Considerations when undergoing personal genotyping

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GENE 210

Disclosures and introductions

- Professor Ormond provided paid consultation for Navigenics GC Task Force (an advisory board) from 7/07-7/09
- Professor Hudgins has no disclosures

The “old” genetics

- Most genetic conditions were seen as rare and serious
- Medical Genetics was mostly practiced in pediatrics or obstetrics

- Testing was usually not available for inherited conditions
- Risk information was often limited

- Newborn screening and carrier testing based on ethnicity were as “population based” as genetics got…

Genetics of Today

- Testing available for several thousand conditions (↑)
  - Still mostly rare, mendelian,
  - based on family history or other risk factors (age, ethnicity)
- Family history is recognized as a key "genetic test"
- Focus shifting from mendelian to complex disease
- Approximately 3,000 genetic counselors and 1,100 medical geneticists in pediatrics, obstetrics, cancer genetics, neurogenetics, cardiogenetics…

Testing strategies: Mendelian conditions

- **Test a relative who is known to be affected first, so that results are most informative**

- Positive results (e.g. identify a pathogenic mutation)
  - Medical management, planning ahead
  - Consider penetrance and variable expression in discussing prognosis
  - Make life decisions (marriage, reproduction, education/career)

- Negative results (e.g. no mutation identified)
  - True negative if mutation identified in family
    - Family members' risks can be adjusted
  - If the person has an unclear phenotype, a negative result remains uninformative
    - They could still carry a mutation in a different gene, or in a part of the gene that was not assessed by the specific genetic test
    - Family members' risks cannot be adjusted

- Uncertain results (dreaded Variant of Uncertain Sig.)
  - Uninformative – you don't know if it is a mutation or a benign polymorphism
    - Family members' risks cannot be adjusted

Clinical example: Clear-cut mutation

- You have a 26 yo patient of Jewish background who comes to you because her 32 year old sister has a diagnosis of *breast cancer*. She does not have breast cancer, and she wants to have a genetic test. Wisely, you suggest her sister be tested first, since she has the clinical diagnosis. She is found to carry a mutation in *BRCA2 (one of the 3 founder mutations).*
    - **This provides diagnostic confirmation, and an explanation for the condition in the family**
    - **The mutation is highly penetrant – 60-80% lifetime risk of breast cancer**
    - **There may or may not be genotype/phenotype correlations**
    - **Can offer targeted surveillance for recurrence, change surgical management for patient's affected sister and offer testing to unaffected relatives**

Predictive Testing: To know or not?

- Family members can now undergo accurate genetic testing
  - Do people WANT to know genetic information if it's uncertain whether and when it will happen?
  - Presymptomatic detection leads to medical recommendations
  - Will you alter your healthcare? Will you alter your life planning?
  - Will you see yourself differently? Will people (including family) treat you differently? In a positive or negative manner?

- You have a 26 yo patient who comes to you because her 32 year old sister has a diagnosis of *breast cancer*. She does not have breast cancer, and she wants to have a genetic test. Wisely, you suggest her sister be tested first, since she has the clinical diagnosis.

- *No mutations are found. You send the sample for full sequencing. The lab finds a novel change, which is called a "Variant of Uncertain Significance."* (VUS)
    - **In contrast to the last case, we don't know if this variant is causally related to the breast cancer in the family.**
    - **Testing family members may not be clinically useful unless you can establish the VUS tracks with the condition**
    - **Predictive algorithms (such as SIFT and PolyPhen are accurate about 50% of the time)**

- *What if we'd only tested the unaffected patient and found a VUS – how do we interpret it?*

Clinical example: VUS (Variant of Uncertain Significance)

Most of the data about how patients think about "variants of uncertain significance" comes from BRCA1/2 testing

- Patients tend to think in a binary fashion and aren't that good at making meaning out of unclear results
- Patients may also be more frustrated and anxious with a variant than with a clearcut mutation

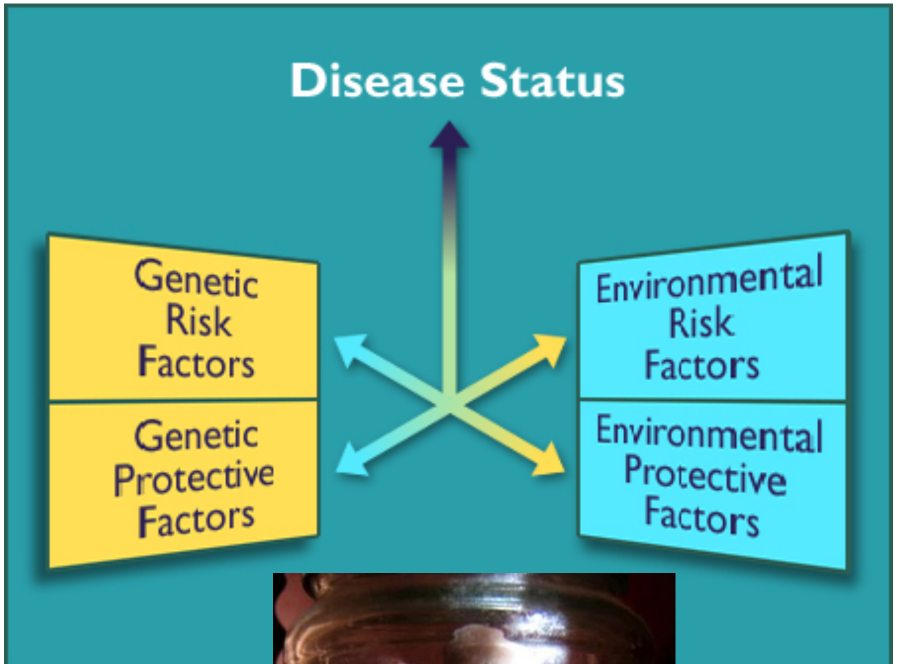
- As the physician, how (if at all) do you alter medical management on the basis of a variant?
- Presymptomatic detection may lead to changed management, but <u>should</u> it? It may inappropriately increase risks to patient

The "new" genetics of today and tomorrow

- Complex genetics 101
  - All the genetic rules are less clear
  - Addressing common conditions of adulthood
  - Involves both genetic and lifestyle components
  - Genome wide testing via SNPs and exome/genome sequencing

- Testing available for more and more conditions, but good prediction still a long way off for most common complex disease

“Multifactorial” Inheritance



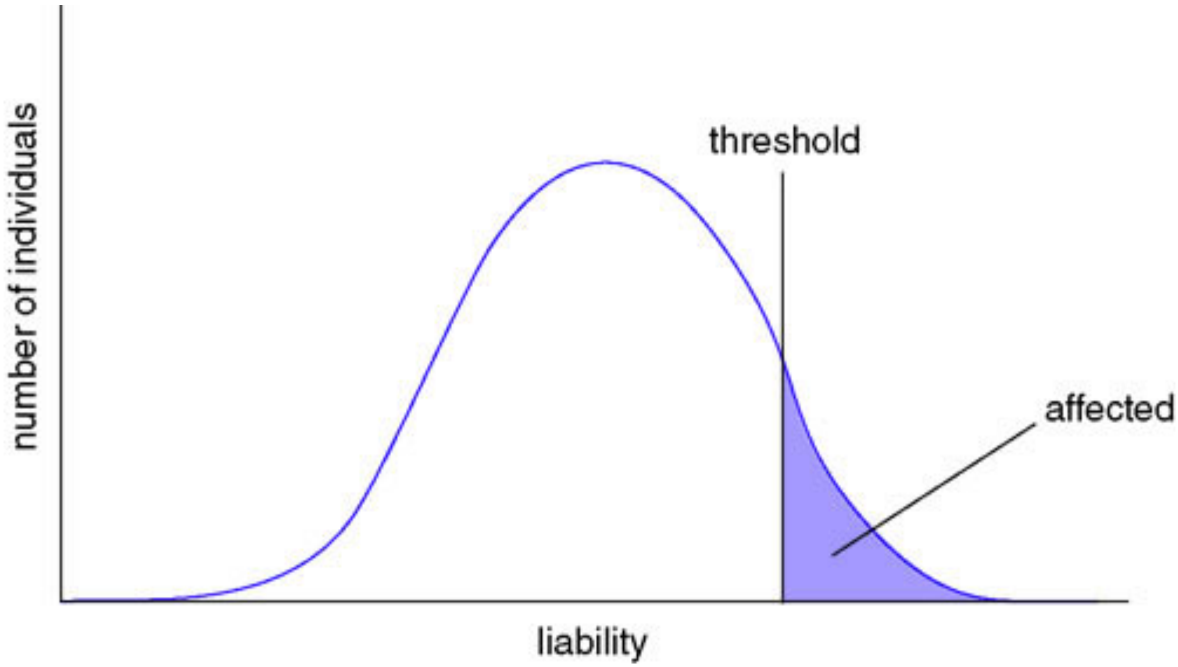
•**Polygenic** – Multiple genes act in concert, with each contributing a small amount to the overall genetic risk

•Often these conditions follow a normal, Gaussian, distribution

•“heritability” (h^2) is the term that addresses the genetic variance

•**Multifactorial** – both genetic and environmental factors contribute to the phenotype

The Threshold/Liability Model

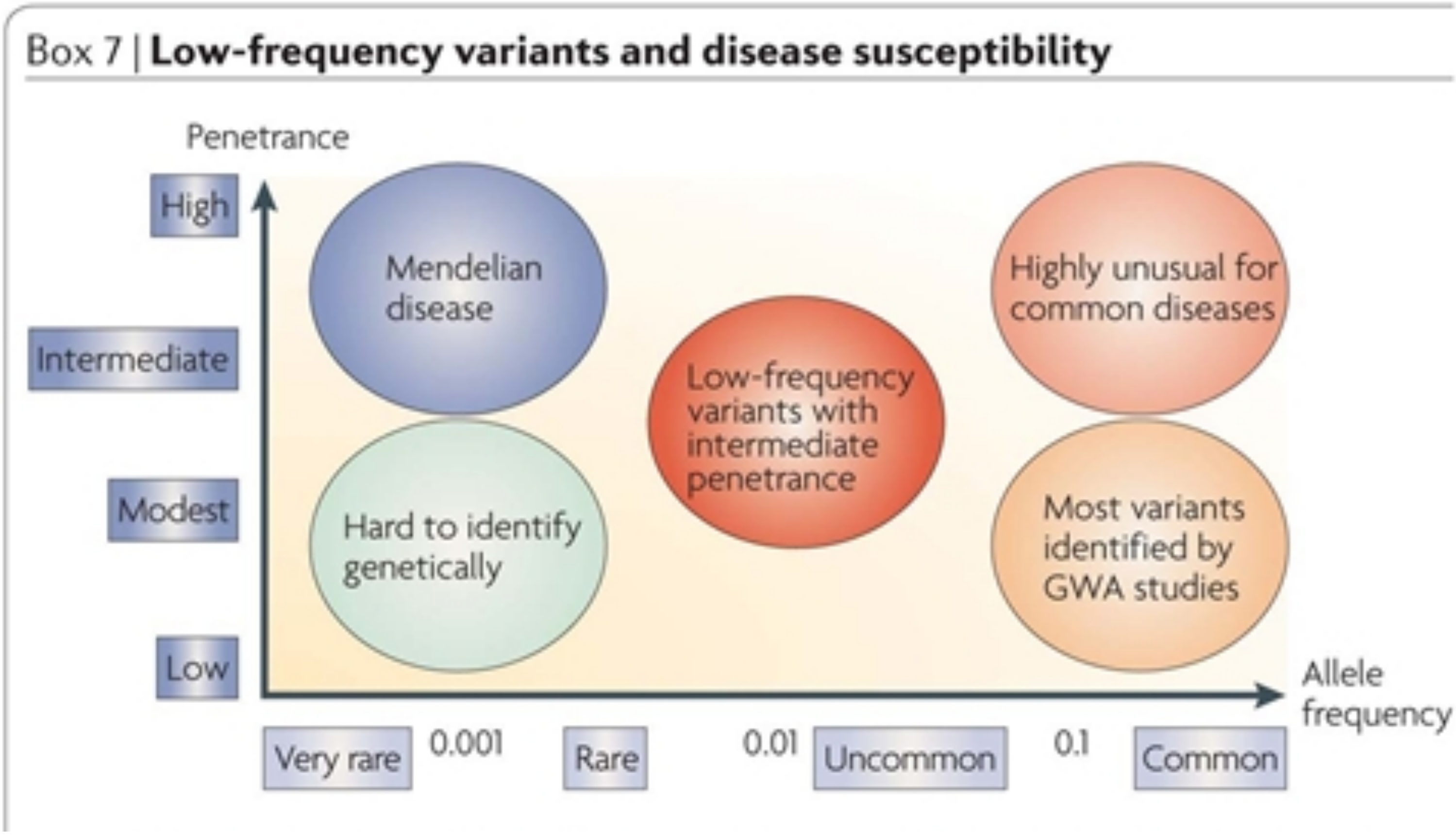


Important Factors
•Severity of disorder in proband
•Gender of proband
  •Less common gender inc. risk
•Number of affecteds in family

•Distance of relationship to proband
•Consanguinity

•Assumes that liability is normally distributed within the population
•Takes into account genetics and environmental liabilities

Single genes and beyond…



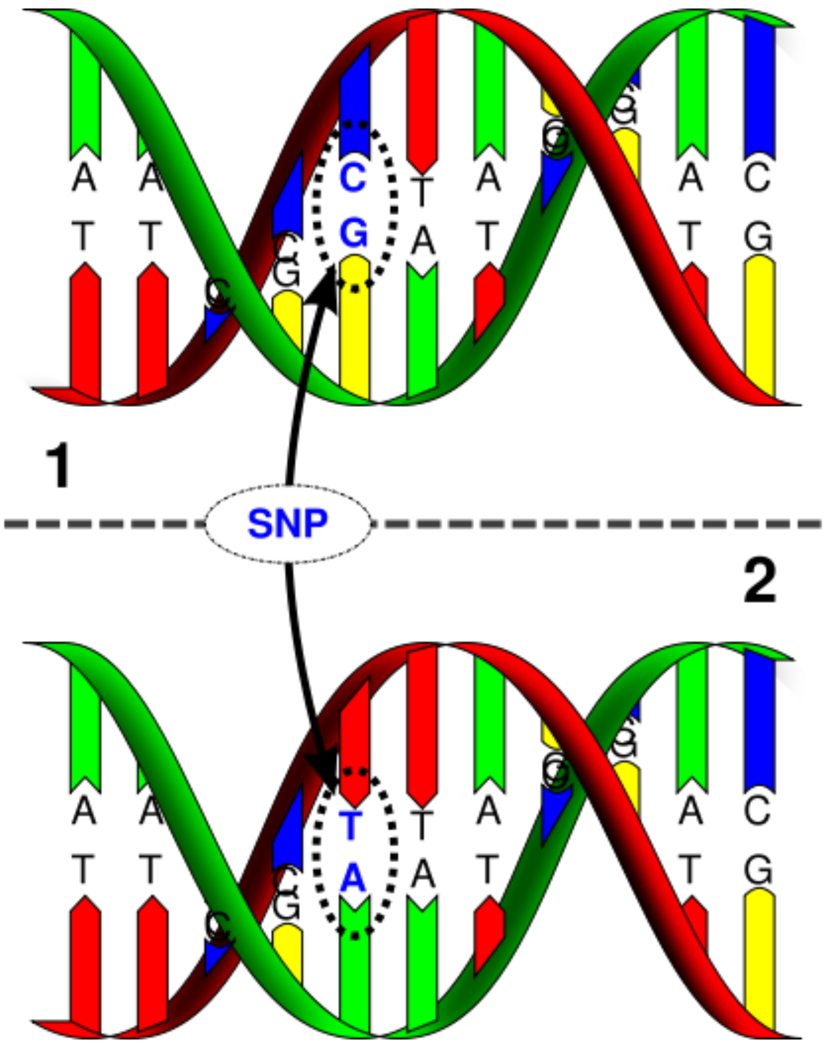
McCarthy et al., 2009

marked disparity between the extent of overall familial aggregation observed for

What is a GWA Study anyway?

- Genome wide association study
- Allows you to “probe” the entire genome
- Find previously unsuspected associations between SNPs and phenotype
- Find lots of associations at the same time

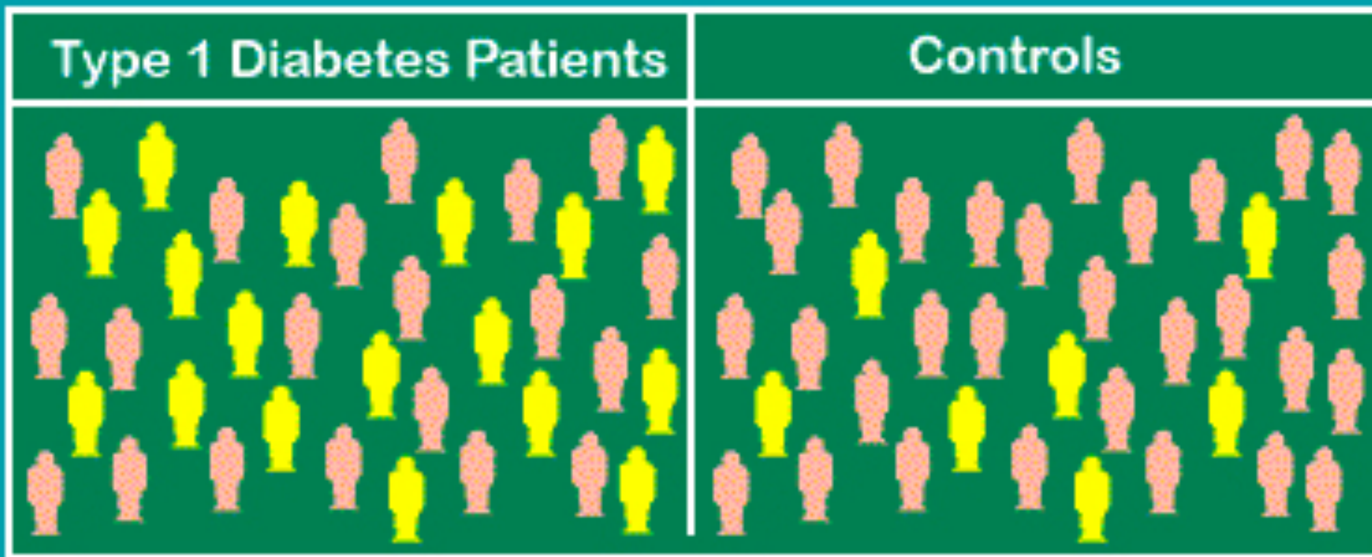
What is a SNP



- Single nucleotide polymorphism
- Estimated ~1/1000 base pairs
- If ~3,300,000,000 bp, that is several <u>million</u> SNPs in the genome!
- ~10 Million validated SNPs in dbSNP already
- dbSNP assigned reference SNP
  - (eg. rs709932)

http://www.ncbi.nlm.nih.gov/About/primer/snps.html for more basic info

Association Studies



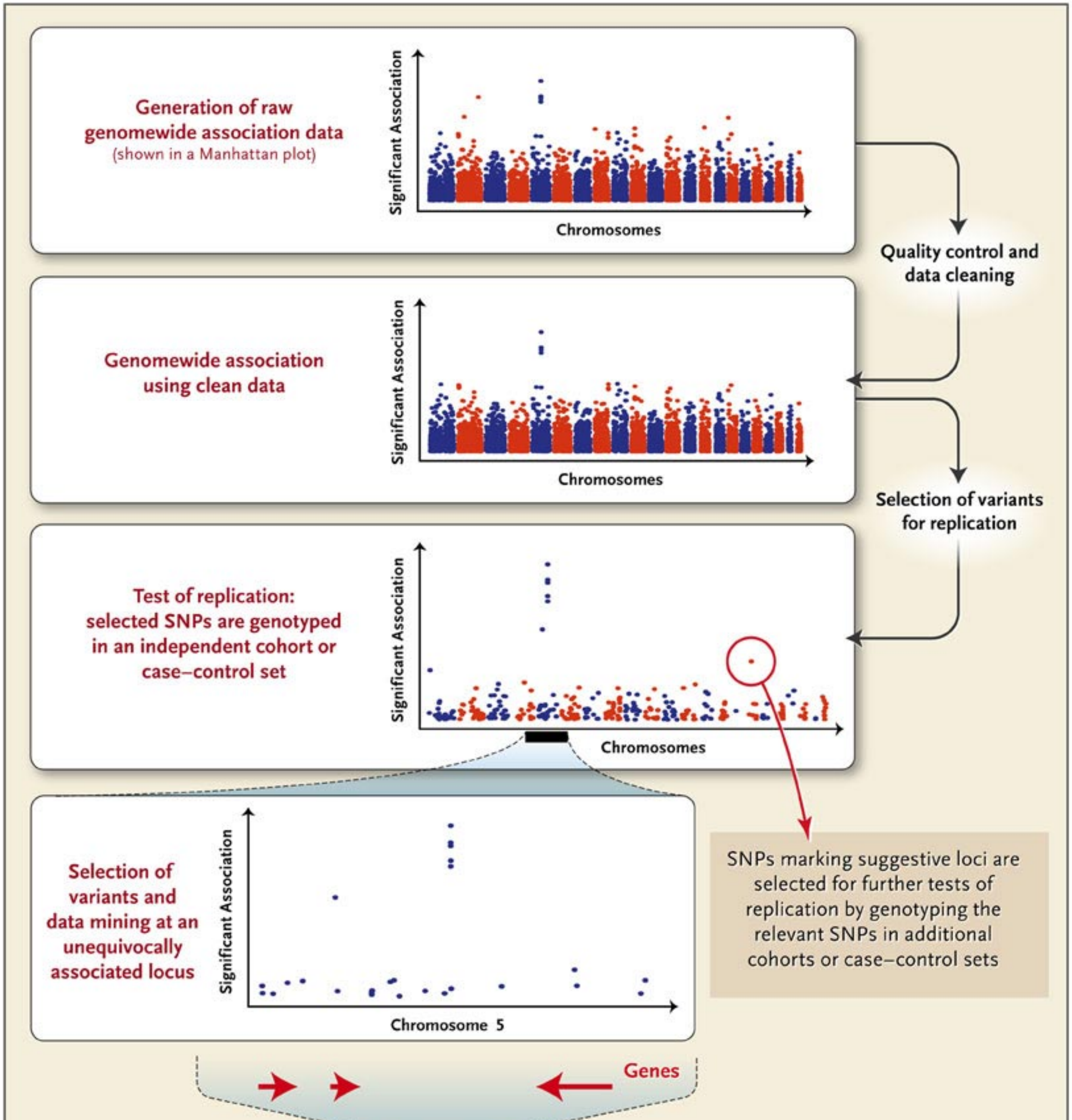
Genotype	Type 1	Controls	Total
HLA DR4	17	7	24
NON-HLA DR4	20	30	50
	37	37	

$X^2_{.05} = 5.377$

$p < 0.025$

 = HLA DR4

 = non-HLA DR4



Generation of raw genomewide association data
(shown in a Manhattan plot)
Significant Association
Chromosomes
Quality control and data cleaning
Genomewide association using clean data
Significant Association
Chromosomes
Selection of variants for replication
Test of replication: selected SNPs are genotyped in an independent cohort or case–control set
Significant Association
Chromosomes
Selection of variants and data mining at an unequivocally associated locus
Significant Association
Chromosome 5
SNPs marking suggestive loci are selected for further tests of replication by genotyping the relevant SNPs in additional cohorts or case–control sets
Genes

Hardy, 2009

Interpreting the data

- If you look at 500,000-1M SNPs, odds are that many of them are going to appear positive just by chance alone…

- How do you know if it's real?

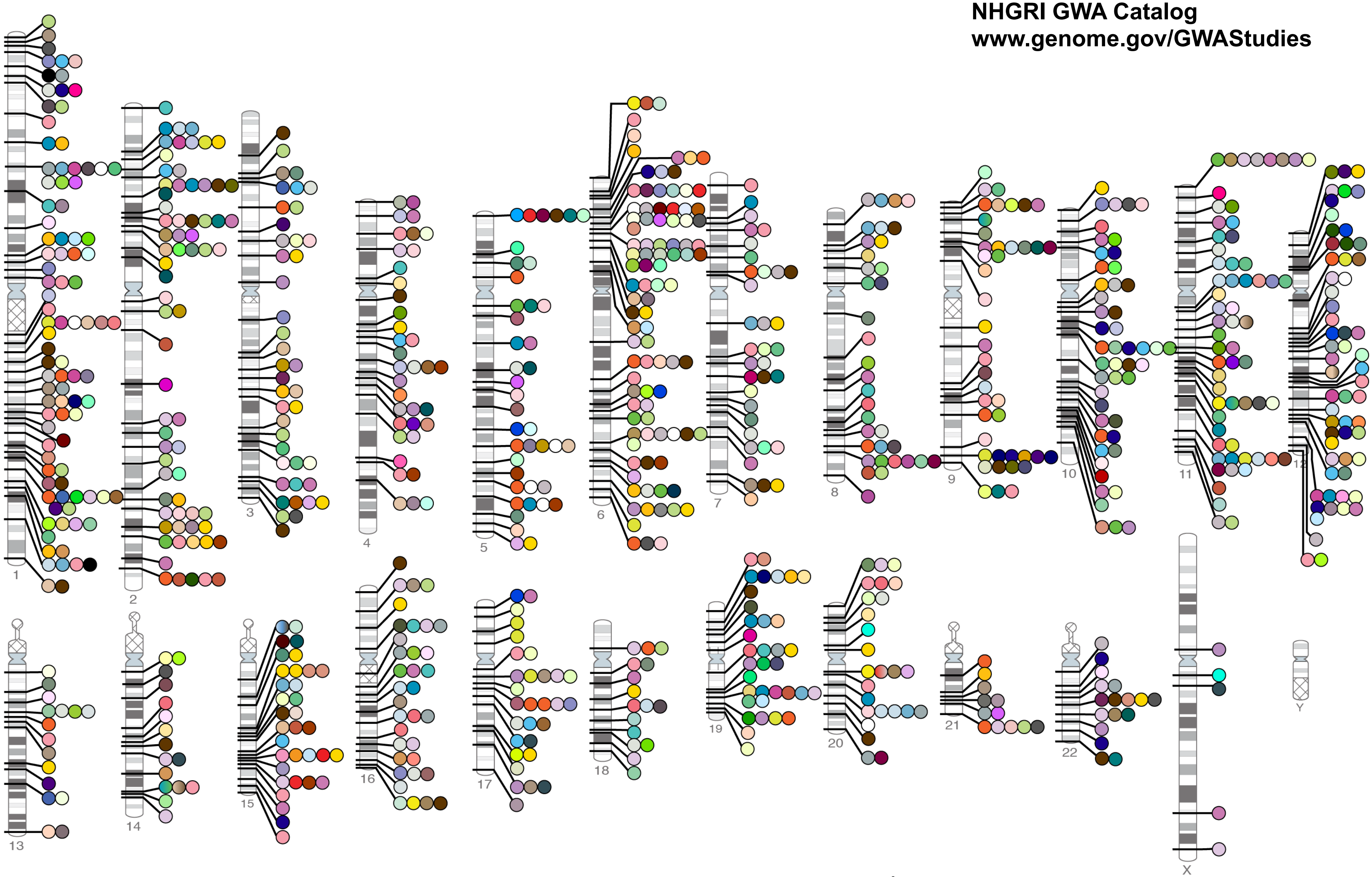
  – Bonferoni corrections - lead to much smaller p values
    - Use 5 X 10-7 (conservative)

  – Replication in similar populations…
    - Hirschorn et al. 2002 – of 166 early GWA studies, only 6 replicated in multiple studies

    - Currently ~1000 **published GWA at p $\leq$ 5 x 10-8**

Published Genome-Wide Associations through 6/2010,
904 published GWA at $p \leq 5 \times 10^{-8}$ for 165 traits

NHGRI GWA Catalog
www.genome.gov/GWAStudies



~500 new associations since 6/09

Challenges interpreting GWA Studies

- Vast majority of data remains based on European Caucasian populations
- Population stratification issues
  - Populations may have different MAFs, which could lead to spurious associations
- Defining the phenotype (and controls) accurately
  - Ascertainment biases
- Study size
- Different platforms assess different things, but generally only pick up SNPs with a relatively 'common' minor allele frequency

"Missing heritability"

- Where's all that "missing heritability"?
  - Age related Macular Degeneration – 5 loci, 50% of heritability
  - Crohn's disease – 35 loci, 20% heritability
  - T2Diabetes – 18 loci, 6% heritability
  - Height – 40 loci, 5% heritability
  - Fasting glucose – 4 loci, 1.5% heritability

- ORs may underestimate actual risks b/c SNPs more distant from causal variant
- Low MAF alleles not currently being assessed

- (Manolio et al, 2009 – 2009 Oct 8;461(7265):747-53)

A primary reason doctors slow to adopt

ARTICLE

Evaluation of risk prediction updates from commercial genome-wide scans

Raluca Mihaescu, MD[1], Mandy van Hoek, MD[1,2], Eric J. G. Sijbrands, MD, PhD[2], André G. Uitterlinden, PhD[2], Jacqueline C. M. Witteman, PhD[1], Albert Hofman, MD, PhD[1], Cornelia M. van Duijn, PhD[1], and A. Cecile J. W. Janssens, PhD[1]

When considering the 5% of the population at highest risk for diabetes (N=5297 total population):

- *TCF7L2* only = 28.0% risk (AUC 0.55)
- All 18 polymorphisms = 29.7% risk (AUC 0.60)
- Clinical factors only (AUC =0.63)
- Clinical + *TCF7L2 (AUC =0.64)*
- All 18 + clinical factors = 36.8% risk (AUC 0.66)

Table 1 Measures of model performance for dichotomizing predicted risk at average risk

	Model based on *TCF7L2* (%)	Model based on 18 polymorphisms (%)	Model based on 18 polymorphisms, age, sex, and body mass index (%)
Sensitivity	55.7	50.8	57.2
Specificity	51.8	62.7	64.5
PPV	21.8	24.7	28.0
NPV	82.9	84.1	86.2

Measurements are based on individuals with complete genotype and clinical information.
PPV, positive predictive value; NPV, negative predictive value.

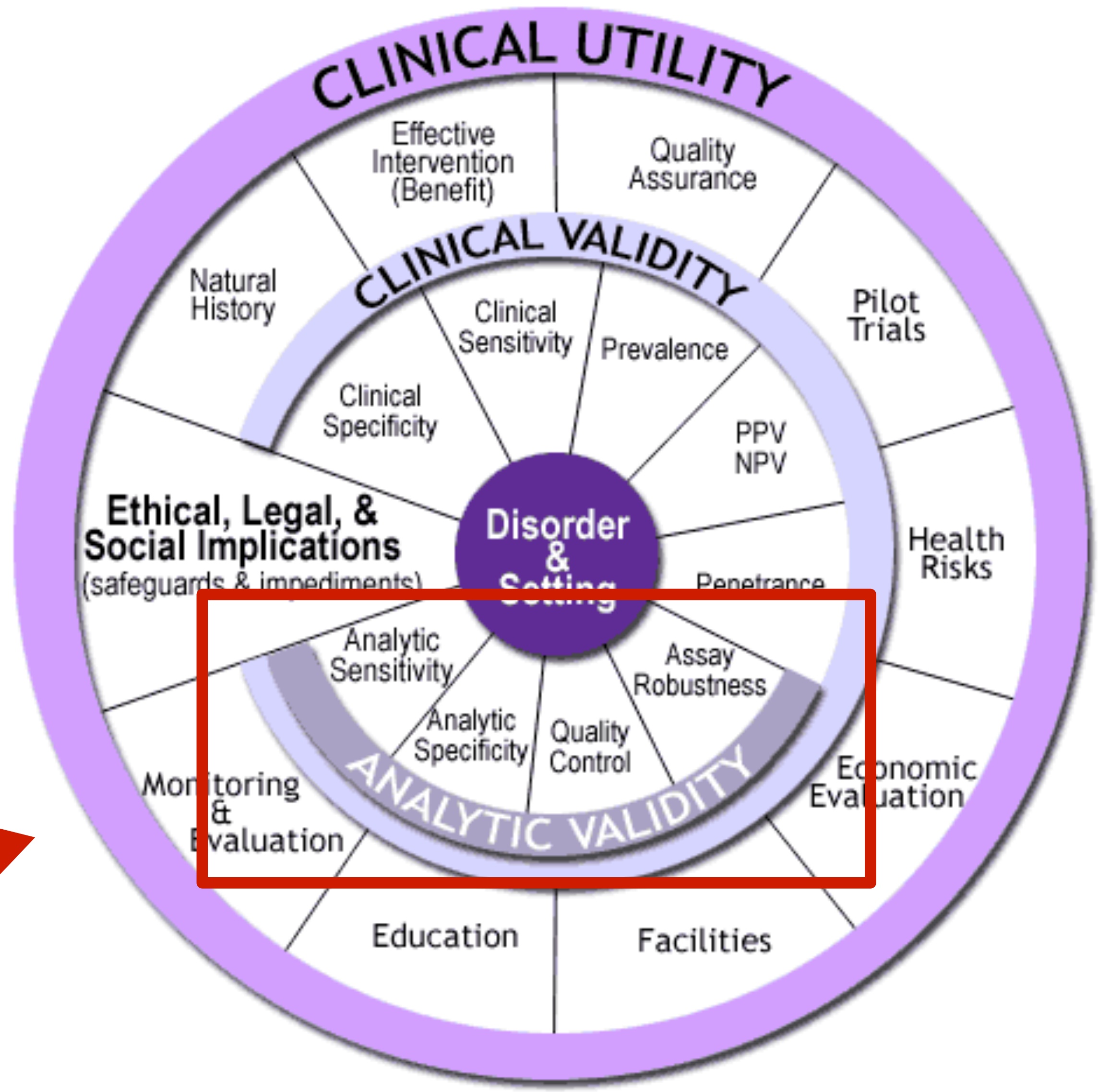
Comparison of individual risk factors for MI

Risk Assessment	Risk Factor	Effect (odds-ratio)
Positive Family History	parent with MI <50 yrs	1.52
Genetic Risk Factors	9p21	1.72
	MTHFD1L	1.53
Environmental Risk Factors	Stage 2-4 hypertension	1.92
	LDL>160	1.74
	HDL<35	1.46
	smoker 12 mos	1.71
	diabetes, type 2	1.47
	no exercise	1.39

- Most individual genotypes will have a relatively low OR, but there is the possibility that in combination the impact will be larger
- Range of effect sizes for genetic risk markers is similar to established environmental and family history risk factors

Modified from a slide by Elissa Levin, MS, CGC

Evaluating the tests…



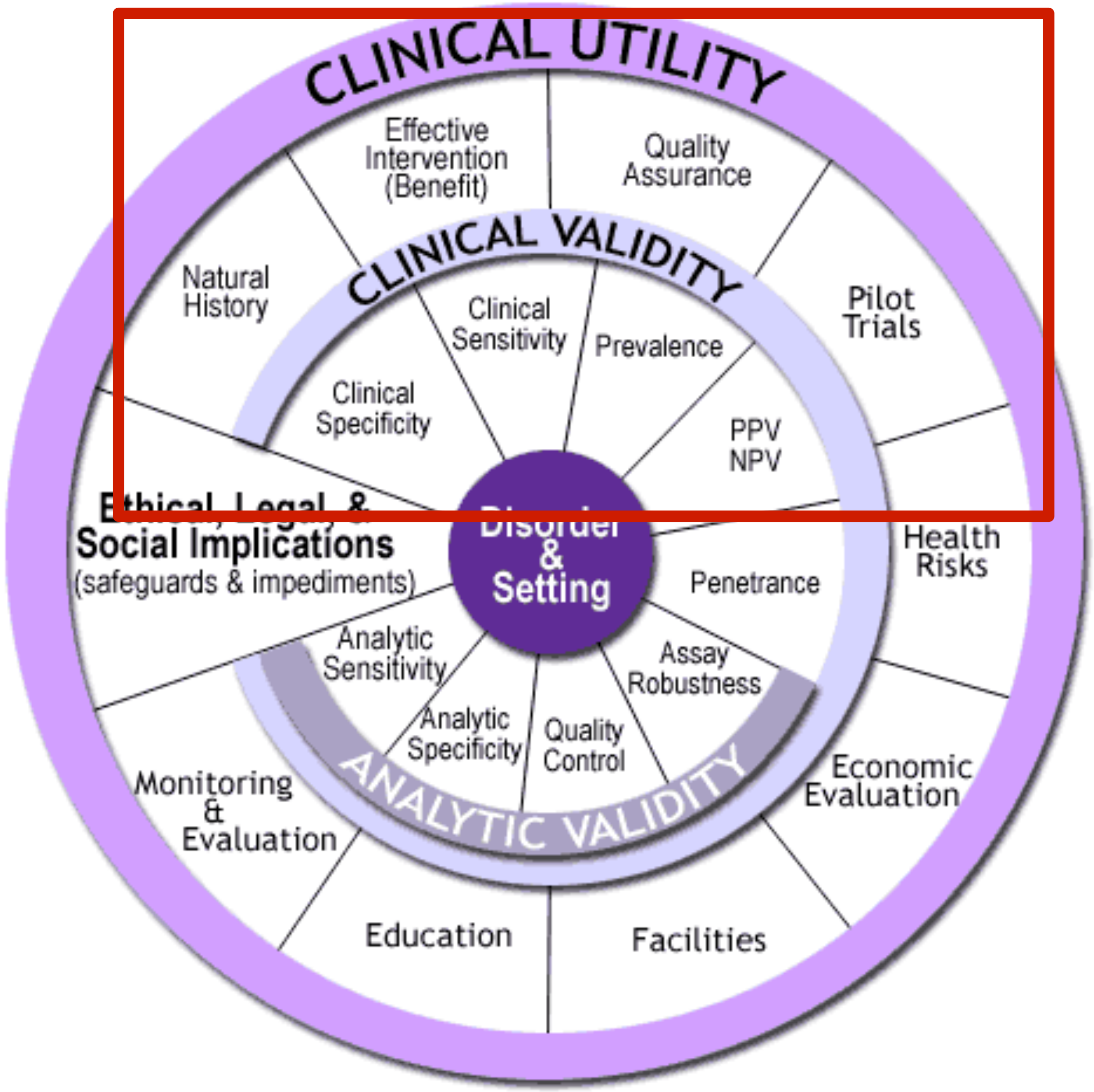
Laboratory focus

Evaluating the tests…

- Sensitivity and Specificity
  - Ability to correctly identify clinically affected persons with positive results and clinically unaffected persons with negative results
- PPV/NPV
  - considers prevalence
- Validation across all relevant populations
- Methods to resolve initial positive results diagnostically

- Knowledge of natural history
- Changes in medical management
- Psychological benefit?

- **The medical "so what"?**



Do SNPs meet the Clinical Validity "Test"? (adapted from cdc.gov)

- How often is the test positive when the disorder is present?
- How often is the test negative when the disorder is not present?
- Are there methods to resolve clinical false positive results in a timely manner?

- What is the prevalence of the disorder in this setting?
- Has the test been adequately validated on all populations to which it may be offered?
- What are the positive and negative predictive values?

- What are the genotype/phenotype relationships?
- What are the genetic, environmental or other modifiers?

Ten Basic Questions to Ask About a Genome-wide Association Study Report

- 1. Are the cases defined clearly and reliably so that they can be compared with patients typically seen in clinical practice?
- 2. Are case and control participants demonstrated to be comparable to each other on important characteristics that might also be related to genetic variation and to the disease?
- 3. Was the study of sufficient size to detect modest odds ratios or relative risks (1.3-1.5)?
- 4. Was the genotyping platform of sufficient density to capture a large proportion of the variation in the population studied?
- 5. Were appropriate quality control measures applied to genotyping assays, including visual inspection of cluster plots and replication on an independent genotyping platform?

Top 10 questions (con't)

- 6. Did the study reliably detect associations with previously reported and replicated variants (known positives)?
- 7. Were stringent corrections applied for the many thousands of statistical tests performed in defining the *P* value for significant associations?
- 8. Were the results replicated in independent population samples?
- 9. Were the replication samples comparable in geographic origin and phenotype definition, and if not, did the differences extend the applicability of the findings?
- 10. Was evidence provided for a functional role for the gene polymorphism identified?
    - For a more detailed description of interpretation of genome-wide association studies, see NCI/NHGRI Working Group on Replication in Association Studies. (taken from *Pearson and Manolio 2008*)

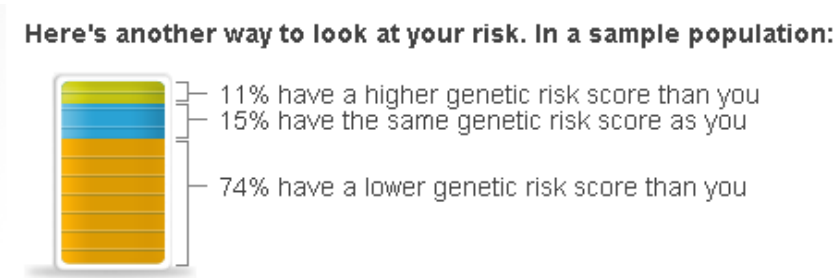
- **What SNPs are included to develop the OR?**
    - **Where does that data come from (size, population variances, etc.)**
    - **How good a job is done "cleaning" the data for spurious associations**
    - **Who/how to decide what is "legit" for inclusion?**
    - **Models for interactions and additive nature of the risk factors are becoming available (Drenos et al. 2007)**
    - **Data changing rapidly at this point – reanalysis? Recontact?**
    - **Do SNPs meet the clinical validity test?**
    - **Just because we can "know it", does that make it useful?**

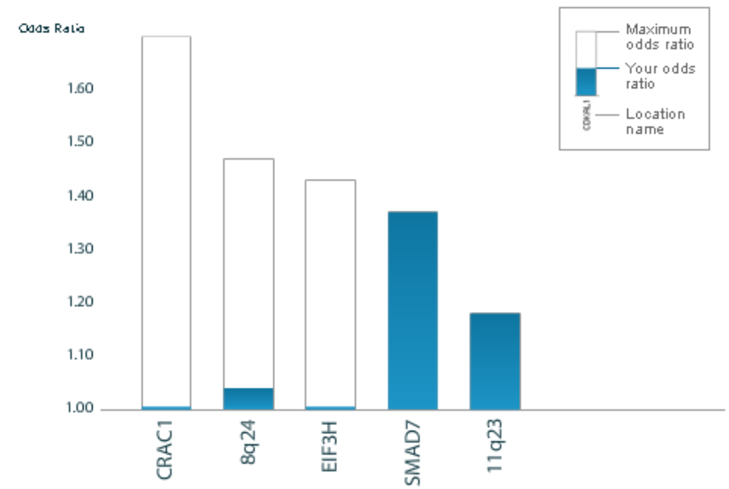
    - **How well phenotyped are the cases and controls**

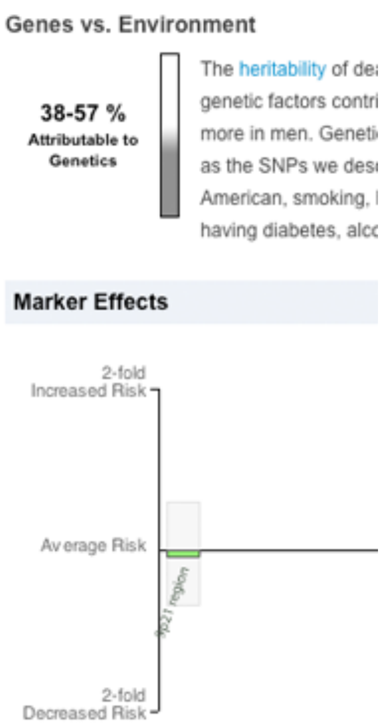
So what will I learn if I undergo personal genotyping?

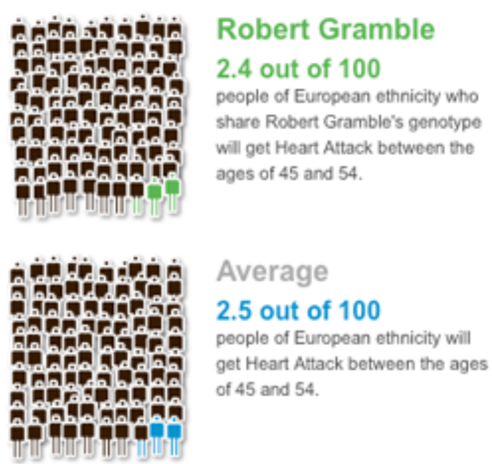
- Depends on the company!
  - (Louanne will discuss further)
- Medical conditions
  - Estimate risk for common complex diseases (may or may not be "actionable")
  - Pharmacogenomic information
  - Some examine carrier status for various conditions
- Traits?
- Ancestry?
- Family relationships?

What sort of data will I get?









Gene or location	Risk marker	Your markers	Odds ratio	Source
9p21	C	GG	1.0	Science, 2007
MTHFD1L	A	GG	1.0	New England Journal of Medicine, 2007

Navigenics.org; 23andme.com

What are the potential benefits of personal genotyping

- You may have some validation that you are at increased risk for specific common disorders present in your family

- If you are found to be at elevated risk, this may help you decide to make some lifestyle or behavioral changes to decrease your risks, or to get screening at an earlier or more frequent age then otherwise

- If you are adopted and don't know your family medical history, this may provide you with some information

What are the potential “risks” to personal genotyping

- There are minimal physical risks (spit in tube)
- There are minimal financial risks
  - Personal cost of test $99
  - Insurance risks? GINA +/-

What are the potential "risks" to personal genotyping

- The emotional risks include:
  - You might learn that you have a high risk for something you were not previously aware of
    - Most risks from GWAS data are small odds ratios – this is not like testing for Huntington disease
    - 23andme does include BRCA1/2 Jewish founder mutations, which ARE highly penetrant
  - Depending on the test, you might learn about your risks for a condition like Alzheimer disease (Navigenics) or psychiatric illness risks for Bipolar or Schizophrenia (23andme)
    - In some cases you can opt out of learning this information if you don't want to learn it
  - You might learn something about your ancestry that makes you uncomfortable
  - If more than one person in your family gets tested, you might learn that family relationships are not what you expected

What about GINA?

- Genetic information nondiscrimination act (signed 5/2008)
- Federal provisions to protect against genetic discrimination in the realms of health insurance (5/09) and employment (11/09)
- No protections for life, disability and long-term care insurance
- Few actual reports of discrimination on the basis of presymptomatic mutation status, but this federal bill will provide additional protections and, hopefully, help patients and families feel more confident undergoing testing
- http://www.genome.gov/10002328

Are there any potential health risks?

- You might find out about an elevated health risk and decide to undergo an invasive screening test that wasn't really necessary, putting yourself at an increased risk for complications.

- You might find out about a decreased health risk and decide you no longer needed to undergo routine screening tests that are recommended to the general population, and there is always a chance you could still develop that condition (and have it detected at a later point, impacting prognosis).

What other factors should be considered

- The companies do both use CLIA approved laboratories, but are not regulated
- Each company uses a different algorithm to calculate your lifetime risks
- Your "risks" will change over time as the companies modify their algorithms and add additional SNPs

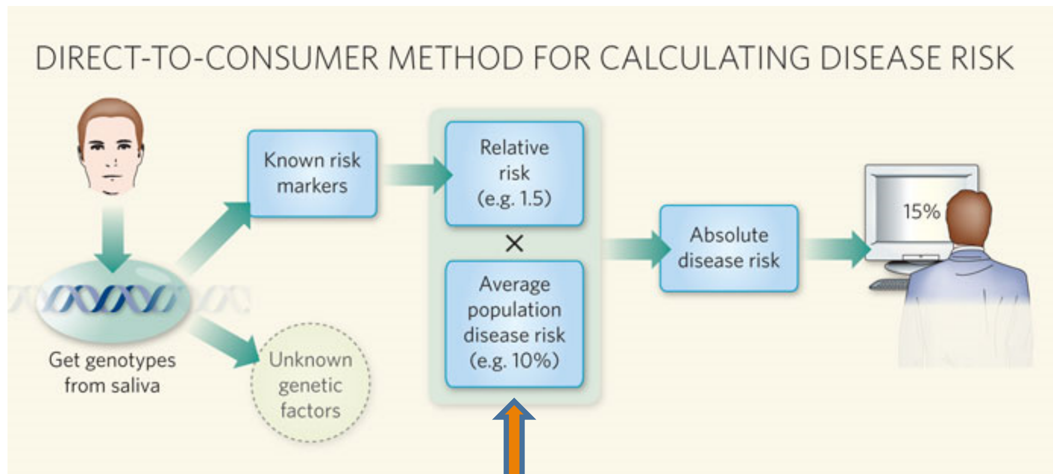
- What happens to your data?
  - Is the company going to use your DNA for future study? Do you opt in or out?
  - What if you decide you want your data removed from their databases?
  - What if the company goes bankrupt? Who gets the data?
  - How secure are the confidentiality protections via the websites?

nature Vol 461|8 October 2009

OPINION

An agenda for personalized medicine

Pauline C. Ng, **Sarah S. Murray**, **Samuel Levy** and **J. Craig Venter** find differences in results from two direct-to-consumer genetics-testing companies. They therefore give nine recommendations to improve predictions.



- Most (all?) of the current GWAS predications are currently being offered by direct-to-consumer companies

- Companies use unique algorithms for calculating risks and selecting which SNPs and population risks to consider in their calculations

99.7% match

Variation in how pop risk calculated (age, gender)

Both companies provide absolute risk

Ng, 2009

21 of 58 risk predictions differed between the two companies

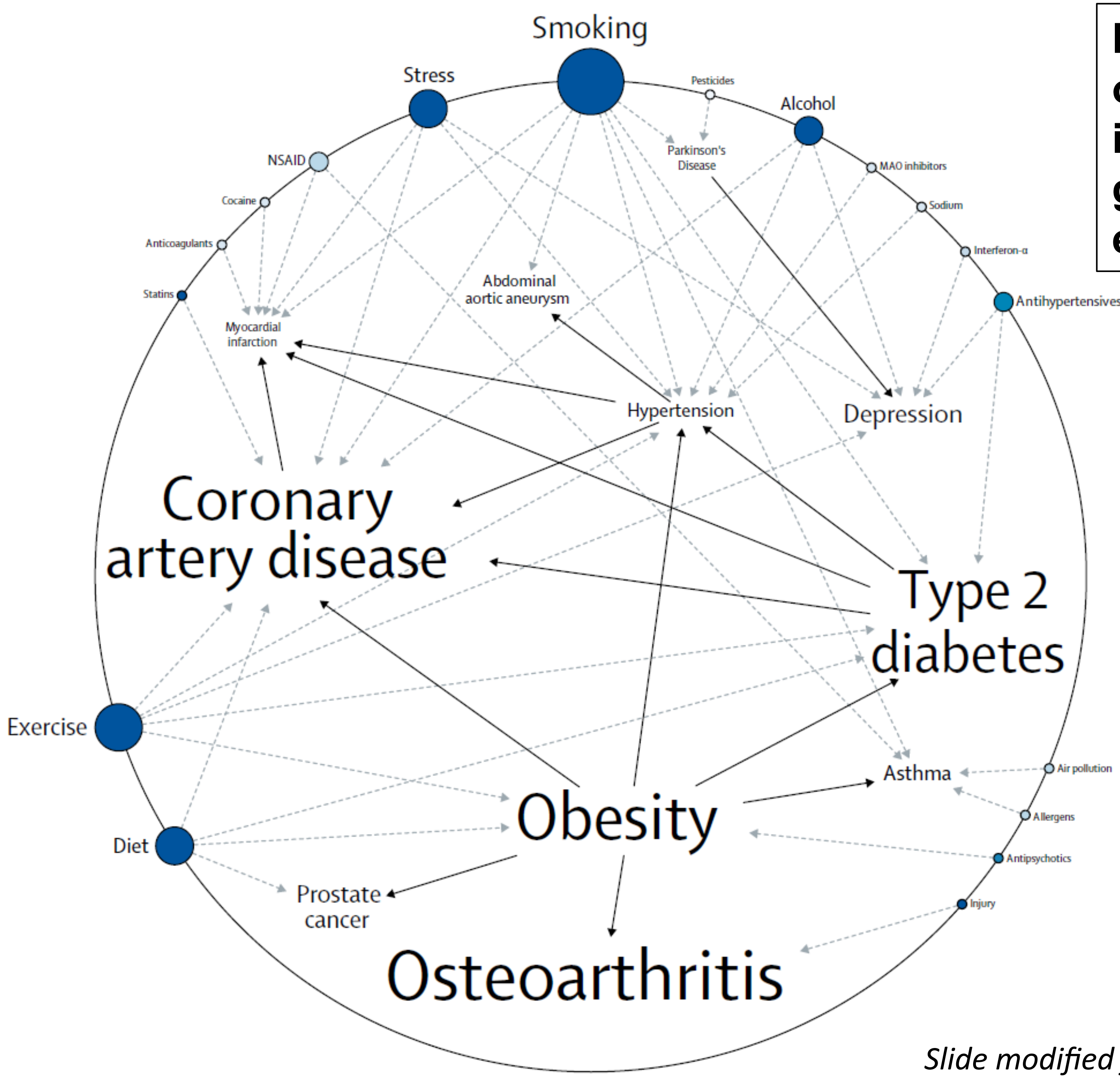
Only 4 diseases provided consistent risk prediction:
- -Breast cancer
- -Celiac disease
- -Multiple sclerosis
- -Rheumatoid arthritis

Mihaescu 2009 showed that if they adjusted the data every time a new marker was added, risks "yo-yo" back and forth, which could lead to patient confusion

TABLE 1: PREDICTIONS FOR DISEASE RELATIVE RISKS FOR FIVE INDIVIDUALS

Disease	Female A	Female B	Female C	Male D	Male E
Breast cancer	↑↑	↑↑	↓↓		
Coeliac disease	↓↓	↓↓	↓↓	↓↓	↓↓
Colon cancer	==	==	=↓	↑↑	=↓
Crohn's disease	↓↑	↓↑	↓↓	↓↓	↓=
Heart attack	↓↓	=↓	=↓	=↓	↑↑
Lupus	↑↓	↓↓	↓↓	↑=	↑=
Macular degeneration	↓↓	↓↓	↑=	↓↓	↓↓
Multiple sclerosis	↑↑		↓↓	↓↓	↓↓
Prostate cancer				↑↑	↓↑
Psoriasis	↓↑		↑↓	↑↑	↓↓
Restless legs syndrome	=↓	↑↑	↓=	↓↑	↑↑
Rheumatoid arthritis	↑↑	↑↑	↓↓	↓↓	↑↑
Type 2 diabetes	↓↓	=↓	↓↓	↑↓	=↓

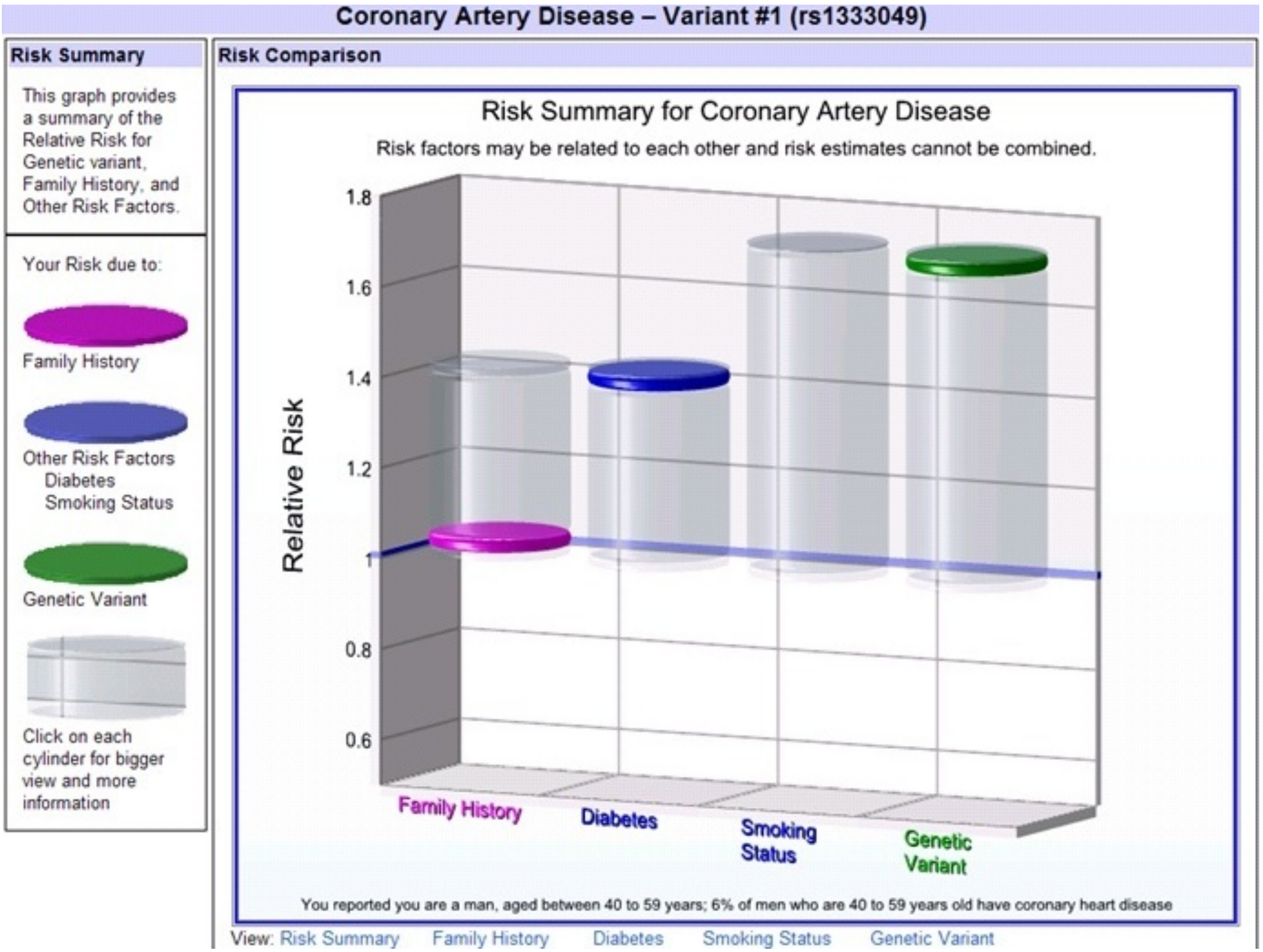
↑ increased risk (RR > 1.05), ↓ decreased risk (relative risk (RR) < 0.95), = average risk (0.95 ≤ RR ≤ 1.05). First prediction is from 23andMe; second prediction is from Navigenics. Different predictions are highlighted in beige.

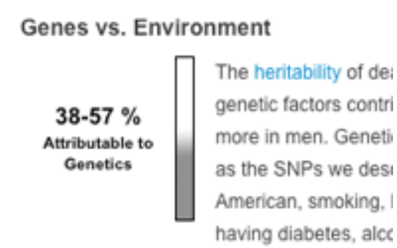


Risks do not occur in isolation, either genetically or environmentally!

Slide modified from Atul Butte, 2010

Environmental risks may be as large, or larger, than genetic risks





Do YOU want to know?

- Is there ANY sort of condition that you would NOT want to know about predictively?

- Fatal vs. Chronic Static vs. Progressive
- Is it treatable?
- Is screening available to promote early diagnosis?
- Is there anything you can do to reduce your risk?
- What is the typical age of onset

- Why might people NOT want to know

Questions you should think about…

- Why do you want to know?
- Why now versus at another time in your life?
  - As a medical student or graduate student, are knowing these risks going to make you more or less likely to worry about them?
  - How does your age, current health, relationship status and parenting status impact your decision?

- Have you told your family you are considering this? What do they think?
    - Is there external pressure to get tested? Is this a good or bad thing?

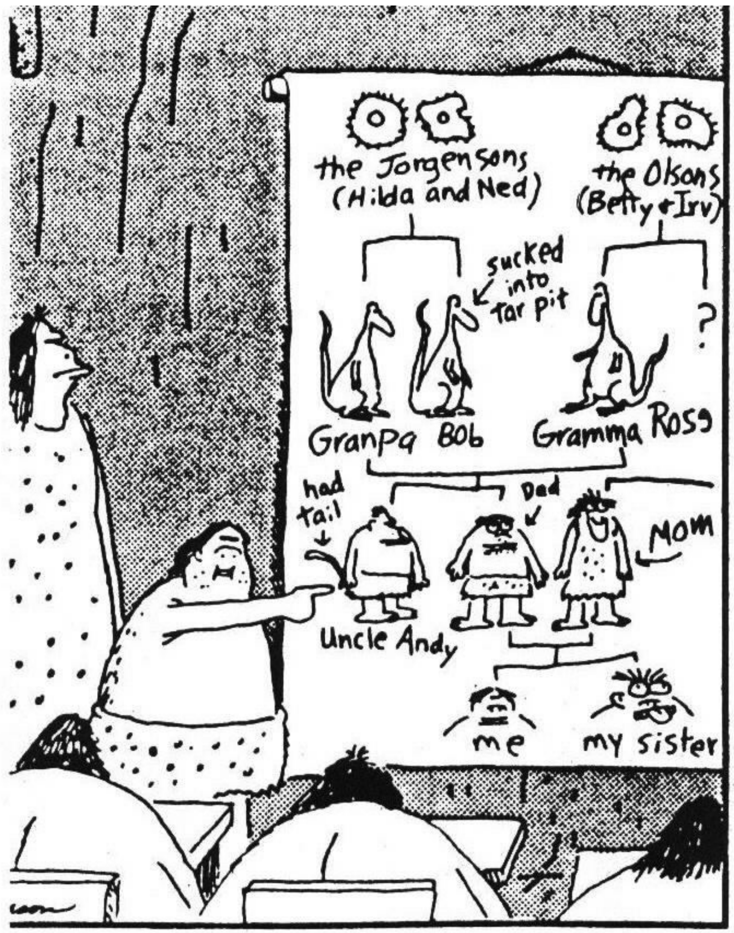
- With whom will you share your results?
  - Family? Partner? Doctor? Friends? Classmates? Teachers?

- What result are you expecting? Why?
- How do they think you will respond if the result is not what you are expecting?

- What, if anything, do you think you will do about the conditions you learn you are at increased risk for?

- Are there behavioral or screening changes you can make without your genotyping results? What factors might be holding you back? How will genotype results *really* interact with the day-to-day barriers we all face for behavior change?

Before you test,
assess your family history!



Dirk brings his family tree to class.

First degree relative means 2-5X risk for disease

Common diseases (age that defines early onset)

- coronary heart disease (60)
- sudden unexpected death (40)
- stroke/TIA (mini stroke) (60)
- hypertension (40)
- diabetes (20)
- blood clots in lungs or legs (40)
- emphysema/lung disease (50)
- kidney disease (50)
- breast, ovarian or endometrial cancer (50)
- prostate cancer (50)
- colon/colorectal cancer (50)
- thyroid cancer (50)
- kidney cancer (50)

Family History Tool

1st draft

Bigger than most GWAS odds ratios!

FHx will predict your GWAS results

CDC

SAFER • HEALTHIER • PEOPLE

Using family history for disease prevention

Classification → Intervention

Family History Tool

- **Average** → **Standard prevention recommendations**
- **Moderate** → **Personalized prevention recommendations**
- **High** → **Referral for genetic evaluation and personalized prevention recommendations**

Using family history for disease prevention

	Classification		Intervention
Family History Tool + GWAS resuluts →	**Average**	→	**Standard prevention recommendations**
	Moderate	→	**Personalized prevention recommendations**
	High	→	**Referral for genetic evaluation and personalized prevention recommendations**

Professional societies on DTC genetic testing

- http://www.nsgc.org/about/position.cfm#DTC
- http://www.acmg.net/StaticContent/StaticPages/DTC_Statement.pdf
- http://www.ashg.org/pdf/dtc_statement.pdf

How to choose a DTC genetic testing service

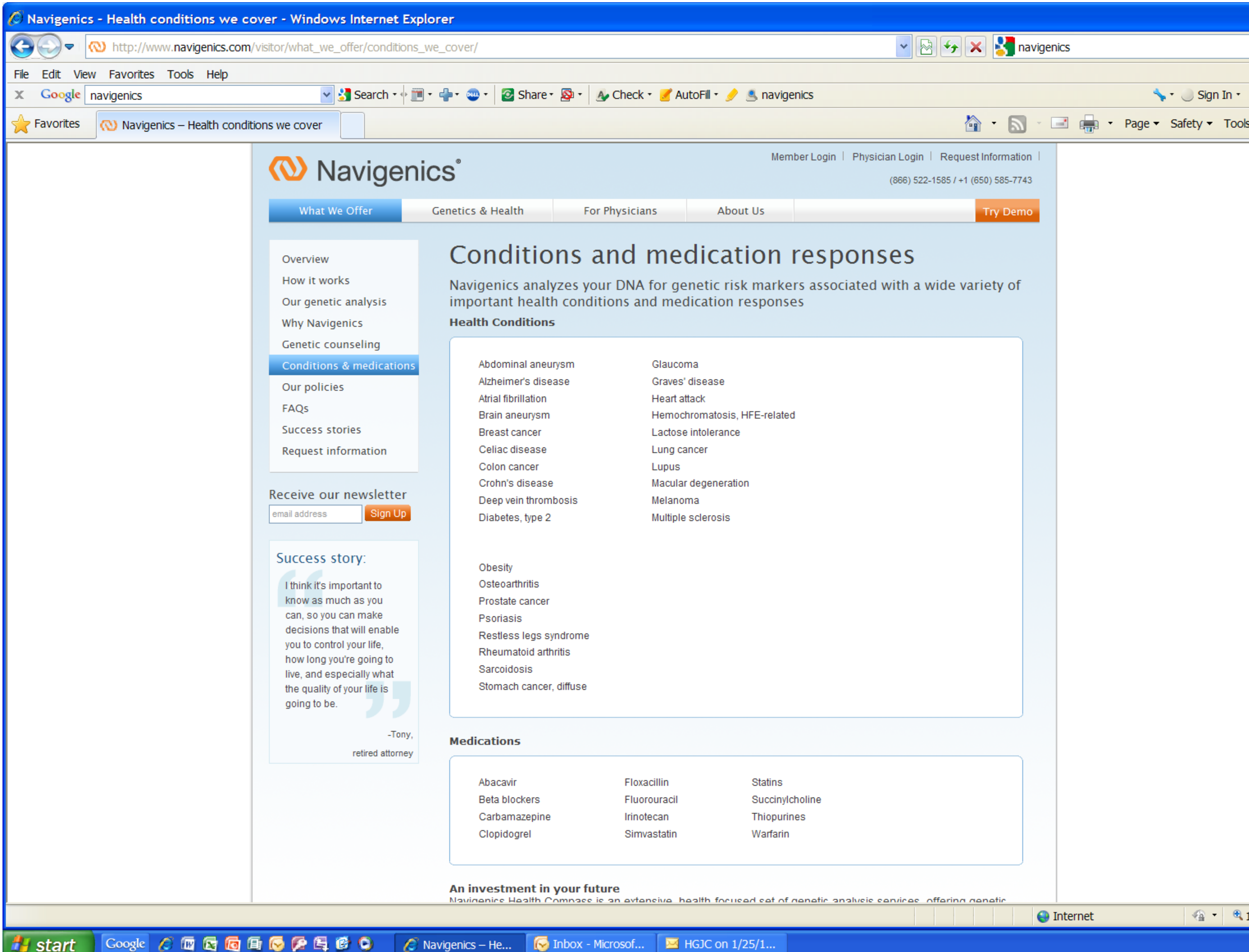
- What do you really want to know?
  - What are the conditions tested for?
    - How serious is each specific condition?
    - What is the age of onset for each specific condition?
  - What does this mean for my health and the health of my family members?
    - Will I change my behavior based on the results?
    - Will the results cause me and/or my family members undue anxiety?
  - Does the company provide someone to talk to if you have questions including a genetic counselor or geneticist?

How to choose a DTC genetic testing service

- How good is the test for each individual condition?
  - In defining risk
  - For my ethnicity

How to choose a DTC genetic testing service

- How accurate is the test for each individual condition
  - In defining risk
  - For my ethnicity



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I think it's important to know as much as you can, so you can make decisions that will enable you to control your life, how long you're going to live, and especially what the quality of your life is going to be.
-Tony, retired attorney
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Navigenics analyzes your DNA for genetic risk markers associated with a wide variety of important health conditions and medication responses
Health Conditions
Abdominal aneurysm
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Atrial fibrillation
Brain aneurysm
Breast cancer
Celiac disease
Colon cancer
Crohn's disease
Deep vein thrombosis
Diabetes, type 2
Glaucoma
Graves' disease
Heart attack
Hemochromatosis, HFE-related
Lactose intolerance
Lung cancer
Lupus
Macular degeneration
Melanoma
Multiple sclerosis
Obesity
Osteoarthritis
Prostate cancer
Psoriasis
Restless legs syndrome
Rheumatoid arthritis
Sarcoidosis
Stomach cancer, diffuse
Medications
Abacavir
Beta blockers
Carbamazepine
Clopidogrel
Floxacillin
Fluorouracil
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- Multiple sclerosis
- Obesity
- Osteoarthritis
- Prostate cancer
- Psoriasis
- Restless legs syndrome
- Rheumatoid arthritis
- Sarcoidosis
- Stomach cancer, diffuse

Medications

- Abacavir
- Beta blockers
- Carbamazepine
- Clopidogrel
- Floxacillin
- Fluorouracil
- Irinotecan
- Simvastatin
- Statins
- Succinylcholine
- Thiopurines
- Warfarin

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-Tony, retired attorney

Alzheimer's disease

View all

- **Fact:** Alzheimer's is not just a devastating illness, causing a frustrating and debilitating loss of memory and brain function. For some who have it, Alzheimer's disease can be fatal.
- **Proportion of risk that's in your genes:** 62 percent.
- **What you can do:** Early detection is critical to controlling Alzheimer's disease. Medication and exercise may temporarily improve memory symptoms and boost mental function. Controlling blood pressure and cholesterol and maintaining social connections are also important. Diet matters, too. Our genetic testing service can help you determine if you are at above-average genetic risk of Alzheimer's.
- **Did you know?** Doing crossword puzzles can help keep your brain in shape; as can physical exercise and eating more fish, fruits and vegetables.

Alzheimer's, the most common form of dementia, is a progressive disease of the brain that causes problems with memory, thinking and behavior. It gradually destroys brain cells, making it increasingly difficult for people to work, participate in hobbies and even care for themselves. It is not a natural part of aging.

As many as 5 million Americans have Alzheimer's. Because the population is living longer, the number of people with this disease is expected to more than triple by 2050.

Although about three-fourths of cases occur in people with no apparent family history, nonetheless genetic changes are likely to play a key role. One of the primary culprits is thought to be the E4 version of the APOE gene This gene carries the code for a protein that helps transport cholesterol in the bloodstream. Those who have 1 or 2 copies of the APOE4 gene variant are known to have a higher risk for Alzheimer's. Our genetic test looks at markers in the APOE gene and determines genetic risk.

Early onset Alzheimer's disease, which begins before age 60, is even more strongly genetic in its cause, but very rare — it represents less than 2 percent of cases. At this time, Navigenics does not test for this rare kind of Alzheimer's. If you have family members who developed the disease at an early age, you should consult a genetic counselor.

Fortunately, exercising your body and your mind may improve blood flow to the brain and increase connections between nerve cells, helping compensate for the brain's degeneration. Recent research suggests you can even generate new brain cells. Trying your hand at the saxophone or Sudoku puzzles can be of benefit in preventing Alzheimer's disease. And seniors with a lively social life are less likely to suffer cognitive decline.

If you begin experiencing serious memory loss or confusion, your doctor can give you a simple mental function test to screen for Alzheimer's disease. Brain imaging can also be a helpful test for Alzheimer's.

Explore other conditions and medications

Health Conditions

Abdominal aneurysm	Glaucoma
Alzheimer's disease	Graves' disease
Atrial fibrillation	Heart attack
Brain aneurysm	Hemochromatosis, HFE-related

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Carrier Status (24)

- Alpha-1 Antitrypsin Deficiency *
- BRCA Cancer Mutations (Selected) *
- Bloom's Syndrome *
- Canavan Disease *
- Connexin 26-Related Sensorineural Hearing Loss *
- Cystic Fibrosis *
- Factor XI Deficiency *
- Familial Dysautonomia *
- Familial Hypercholesterolemia Type B *
- Familial Mediterranean Fever *
- Fanconi Anemia (FANCC-related) *
- G6PD Deficiency *
- Gaucher Disease *
- Glycogen Storage Disease Type 1a *
- Hemochromatosis *
- Limb-girdle Muscular Dystrophy *
- Maple Syrup Urine Disease Type 1B *
- Mucolipidosis IV *
- Niemann-Pick Disease Type A *
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- Rhizomelic Chondrodysplasia Punctata Type 1 (RCDP1) *
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- Torsion Dystonia *

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- Abacavir Hypersensitivity *
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- Pseudocholinesterase Deficiency *
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Traits (47)

- Adiponectin Levels
- Alcohol Flush Reaction *
- Asparagus Metabolite Detection
- Avoidance of Errors

Disease Risk (94)

- Abdominal Aortic Aneurysm
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- Atrial Fibrillation: Preliminary Research
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- Breast Cancer Risk Modifiers
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- Esophageal Squamous Cell Carcinoma (ESCC) *
- Essential Tremor
- Exfoliation Glaucoma *
- Follicular Lymphoma
- Gallstones
- Generalized Vitiligo
- Gestational Diabetes
- Gout
- Hashimoto's Thyroiditis
- Heart Attack *
- High Blood Pressure (Hypertension)
- Hodgkin Lymphoma
- Hypertriglyceridemia
- Intrahepatic Cholestasis of Pregnancy
- Keloid
- Kidney Disease
- Larynx Cancer
- Lou Gehrig's Disease (ALS)
- Lung Cancer *

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Hodgkin Lymphoma
Hypertriglyceridemia
Intrahepatic Cholestasis of Pregnancy
Keloid
Kidney Disease
Larynx Cancer
Lou Gehrig's Disease (ALS)
Lung Cancer *

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About Canavan Disease

Canavan disease is caused by mutations in the ASPA gene, which encodes the aspartoacylase enzyme. These mutations cause a deficiency in enzyme activity, leading to a buildup of the chemical N-acetylaspartic acid (NAA) in the cells of the body. For unknown reasons, excess NAA results in a breakdown of the myelin, a major part of white matter, in the brain. Canavan disease is inherited in a recessive manner, meaning that only a child who receives two mutated copies of the ASPA gene (one from each parent) will get the disease. Symptoms include mental retardation, loss of motor skills, abnormal muscle tone, visual degeneration and a rapidly increasing head circumference. Most people with Canavan disease die in childhood, but some survive to adolescence or adulthood. Although anyone can be a carrier for a mutation that causes Canavan disease, they are most common in people with Ashkenazi Jewish ancestry.

1 of 2. Canavan disease is caused by mutations that lead to a breakdown of the white matter in the brain.

Learn more about the biology of Canavan Disease...

Example Genetic Data

Who	What It Means
	Has Canavan disease.
	Most likely does not have Canavan disease, but can pass mutation to offspring. May have Canavan disease due to other mutations in the ASPA gene (not reported here).
Greg Mendel (Dad)	Does not have any of the three Canavan disease mutations reported by 23andMe. Most likely no disease and not a carrier. May still be a carrier due to other mutations in the ASPA gene (not reported here).

Learn more about your genotype...

Genes vs. Environment

Canavan disease is inherited in a recessive manner, meaning that only a child who receives two mutated copies of the ASPA (one from each parent) will get the disease. Many mutations in the ASPA gene have been documented. 23andMe reports data for the three that account for about 99% of mutations found in Ashkenazi Jews and 40-60% of mutations found in non-Jewish populations. This means you may still have an ASPA mutation even if your data indicates that you are a non-carrier. If you are concerned about Canavan disease, consult a health professional.

A genetic counselor can help you understand more about your 23andMe reports and respond to your genetic health questions. 23andMe is collaborating with Informed Medical Decisions, Inc., to give you direct access to board-certified genetic counselors that have been specifically trained to guide you through your 23andMe results. Click here to learn more about their independent genetic counseling services

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Lou Gehrig's Disease (ALS)
Lung Cancer *

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About Limb-girdle Muscular Dystrophy

Muscular dystrophy is a broad category of disorders characterized by progressive muscle degeneration due to abnormal muscle proteins. Limb-girdle muscular dystrophy is a specific type of muscular dystrophy that mainly affects the muscles around the hips and shoulders, as well as the muscles in the upper parts of the arms and legs. Limb-girdle muscular dystrophy can be caused by mutations in many different genes. Symptoms vary and depend on which gene is mutated and what type of mutation is present. Some people with limb-girdle muscular dystrophy lose the ability to walk and suffer from serious disability, while others have minimal disability even after many years. Between one out of every 14,500 and one out of every 123,000 people worldwide is affected with by some form of LGMD.

1 of 2. Physical therapy and stretching exercises can help maintain mobility in people with limb-girdle muscular dystrophy

Learn more about the biology of Limb-girdle Muscular Dystrophy...

Example Genetic Data

Who	What It Means
	Has limb-girdle muscular dystrophy.
	Most likely does not have limb-girdle muscular dystrophy, but can pass mutation to offspring. May have limb-girdle muscular dystrophy due to the presence of other mutations (not reported here).
Greg Mendel (Dad)	Does not have any of the three limb-girdle muscular dystrophy mutations reported by 23andMe. Most likely no disease and not a carrier. May still be affected or a carrier due to the presence of other mutations (not reported here).

Genes vs. Environment

23andMe reports data for three specific mutations associated with recessively inherited LGMD: the R77C mutation in the SGCA gene (LGMD2D), the T151R mutation in the SGCB gene (LGMD2E), and the L276I mutation in the FKRP gene (LGMD2I). A child who receives two copies of one of these mutations will have limb-girdle muscular dystrophy. There are many other mutations in these genes, as well as in other genes, that can cause limb-girdle muscular dystrophy. If you are concerned about this disease, consult a medical professional.

A genetic counselor can help you understand more about your 23andMe reports and respond to your genetic health questions. 23andMe is collaborating with Informed Medical Decisions, Inc., to give you direct access to board-certified genetic counselors that have

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Limb-Girdle Muscular Dystrophy Overview - GeneReviews - NCBI Bookshelf - Windows Internet Explorer

http://www.ncbi.nlm.nih.gov/books/NBK1408/

Table 1. Autosomal Recessive Limb-Girdle Muscular Dystrophy (LGMD): Molecular Genetics

% of Individuals with AR LGMD	Disease Name	Populations with Founder Mutations	Locus Name	Gene Symbol	Locus	Protein Product
Up to 68% of individuals with childhood onset and ~10% with adult onset [1]	Alpha-sarcoglycan-opathy	None	LGMD2D	*SGCA*	17q12-q21.3	Alpha-sarcoglycan
	Beta-sarcoglycan-opathy	Amish	LGMD2E	*SGCB*	4q12	Beta-sarcoglycan
	Gamma-sarcoglycan-opathy (formerly SCARMD) [2]	North Africans; Gypsies [3]	LGMD2C	*SGCG*	13q12	Gamma-sarcoglycan
	Delta-sarcoglycan-opathy	Brazilian [4]	LGMD2F	*SGCD*	5q33	Delta-sarcoglycan
~10%-80% [5]	Calpainopathy	Amish, La Reunion Island, Basque (Spain), Turkish	LGMD2A	*CAPN3*	15q15.1-q21.1	Calpain-3
~10%	Dysferlinopathy, Miyoshi distal myopathy	Libyan Jewish	LGMD2B	*DYSF*	2p13.3-p13.1	Dysferlin
3%	Telethonin-opathy	Italian (?)	LGMD2G	*TCAP*	17q12	Telethonin
Unknown	LGMD2H	Manitoba Hutterites only	LGMD2H	*TRIM32*	9q31-q34.1	Tripartite motif protein 32
6% [6]	LGMD2I	Unknown	LGMD2I	*FKRP*	19q13.3	Fukutin-related protein
Unknown	LGMD2J	Finland	LGMD2J	*TTN*	2q24.3	Titin
Unknown	LGMD2K	Turkish	LGMD2K	*POMT1*	9q34.1	Protein O-mannosyl-transferase 1
Unknown	LGMD2L	Unknown	LGMD2L	*FKTN*	9q31	Fukutin
Unknown	LGMD2M	Unknown	LGMD2M	*POMGNT1*	1p34-p33	Protein O-linked-mannose beta-1,2-N-acetylglucosaminyltransferase 1
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	Protein O-mannosyl-transferase

14 genes

weakness. Distal weakness occurred late. A juvenile-onset form and an adult-onset form were observed; the more rapid progression seen in the juvenile-onset form is thought to result from anticipation. A subset of individuals with the juvenile-onset form show scapular winging and facial muscle weakness. No calf hypertrophy, eye involvement, or intellectual impairment has been observed [Gamez et al 2001].

LGMD1G. While symptoms are slowly progressive, all but one individual were still ambulatory ten years after diagnosis. No other joint limitation, aside that noted in Table 4, was observed.

Evaluation Strategy

Go to: Top ▲

Establishing the type of LGMD can be useful in discussions of the clinical course of the disease and for genetic counseling purposes.

Establishing the specific type of LGMD in a given individual usually involves obtaining the medical history and family history, performing a physical examination, and laboratory testing (see Table 5) including serum CK concentration and muscle biopsy for histologic examination and protein testing [Pogue et al 2001].

Note: (1) Only dysferlin immunoblotting of muscle is currently thought to be specific and sensitive. (2) Results of immunostaining of muscle should be confirmed with molecular genetic testing when it is available.

Use of molecular genetic testing to establish the specific type of LGMD is problematic:

- Many causative genes are involved.
- Mutations in no one gene account for the majority of cases.
- Few clinical or laboratory findings help identify the causative gene for a given individual.
- The lack of common mutations prevents efficient screening by genotype.
- About 50% of currently identified LGMD would have no molecular diagnosis, even if all 14 currently known genes were fully sequenced.

Table 5. Testing Used to Establish LGMD Type

Type	Serum CK Concentration	Muscle Biopsy Histology	Muscle Protein (Biochemical) Testing [1, 2]	Test Availability: Molecular Genetic Testing	Test Availability: Protein (Biochemical) Testing
Autosomal Recessive					
Alpha-sarcoglycanopathy	Mildly to greatly elevated	Myopathic changes	Reduced or complete absence of sarcoglycan antibodies [3]	Clinical Testing	Clinical (immuno-histochemistry)
Beta-sarcoglycanopathy				Clinical Testing	
Gamma-sarcoglycanopathy				Clinical Testing	

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- Food Preference
- Freckling
- HDL Cholesterol Level
- HIV Progression
- Hair Color
- Hair Curl *
- Hair Curl: Preliminary Research
- Hair Thickness
- Height
- Lactose Intolerance *
- Leprosy Susceptibility
- Longevity
- Malaria Complications
- Malaria Resistance (Duffy Antigen) *
- Male Pattern Baldness *
- Measures of Intelligence
- Measures of Obesity
- Memory
- Menarche
- Menopause
- Muscle Performance *
- Non-ABO Blood Groups *
- Norovirus Resistance *
- Odor Detection
- Pain Sensitivity
- Persistent Fetal Hemoglobin
- Photic Sneeze Reflex
- Prostate-Specific Antigen
- Reading Ability
- Refractive Error
- Resistance to HIV/AIDS *
- Response to Diet and Exercise
- Sex Hormone Regulation
- Smoking Behavior *
- Tuberculosis Susceptibility

- Lung Cancer *
- Lupus (Systemic Lupus Erythematosus) *
- Male Infertility
- Melanoma *
- Melanoma: Preliminary Research
- Multiple Sclerosis *
- Nasopharyngeal Carcinoma
- Neural Tube Defects
- Neuroblastoma
- Nicotine Dependence
- Nonalcoholic Fatty Liver Disease
- Obesity *
- Obesity: Preliminary Research
- Obsessive-Compulsive Disorder
- Oral and Throat Cancer
- Osteoarthritis
- Otosclerosis
- Paget's Disease of Bone
- $\boxed{\text{Parkinson's Disease *}}$
- Parkinson's Disease: Preliminary Research
- Peripheral Arterial Disease
- Placental Abruption
- Polycystic Ovary Syndrome
- Preeclampsia
- Primary Biliary Cirrhosis
- Progressive Supranuclear Palsy
- Prostate Cancer *
- Psoriasis *
- Restless Legs Syndrome *
- Rheumatoid Arthritis *
- Schizophrenia
- Scleroderma (Limited Cutaneous Type) *
- Selective IgA Deficiency
- Sjögren's Syndrome
- Stomach Cancer (Gastric Cardia Adenocarcinoma) *
- Stomach Cancer: Preliminary Research
- Stroke
- Tardive Dyskinesia
- Thyroid Cancer
- Tourette's Syndrome
- Type 1 Diabetes *
- Type 2 Diabetes *
- Ulcerative Colitis *
- Uterine Fibroids
- Venous Thromboembolism *

The genotyping services of 23andMe are performed in LabCorp's CLIA-certified laboratory. The tests have not been cleared or approved by the FDA but have been analytically validated according to CLIA standards. The information on this page is intended for research and educational purposes only, and is not for diagnostic use.

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Parkinson's Disease - Genetic Testing - 23andMe - Windows Internet Explorer

https://www.23andme.com/health/Parkinsons-Disease/

possible genotypes at the marker.

2-fold
Decreased Risk

LRRK2 **Marker:** rs34637584

Mutations in the LRRK2 gene are the most common known genetic cause of Parkinson's disease (PD).

More than 50 variations are known in the LRRK2 gene. Several of these have been associated with PD. The variant reported by 23andMe, rs34637584, also known as the G2019S mutation, is the best-studied LRRK2 SNP related to Parkinson's.

Parkinson's is a fairly rare disease. The average person has a 1-2% chance of developing the disease during their lifetime. The chance that a person with the G2019S mutation will develop Parkinson's is much higher and increases with age. One recent study found that a person who inherits this mutation from either parent has a 28% chance of developing Parkinson's by the age of 59, 51% by the age of 69 and 74% by the age of 79.

Few people with Parkinson's have the G2019S mutation, but it is present at high levels in patients from some ethnic groups. Up to 40% of people with PD who are of Arab-Berber ancestry and 20% of Ashkenazi Jewish people with PD have this mutation.

Scientists do not know why only some people with the G2019S mutation get PD. There may be unknown effects due to other genes or environmental factors. Such unknown factors may also explain why not all people with the G2019S mutation have the same symptoms.

Mutations in the LRRK2 gene tend to be dominant; that is, they appear to increase Parkinson's risk whether a person inherits the mutation from just one parent or both.

Citations

Schapira (2006) . "The importance of LRRK2 mutations in Parkinson disease." *Arch Neurol* 63(9):1225-8.

Klein et al. (2007) . "Deciphering the role of heterozygous mutations in genes associated with parkinsonism." *Lancet Neurol* 6(7):652-62.

Healy et al. (2008) . "Phenotype, genotype, and worldwide genetic penetrance of LRRK2-associated Parkinson's disease: a case-control study." *Lancet Neurol* 7(7):583-90.

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23andMe is a genetic testing service that provides information and tools to understand your DNA.
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How to choose a DTC genetic testing service

- What do you really want to know?
  - What are the conditions tested for?
    - How serious is each specific condition?
    - What is the age of onset for each specific condition?
  - What does this mean for my health and the health of my family members?
    - Will I change my behavior based on the results?
    - Will the results cause me and/or my family members undue anxiety?
  - Does the company provide someone to talk to if you have questions including a genetic counselor or geneticist?

Resources

- Company's website
- Gene Tests/Gene Reviews: genetests.org
- http://www.accessdna.com/blog/2010/02/personal-genomic-company-test-comparisons/

- OMIM: http://www.ncbi.nlm.nih.gov/omim/

Navigenics - Conditions we cover - Breast cancer - Windows Internet Explorer
http://www.navigenics.com/visitor/what_we_offer/conditions_we_cover/breast_cancer/
File Edit View Favorites Tools Help
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Favorites Navigenics – Conditions we cover – Brea...
Find: Previous Next Options

Overview
How it works
Our genetic analysis
Why Navigenics
Genetic counseling
Conditions & medications
Our policies
FAQs
Success stories
Request information

Breast cancer

View all

- **Fact:** Breast cancer strikes one in eight women during their lives. It kills more American women than any other cancer except lung cancer.
- **Proportion of risk that's in your genes:** 27 percent.
- **What you can do:** Our gene test gauges the extent of your genetic risk. Exercising more, smoking less, maintaining a healthy weight and avoiding long-term hormone replacement therapy can help prevent breast cancer. Early detection of the disease through regular mammograms and breast self-examinations can detect the cancer when it is small and has not spread, significantly increasing the chances of survival.
- **Did you know?** Drinking two alcoholic drinks a day increases your risk of developing breast cancer.

Breast cancer is a disease in which cells in the breast grow out of control. These extra cells can form a mass of tissue called a tumor, and sometimes break away and invade and damage nearby tissues and organs.

Women in North America have the highest rate of breast cancer in the world, with more than 180,000 new cases diagnosed every year.

For most women, genes play only a minor role in their breast cancer risk, with lifestyle, environment and behavior playing a much more important part. You've probably heard about the BRCA genes, the first genes linked to familial breast and ovarian cancer that are most commonly found in women of Ashkenazi (Eastern European) Jewish descent. Navigenics does not currently test for the BRCA variants, because the bulk of a woman's inherited risk appears to result from combinations of more common genetic variants. The Navigenics DNA tests currently look for these more common genetic variants.

Being at high risk of breast cancer is not a death sentence. If caught early enough, the health condition is highly treatable, and today more than 2.5 million American women can call themselves breast cancer survivors.

Genetic testing can help you understand whether you have an above-average genetic risk of breast cancer. Those at extremely high risk for the disease can talk to their doctor about early detection strategies and aggressive preventive measures, including surgery to remove the breasts or preventive medication. The average woman, however, can be well served by maintaining a healthy weight, exercising, limiting alcohol, eating nutritious meals that are low in animal fat, and following recommended breast cancer screening guidelines. Breast cancer tests include ultrasounds, mammograms and MRIs.

Explore other conditions and medications

Health Conditions

Abdominal aneurysm	Glaucoma	Obesity
Alzheimer's disease	Graves' disease	Osteoarthritis
Atrial fibrillation	Heart attack	Prostate cancer
Brain aneurysm	Hemochromatosis	Psoriasis
Breast cancer	Lactose intolerance	Restless legs syndrome
Celiac disease	Lung cancer	Rheumatoid arthritis

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Success story:

I think it's important to know as much as you can, so you can make decisions that will enable you to control your life, how long you're going to live, and especially what the quality of your life is going to be.

-Tony,
retired attorney

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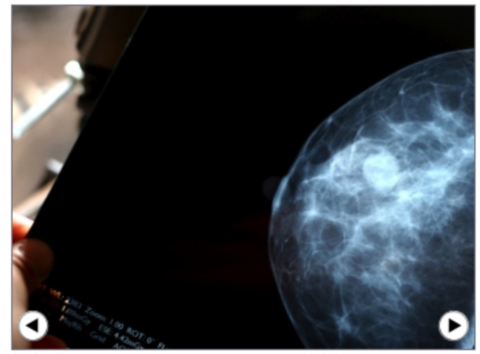
try a demo

About Breast Cancer

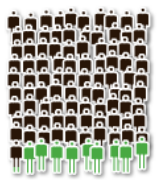
Breast cancer can affect both sexes, but it is mainly a concern for women— one in eight will face the disease at some point in their lifetimes. Next to lung cancer, it is the second leading cause of cancer -related deaths in women. The good news is that the number of these deaths is steadily decreasing. Medicine is making great strides against the disease thanks to early detection and better treatments.

Learn more about the biology of Breast Cancer...
Major discoveries in Breast Cancer...


1 of 4. Having a regular mammogram can help detect breast cancer early, allowing more treatment options.

Example Genetic Data

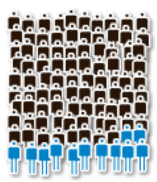
Information for **Lilly Mendel (Mom)** assuming **European** ethnicity and an age range of 30-79



Lilly Mendel (Mom)

9.1 out of 100

women of European ethnicity who share Lilly Mendel (Mom)'s genotype will get Breast Cancer between the ages of 30 and 79.



Average

12.5 out of 100

women of European ethnicity will get Breast Cancer between the ages of 30 and 79.

What does the Odds Calculator show me?

Use the ethnicity and age range selectors above to see the estimated incidence of Breast Cancer due to genetics for women with **Lilly Mendel (Mom)**'s genotype. The 23andMe Odds Calculator assumes that a person is free of the condition at the lower age in the range. You can use the name selector above to see the estimated incidence of Breast Cancer for the genotypes of other people in your account.

The 23andMe Odds Calculator only takes into account effects of markers with known associations that are also on our genotyping chip. Keep in mind that aside from genetics, environment and lifestyle may also contribute to one's chances of developing breast cancer (if you are a woman).

Genes vs. Environment

27-40 %
Attributable to Genetics

The heritability of breast cancer is estimated to be 27-40%. This means that environmental factors contribute more to differences in risk for this condition than do genetic factors. Genetic factors that play a role in breast cancer include both unknown and known factors. Known factors include the rare but high-risk mutations in the BRCA1 and BRCA2 genes as well as the SNPs described here. Other factors that can increase your risk include being female, being older, a family history of breast or ovarian cancer, an abnormal breast biopsy, previous chest radiation, early menarche or late menopause, exposure to diethylstilbestrol (DES) in utero, not having children or having children after the age of 30, recent oral contraceptive use, long term post-menopausal hormone therapy

BRCA1 and BRCA2 Hereditary Breast/Ovarian Cancer -- GeneReviews -- NCBI Bookshelf - Windows Internet Explorer
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Find: Previous Next Options

Summary

Disease characteristics. Mutations in *BRCA1* or *BRCA2* predispose to breast cancer and ovarian cancer as well as prostate cancer *(BRCA1)* and other cancers *(BRCA2)*. The risk of developing cancer that is associated with a *BRCA1* or *BRCA*
predisposing mutation is not known and appears to be variable even within families of similar ethnic background with the same mutation. Estimates of breast cancer and ovarian cancer risks have been derived from families with multiple a
individuals as well as from families with few affected individuals and from population-based studies. Prognosis for breast cancer survival depends upon the stage at which breast cancer is diagnosed. Prognosis for individuals with *BRCA1* c
cancer-predisposing mutations may not be different from that for controls.

Diagnosis/testing. Molecular genetic testing for *BRCA1* and *BRCA2* cancer-predisposing mutations is available on a clinical basis for probands who are identified to be at high risk for a *BRCA1* or *BRCA2* cancer-predisposing mutation and fo
relatives of an individual with an identified *BRCA1* or *BRCA2* cancer-predisposing mutation. No currently available technique can guarantee the identification of all cancer-predisposing mutations in the *BRCA1* gene or in the *BRCA2* gene. Fur
mutations of uncertain clinical significance may be identified.

Management. *Treatment of manifestations:* Treatment of breast and ovarian cancer in individuals with *BRCA1*- or *BRCA2*-related tumors is similar to that for sporadic forms of these cancers. *Prevention of primary manifestations:* Prophylactic
and/or oophorectomy and chemoprevention using tamoxifen (a partial estrogen antagonist) have been used, but have not been assessed by randomized trials or case-control studies in high-risk women. *Surveillance:* Recommended canc
strategies, which need to be modified based on the earliest age of onset in family, have not been assessed by randomized trials or case-control studies. Breast cancer screening in women and men relies on a combination of monthly brea
examination, annual or semiannual clinical breast examination, annual mammography, and breast MRI. Ovarian cancer screening relies on a combination of annual or semiannual pelvic examination, annual or semiannual transvaginal ultra
examination with color Doppler, and annual serum CA-125 concentration. Prostate cancer screening relies on annual digital rectal examination and prostate-specific antigen (PSA) testing. *Testing of relatives at risk:* Once a *BRCA1* or *BRCA2*
been identified in an individual, testing at-risk relatives can identify those family members with the family-specific mutation who will benefit from surveillance and early intervention when a cancer is identified.

Genetic counseling. Cancer-predisposing mutations in the *BRCA1* and *BRCA2* genes are inherited in an autosomal dominant manner. Each offspring of an individual with a *BRCA1* or *BRCA2* cancer-predisposing mutation has a 50% chance
the mutation. Molecular genetic testing of asymptomatic family members at risk of inheriting either a *BRCA1* or *BRCA2* cancer-predisposing mutation is possible once the family-specific mutation has been identified. Prenatal testing is possi
pregnancies at increased risk; however, requests for prenatal diagnosis of adult-onset diseases are uncommon and require careful genetic counseling.

Diagnosis

Clinical Diagnosis

BRCA1 or *BRCA2* hereditary breast/ovarian cancer is suspected in an individual who has one or more of the following:

- A personal history of early-onset (before age 50 years) breast cancer or early-onset breast and ovarian cancer at any age and/or bilateral (or multifocal) disease
- A family history of breast cancer or breast and ovarian cancer consistent with autosomal dominant inheritance
- A personal or family history of male breast cancer

Probability models have been developed to estimate the likelihood that an individual or family has a mutation in *BRCA1* or *BRCA2*.

- Four older prior probability models [Couch et al 1997, Shattuck-Eidens et al 1997, Frank et al 1998] and BRCAPRO [Parmigiani et al 1998] are available. Each has unique attributes determined by the methods, sample size, and po
to create the model.

  Note: The BRCAPRO model is frequently updated; this is not reflected in the date of the citation.

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: Company Test Comparisons - Windows Internet Explorer
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By Jordanna Joaquina, MS, CGC

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« MD calls for widespread recognition of genetic counselors

Media Returns Focus to Classic Genetic Diseases »

Personal Genomic Company Test Comparisons

February 10th, 2010 | Author: jordannajoaquina

SNPs are small variations in a single "letter" of DNA that can be found throughout our entire genetic make-up. Personal genomic companies, such as 23andMe, Navigenics, Pathway Genomics, Gene Essence, and deCODEme, analyze thousands of SNPs at once related to various diseases and traits.

Because a number of individuals have shared their personal risk analyses and genotypes, we know that there are differences between personal genomic companies' disease risk predictions. These discrepancies are largely due to the absence of accepted standards for selecting disease risk markers.

To easily compare testing options presently available directly to consumers, the following charts highlight the wide variation between SNPs analyzed by these companies. To be complete, Coriell Personalized Medicine Institute, who in contrast tests for very few SNPs, is included in the review comparison.

Reported risk markers change frequently. Consequently, these charts will be updated periodically. Comments and suggestions are appreciated.

Lung Cancer Overview:

- Whole genome scan home DNA tests for SNPs associated with lung cancer.

Alzheimer's Disease Overview:

- Whole genome scan home DNA tests for SNPs associated with Alzheimer's disease.

Breast Cancer Overview:

- Whole genome scan home DNA tests for SNPs associated with breast cancer.

About AccessDNA

AccessDNA is the leading online consumer resource for genetics. The company combines high-quality content about genetics with access to, and evaluation of, relevant testing, counseling and support services.

By providing insight into the genetics of disease, AccessDNA helps people better understand their treatment, management and prevention options.

About Jordanna Joaquina

Jordanna Joaquina, MS, CGC is Director of Genetics and a Co-Founder of AccessDNA. She has a clinical background in multiple disciplines of genetics, including prenatal, adult onset and pediatric.

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