Genetic Epidemiology at the intersection between function and disease

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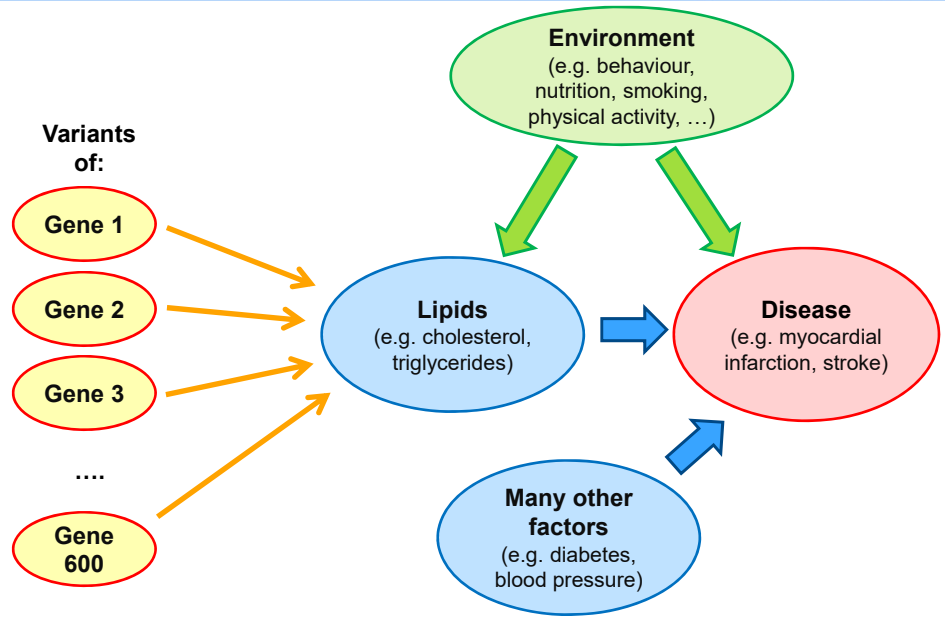
Overview

1. **Background**
2. Association studies
3. Genomewide association studies (GWAS)

GENEPI INNSBRUCK

How is health and disease determined?



GENEPI INNSBRUCK

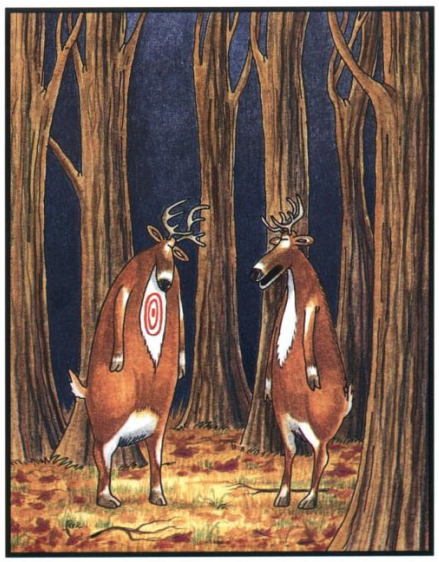
Why are we interested in "new" genes?

By Victor A. McKusick, M.D., Baltimore, Maryland

Ann. Int. Med. 49:556-567, 1958

Study of genetic factors is important:

(1) because potentially it will permit **recognition of genetic susceptibles**, for more effective application of preventive measures,



"Bummer of a birthmark, Hal."

GENEPI INNSBRUCK

Why are we interested in "new" genes?

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Study of genetic factors is important:

(2) because from our **understanding of the mechanism** whereby the gene or genes operate in these disorders can come preventive or therapeutic measures for breaking the chain leading to disease.

"This could be the discovery of the century. Depending, of course, on how far down it goes."

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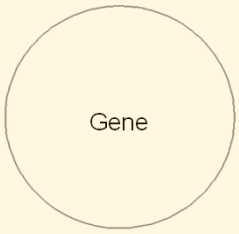
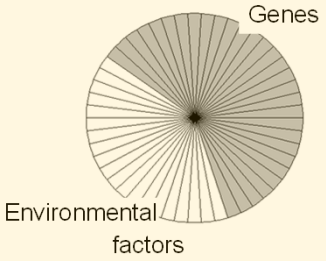
Monogenic and complex diseases



Monogenic diseases:
e.g. Morbus Huntington



Complex diseases:

e.g. Diabetes, myocardial infaction, overweight, cancer, …

Environmental factors are e.g. smoking, physical activity, nutrition, education, sun exposition, ….

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Searching for genes for complex diseases

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Knockout versus small changes by polymorphisms

Knock-out

- Pronounced effects
- Animals: great models but not necessarily to extrapolate to humans
- Humans: often very rare cases

Polymorphism

- Small effects
- Usually investigated in humans
- Real in vivo conditions
- Thousands of people can be studied easily
- Sample sizes of thousands are required

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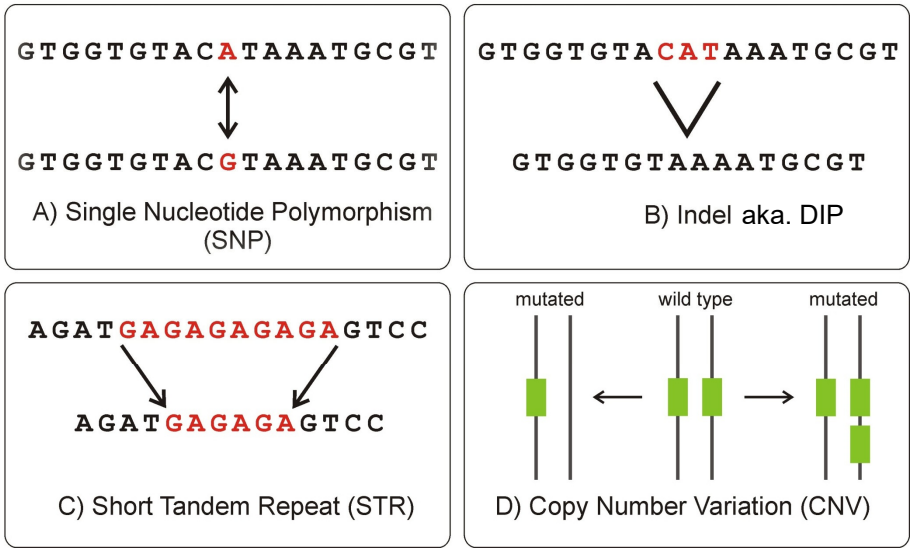
Genetic variability



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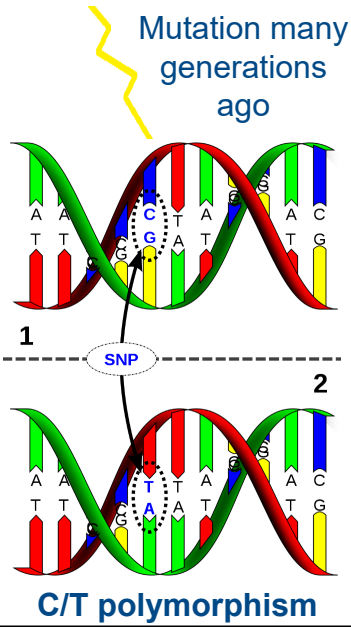
Single Nucleotide Polymorphisms (SNPs)

- Variations of single base pairs (bp) in the DNA sequence
- Heritable and stable.
- Account for 90% of the genetic variability
- Every 300 – 1000 bp
- At least 3 – 4 million SNPs per individual
- 10,000 – 11,000 non-synonymous SNPs per individual
- 700 million SNPs are described in databases



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Single Nucleotide Polymorphism (SNP)

- **Coding SNPs within a gene**
  - synonymous exchanges: without influence on protein
  - non-synonymous exchanges: resulting in an AA exchange
- **SNPs within the regulatory regions:**
  - when and why a gene will be switched on or off
  - effect on quantity of protein production
- **SNPs within the untranslated regions**
  - with influence on mRNA stability
- **SNPs in intergenic regions**
  - functional consequences have to be evaluated

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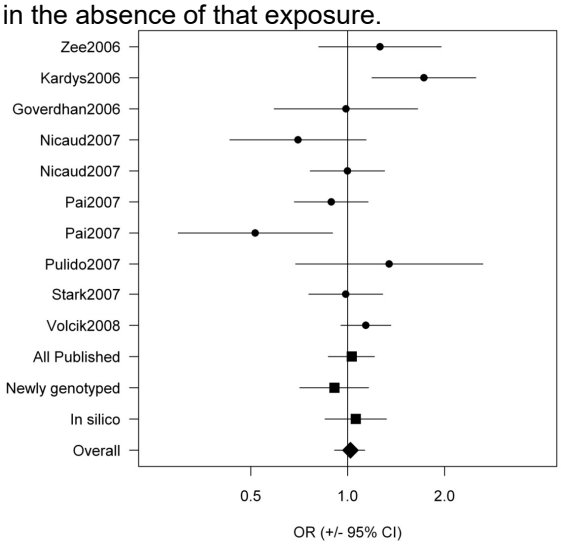
Some basics from epidemiology

- **Odds ratio**
  - Represents the odds that an outcome will occur given a particular exposure, compared to the odds of the outcome occurring in the absence of that exposure.
  - Values between 0 and infinite (∞)
  - 1.00 = same odds
  - 1.50 = 50% higher odds
  - 2.00 = 100% higher odds
  - 0.50 = 50% lower odds
- **95% confidence interval (CI)**
- **Hazard ratio**
  - In case of prospective studies
- **Meta-analysis**
  - Combining data from more than one study



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Overview

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2. **Association studies**
3. Genomewide association studies (GWAS)

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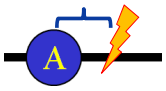
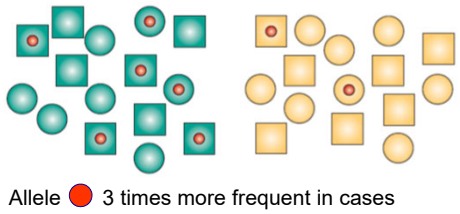
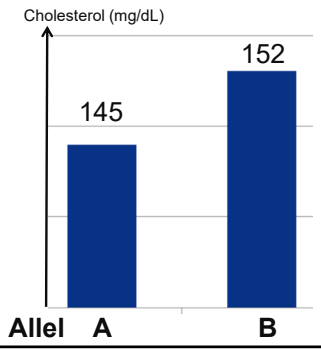
Principle of association studies



- **Qualitative analysis:**
  Preferential association of an allele with a disease status



- **Quantitative analysis:**
  Carriers of a various alleles differ in the mean values of the investigated parameter (e.g. cholesterol level)



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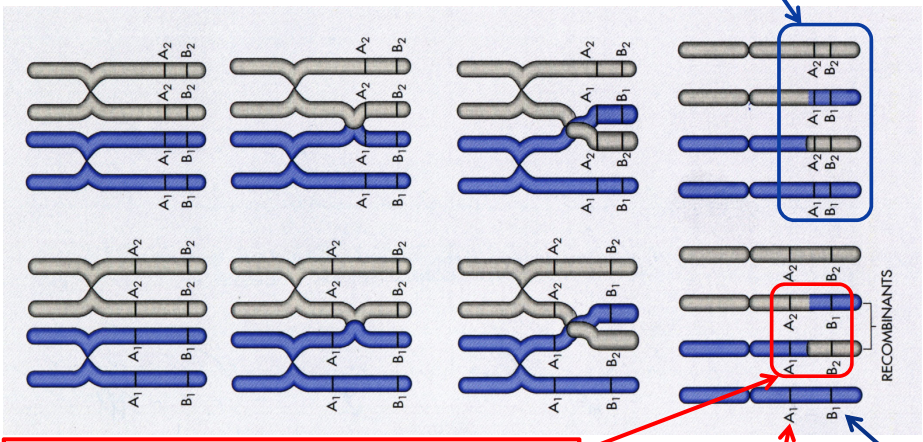
Remember: crossover and recombination during meiosis I

No recombination of alleles of the gene loci A and B since crossover outside the region between A and B



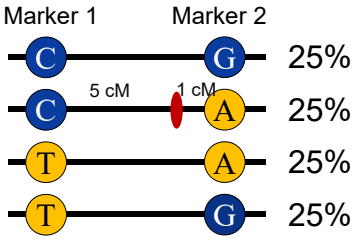
Recombination of alleles in the two gametes due to crossover

"Wanted" disease locus

Genotyped marker locus

Jorde, Carey, Bamshad, White: Medical Genetics

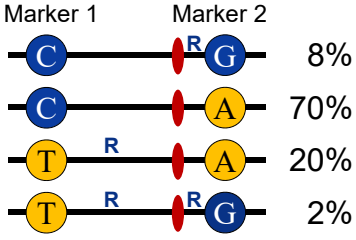
Basis of association: Linkage disequilibrium



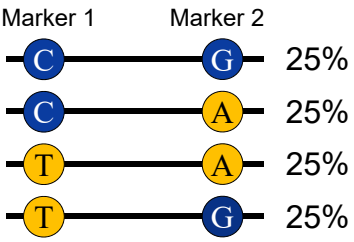
	Patients	Controls
Allele 2A	**90%**	**50%**
Allele 1C	78%	50%

After many generations

Patients



Controls



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R … Recombination

What does a significant genetic association mean?

- **Direct association**
  - The investigated genetic variant is indeed the causal disease-causing variant
  - This is rarely the case
  - Optimum pocedure: functional characterisation goes hand in hand
- **Indirect association**
  - The investigated genetic variant is in linkage disequillibrium with the causal variant

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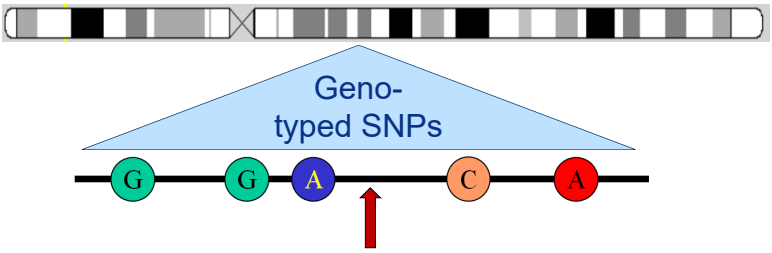
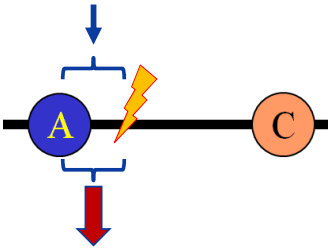
Indirect association



Disease-causing variant we are searching

Due to the small distance there are rarely crossovers and recombinations during meiosis



Allele A can be observed more frequently with the disease

ACTAGAGCTACTACGAGGGACTAC...TACGAGCATCGACTA...GAGG
TAGAGCTATA...TTCT AGGCTA...CTACGATCGATC...ACGTAG...

High correlation

The genotyped SNP is a marker of the „non-genotyped“ disease-causing variant we are searching

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What does a significant genetic association mean?

- **Direct association**
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  - This is rarely the case
  - Optimum pocedure: functional characterisation goes hand in hand
- **Indirect association**
  - The investigated genetic variant is in kinkage disequillibrium with the causal variant
- **False-positive finding (spurious association)**
  - Random finding (sample size!)
  - Confounding: e.g. population stratification
  - Often observed in small studies without replication

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→ replicate, replicate, replicate!

Mendelian Randomization study

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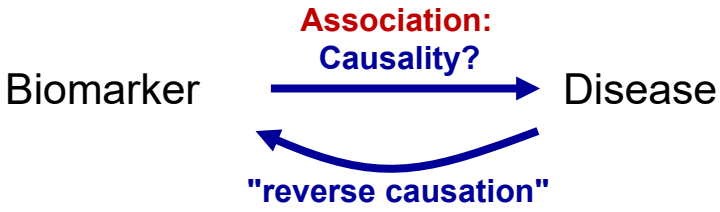
Biomarker for diseases: causality or consequence?



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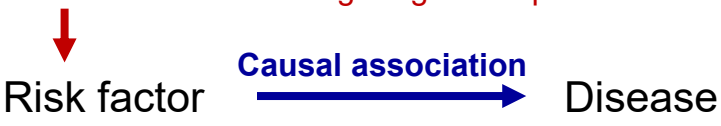
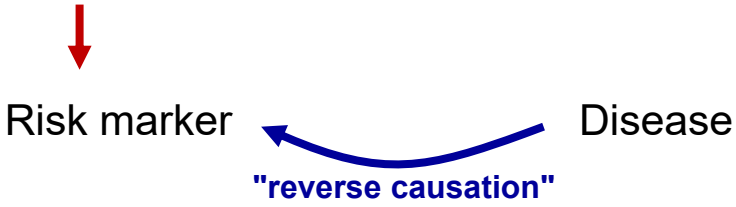
Biomarker for diseases: causality or consequence?

- Intervention including drug development



- No direct reason for intervention or drug development
- Useful for diagnostic purposes?



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The big question for biomarkers

- You found an association with a disease
- **Risk factor or risk marker?**
- Classical epidemiological studies with prospective observation will last a long time and will not prove causality
- You have to decide now whether to go for drug development or not
- Worst case scenario: after 10-15 years of development the drug flops
- One reason might be that it is only a risk marker and not a risk factor.

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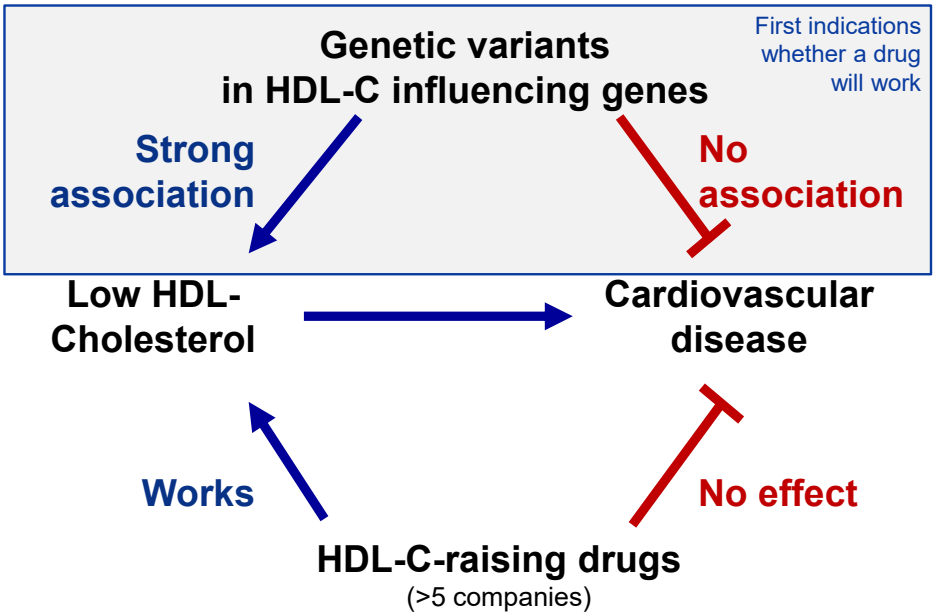
Example of a flop: CETP inhibitors



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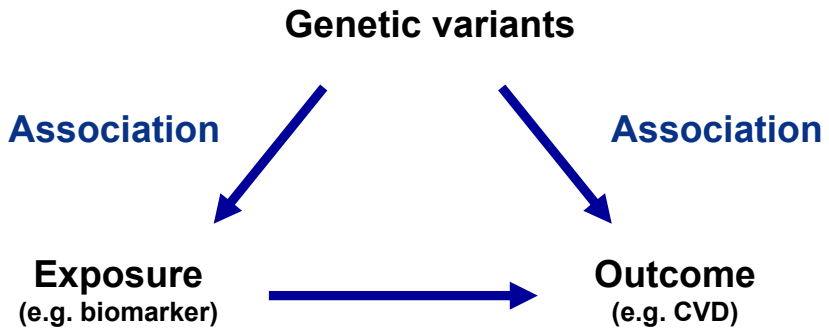
Kronenberg: Kidney Int. 89:747-9, 2016

Mendelian randomization approach



→ Strong support for causality

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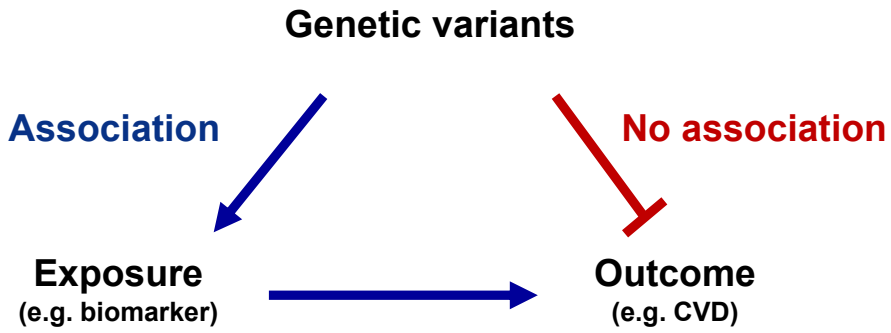
Mendelian randomization approach



→ Causality is unlikely if the study is sufficiently powered

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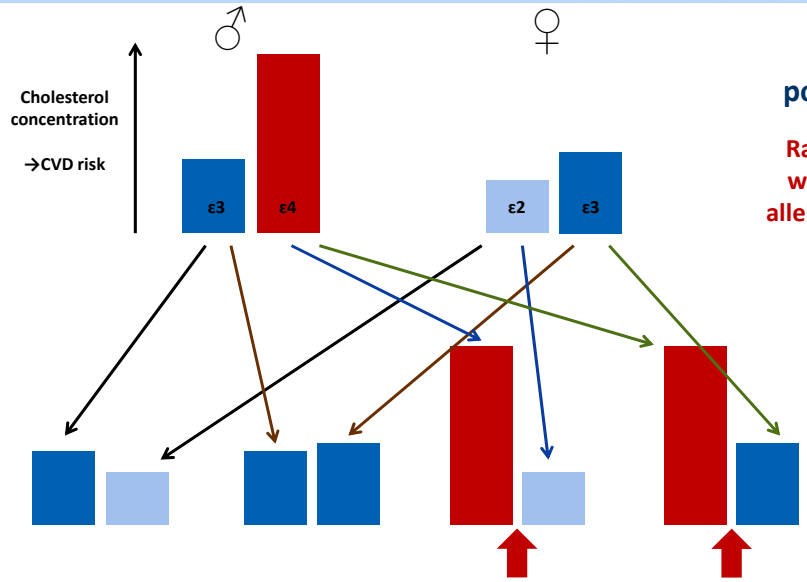
Mendelian randomization at the time of conception



ApoE polymorphism

Random decision which of the two alleles is transmitted to the child

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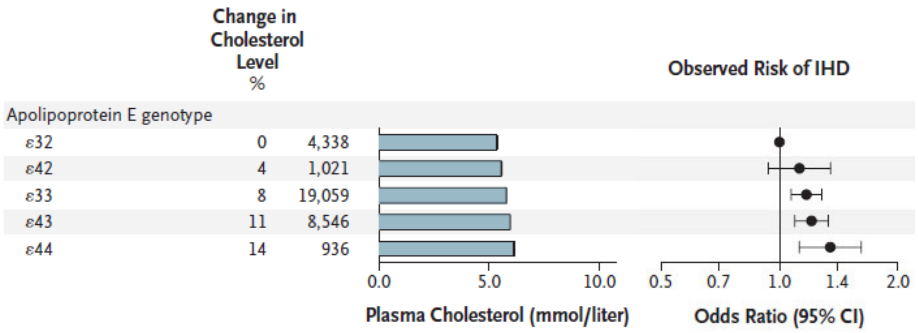
Adapted from Cardiovasc.Drugs Ther. 30:87-100, 2016

Increased risk for CVD due to lifelong exposure to higher cholesterol concentrations

ApoE, cholesterol and risk for CVD



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Zacho et al.: NEJM 359:1897-1908, 2008

Example: Lipoprotein(a)

Lp(a)

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Experience of a young widow

- Husband 39 years of age
- Loses consciousness, cardiac arrest, revival not successful

- No classical risk factors
- Healthy lifestyle, physically active
- Health checkup on a yearly basis

- Autopsy: most severe heart disease
- **Very high Lp(a) concentrations**

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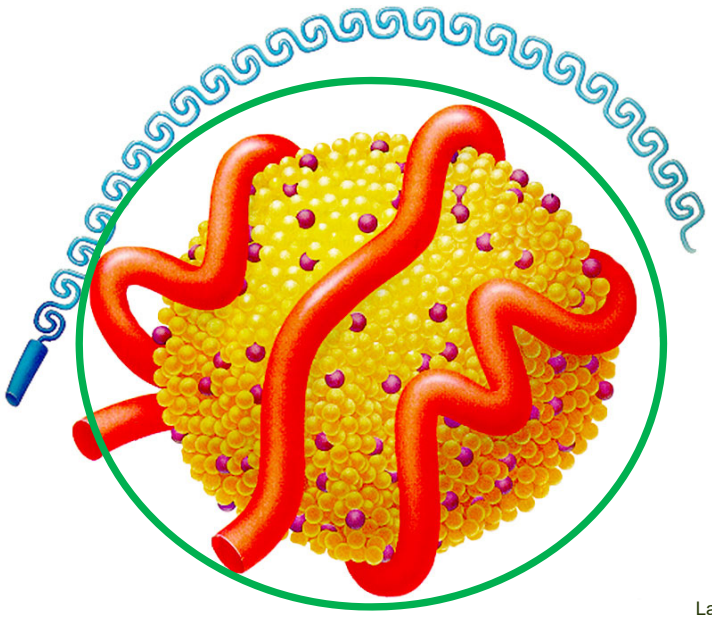
Lp(a) – the mysterious brother of LDL



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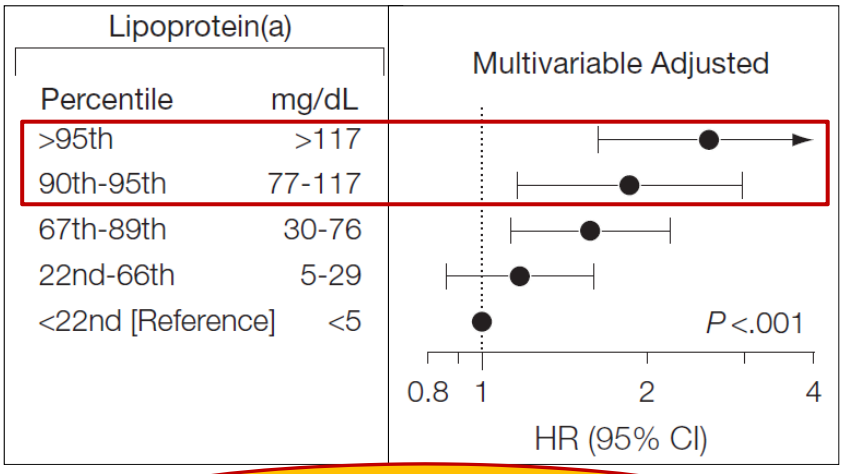
Lawn; Sci.Am. 266:54-60, 1992

Lp(a) and risk for myocardial infarction

Results from the Copenhagen City Heart Study



Ist this association causal?

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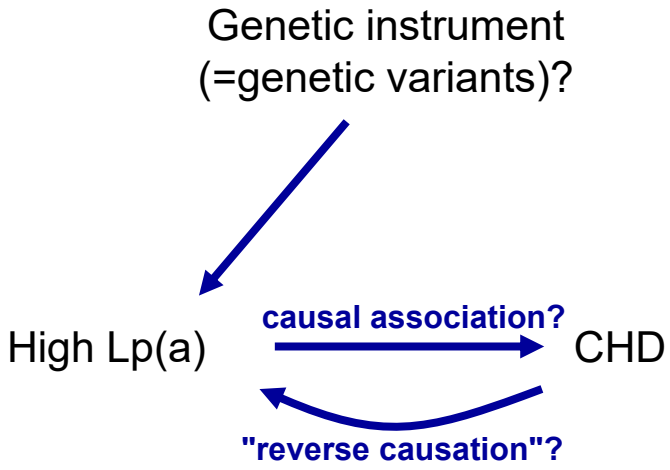
Kamstrup et al.: JAMA 301:2331-9, 2009

Lp(a) and CHD: truth or consequence?



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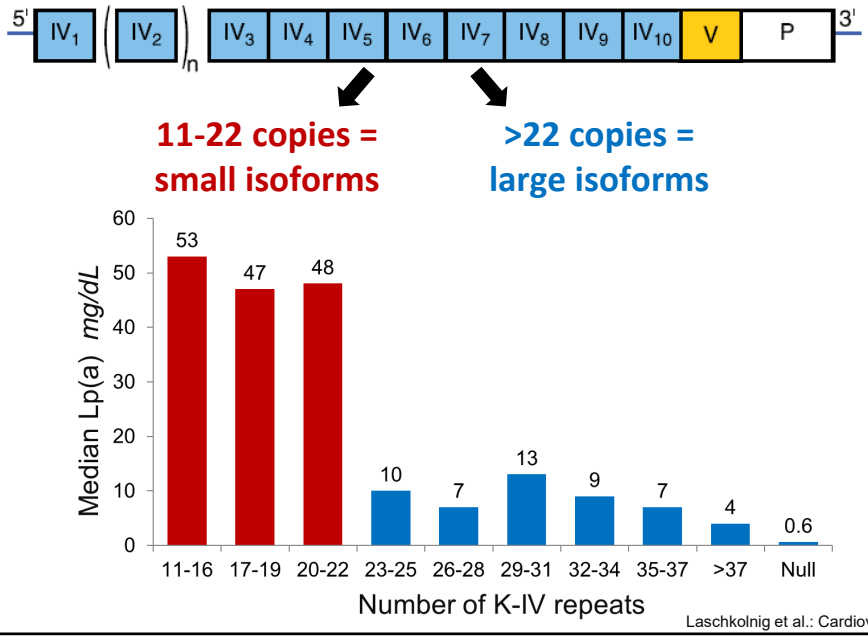
Apolipoprotein(a) - Mr 300-800 kDa



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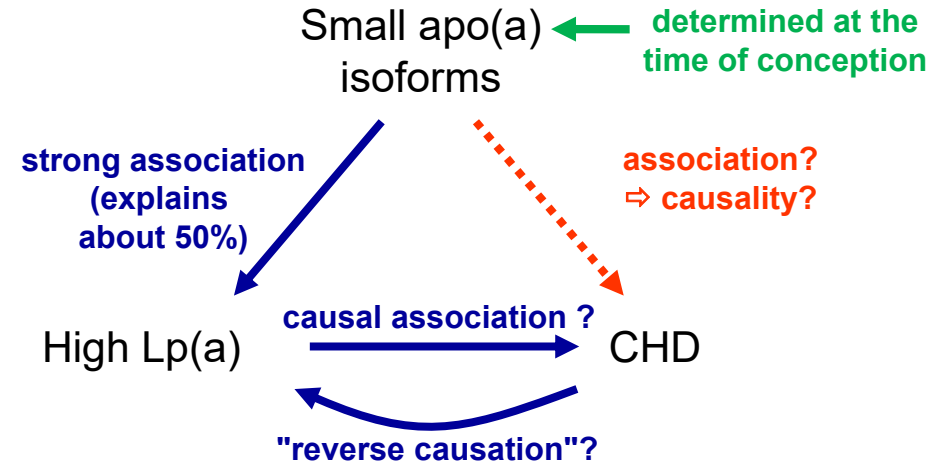
Laschkolnig et al.: Cardiovasc Research 103: 28-36, 2014

Lp(a) and CHD: Mendelian randomization



Do carriers of small apo(a) isoforms more often have CHD?

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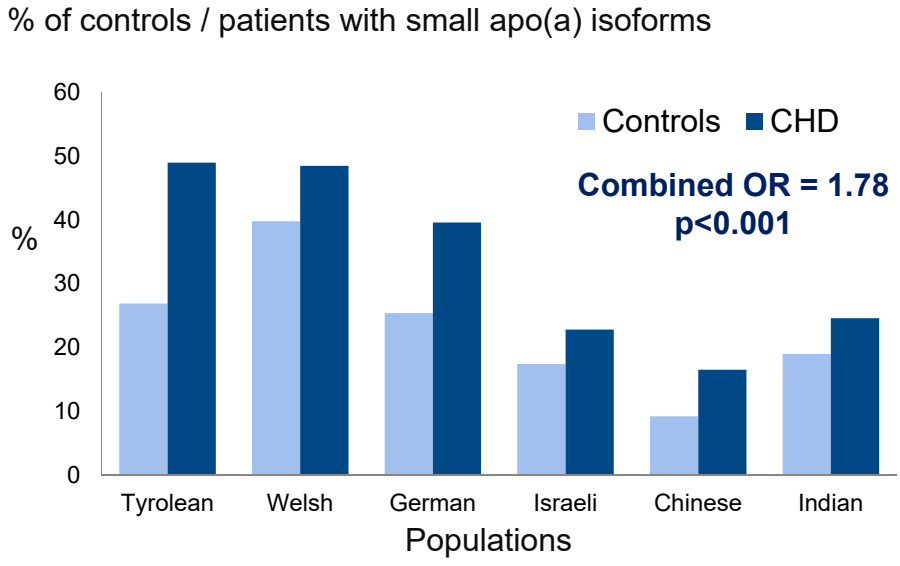
Apo(a) isoforms and risk for CHD



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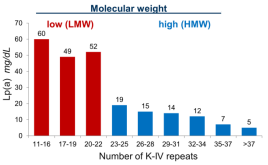
Sandholzer et al.: Arterioscler Thromb 12: 1214-26, 1992

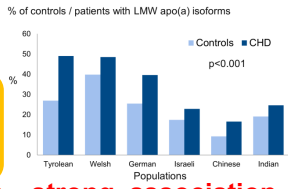
Lp(a) concentrations, apo(a) isoforms and CVD



strong association
(explains about 50%)

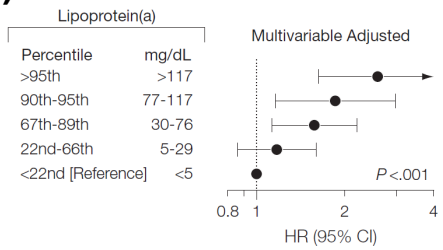
Small apo(a) isoforms

25-35% of the population



strong association

High Lp(a) → causal association → **CVD**



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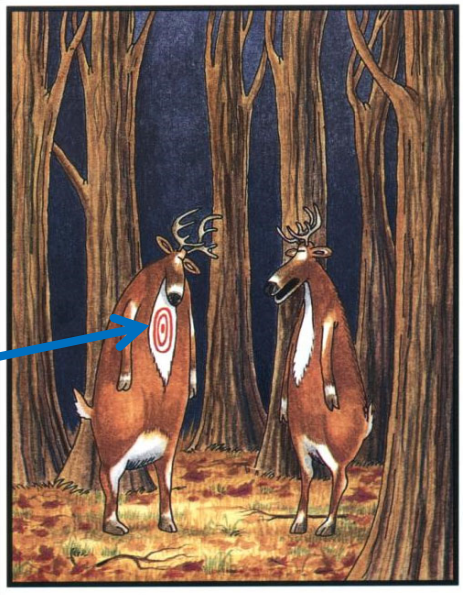
Cardiovasc.Drugs Ther.: 30:87-100, 2016

Lp(a) concentrations and apo(a) isoform as a risk factor

Having a small apo(a) isoform doubles the odds for CVD in 25-35% of the population

→ strongest genetically determined risk factor for CVD



"Bummer of a birthmark, Hal."

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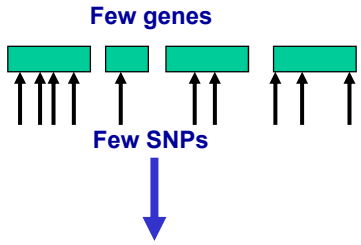
Candidate gene approach vs. GWAS

Candidate gene approach



- Hypothesis-driven
- Biochemical or physiological *a priori* knowledge
- Few genes identified

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Overview

1. Background
2. Association studies
3. **Genomewide association studies (GWAS)**

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Systematic against the hopelessness

Genome-wide association studies (GWAS)
(say: "GiWAS")

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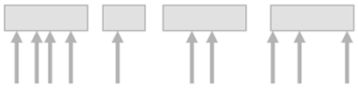
Candidate gene approach vs. GWAS

Candidate gene approach

Few genes



Few SNPs

Association with phenotype

- Hypothesis-driven
- Biochemical or physiological *a priori* knowledge
- Few genes identified

Genomwide association study GWAS

23 chromosomes

0.5 – 10 million SNPs

Association with phenotype

- **"Hypothesis-free"** (unbiased)
- No *a priori* knowledge
- New pathways
- Small effects detectable
- **Very large sample sizes required**

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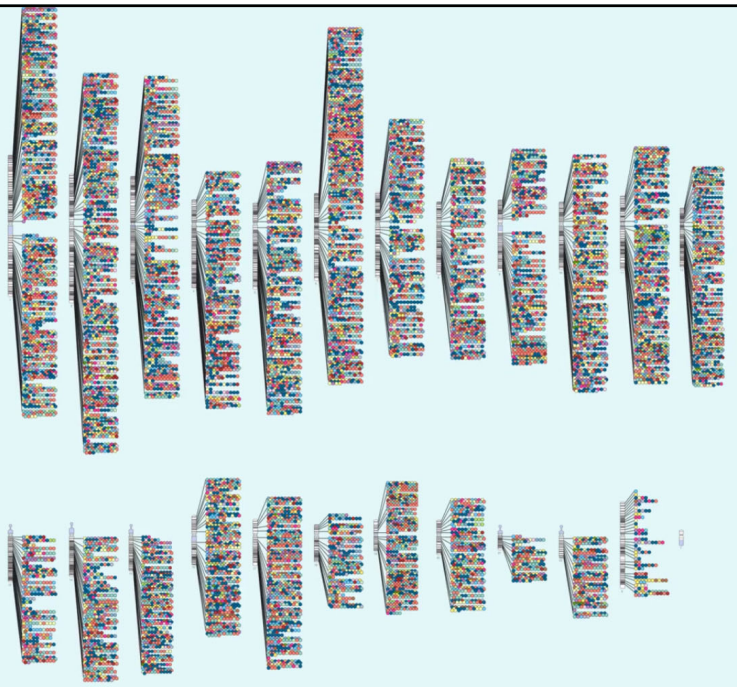
2018 Apr

Associations: 69,885

Studies: 5,152

Papers: 3,378



www.ebi.ac.uk/gwas

Gain in detected genes by GWAS

Examples for metabolic traits

Disease	before 2007	2007 onward
Type 2 DM	3	50
Body mass index	1	30
Glucose or insulin	1	15
Fat distribution	0	20
Lipids	16	95
Total	**21**	**202**

7 examples of autoimmune diseases

Disease	before 2007	2007 onward
Ankylosis spondylitis	1	13
Rheumatoid arthritis	3	30
Systemic lupus eryth.	3	31
Type 1 DM	4	40
Multiple sclerosis	1	51
Crohn's disease	4	67
Ulcerative colitis	3	44
Total	**19**	**277**

Since 2012 the number of known genes has further increased by 5- to 10-fold

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Visscher et al.: Am.J.Hum.Genet. 90:7-24, 2012 (updated)

Design and cost-performance ratio

Cohort
(population-based or case-control studies)

Consortia:
Team-up with other cohorts for meta-analyses:
GWAMA

Genotyping of up to 10 million SNPs with microarrays

- Costs for 500.000 arrays used worldwide up to 2011: $250 million
- Same costs as for 1-2 stealth fighter jets
- ½ atomic submarine

Association with phenotypes (e.g.)

- BMI
- Waist
- Blood pressure
- QT interval
- Smoking

Lab values

- Lipids
- Kidney function
- CRP
- Hemoglobin
- …

Diseases

- CAD
- Stroke
- Ankle-brachial-index
- Cancer types

Whatever has a genetic component and is measured

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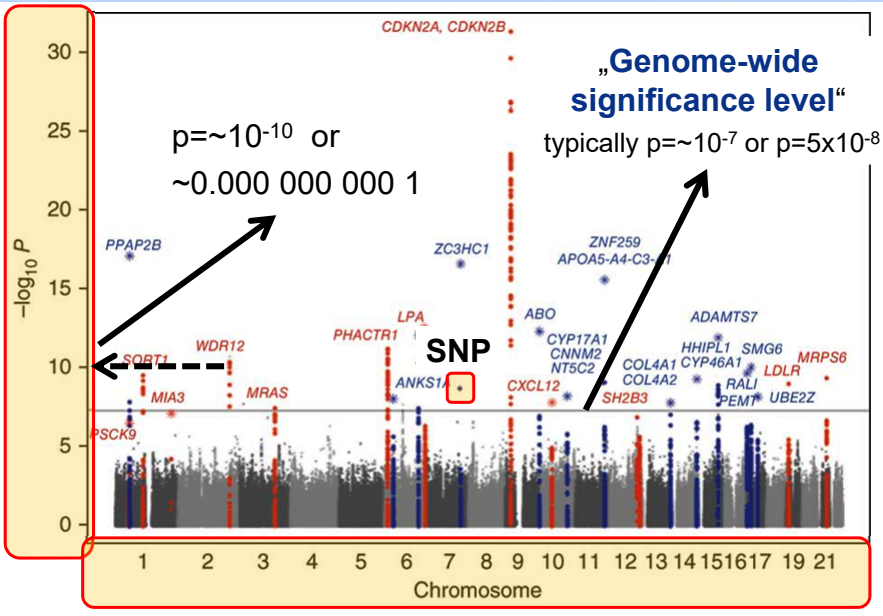
The Manhattan Plot



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Schunkert et al.: Nature Genetics 43:333-338, 2011

Genome-wide association studies (GWAS)

- **Study design**
- **Examples:**
  - Lipids
  - Type 2 diabetes mellitus
  - Blood pressure
  - Kidney function
  - Addiction (smoking quantity)
  - BMI

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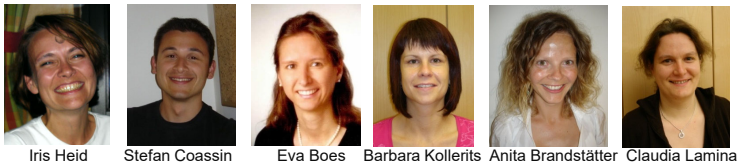
GWAS: Lipids

- **Consortium:**
  - Established during fall 2005
  - Together with Helmholtz-Zentrum München
  - 11 members studying various phenotypes
- **Innsbruck Group:**
  - Lipid metabolism
  - HDL-C as a starting point
  - Quantitative trait considered more powerful
- **Population and Genotyping:**
  - 1644 population-based subjects from KORA
  - Affymetrix 500K SNP chip


Iris Heid Stefan Coassin Eva Boes Barbara Kollerits Anita Brandstätter Claudia Lamina

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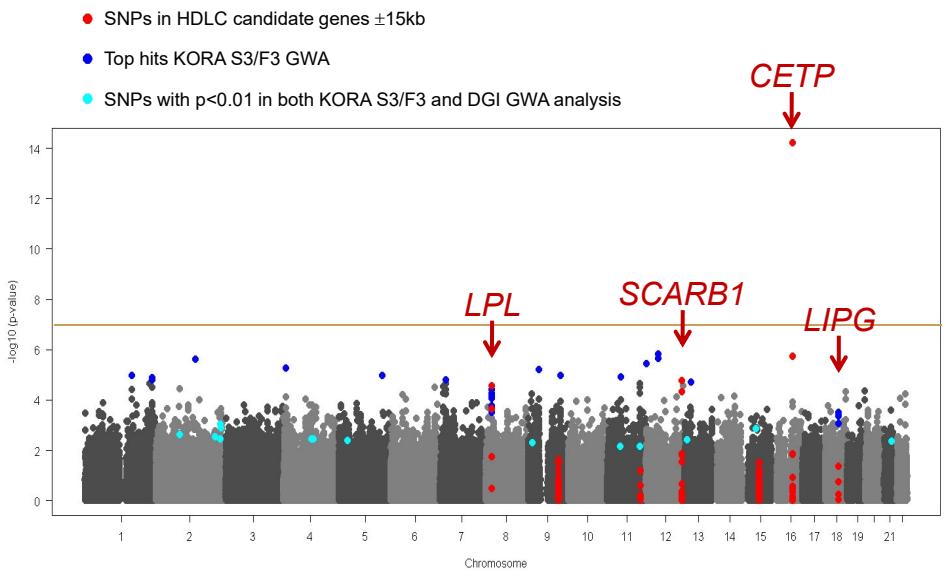
GWAS: HDL cholesterol



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Heid et al.: Circ. Cardiovasc. Genet. 1:10-20, 2008

GWAS on Lipids (TC, HDLC, LDLC, TG): next steps

- **First own GWAS** *(Circ. Cardiovasc. Genet. 2008)*
  1644 probands: found nothing new
- **Engage Consortium:** *(Nature Genetics 2009)*
  - 22,000 probands: **22 genes found associated**
- **Global Lipids Genetics Consortium:** *(Nature 2010)*
  - >100,000 probands: **95 genes found associated**
- **Global Lipids Genetics Consortium:** *(Nature Genetics 2013)*
  - >188,000 probands: **roughly 155 genes found associated**
- **Global Lipids Genetics Consortium:** *(Nature 2021)*
  - 1,65 million probands: **>900 Gene**

Functional characterisation for most of the genes has to be done

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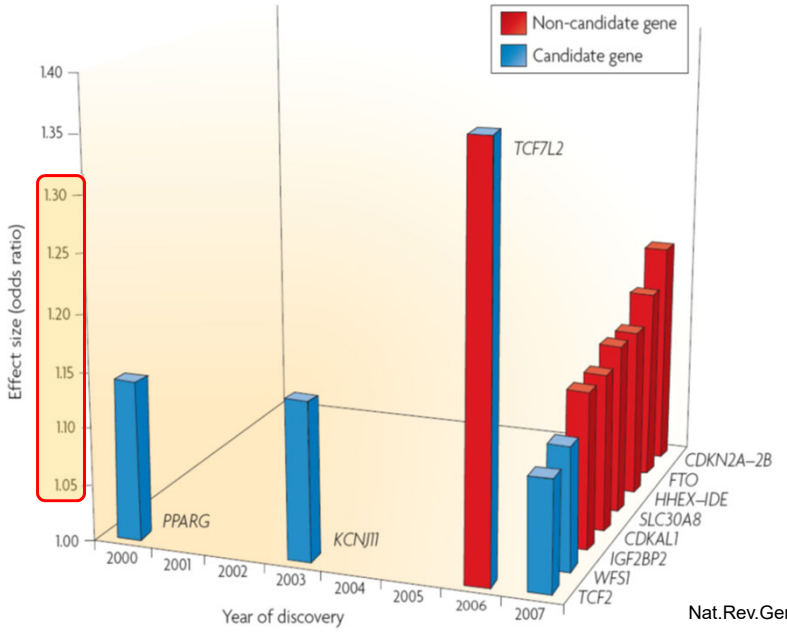
GWAS: Type 2 diabetes mellitus



2017:

≈ 86 genes

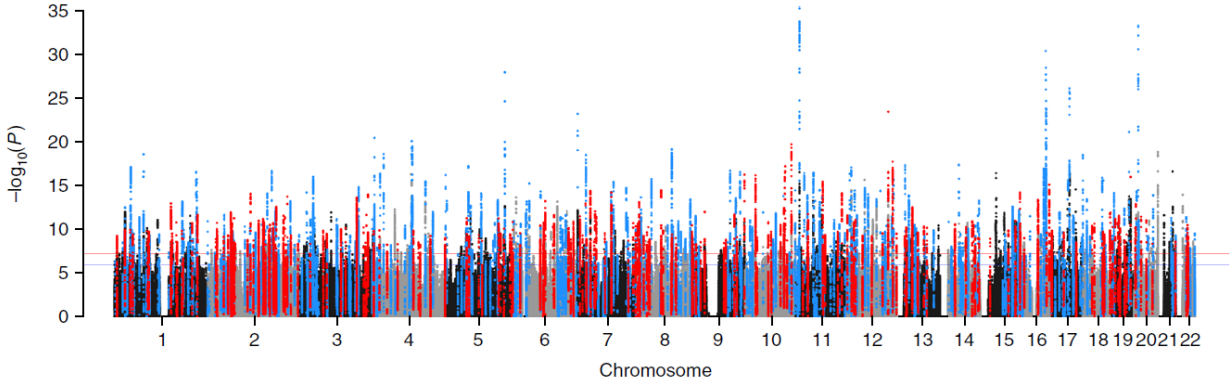
2019:

≈ 250 genes

T. Frayling:
Nat.Rev.Genet. 8:657-62, 2007

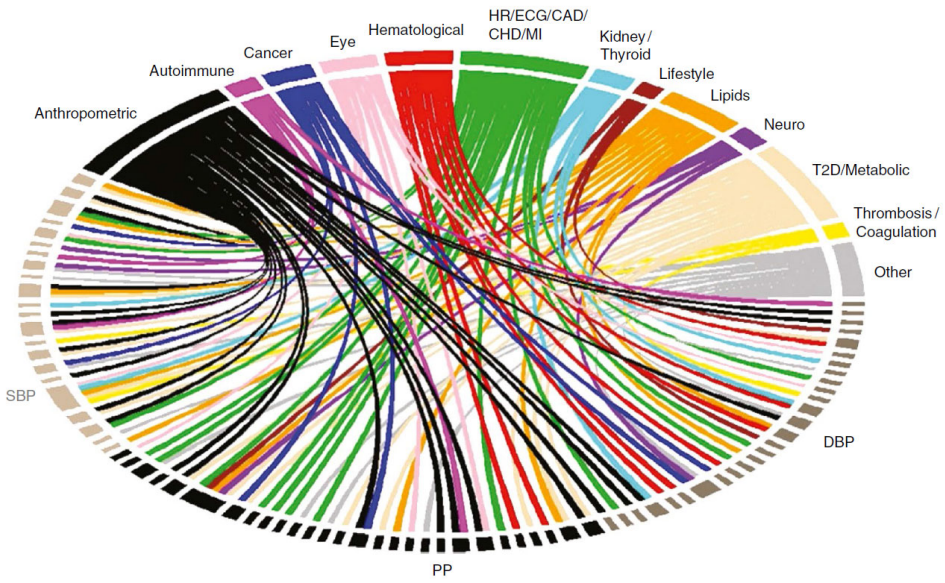
GWAS and blood pressure traits

- Phenotypes: systolic and diastolic BP, pulse pressure
- > 1 million study participants
- 901 genetic loci in total (535 novel)



Evangelou et al.: Nature Genet. 50:1412-25, 2018

Association of BP loci with other diseases



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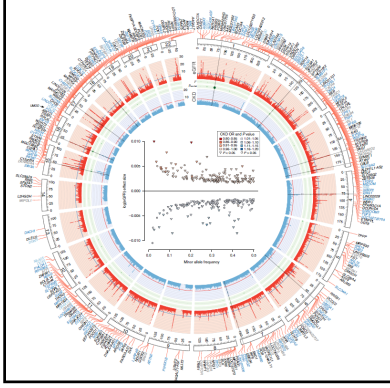
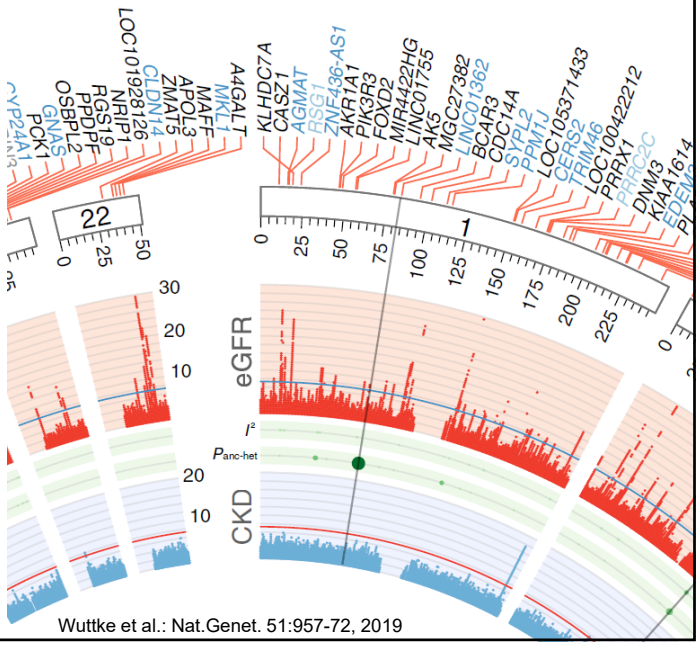
Evangelou et al.: Nature Genet. 50:1412-25, 2018

GWAS on kidney function

- **CKDGen consortium**
  - 1,046,070 persons
  - 264 associated loci (166 new)
  - Circos plot
  - comprehensive priority list of molecular targets for translational research

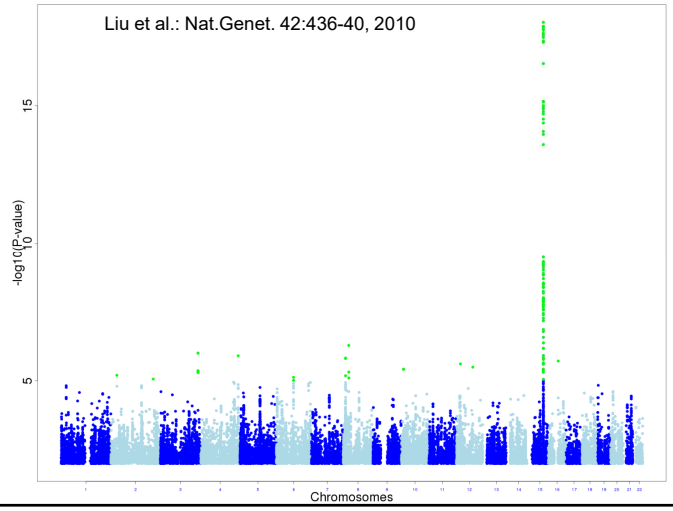




Wuttke et al.: Nat.Genet. 51:957-72, 2019

GWAS on smoking (quantity)

- Addiction research
- >40,000 persons
- Neuronal nicotinic acetylcholine receptor subunits
- Same region was found for lung cancer, COPD,lung function and PAD



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Genes for body mass index and overweight

Own behavior (lifestyle)

Genetics

- 536 genetic loci detected
- Many of them play a role in the brain by
  - ⇨ **Regulation of appetite**
  - ⇨ Neuronal component of overweight
- Explain roughly 5% of BMI

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Contribution of single genes to overweight

- **Very few with strong effects:** risk increase by 10 to 30% per allele
- **More with moderate effects:** risk increase by 3 to 10% per allele
- **Many more with tiny effects:** risk increase by 0.1 to 3% per allele

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Development of SNP-Risk-Scores

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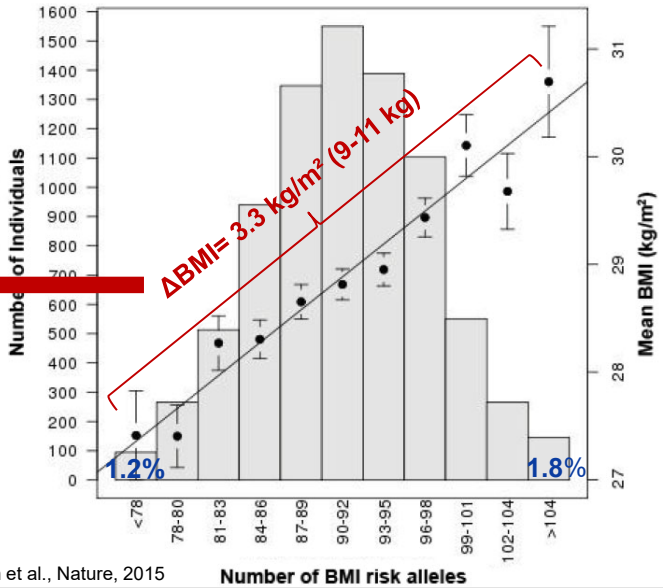
Risk score of 97 SNPs for BMI: 0-194 risk variants



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Shungin et al., Nature, 2015

Risk score for 65 SNPs for diabetes

Many risk variants (top quintile)

2.7-fold increased risk to develop a diabetes in the future

Few risk variants (bottom quintile)

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Talmud et al., Diabetes 64:1830-40, 2015

Where is the reward?

Can a single gene explaining less than 1% of the traits' variance still be useful for anything?

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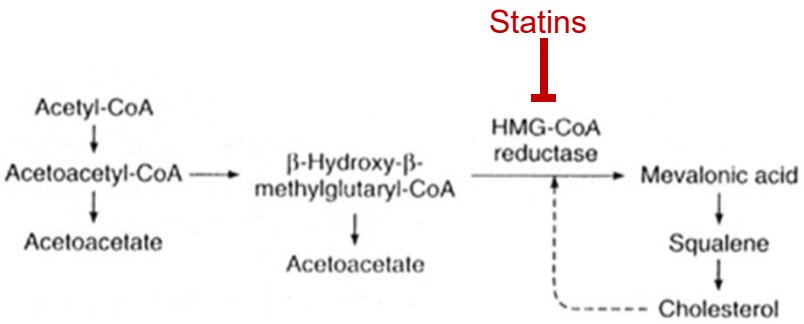
Statins: HMG-CoA-Reductase-Inhibitors

- **Mechanism of action**
  - Inhibition of HMG-CoA-Reductase: this enzyme catalyzes the conversion of HMG-CoA to mevalonic acid: an early and rate-limiting step in cholesterol biosynthesis.
  - Results in higher expression of LDL receptor which decreases LDL cholesterol



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Polymorphisms in HMG-CoA-R gene region

- **GWAS results for HMG-CoA-reductase**
  - Very small effects
  - Were not detected in the first GWAS
  - This gene was only detected after investigation of at least 10.000 subjects
  - Single polymorphisms explain far less than 1% of the cholesterol concentrations within a population
  - Nevertheless, the most sucessful drug target for lipid metabolism
- **Other drug targets within the 157 lipid genes?**
  - CETP, ABCA1, PCSK9
  - Others?

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Conclusions on GWAS

- An **hypothesis-free approach**
- Never before such a gain in gene-phenotypic information
- New genes for CAD, diabetes, cancer, kidney function…
- Odds ratios between 1.02 and 1.40
- To have the equipment is only the smallest step
- Very large studies of well phenotyped cohorts are necessary
- Works only within a very well constructed network between genetics, epidemiology, statistics, informatics, genomics
- Data sharing (a lot is already on the web)
- Non-coding SNPs and "gene deserts" can no longer be neglected
- A lot to learn about regulatory regions
- Functional characterization of "new" genes will need decades

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Why are we searching these many genes?

Improvement of risk prediction (gene risk scores)

Identification of new drug targets

- PCSK9 increases LDL cholesterol: discovered by genetic studies
- PCSK9 inhibitors lower LDL cholesterol by 60%

Exclusion of drug targets

- CETP increases the "good" cholesterol
- Development of CETP inhibitors to increase HDL cholesterol
- Billions of investment without lowering of heart attacks
- Genetic studies would have predicted the failure of these drugs

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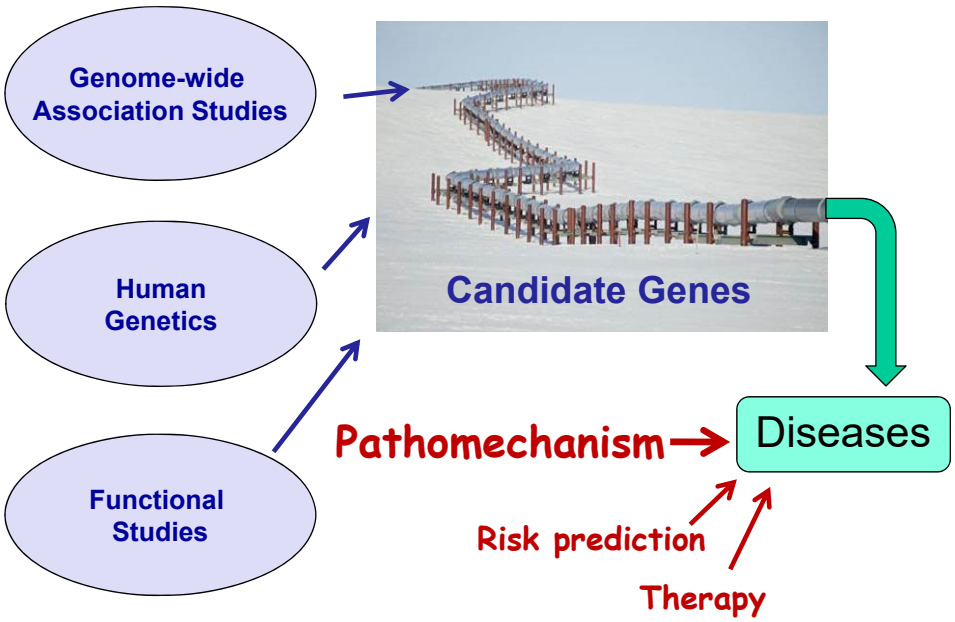
Gene hunting: an interdisciplinary approach



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