethan M. Lange · Lingsi Lu · Siqun L. Zheng · Zhong Wang · Stephen N. Thibodeau · Lisa A. Cannon-Albright · Craig C. Teerlink · Nicola J. Camp · Anna M. Johnson · Kimberly A. Zahlke · Janet L. Stanford · Elaine A. Ostrander · Kathleen E. Wiley · Sarah D. Isaacs · Patrick C. Walsh · Christiane Maier · Manuel Luedeke · Walther Vogel · Johanna Schleutker · Tiina Wahlfors · Teuvo Tammela · Daniel Schaid · Shannon K. McDonnell · Melissa S. DeRycke · Geraldine Cancel-Tassin · Olivier Cussenot · Fredrik Wiklund · Henrik Grönberg · Ros Eeles · Doug Easton · Zoofa Kote-Jarai · Alice S. Whittemore · Chih-Lin Hsieh · Graham G. Giles · John L. Hopper · Gianluca Severi · William J. Catalona · Diptarsi Mandal · Elsa Ledet · William D. Foulkes · Nancy Hamel · Lovise Mahle · Pal Moller · Isaac Powell · Joan E. Bailey-Wilson · John D. Carpten · Daniela Seminara · Kathleen A. Cooney · William B. Isaacs · International Consortium for Prostate Cancer Genetics

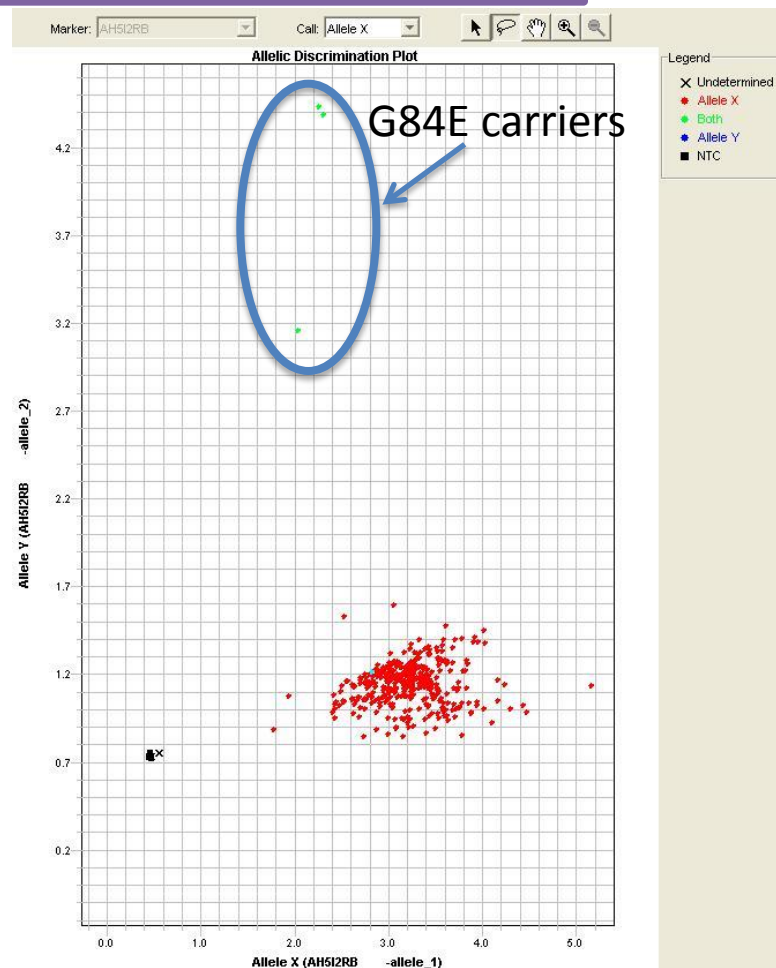
Received: 13 July 2012 / Accepted: 15 September 2012 / Published online: 12 October 2012
© The Author(s) 2012. This article is published with open access at Springerlink.com

- In this study of 2443 prostate cancer families of European descent the G84E mutation was found in 4.6% of families.
- The proportion was highest in families from the Nordic countries of Finland (22.4 %) and Sweden (8.2 %) and lower in North America (0–6.1 %) and Australia (2.6 %).
- The odds ratio (OR) for prostate cancer was **4.4** for the G84E mutation carriers.
- The mean age at diagnosis of carriers was **62.8 years** compared with patients without the mutation (**64.4 years**)

TaqMan assay

(Applied Biosystem/Life Technologies)

- genotyping data for 8652 PrCa cases (UKGPCS) and 5252 controls (ProtecT)
- 2 duplicate samples and 4 positive and 4 negative controls were included on each 384 well plate



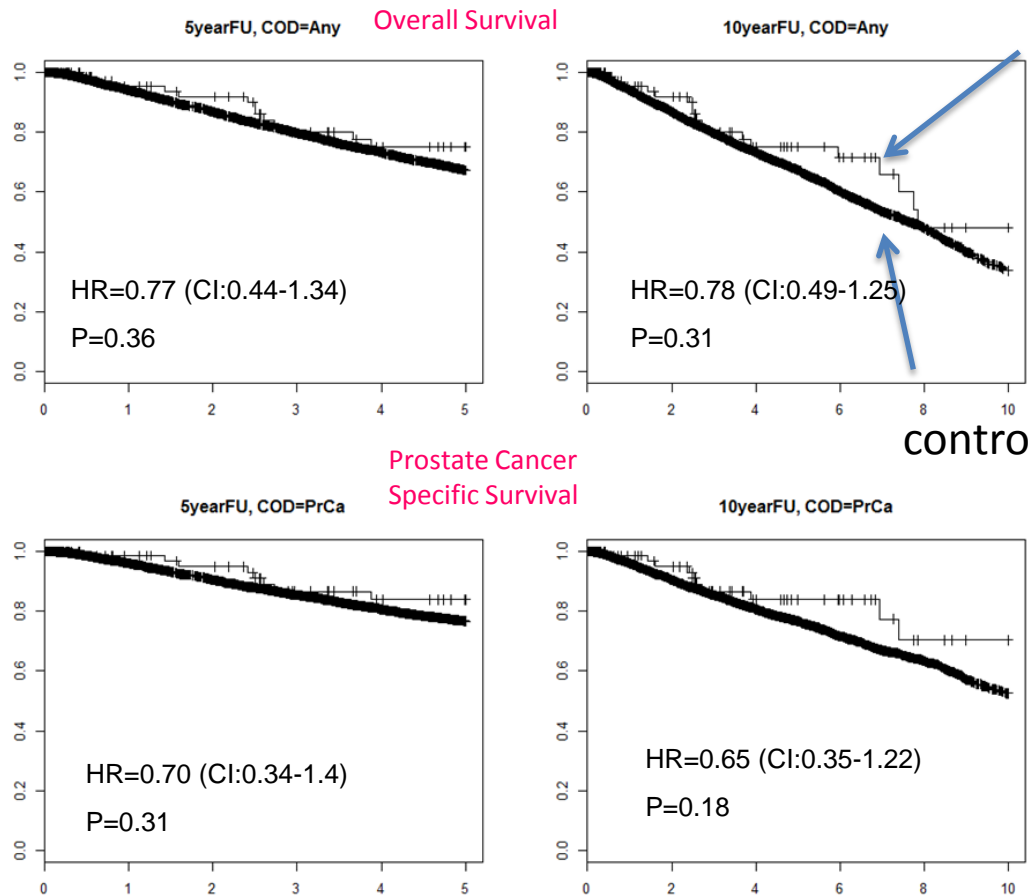
- *HOXB13* G84E identified in **0.5%** of healthy controls vs. **1.5%** of prostate cancer (PrCa) cases.
- OR=2.93 (95%CI: 1.94-4.59) relative risk of PrCa
- OR=4.53 (95%CI:2.86-7.34) relative risk of familial PrCa
- OR=3.11(95%CI:1.98-5) relative risk of early-onset PrCa (under 55 years)

There was no significant association of HOXB13G84E with:

1. Gleason Score
2. Presenting PSA
3. TNM stage
4. NCCN risk

Characteristic	Carriers N	Carriers %	Noncarrier s N	Noncarrier s %	P(carriers vs noncarriers)
Age					
Median	59		59		0.735
Range	37-79		36-89		
Median PSA	8.625		8.3		0.363
FH					
No	60	47.6	4847	64.1	<0.001
Yes	66	52.4	2718	35.9	
Unknown	8	6	953	11.2	
TStage					
T1	26	23.4	1845	27.3	0.836
T2	49	44.1	2608	38.6	
T3	32	28.8	2008	29.8	
T4	4	3.6	287	4.3	
Unknown	23	17.2	1770	20.8	
NStage					
N0	76	91.6	4444	90.2	0.826
N1	7	8.4	481	9.8	
Unknown	51	38.1	3593	42.2	
MStage					
M0	70	92.1	4222	86.4	0.206
M1	6	7.9	662	13.6	
Unknown	58	43.3	3634	42.7	
NCCN					
Low	24	19.8	1428	19.6	0.079
Intermediate	51	42.1	2420	33.2	
High	30	24.8	2013	27.6	
VeryHigh	5	4.1	466	6.4	
Metastatic	11	9.1	966	13.2	
Unknown	13	9.7	1225	14.4	

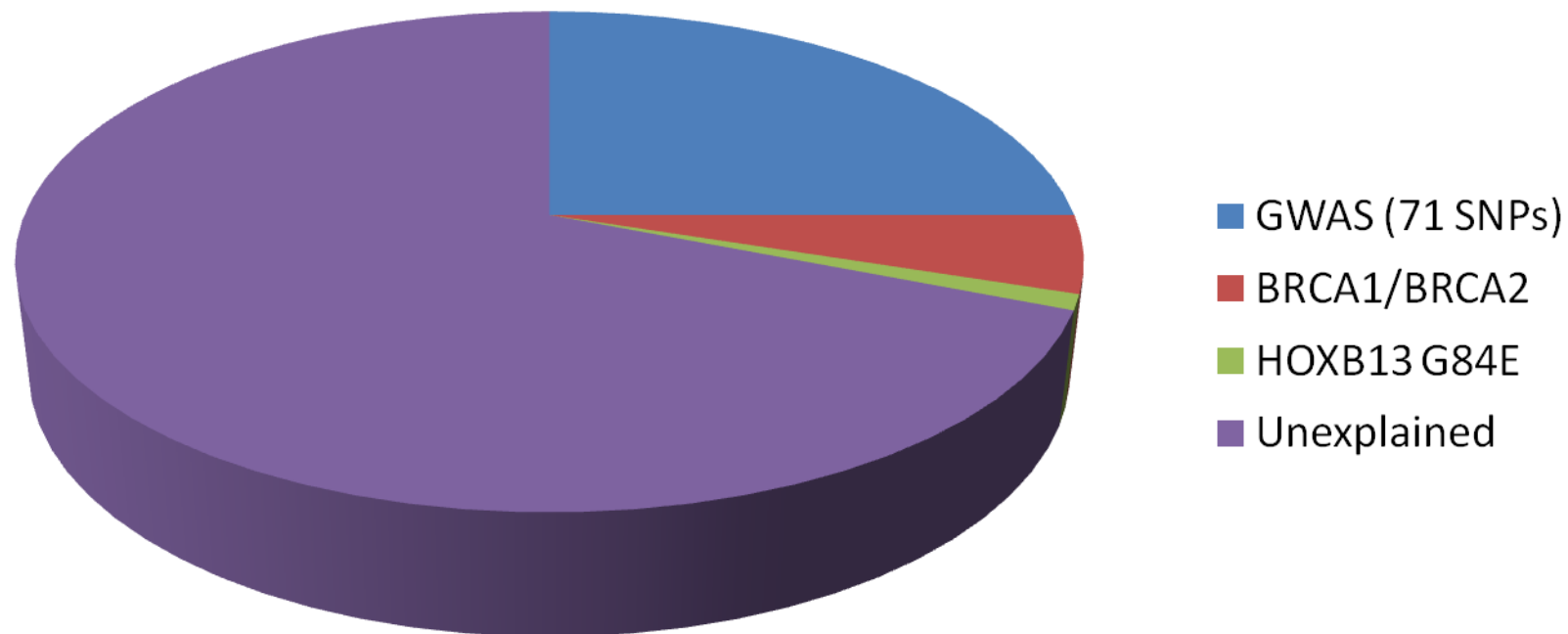
- No impact on overall and prostate cancer specific survival



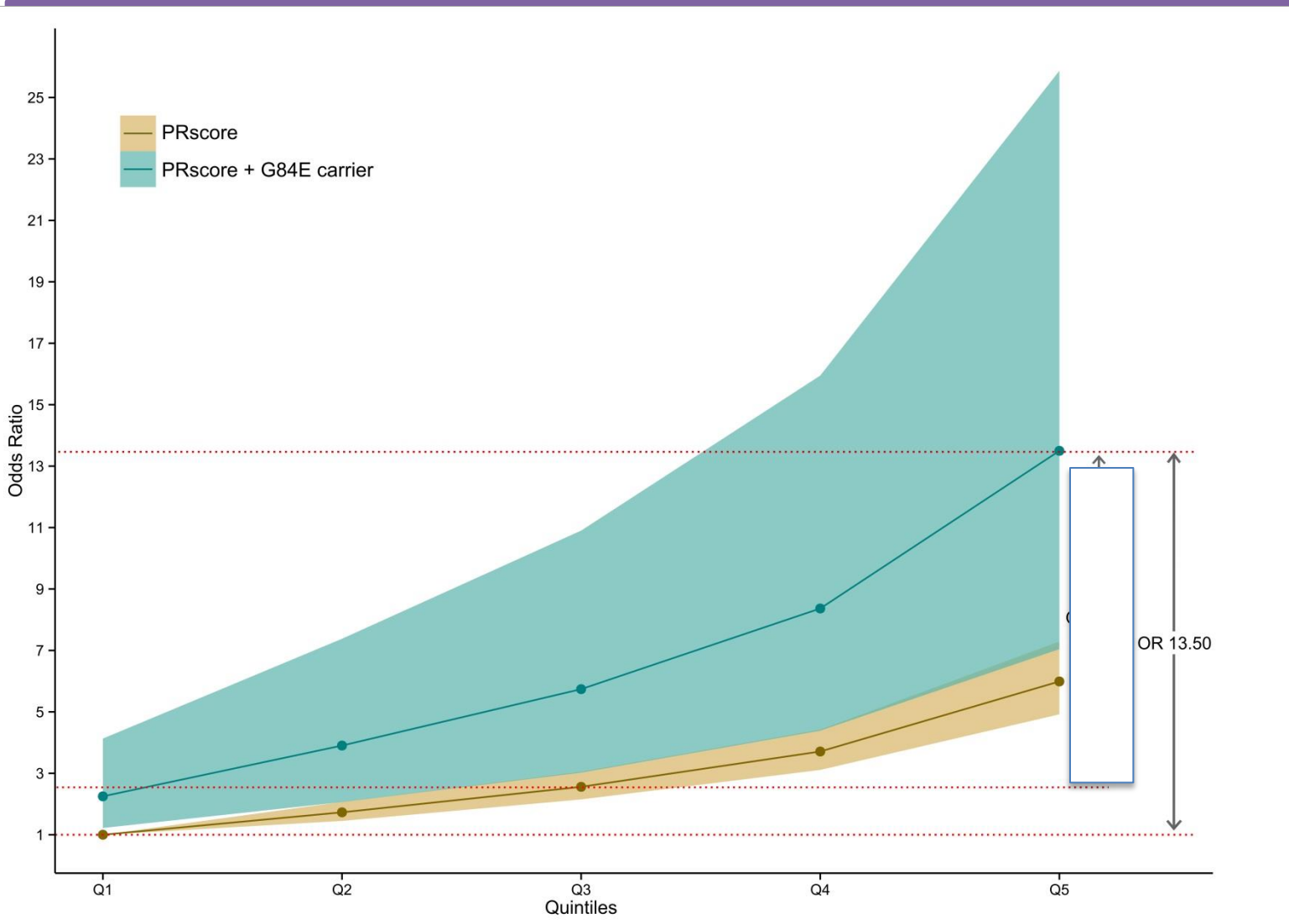
G84E carrier

HOXB13 G84E impact on PrCa genetic risk

PrCa Inheritance



Polygenic Risk Score



Conclusions

- 1.5% of PrCa cases in the UK harbour G84E mutations
- In men with a high polygenic risk score who also have a G84E mutation, their PrCa relative risk is 13.5
- Testing more applicable to Nordic Countries in families with PrCa cases
- Associated with early onset and familial PrCa
- No obvious phenotypic association
- No impact on survival

Christos Mikropoulos¹, Zsofia Kote-Jarai¹, Tokhir Dadaev¹, Daniel A. Leongamornlert¹, Malgorzata Tymrakiewicz¹, Edward J. Saunders¹, Michael Jones¹, Sarah Jugurnauth-Little¹, Koveela Govindasami¹, Michelle Guy¹, , Freddy Hamdy³, Jenny Donovan⁴, David Neal², J. Athene Lane², David Dearnaley¹, Rosemary A. Wilkinson¹, Emma J. Sawyer¹, Angela Morgan¹, The UK Genetic Prostate Cancer Study Collaborators, and the ProtecT Study Group Antonis C. Antoniou⁵, Rosalind A. Eeles^{1, 6}

¹ Institute of Cancer Research, 123 Old Brompton Rd, London SW7 3RP

² Surgical Oncology (Uro-Oncology: S4), University of Cambridge, Box 279, Addenbrooke's Hospital, Hills Road, Cambridge, UK and Cancer Research UK Cambridge Research Institute, Li Ka Shing Centre, Cambridge, UK

³ Nuffield Department of Surgical Sciences, University of Oxford, Oxford, UK, Faculty of Medical Science, University of Oxford, John Radcliffe Hospital, Oxford, UK

⁴ School of Social and Community Medicine, University of Bristol, Canynge Hall, 39 Whatley Road, Bristol, BS8 2PS, UK

⁵ Centre for Cancer Genetic Epidemiology, Department of Public Health and Primary Care, University of Cambridge, Strangeways Laboratory, Worts Causeway, Cambridge, UK

⁶ The Royal Marsden NHS Foundation Trust, Fulham Road, London, UK