Introduction to Psychiatric Genetics

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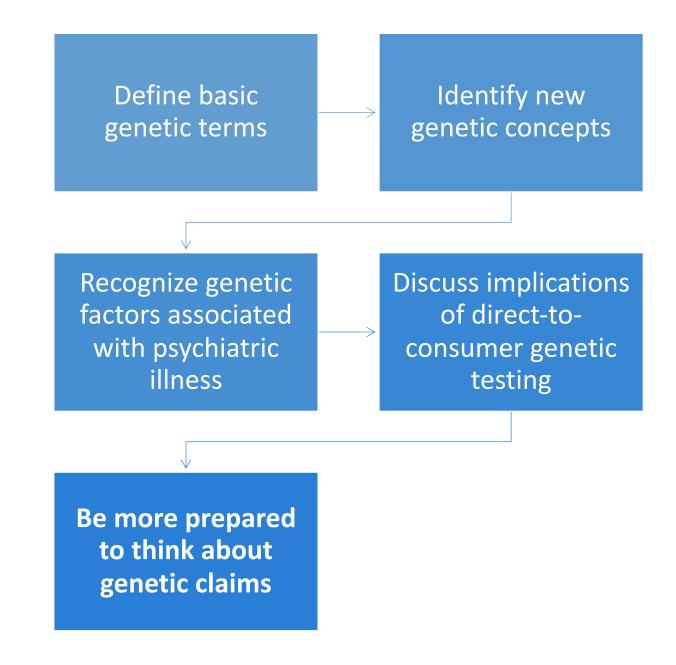
Disclosures:

No financial Disclosures

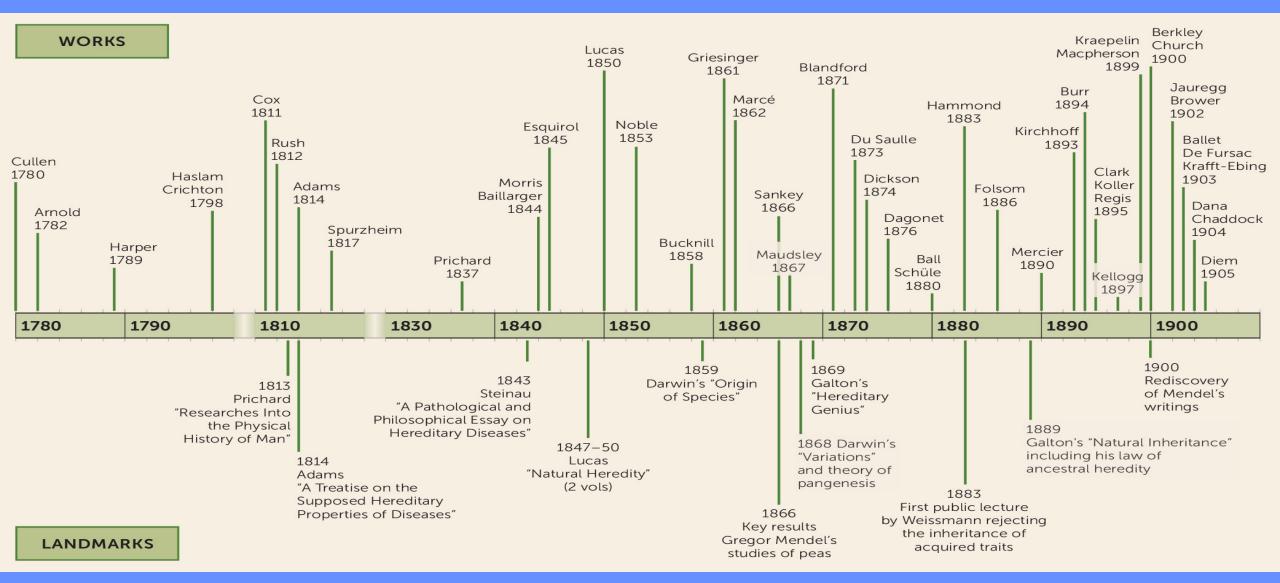
I am no expert, just curious

Learning Objectives

At the conclusion of this activity the participant will be able to:



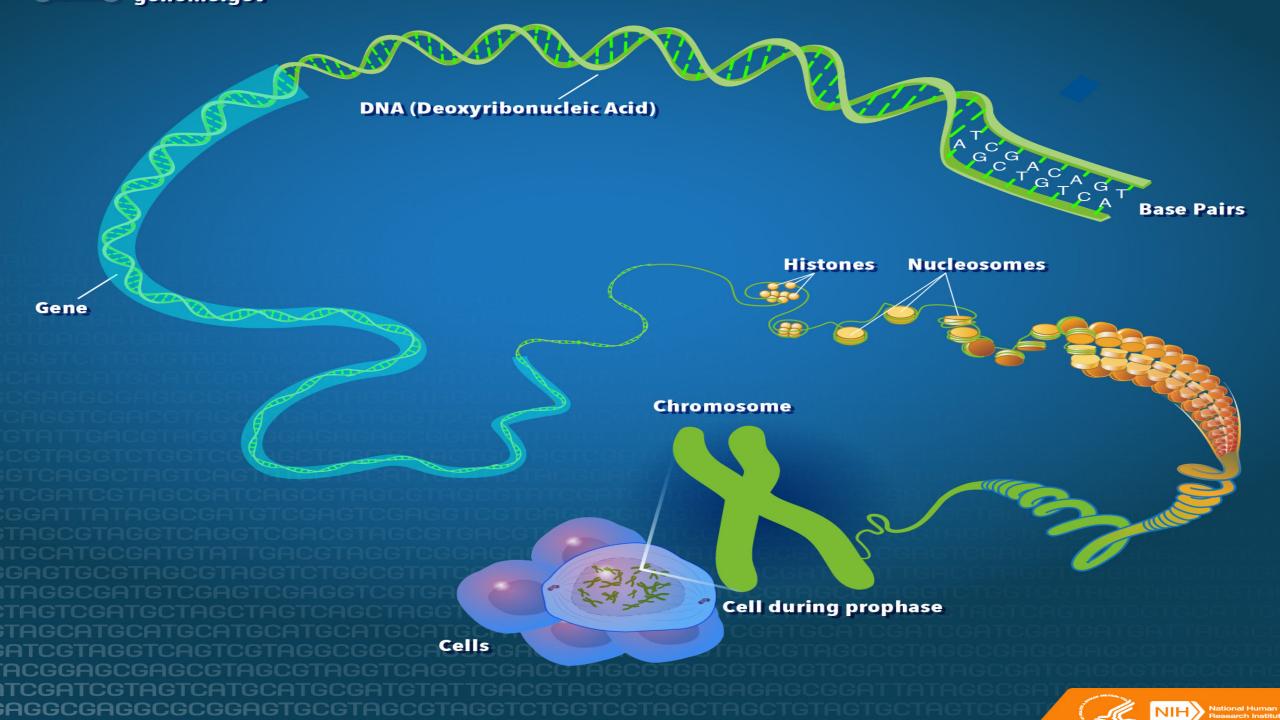
The Prehistory of Psychiatric Genetics: 1780-1910



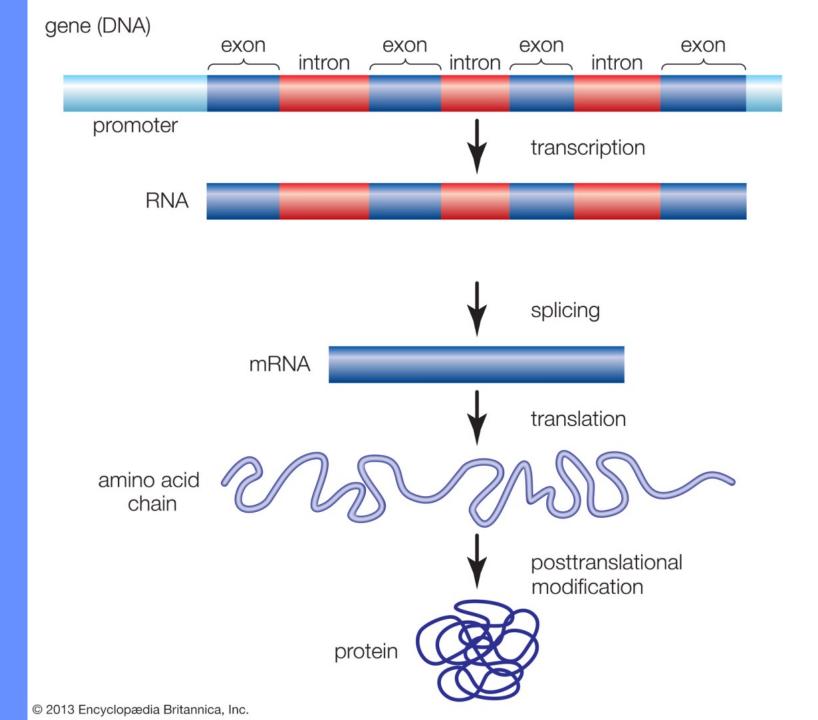
(Kendler 2020)

Genes influence:

- metabolism of medications
- risk of developing illness
- response to treatment
- side effects



Protein synthesis



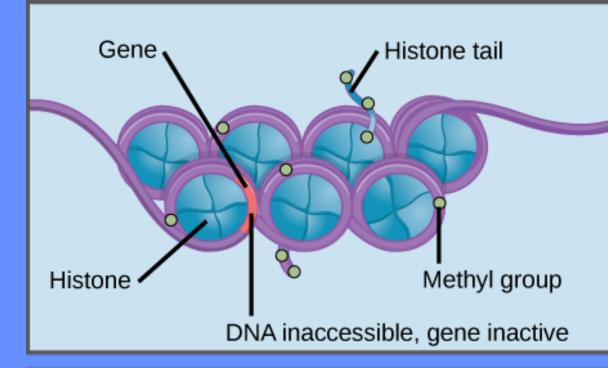
https://www.britannica.com/science/gene

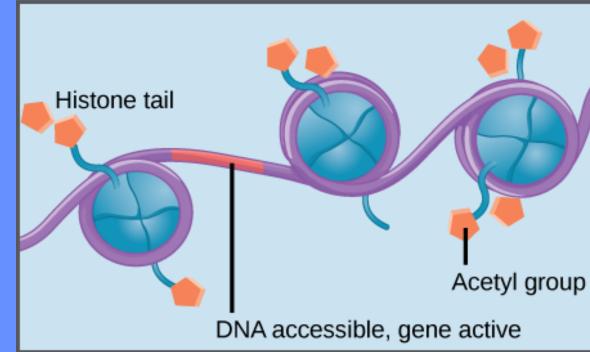
Epigenetics

 Regulating genes without changing DNA sequence

- DNA methylation
 - Mutes gene
- Histone acetylation
 - Gene accessible

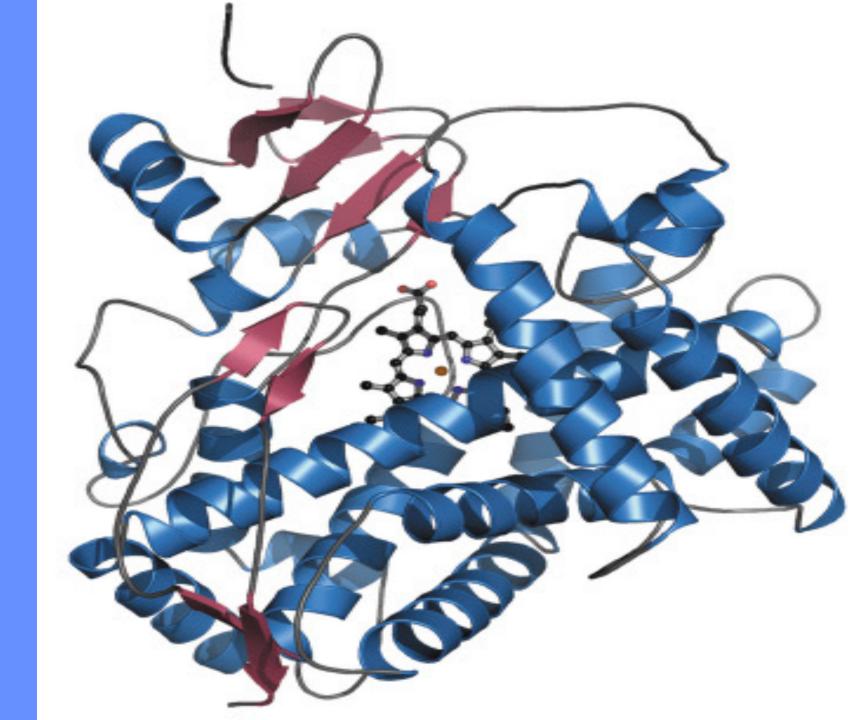
https://commonfund.nih.gov/sites/def ault/files/epigeneticmechanisms.pdf





Cytochrome P450 2D6

~500 Amino acids Heme group



(Rowland et al., 2006)

What is a Cytochrome?

What does it do?

- Transfer electrons
- Make molecules more polar and easier to excrete
- Why named P450?

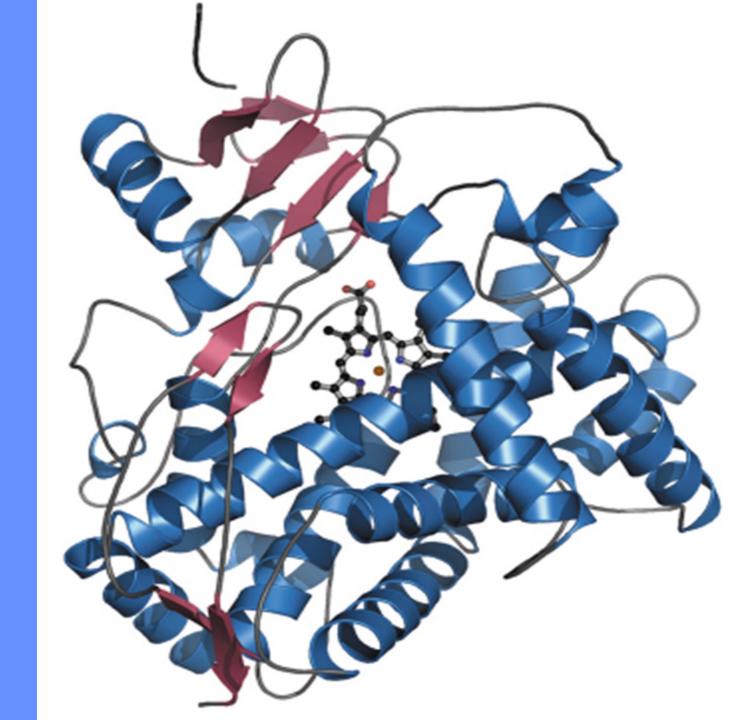
Who has them?

- Mammals?
- All animals?
- Plants?
- Fungi?
- Bacteria?
- Viruses?

(Werck-Reichhart & Feyereisen, 2000) (Ingelman-Sundberg, 2005)

CYP2D6

- Duplication
- Deletion
- Frame shift
- Splice defect
- Codon
 - SNP



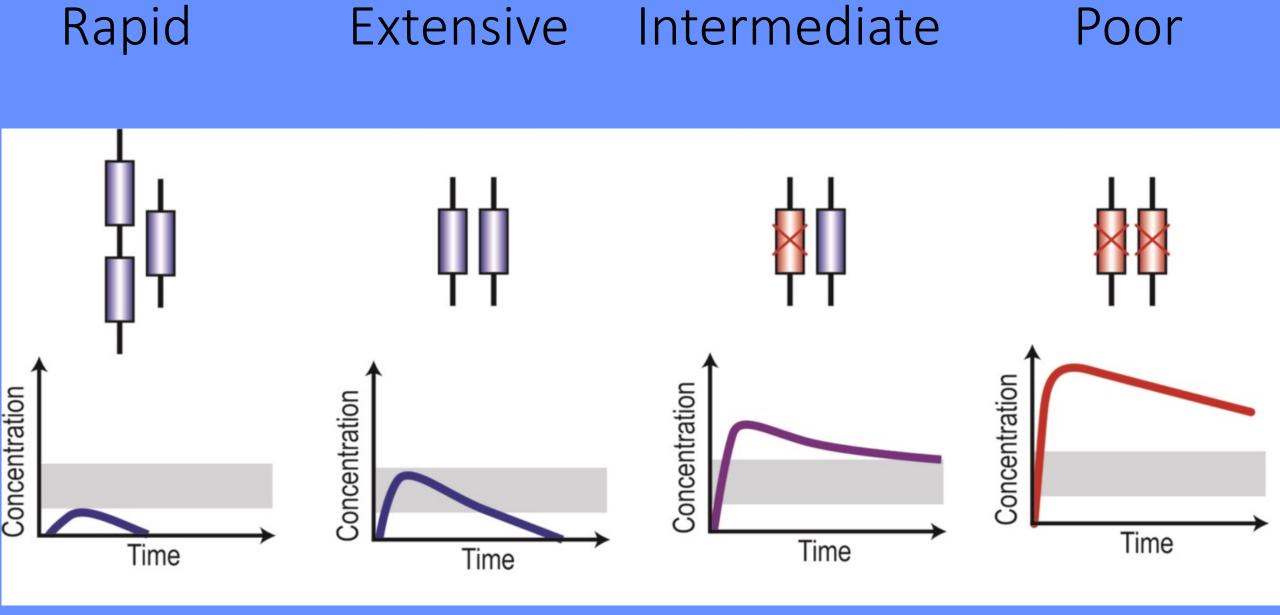
Single Nucleotide Polymorphism

- Nonfunctional enzyme
- Decreased function enzyme
- Equivalent function enzyme
- Increased function enzyme
- Promoter change



How many genetic variants of cytochrome 2D6 have been identified in humans?

- A. 10-25
- B. 25-50
- C. 50-100
- D. >100



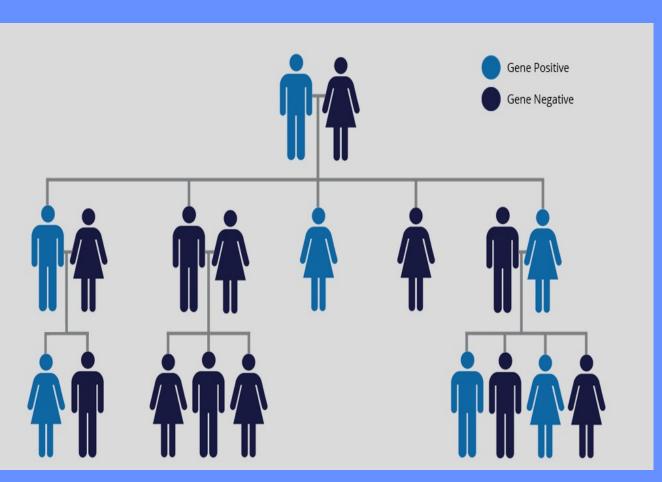
(Nagele & Liggett, 2011)



Genes and diagnoses

Simple and Complicated

Risk of developing Huntington's Disease



- Autosomal Dominant
- HTT gene codes for huntingtin protein
- CAG codon = Glutamine
 - Gets repeated excessively

(https://hdsa.org/what-is-hd/history-and-genetics-of-huntingtons-disease/who-is-at-risk)

Genome wide association study (GWAS)

calculate

$$Z_{j,meta} = rac{\sqrt{ ilde{N}_{1j}}Z_{1j} + \sqrt{ ilde{N}_{2j}} ilde{Z}_{2j}}{\sqrt{ ilde{N}_{1j} + ilde{N}_{2j}}}$$

where

$$ilde{Z}_{2j} = sign\left(r_g
ight) rac{Z_{2j}}{\sqrt{1+\left(1-r_g^2
ight)N_{2j}h_2^2l_j/M}}$$

$$ilde{N}_{1j} = N_{1j} rac{P\left(1-P
ight)\phi\left(\Phi^{-1}\left[K
ight]
ight)^{2}}{\left[K\left(1-K
ight)
ight]^{2}}$$

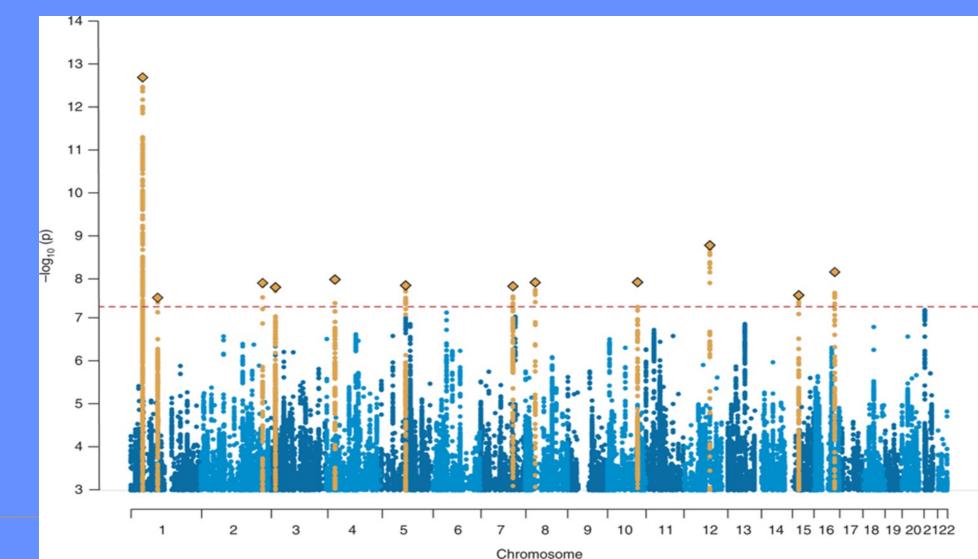
$$ilde{N}_{2j} = N_{2j} rac{r_g^2 h_2^2/h_1^2}{1 + (1 - r_g^2) N_{2j} h_2^2 l_j/M}$$

(Demontis et al., 2019)

Genome wide association study-ADHD

20K subjects 35K controls

12 loci found



(Demontis et al., 2019)

Genome wide association study- ADHD

Heritability 70-80%

Genetic overlap with:

- Antisocial personality
- Cognitive impairment
- Autism spectrum disorder
- Schizophrenia
- Bipolar disorder
- Major depressive disorder

Genes and treatment response in ADHD

Methylphenidate

- 36 studies (3647 children)
- 9 genes reviewed
 - 6 positive
 - 3 no effect

Atomoxetine

- Really likes 2D6
- Does not like any other cytochromes
- 10x higher exposure in "poor metabolizers"

Polygenic risk scores

- PRS= Summary of a person's total genetic risk for that disorder
- How many risk variants are present x How strong is each one

Genetics and Epigenetics of Suicide



GWAS of Suicide Attempt in major depressive disorder, bipolar disorder, and schizophrenia

	major depression	bipolar disorder	schizophrenia
10 SNPs for suicide attempt in mood disorders			NO
loci for suicide attempt	Yes	Yes	NO
Depression PRS associated with risk of suicide attempt	Yes	Yes	Yes
Counterpoints	not replicated in other cohorts		

Review of 52 studies of suicide epigenetics

- DNA methylation
- histone modifications
- microRNA (miRNA)

- complex interplay of environmental risk factors with genetic risk factors
- Hard to distinguish suicide specific effects from adverse childhood experiences and psych diagnosis

MicroRNA may mediate Early Life Stress (ELS) vulnerability to depression and suicidal behavior

- MiRNAs influence:
 - gene expression
 - messenger RNA (mRNA)
 - altering protein production
 - individual miRNAs can have hundreds of targets
 - neuronal development and brain physiology
 - HPA axis
- ELS may induce changes in miRNA function

What is the estimated genetic contribution to risk of developing autism?

- A. <25%
- B. 25-50%
- C. 50-75%
- D. >75%

Genetics of Autism Etiology of Autism Spectrum Disorders and Autistic Traits Over Time

	Swedish Twin Registry (STR)	Child and Adolescent Twin Study in Sweden (CATSS)
Twin pairs	23K	15K
Participants born	1982-2008	1992-2008
Data	Dx from National Patient Register	Screening with a structured, parental telephone interview
Heritability	.8897	.75-93

- Highly Heritable
- Contribution of environmental factors remained relative constant

All major psychiatric disorders have a heritable component

- Heritability 20% to 45%
- anxiety disorders
- obsessive-compulsive disorder
- posttraumatic stress disorder
- major depressive disorder
- Heritability 50% to 60%
- alcohol dependence
- anorexia nervosa

- Heritability >75%
- autism spectrum disorder (ASD)
- attention deficit hyperactivity disorder (ADHD)
- schizophrenia
- bipolar disorder

Depression Genetics

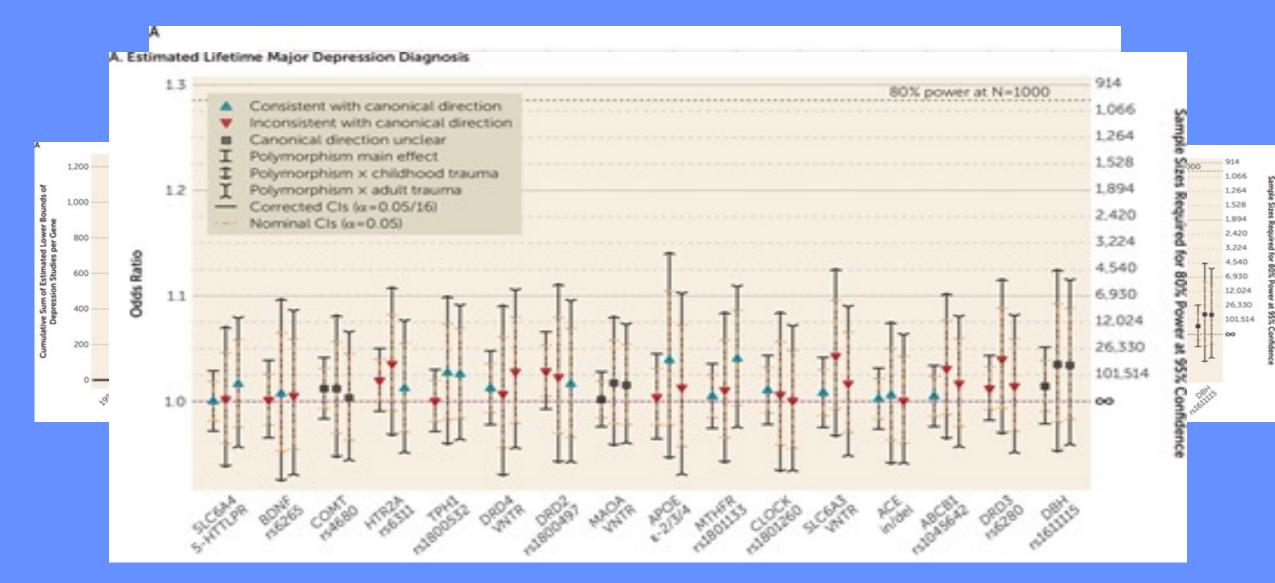
Development
And
Treatment



Which Gene shows a consistent association with risk of Depression?

- A. Serotonin reuptake pump
- B. Serotonin receptors
- C. Brain Derived Neurotrophic Factor
- D. None of the above

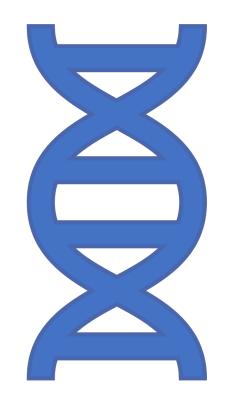
Genetics of Depression Risk



(Border et al., 2019)

Genetics of Depression Risk

- No evidence was found for:
 - any candidate gene
 - any gene-by-environment effects
- Early hypotheses about depression candidate genes were incorrect

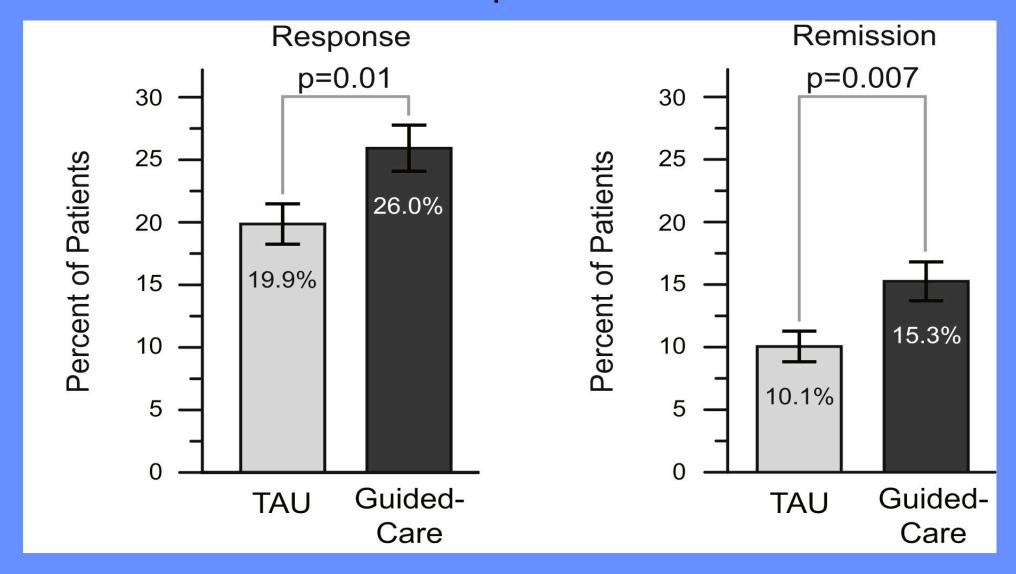


Letter to Editor and Author's response

- They mismeasured environments, so they are wrong
 - Vrshek-Schallhorn et al.
- We did not mismeasure environments and even if we did it would not change the results
 - Border et al

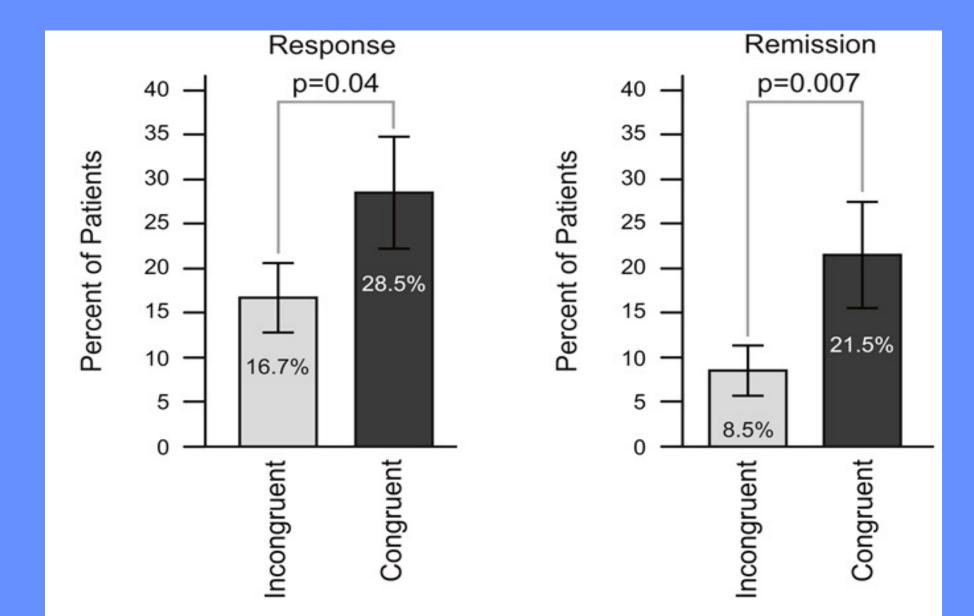
(Vrshek-Schallhorn et al., 2019) (Border et al., 2019)

Genetic-Guided Depression Treatment



(Greden et al., 2019)

Genetic-Guided Depression Treatment



Pharmacogenomic test-guided treatment versus treatment as usual for major depressive disorder

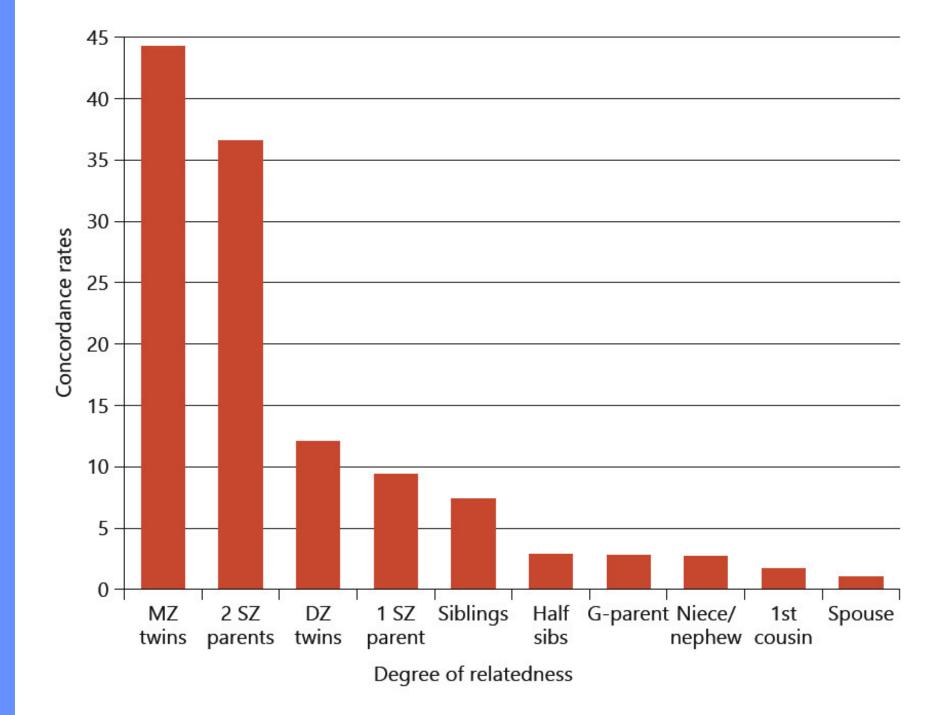
No better when providers were unconstrained by the results

Was better when treatment was concordant with assay results

Gene variants and antidepressant response

- 16 studies-2257 patients with MDD. Seven Asian. Nine Caucasian.
- 8 SNPs were analyzed:
 - 5-HTTLPR
 - 5HTR2A (rs6311, rs6314, rs7997012 and rs6313)
 - 5HTR1A (rs6295)
 - BDNF (rs6265)
 - 5HTTSTin2
- None associated with antidepressant response

Schizophrenia Concordance



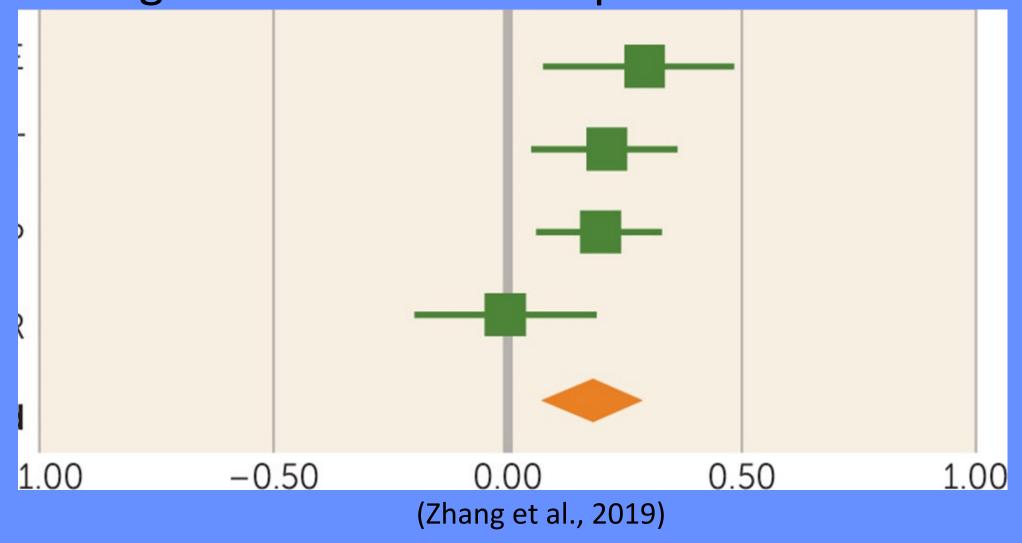
(Avramopoulos, 2018)

Genetics of Schizophrenia

- Velo-Cardio-Facial Syndrome (VCFS)
 - deletion in chromosomal band 22q11.2
- deletion increases the risk of schizophrenia ≈ **70 times**
- present in 1 out of 300 individuals with schizophrenia

- GWAS- 248 genome-wide significant loci
- GWAS variants are mostly non-coding

Polygenic Risk score in first episode treatment more genetic risk = less response to treatment



Polygenic risk score for schizophrenia: Ancestry > Diagnosis

- Difference between some ancestral groups was 10 times the difference between European cases and controls
- PRS derived from Europeans cannot be applied to non-Europeans
- Limits potential usefulness in clinical settings

A polygenic resilience score moderates the genetic risk for schizophrenia

- Some rare gene variants provide resistance to simple genetic disease
- Some gene variants protect from complex diseases (Chen)
- Resilience has been traditionally viewed as a psychological construct
- Genetic Resilience = heritable variation that promotes resistance to disease by reducing the impact of risk loci
- Resilience and risk loci operate independently

(Hess et al., 2019) (Chen et al., 2016)

Genetics of Alzheimer's

Autosomal Dominant

- If you get one copy you get early Alzheimer's
 - APP-amyloid precursor protein
 - PSEN1
 - PSEN2

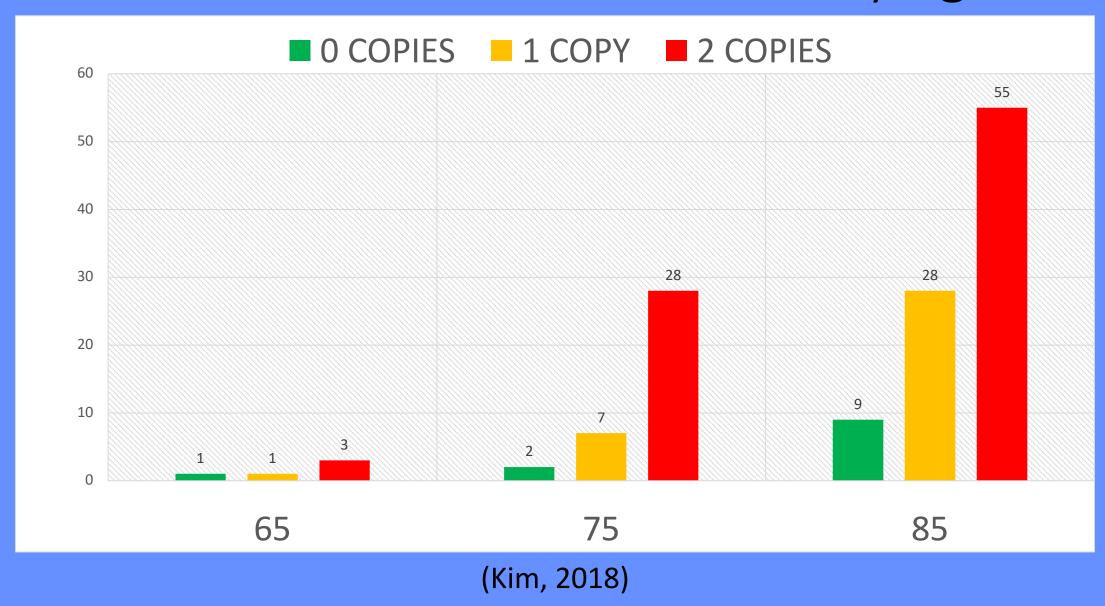
Polygenic Risk Score

- GWAS
- APOε and >20 others carry similar risk
- Heritability 80%

Genetics of Alzheimer's 23 and Me only examines APOε 4

- "Does **not** include all possible variants or genes associated with late-onset Alzheimer's disease.
- Does **not** include *any* variants or genes linked to early-onset Alzheimer's disease.
- Does **not** determine a person's full APOE genotype."

APOE4 and Alzheimer's risk by age



Direct-to-consumer genetic tests are sold for:

- Intelligence
- Diet
- Wine Preference
- Caffeine sensitivity
- Cancer risk
- Sunburn risk

- Selection of exercise
- Alzheimer risk
- Parkinson risk
- Drug metabolism
- Celiac disease
- Gut microbiome

Direct to consumer cancer genes

30 gene panel

- colorectal
- male breast
- prostate
- stomach
- melanoma
- pancreatic

"You tested negative, and

85-90% of all cancers have a

non-genetic cause"

"Early detection improves survival"

(Color.com Male Cancer genes)

Is there Value in Knowing?

Knowing my genetic risk would change my behavior

T/F

Other people knowing *their* risk would change *their* behavior

T/F

All of these were *unchanged* with genetic information about risk:

- Smoking
- Diet
- Physical activity
- Alcohol use

• Little or no effect on riskreducing health behavior

 If you expect that genetic information will play a major role in motivating behavior, prepare to be disappointed



non-coding RNAs (ncRNAs)

microRNAs (miRNAs)	(~22 nucleotides)	modulating synaptic functions and neural structures
small interfering RNAs (siRNAs)	(~20-24 nucleotides)	double-stranded RNAs (dsRNAs) interfere in the translation of proteins
piwi-interacting RNAs (piRNAs)	(26–32 nucleotides)	regulation of transposable elements in germlines
small nuclear RNAs (snRNAs)	(~150 nucleotides)	snRNAs remove the pre-mRNA regions (intron)
small nucleolar RNAs (snoRNAs)	(~60-140 nucleotides)	modify rRNAs, tRNAs, and snRNAs

(Yoshino & Dwivedi, 2020)

long non-coding RNAs (LncRNAs) >200 nucleotides)

'sponges' that prevent miRNA functions

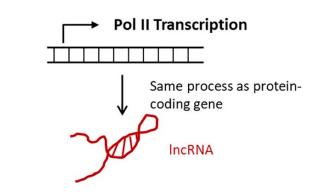
Modify chromatin

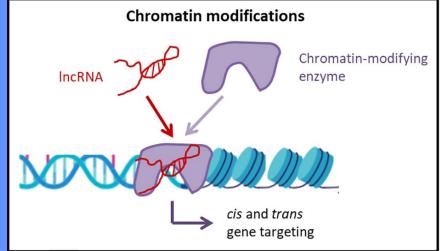
scaffolds that provide docking sites for proteins

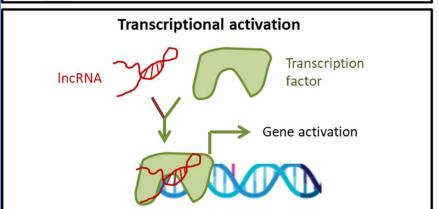
activators and suppressors of mRNA transcription

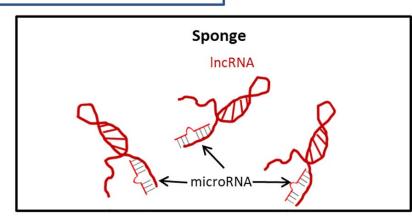
(Yoshino & Dwivedi, 2020)

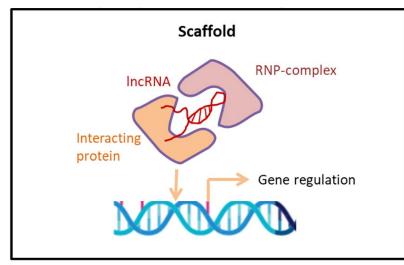
Long non-coding RNA biogenesis and functions

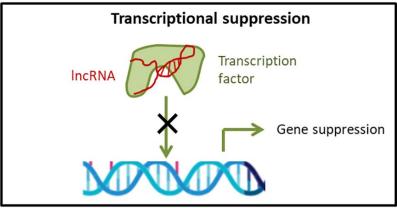








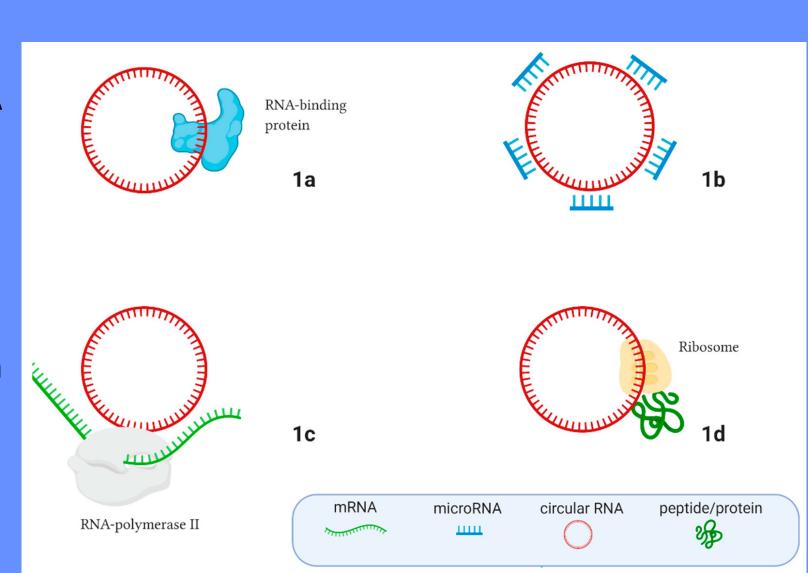




Circular RNAs (circRNAs)

- are endogenous, singlestranded, non-coding RNA (ncRNA)
- interact with RNA-binding proteins (RBPs)
- affect microRNA
- modulate gene expression
- translate proteins by themselves

(Nedoluzhko et al., 2020)





Conclusions

- 1. Huge amount of new data being generated
- 2. Will influence our understanding of Psychiatric Disorders
- 3. It's complicated and cool
- 4. Remember to temper enthusiasm with evidence

Which concept did you find most interesting?

- A. Cytochromes
- B. GWAS
- C. Epigenetics
- D. Polygenic Risk Score
- E. Noncoding RNA

Questions?

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