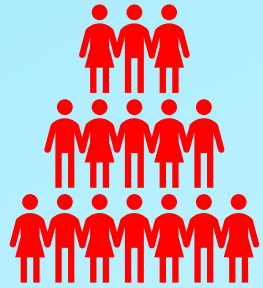
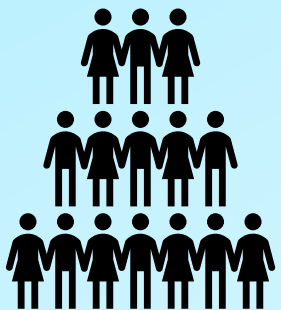


GWAS Are Used to Identify Novel AD Candidate Genes Using Large-Scale Genetic Information



AD population
Disease phenotype



Control population
Without the disease phenotype

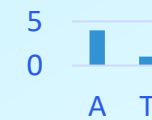
STEPS in GWAS:

- Enroll a large population of people that differ in the trait of interest
- Do a careful phenotype analysis
- Survey each person's genome for variation (called single-nucleotide polymorphisms, SNPs) in the genetic code
- Look for variants that are significantly more common in the disease population than in the control population
- These variants are map posts on the chromosome that are used to explore the nearby genes as candidate genes for AD
- **GWAS are useful for nominating candidate genes, but typically are unable to establish disease causality** (due to genetic linkage, lack of statistical power, multiple causative variants or genes).¹ Functional validation is needed through cell biology or animal studies

Identify single-nucleotide polymorphisms (differences) between populations

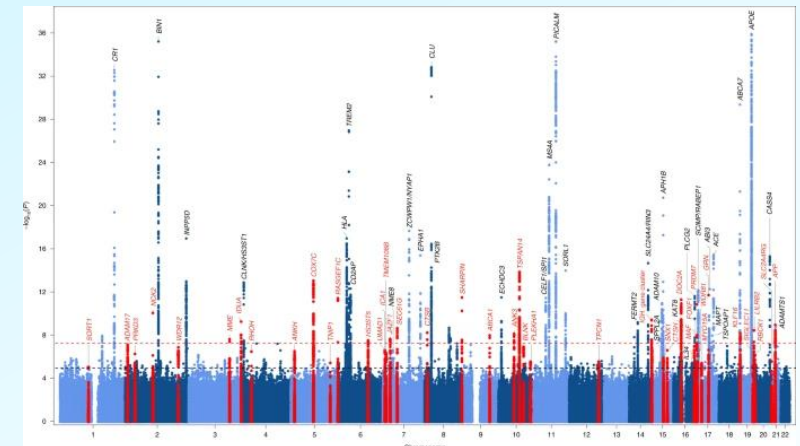
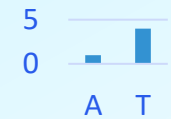
Control population

...CCTATGCTAC...
...CCTATGCTAC...
...CCTATGCTAC...
...CCTTTGCTAC...
...CCTATGCTAC...



AD population

...CCTTTGCTAC...
...CCTTTGCTAC...
...CCTTTGCTAC...
...CCTATGCTAC...
...CCTTTGCTAC...



Bellenguez et al, CC by 4.0²

GWAS, genome-wide association studies.

1. Flister M et al. *Genome Res.* 2013;23:1996-2002; 2. Bellenguez C et al. *Nat Genet.* 2022;54:412-436.

GWAS Have Significantly Increased the Pace of AD Gene/Risk Loci Discovery

Genome-wide association studies identify regions of the genome associated with LOAD. Fine mapping is needed to identify specific genes.

1987
APP
sequenced
A β 42 and
43

1988
TAU
sequenced

1993
Gene:
ApoE2
and E4

1995
Gene:
1st PS-1
mutation

1999
BACE 1
cloned, β
secretase

1991
1st APP
mutation
identified

2007
1st AD
GWAS

2009
Gene:
CLU
PICALM
CR1

2008
Gene:
CD33

2010
Gene:
ADAM10

2010
Gene:
BIN1

2013
22 risk loci
identified

2011
Gene:
ABCA7
MS4A6A

2012
Gene:
TREM2

2018
4 risk loci
identified

2019
5 risk loci
identified

2021
Genes:
SPRED2
CLEC7A
FLT3
IRF8
SLC24A4
SLC24A5
SLC2A9
SORL1

2022
75 risk loci
identified,
42 new

1990

2000

2010

2020

Susceptibility Loci Help Pinpoint Major Molecular Pathways Associated With LOAD

Gene	Molecular Pathway
ApoE, SORL1, CLU, CR1, PICALM, BIN1, ABCA7, CASS4, PLD3	Amyloid pathway
CLU, CR1, EPHA1, ABCA7, MS4A4A/MS4A6E, CD33, CD2AP, HLA-DRB5/DRB1, INPP5D, MEF2C, TREM2/TREML2	Immune system/inflammation
ApoE, CLU, ABCA7, SORL1	Lipid transport and metabolism
CLU, PICALM, BIN1, EPHA1, MS4A4A/MS4A6E, CD33, CD2AP, PTK2B, SORL1, SLC24A4/RIN3, MEF2C	Synaptic cell functioning/endocytosis
BIN1, CASS4, FERMT2	Tau pathology
PTK2B	Cell migration
MEF2C, PTK2B	Hippocampal synaptic function
CELF1, NME8, CASS4	Cytoskeletal function and axonal transport
INPPD5	Microglial and myeloid cell function
FBXL7	Phosphorylation-dependent ubiquitination