Clues From The Pathway-Driven Approach

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U.S. DEPARTMENT OF HEALTH AND HUMAN SERVICES

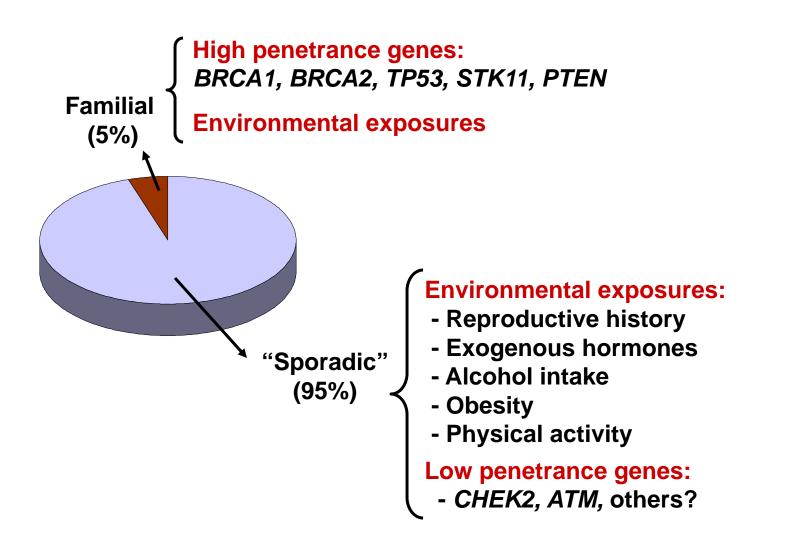
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Overview

- Breast Cancer:

- Case-control and Cohort Breast Cancer Studies
- Breast Cancer Association Consortium
- Bladder Cancer:
 - Spanish Bladder Cancer Study
 - International Consortium of Case-control Studies of Bladder Cancer

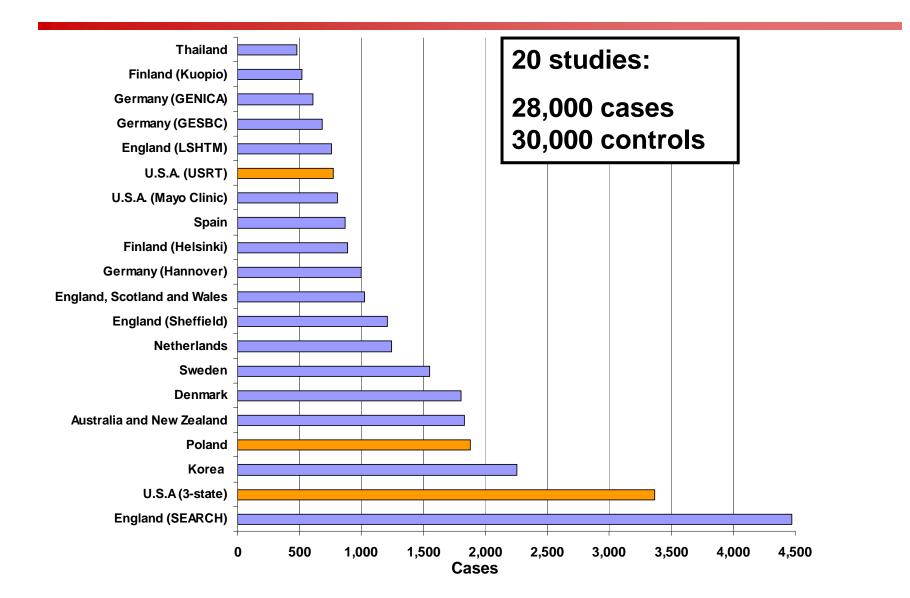
Breast Cancer Etiology



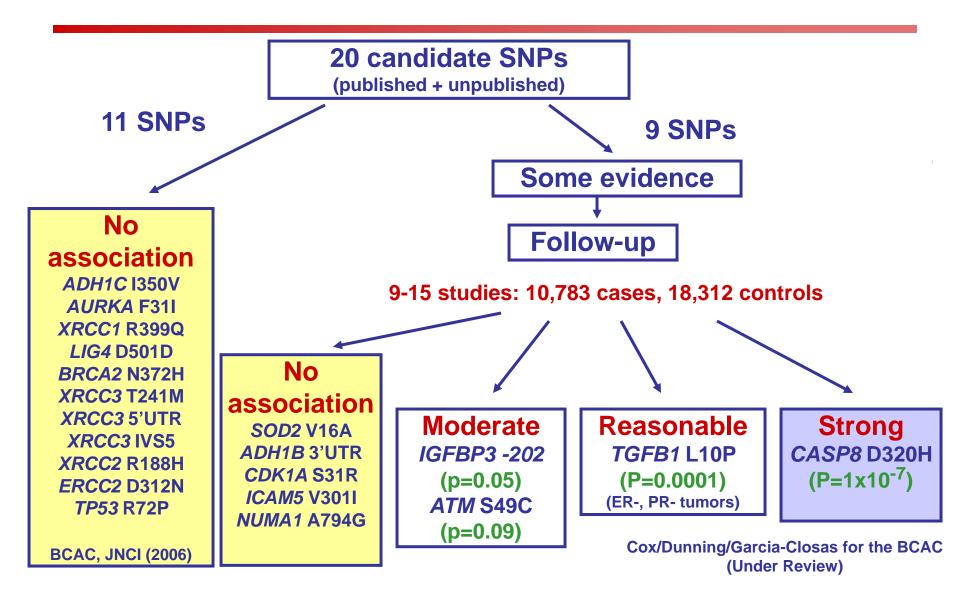
Pathways of Interest in Breast Cancer

- Established or possible risk factors:
 - Hormone biosynthesis, metabolism, and action
 - Obesity
 - Alcohol metabolism
 - Carcinogen metabolism
 - Inflammation
- Carcinogenic processes:
 - DNA repair, cell cycle control, and apoptosis
 - Cell signaling pathways
 - Telomere length
 - Gene expression studies
 - Somatic mutations

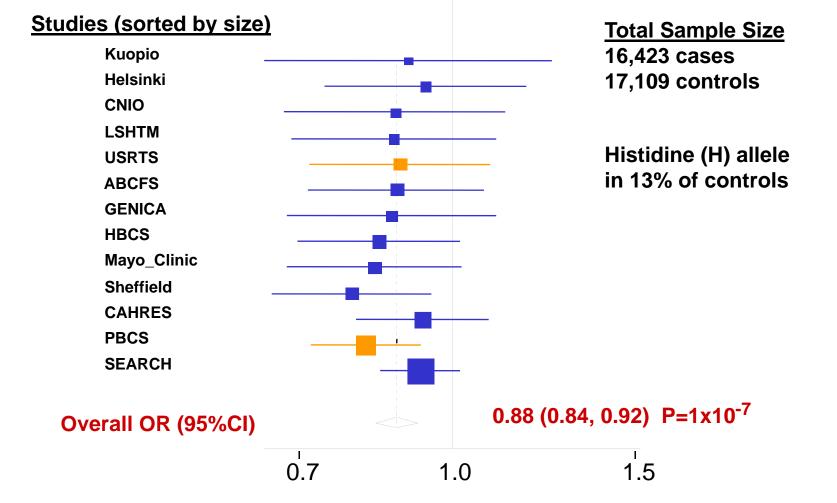
Breast Cancer Association Consortium



Breast Cancer Association Consortium: Findings to Date



Caspase 8 (CASP8) D302H Variant Decreases Breast Cancer Risk



Cox A/Dunning A/Garcia-Closas M* for the BCAC (Under Review) * in alphabetical order

Caspase 8 and Breast Cancer: Plausibility and Significance of Findings

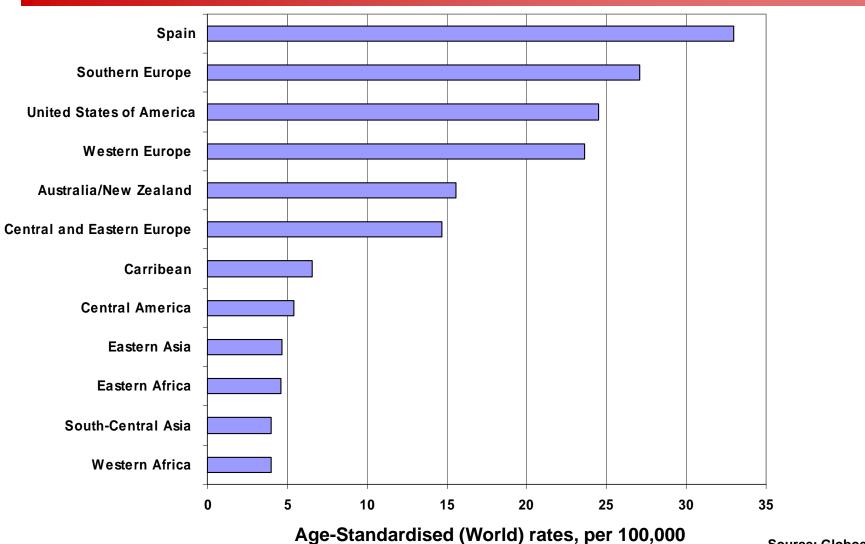
- CASP8 D302H is the first common variant with convincing evidence of an association with breast cancer.
- Caspase 8 is a critical initiator of death receptor mediated apoptosis.
- Follow-up:
 - Fine mapping to dissect genetic variants in CASP8.
 - Functional significance of variants.

Bladder Cancer

Excellent model to evaluate genetic susceptibility and gene-environment interactions:

- Relatively homogenous histology.
- Well-known non-genetic causes:
 - Tobacco smoking
 - Occupational exposure to aromatic amines
- Good understanding of genetic variation in carcinogen metabolism.
- Familial association not yet explained.

Bladder Cancer Incidence Rates



Source: Globocan 2002

Spanish Bladder Cancer Study



Hospital-based case-control study in 5 areas of Spain (1998-2001)

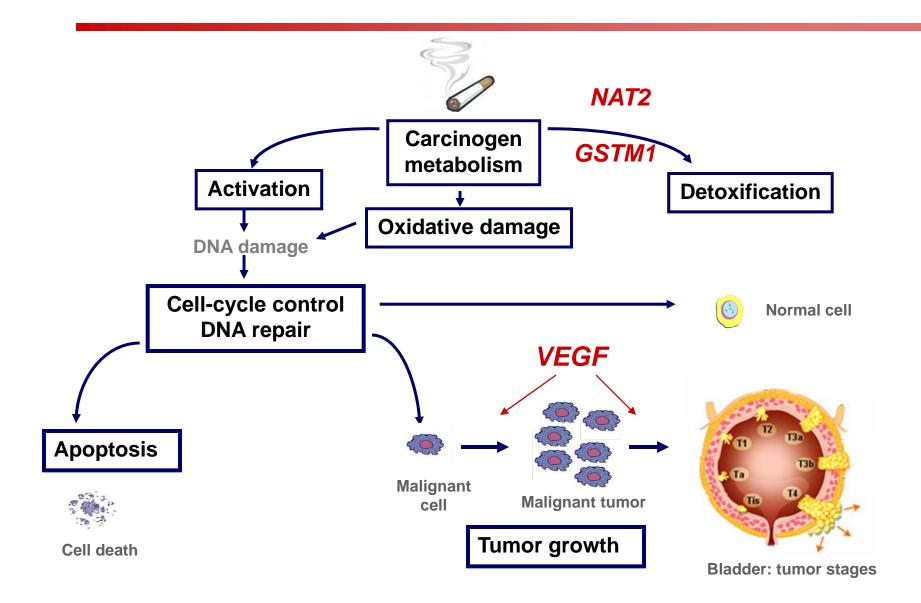
1219 cases (85% of eligibles)

1271 controls (88% of eligibles)

Why Spain?

- Higher incidence rates
- Higher prevalence of tobacco and occupational exposures
- Higher participation rates, lower cost

Candidate Pathways for Bladder Cancer



NAT2 and **GSTM1:** Strong Candidate Genes for Bladder Cancer

- Metabolism of bladder carcinogens.
- Meta-analyses of previous studies:
 - Suggested associations with bladder cancer risk
 - Relatively small studies (23 to 374 cases)
 - Concerns about publication bias and heterogeneity
- Interactions with cigarette smoking:
 - Strong biological rationale for NAT2

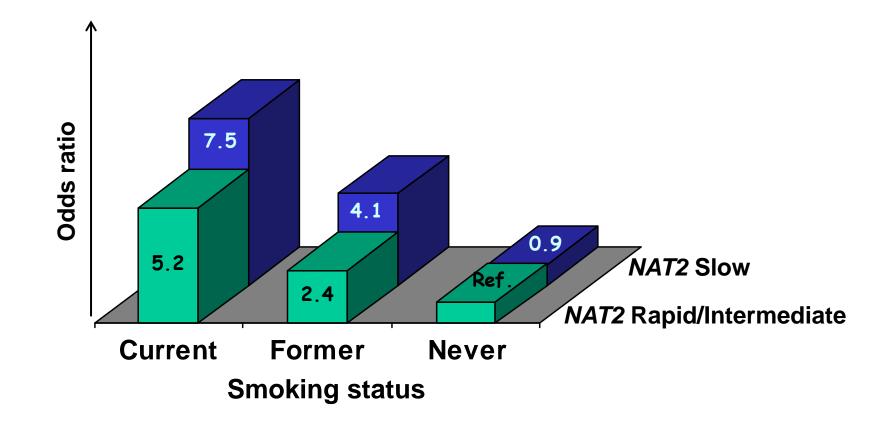
NAT Slow Acetylation and GSTM1 Null Genotypes Increase Bladder Cancer Risk

Spanish Bladder Cancer Study

	Phenotypes*	Cases	Controls	OR	95%CI	p-value
NAT2	Rapid/Intermediate	406	493	1.0		
	Slow	728	637	1.4	(1.2-1.7)	0.0002
GSTM	1 Present	786	561	1.0		0
	Null	716	571	1.7	(1.4-2.0)	1x10 ⁻⁸

* Inferred from genotype data

Stronger Effect of Smoking on Bladder Cancer Risk for NAT2 Slow Acetylators



Garcia-Closas M et al. *Lancet*, 2005; 366: 649-658.

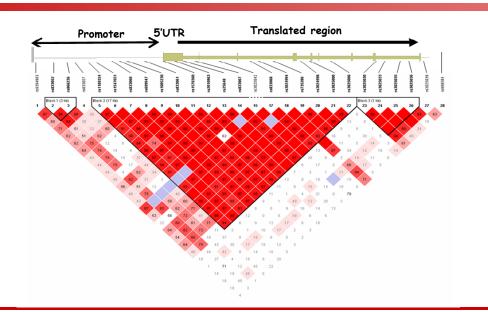
Large-scale Evaluation of Candidate Genes for Bladder Cancer

• 1,433 SNPs within or near 386 genes.



- Most notable finding for a 5'UTR variant in the vascular endothelial growth factor (*VEGF*) gene:
 - Major role in angiogenesis.
 - VEGF tumor and urinary levels related to bladder cancer recurrence and progression.
 - Variants associated with VEGF plasma levels, promoter activity, bladder cancer aggressiveness.

Detailed Characterization of VEGF Variants in the Spanish Bladder Study



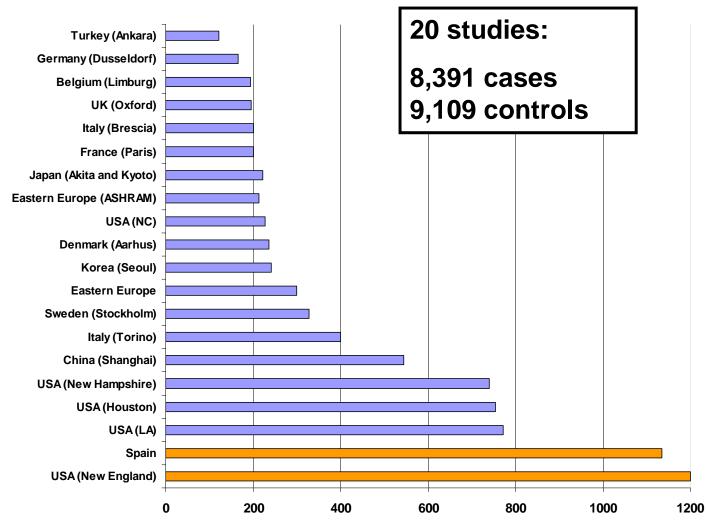
	Location	MAF	Heterozygous OR (95%CI)	Homozygous OR (95%CI)	Ρ
rs833052	Promoter	0.12	1.1 (0.9-1.4)	2.5 (1.1-6.0)	0.04
rs1109324	Promoter	0.14	1.1 (0.9-1.4)	2.7 (1.3-6.0)	0.01
rs1547651	Promoter	0.14	1.1 (0.9-1.4)	3.0 (1.4-6.6)	0.006
rs25648	5'UTR	0.14	1.1 (0.9-1.4)	5.1 (2.3-11.2)	0.00005

Garcia-Closas M et al. (Under Review)

Investigator Web Portal

Bladder Cancer Consortium

International Consortium of Case-Control Studies of Bladder Cancer



Concluding Remarks

- Starting to identify associations with genetic variants unlikely to be false positives:
 - Large, good quality individual studies
 - Collaborative efforts through consortia
 - Robust and affordable genotyping technology
- From candidate pathways based on current understanding of etiology to genome-wide scans.

Collaborative Research Program

Breast Cancer Studies Louise Brinton, HREB, DCEG Mia Gaudet, HREB, DCEG Mark Sherman, HREB, DCEG

William Anderson, BB, DCEG Rose Yang, GEB, DCEG Jeff Struewing, LPG, CCR Stephen Hewitt, TRAP, CCR

Jolanta Lissowska, Warsaw Poland Beata Peplonska, Lodz, Poland

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Core Genotyping Facility Stephen Chanock, CGF, DCEG Meredith Yeager, CGF, DCEG Robert Welch, CGF, DCEG

Statistics Nilanjan Chatterjee, BB, DCEG Jay Lubin, BB, DCEG Sholom Wacholder, BB, DCEG