Human Cancer Genetics Laboratory

est. February 2008

LUDWIG CANCER RESEARCH

The Ambition



SNPs Single Nucleotide Polymorphisms

Understanding genetic variation could be a key for Personalized Medicine

- Single Nucleotide Polymorphisms (SNPs) are one of the most common form of genetic variation (>13 M in dbSNP & 6.9 M validated by multiple investigators)
- SNPs occur when a single nucleotide (A, T, C or G) is replaced with another MAF >1%



Genome Wide Association Studies (GWAS)





1,161 SNPs associated with app. 68 different cancers/cancer subtypes in 228 GWASs

• median 1.2 OR

The p53 Network

p53 does not work in isolation



A SNP in the p53 Network LFS

MDM2 SNP309





Bond, Wu et al., Cell, 2004

MDM2 SNP309 in the p53 Network LFS



MDM2 SNP309 Survival

In Mice



Has GWAS identified more p53 network SNPs?

Post et al., Cancer Cell, 2010

Has cancer GWAS found more p53 pathway SNPs?



Cancer GWAS SNPs in European Populations



From SNPs to genes

Cancer SNPs (2,819 SNPs)

Tags + Linked SNPs
* 1000 Genomes Phase 1
* EUR populations
* MAF ≥ 0.01
* r2=1



From SNPs to genes

Cancer SNPs (2,819 SNPs)

Tags + Linked SNPs
* 1000 Genomes Phase 1
* EUR populations
* MAF ≥ 0.01
* r2=1



Cancer Susceptibility Genes (CSGs)

are genes having ≥ 1 cancer SNP within ± 10 Kb from its boundaries.

• 458 CSGs in the genome



From genes to pathways

Genes were assigned to pathways using the KEGG pathway annotation

- 214 pathways
- 5 major categories: Metabolism, Genetic Information Processing. Environmental Information Processing, Cellular Processes, Organismal Systems



From genes to pathways

Genes were assigned to pathways using the KEGG pathway annotation

- 214 pathways
- 5 major categories: Metabolism, Genetic Information Processing. Environmental Information Processing, Cellular Processes, Organismal Systems



Does the p53 pathway have more CSGs than expected by chance?

- Hypergeometric enrichment test
- P-values adjusted for multiple hypothesis testing by permutations.

10 out of 67 p53 pathway genes are CSGs: is this a lot?



CSGs are enriched in p53 pathway genes



CSGs are enriched in p53 pathway genes





- 3/214 KEGG pathways show significant enrichment:
 - * p53
 - * Adherens Junction
 - * PI3K-AKT

p53 Genes are not enriched in Susceptibility Loci for Other ICD10 Disease Groups



p53 pathway CSGs are somatically mutated genes



Potential Insights

 p53 signaling pathway is highly sensitive to SNPs, and it can contribute to the observed heterogeneity of cancer risk in the broader population and in LFS.

- Potential utility in risk assessment for a broad range of cancers to aid asymptomatic screening protocols.
- Many genes in the p53 pathway are highly sensitive to both heritable and somatic genetic variants, highlighting their central roles in regulating or affecting p53 signaling.
- Targeting these genes could be an efficient method to modulate p53 signaling in the clinic.

•

•

- We will need to incorporate somatic and inherited genetics of these genes and their interactors to maximize treatment efficacy.
- Genetic variants in the p53 pathway primarily affect susceptibility to cancer and not the other major disease groupings we tested.
- As agents that modulate the levels of p53 signaling are entering the clinic, such information could be useful to predict and monitor potential side effects.

Brazilian Li-Fraumeni Syndrome

There are roughly 200-300,000 individuals that carry a lower penetrant p53 mutation in Southern Brazil

- 1 in 30 will develop adrenal corticoid carcinoma by the age of 15 years.
- There are seemingly low and high risk families (breast, brain, gastric and sarcomas).
- One third of the families have no cancer history.
- Recently 172,000 newborns were screened and clinical follow up was able to identify early stage tumors with good prognosis.
- Teaming up with Bonald Figueiredo to explore if p53 pathway SNPs could serve as modifiers of penetrance to better risk estimation.

Custodio et al., JCO 3013

Acknowledgements

Ludwig Institute For Cancer Research

Giovanni Stracquadanio Jorge Zeron Emmanouela Repapi Anna Grawenda Juliet Hewitt Ross Worrall Elleke Peterse Elisabeth Bond

> Sarah De Val Natalia Sacilotto Colin Goding

Wellcome Trust for Human Genetics

Ian Tomlinson Francesc Castro-Giner Benjamin Davies

National Institute of Environmental Health Sciences, NIH

Douglas Bell Xuting Wang Michelle Campbell Dan Su

Queensland Institute of Medical Research Graeme J. Walker

Statistics Department, University of Oxford

Nicolai Meinshausen

University of Colorado Denver Neil Box