

ADGC and NIAGADS Update

October 2014 ADC Director's Meeting

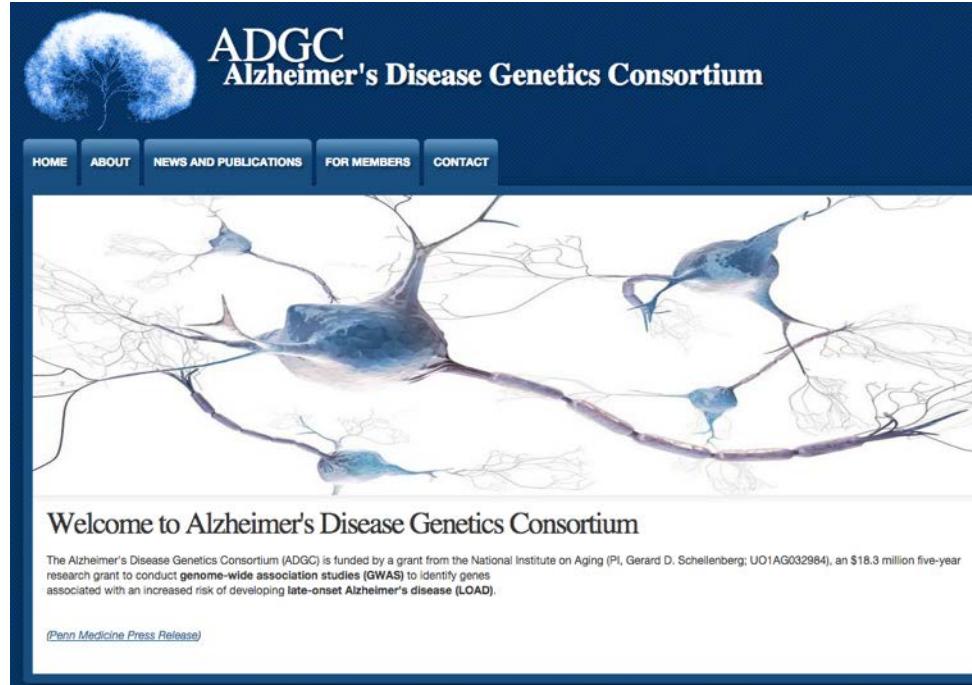
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ADGC

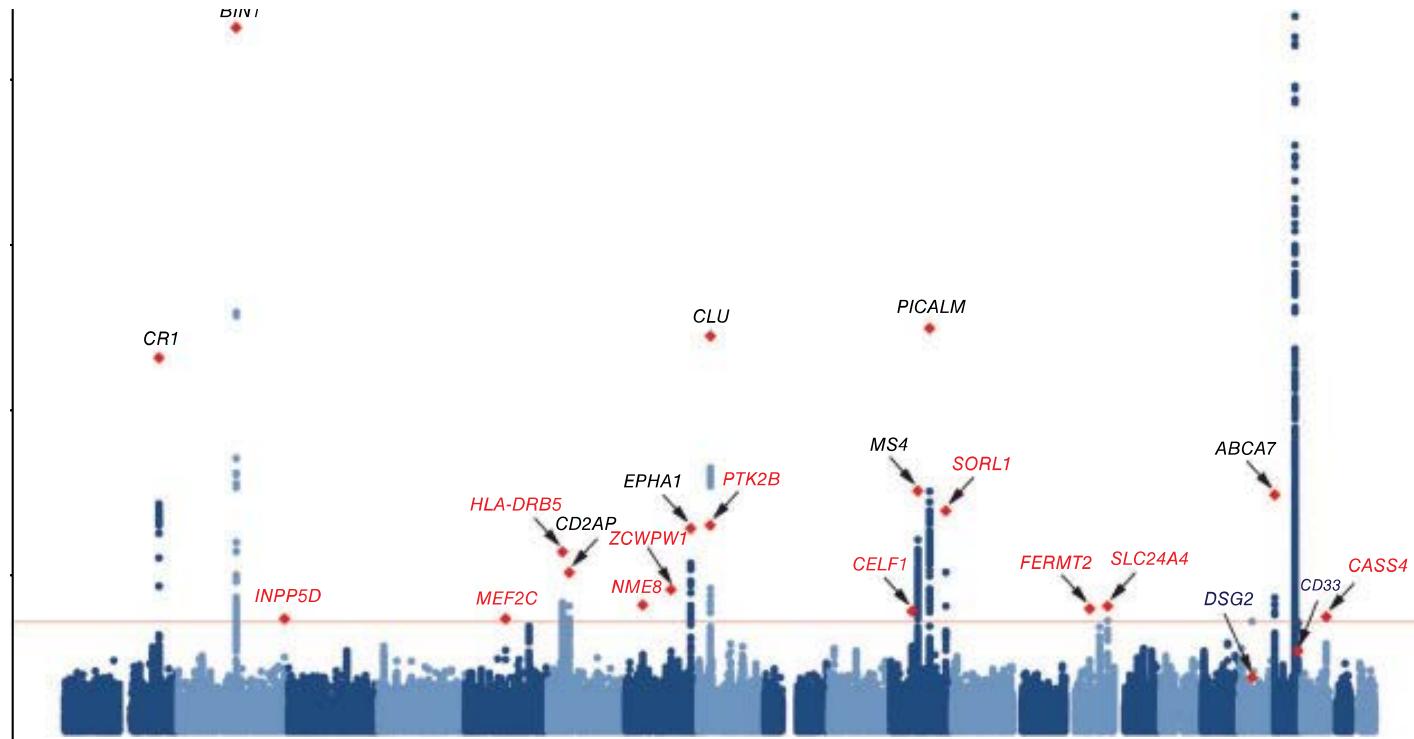


The Alzheimer's Disease Genetics Consortium (ADGC) is funded NIA (PI: Gerard Schellenberg) to conduct genome-wide association studies (GWAS) to identify genes associated with an increased risk of developing late-onset Alzheimer's disease (LOAD).

ADGC / ADC Sample Update

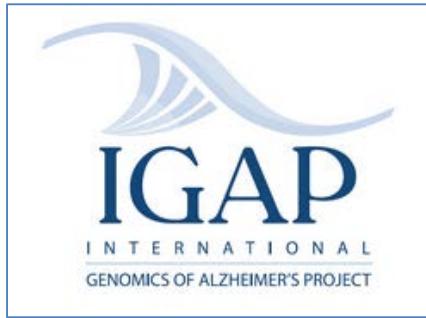
- GWAS Phase I: **4,464** ADC subjects
 - Data available via **NACC** (relabelled to patient IDs) and **NIAGADS** (using NACC IDs)
- GWAS Phase II: As of October 3, 2014, total **11,376** ADC subjects genotyped by ADGC GWAS

Lambert et al 2013 IGAP GWAS



Lambert 2013

IGAP



LETTERS

nature
genetics

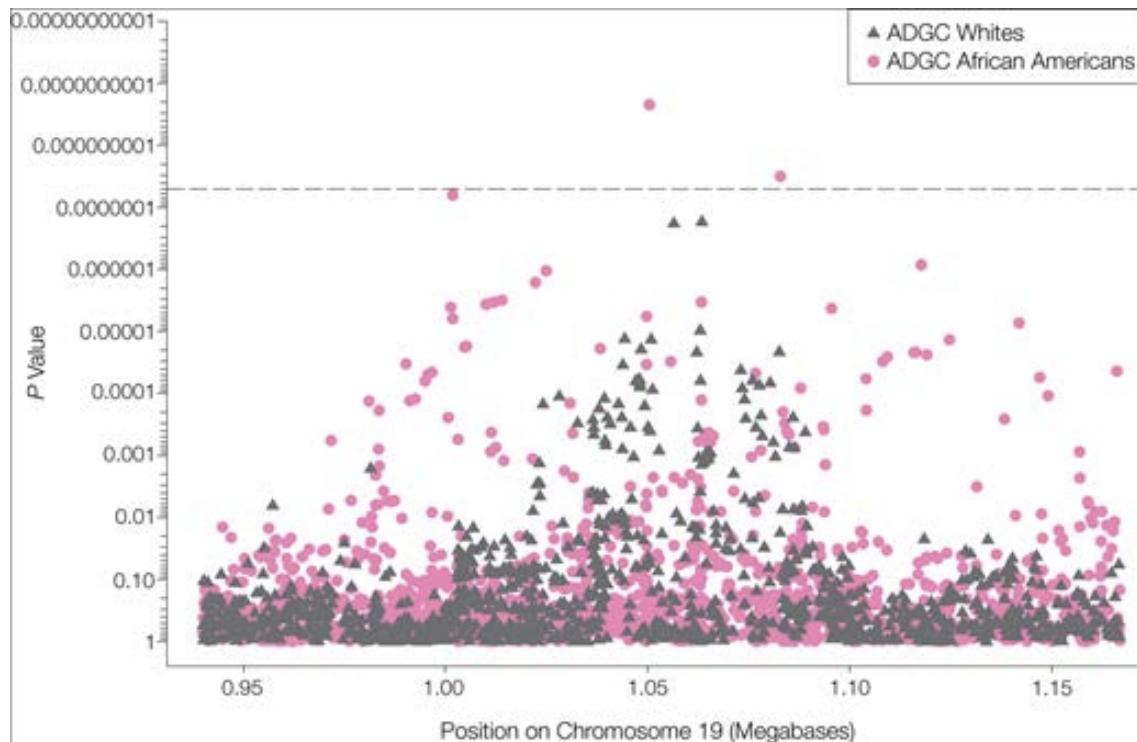
Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease

- ❑ IGAP (Lambert et al. Nature Genetics 2013)
- ❑ Genome-wide summary statistics with non-identifiable information: P-value / HapMap Allele frequency / OR
- ❑ go.nature.com/tumaG2 has the following URL to data access

http://www.pasteur-lille.fr/en/recherche/u744/Igap_stage1.zip

- ❑ NIAGADS is working to cross-list the dataset

Reitz 2013 GWAS on African American population



Effect size for rs429358
(in ABCA7) comparable
with APOE ϵ 4-SNP

OR: 2.31 [95% CI, 2.19-2.42]
 $P = 5.5 \times 10^{-47}$



Reitz 2013

36 publications since 2009

16 published or in press in 2014; 10 submitted and under review

Benitez et al. Missense variant in TREML2 protects against Alzheimer's Disease. *Neurobiol Aging*. 2014 Jun;35(6):1510.e19-26.

- ◆ Ruitz et al. International Genomics of Alzheimer's Disease Project identifies TRIP4 as a novel susceptibility gene. *Transl Psychiatry* 2014 Feb 4;4:e358. ◆ Escott-Price et al. Gene-wide analysis detects two new susceptibility genes for Alzheimer's disease. *PLOS One* 2014 Jun 12;9(6):e94661. ◆ Naj et al. Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease: A Genome-Wide Association Study. *JAMA Neurol*. 2014 Sep 8. ◆ Nelson et al. ABCC9 gene polymorphism is associated with hippocampal sclerosis of aging pathology. *Acta Neuropathologica* 2014 Jun;127(6):825-43. ◆ Allen et al. Association of MAPT haplotypes with Alzheimer's disease risk and MAPT brain gene expression levels. *Alzheimer's Research and Therapy* (in press) ◆ Jones et al. Convergent genetic and expression data implicate immunity in Alzheimer's disease. *Alzheimers and Dementia* (in press) ◆ Wang et al. APP Mutation A673T: A protective variant for Alzheimer's disease in the United States? *JAMA Neurology* (in press) ◆ Beecham et al. Genome-wide association meta-analysis of neuropathologic features of Alzheimer's disease and related dementias. *PLOS Genetics*. 2014 Sept 4;10(9) ◆ Jun et al. PLXNA4 is Associated With Alzheimer Disease Risk and Modulates Tau Protein Phosphorylation. *Ann Neurol*. 2014 Sep;76(3):379-92. ◆ Logue et al. Two Rare AKAP9 Missense Variants are Associated with Alzheimer Disease in African Americans. *Alzheimers Dement*. 2014 Aug 26. ◆ Ramirez et al. SUCLG2 identified as both a determinator of CSF A β 1-42-levels and an attenuator of cognitive decline in Alzheimer's disease. *Hum Mol Genet*. 2014 Jul 15 ◆ Barral et al. Genetic variants in a 'cAMP element binding protein' (CREB)-dependent histone acetylation pathway influence memory performance in cognitively healthy elderly individuals. *Neurobiol Aging*. 2014 Jun 28. ◆ Barral et al. Common genetic variants on 6q24 associated with exceptional episodic memory performance in the elderly. *JAMA Neurology* (In press). ◆ Wetzel-Smith et al. A rare mutation in UNC5C predisposes to Alzheimer's disease and increases neuronal cell death. *Nature Medicine* (In press). ◆ Schreiber et al. Alzheimer's Disease Genetics. *Current Behavioral Neuroscience Reports* (In press).

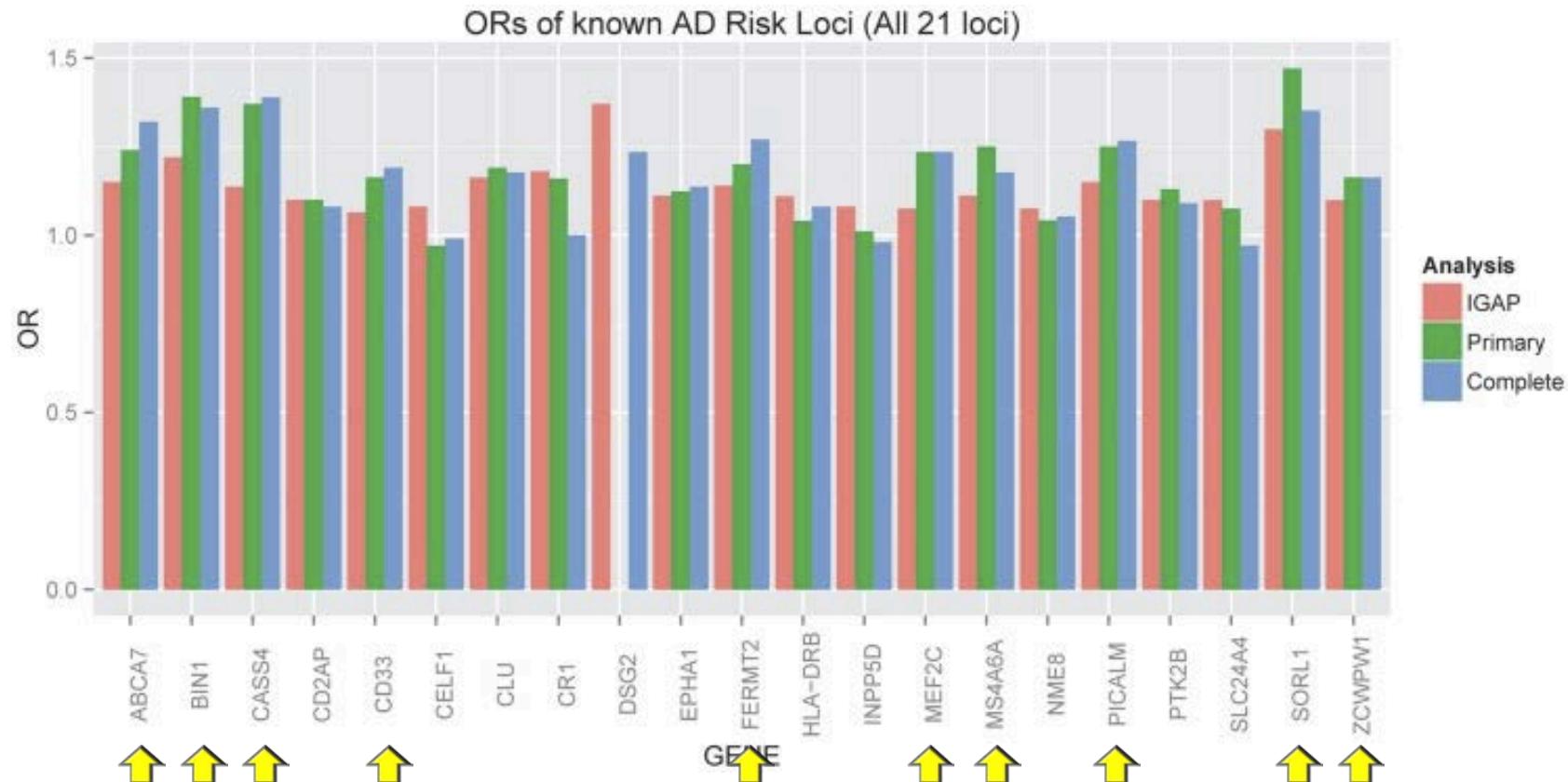
New findings

- ❑ Follow-up of IGAP study
 - ❑ **TRIP4** (rs74615166)
 - ❑ **TP53INP1** and **IGHV1-67** via gene-wise analysis
- ❑ **TREML2** (rs3747742) is a protective variant
- ❑ **ABCC9** (rs704178) associated with hippocampal sclerosis
- ❑ **PLXNA4**: NIA-LOAD and Framingham family studies
- ❑ **SUCLG2** associated with A β_{1-42} and cognitive decline in AD
- ❑ Rare variants in **AKAP9** associated with AD in African Americans
- ❑ GWAS using neuropath-confirmed subjects with stronger effect sizes
- ❑ **CR1**, **BIN1**, and **PICALM** associated with age at onset

Association with age at onset [Naj 2014]

SNP	CH:MB	Age at Onset										LOAD Risk	
		Nearest Gene	Minor Allele	MAF	Minimal Adjustment Model			Extended Adjustment Model			<i>P</i> Value for Het		
					β (95% CI)	<i>P</i> Value	<i>P</i> Value for Het	β (95% CI)	<i>P</i> Value	<i>P</i> Value for Het			
rs6701713	1:207.8	CR1		A	0.24 (-0.65 to -0.17)	-0.41 (-0.65 to -0.17)	7.2 × 10 ⁻⁴	.405	-0.41 (-0.69 to -0.12)	4.9 × 10 ⁻³	.422	1.16 (1.11 to 1.22)	4.6 × 10 ⁻¹⁰
rs7561528	2:127.9	BIN1		A	0.37 (-0.52 to -0.09)	-0.31 (-0.52 to -0.09)	4.8 × 10 ⁻⁴	.855	-0.32 (-0.57 to -0.08)	9.9 × 10 ⁻³	.684	1.17 (1.13 to 1.22)	4.2 × 10 ⁻¹⁴
rs9349407	6:47.5	CD2AP		C	0.32 (-0.25 to 0.19)	-0.03 (-0.25 to 0.19)	.765	.266	-0.14 (-0.40 to 0.11)	.273	.860	1.12 (1.07 to 1.18)	1.0 × 10 ⁻⁶
rs11767557	7:143.1	EPHA1		C	0.18 (-0.26 to 0.32)	0.03 (-0.26 to 0.32)	.830	.861	0.07 (-0.24 to 0.39)	.659	.657	0.87 (0.83 to 0.92)	2.4 × 10 ⁻⁷
rs1532278	8:27.5	CLU		T	0.37 (-0.18 to 0.28)	0.05 (-0.18 to 0.28)	.661	.137	0.0038 (-0.26 to 0.27)	.977	.108	0.89 (0.85 to 0.93)	8.3 × 10 ⁻⁸
rs4938933	11:60.0	MS4A4A		C	0.36 (-0.14 to 0.31)	0.09 (-0.14 to 0.31)	.448	.454	0.018 (-0.23 to 0.27)	.887	.584	0.88 (0.85 to 0.92)	1.7 × 10 ⁻⁹
rs561655	11:85.8	PICALM		G	0.38 (-0.12 to 0.55)	0.33 (-0.12 to 0.55)	2.2 × 10 ⁻³	.915	0.32 (0.07 to 0.57)	.011	.957	0.87 (0.84 to 0.91)	7.0 × 10 ⁻¹¹
rs3752246	19:1.1	ABCA7		G	0.34 (-0.55 to 0.02)	-0.27 (-0.55 to 0.02)	.064	.700	-0.19 (-0.51 to 0.13)	.242	.748	1.15 (1.09 to 1.21)	5.8 × 10 ⁻⁷
Haplotype rs7412/ rs429358	19:45.4	APOE		ϵ 4	0.35 (-2.68 to -2.21)	-2.45 (-2.68 to -2.21)	3.3 × 10 ⁻⁹⁶	.094	-0.24 (-0.75 to 0.27)	.360	.874	3.02 (2.86 to 3.20)	2.2 × 10 ⁻³²⁰
rs3865444	19:51.7	CD33		A	0.20 (-0.13 to 0.33)	0.10 (-0.13 to 0.33)	.377	.596	0.13 (-0.13 to 0.38)	.338	.872	0.89 (0.86 to 0.93)	1.1 × 10 ⁻⁷

Stronger effect size using neuropath-confirmed subjects [Beecham 2014]



ADGC GWAS Data available at NIAGADS

- ❑ 13 ADGC GWAS datasets from Naj et al. (2011) and Lambert et al (2013) available at NIAGADS
- ❑ GWAS data
- ❑ Phenotype
- ❑ Imputation
- ❑ *Naj et al. Nature Genetics 2011 Summary Statistics*

Round	Platform	Cases/Controls	Link
Discovery (Stage 1)			
ACT	Illumina Human660	354/1981	NG00034
ADC1	Illumina Human660	1566/515	NG00022
ADC2	Illumina Human660	738/160	NG00023
ADNI	Illumina Human610	268/173	Access Data
GenADA	Affymetrix 500	669/713	Coming Soon!
Genetic Differences	Illumina Human660	213/0	NG00034
UM			Coming Soon!
VU	Illumina Human660/1M Duo/Affymetrix 6.0	1186/1135	Coming Soon!
MSSM			Contact PI
MIRAGE	Illumina Human610/330	509/753	NG00031
NIA-LOAD	Illumina 610	1852/1991	NG00032
OHSU	Illumina HumanCNV370v1_C	647	NG00017
TGEN2	Affymetrix 1M	864/493	NG00028
Replication (Stage 2)			
ADC3	Illumina OmniExpress	897/588	NG00024
MAYO	Affymetrix 6.0	728/1173	Coming Soon!
ROSMAP	Affymetrix 6.0	296/776	NG00029
UPitt	Illumina HumanOmni1-Quad	1440/1000	NG00026
WashU	Illumina Human610	403/225	NG00030

ADGC vs NIAGADS: Data Access

	ADGC	NIAGADS
Objective	AD genetics research	AD genetics / genomics data resource
Data control jurisdiction	Collaborators contribute data. New analysts NEED approval from original data contributors	Data delegated to NIAGADS via <i>NIA data sharing plan</i> . New analysts DO NOT NEED approval from original data contributors
Apply for data access	As ADGC collaborator with a specific analysis plan. Needs sponsoring ADGC member. No-surprises, no overlap with primary analysis	As an independent Investigator . Data access application
Type of data	Access to pre-publication data	Only published data
Manuscript review	Reviews findings and methodology	Only check for acknowledgement
Authorship & Acknowledgment	ADGC as co-author. Acknowledge ADGC and study funding	NIAGADS is not co-author. Acknowledge study funding and NIAGADS

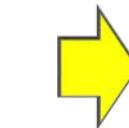
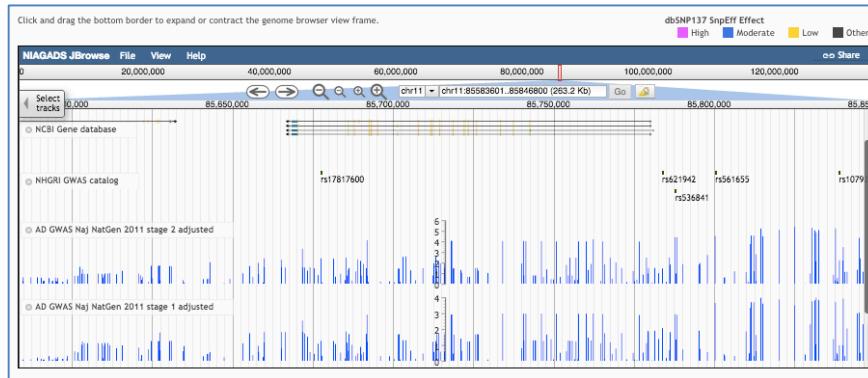
ADGC ADC data types

- ❑ Complete data
 - ❑ GWAS
 - ❑ Phenotype
 - ❑ Imputation
 - ❑ Genome-wide association results
- ❑ Specific subset
 - ❑ Genotypes for top SNPs (in preparation, will be available via NACC)
 - ❑ Association results for specific SNPs are available via NIAGADS Genomics DB

<https://www.niagads.org/genomics/>



Genome Browser



Gene / SNP report

dbSNP rs6656401

Unless otherwise annotated, SNP Information was obtained from NCBI dbSNP [Sherry ST, et al. (2001). dbSNP: the NCBI database of genetic variation. *Nucleic Acids Res.* 29:308-11. PMID:11125122]

Add to Favorites ★

Related Links • NCBI dbSNP

Sections ▾ Genomic Context ▾ NIAGADS GWAS Datasets ▾ NHGRI GWAS Catalog ▾ SnpEff Annotations and Effects ▾ Allele Frequency ▾ Quality Confidence ▾ Additional Annotation

Genomic Context Hide

View rs6656401 in the genome browser

Location (in hg19) chr1: 207,692,250

dbSNP137 SnpEff Effect

- High
- Moderate
- Low
- Other

rs6656401

rs148978218

rs151110404

rs1113531714

rs12003429

rs141109406

NCBI Gene database

Location (in hg19) chr1: 207,692,249

Alternate Allele(s) (dbSNP build 137) G

Reference Allele (dbSNP build 137) A

Back to Top

Alzheimer's GWAS Results Show

Back to Top

SnpEff generated annotations and effects Hide

Cingolani P et al. (2012) SnpEff: A program for annotating and predicting the effects of single nucleotide polymorphisms. SnpEff: SNPs in the genome of Drosophila melanogaster strain w1118; Iso-2; Iso-3. Platts A, Wang le L, Coon M, Nguyen T, Wang L, Land SJ, Lu X, Ruden DM. *Fly (Austin)*, 6(2):80-92. PMID:22728672

Effect	Effect Impact	Functional Class	Codon Change	Amino Acid Change	Amino Acid Length	Gene	Transcript Bio Type	Gene Coding	Transcript Id	Exon Rank	Genotype Number
INTRON	MODIFIER	N/A	N/A	N/A	2039	CR1	N/A	CODING	NM_000573.3	4	1
INTRON	MODIFIER	N/A	N/A	N/A	2489	CR1	N/A	CODING	NM_000651.4	4	1

Allele Frequency Hide

Attribute	Value	Definition
G5	true	>5% minor allele frequency in 1+ populations
GMAF	0.0879	Global Minor Allele Frequency [0, 0.5]; global population is 1000GenomesProject phase 1 genotype data from 629 individuals, released in the 11-23-2010 dataset

Back to Top

View
genomic
context

AD Sequencing Project

- Announced in February 2012 by DHHS and NIH



- Participants
 - NIA, NHGRI
 - LSSP sequencing centers (Broad/Baylor/WashU)
 - ADGC and CHARGE
 - NIAGADS (data coordinating center)
- Study design available at www.niagads.org/adsp

Photo from http://nihrecord.od.nih.gov/newsletters/2012/03_02_2012/story5.htm

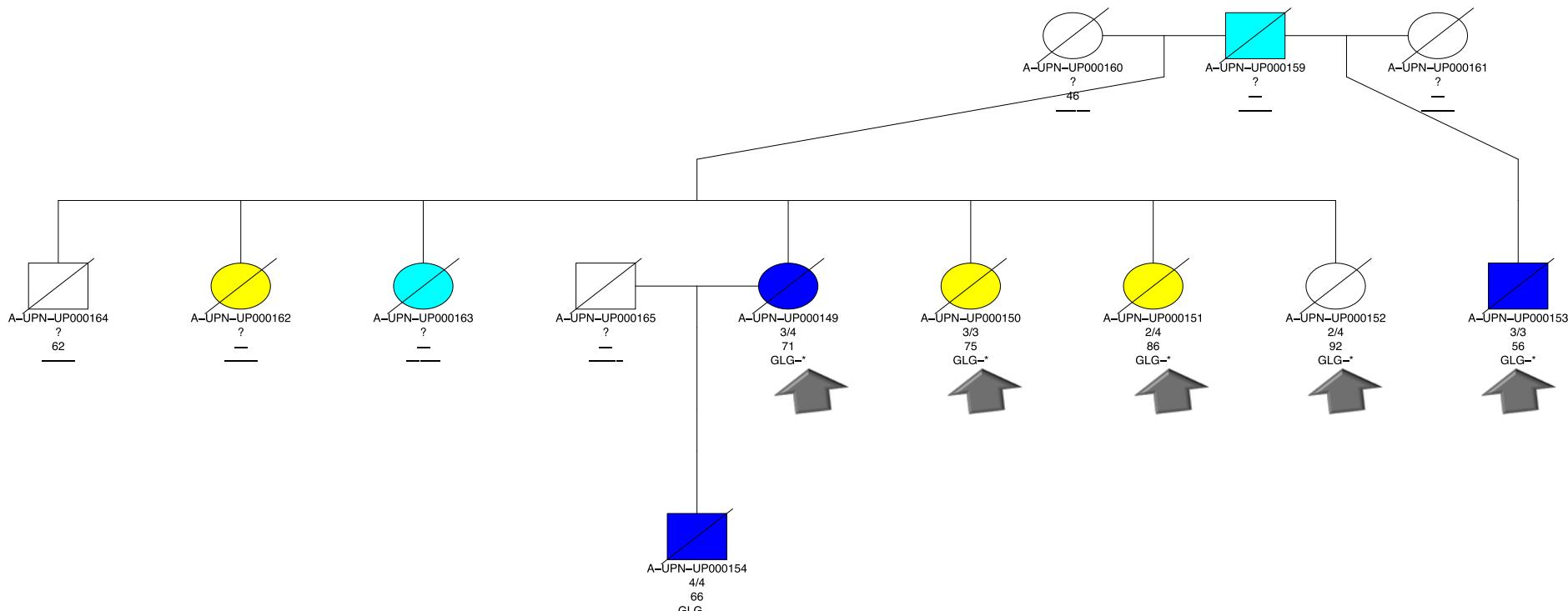
ADSP Progress

- 578 whole genomes from 111 multiplex families available in March 2014
- 10,939 samples/10,959 subjects with Whole Exome Sequencing will be available late October
- 3,264 are ADC subjects
- See ADSP website (www.niagads.org/adsp) for more information on
 - Study design
 - Apply for data access

The screenshot shows the homepage of the Alzheimer's Disease Sequencing Project (ADSP). The header features the 'adsp' logo with 'Alzheimer's Disease Sequencing Project' underneath, accompanied by a stylized DNA double helix graphic. The navigation menu includes links for HOME, ABOUT, DATA ACCESS, STUDY INFO, CONTACT US, LINKS, and ADSP SITE LOGIN. A 'News' sidebar on the right lists two items: 'Second batch of ADSP data released. Whole-genome sequencing data of all 584 subjects available.' and 'First batch of whole-genome sequencing data for Alzheimer's disease available.' Below the menu, a section titled 'Welcome to the Alzheimer's Disease Sequencing Project' describes the project's goals: identifying genomic variants contributing to risk and protection against Alzheimer's Disease, providing insight into why some individuals with known risk factors escape the disease, and examining factors in multi-ethnic populations for prevention. At the bottom, three buttons provide links to 'Study Design', 'Apply for Data', and 'Access Data'.

Example ADSP pedigree

FID = UP0004F, N = 13



Diagnosis

■ ConfirmedAD

■ ProbableAD

■ PossibleAD

■ Family Report AD □ Other

ADSP Whole-Exome Sequencing Data

Apply for data access



Download data



Convert ADSP ID to patient ID

- ❑ ~10,939 subjects, 3,264 are ADC subjects
 - ❑ BAM (raw sequences) end of October
 - ❑ VCF (SNPs and indels) at later date
- ❑ **Apply for access now!** Contact NIAGADS for help
- ❑ **ADSPID to ADC PatientID mapping** via NACC for each center (A NACC/NCRAD/ADGC/NIAGADS Collaboration!)

See www.niagads.org/adsp for more information

Or just contact NIAGADS data@niagads.org

Apply for ADSP data access

Go to www.niagads.org/adsp, click **Apply for Data**



- ❑ All applications will be submitted to dbGaP and reviewed by NIH
- ❑ The dbGaP dataset ID for ADSP is **phs000572**.
- ❑ ADSP requires the following additional information:
 - ❑ **Description of the secondary data** that will be generated by your study and deposited into NIAGADS
 - ❑ Signed **NIA Data Sharing Plan** and **NIAGADS Data Distribution Agreement** for ADSP
- ❑ Contact NIAGADS (data@niagads.org) for data application, we'd be glad to help step-by-step

University of Pennsylvania

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Laura Cantwell
Beth Dombroski
Sherry Beecher

Familial AD

Richard Mayeux
Deborah Blacker

Clinical Group

John Morris
Debbie Tsuang

Neuropathology Group

Tom Montine
Eric Reiman

Biomarker Group

Alison Goate
Andy Saykin

Prospective Cohort Group

David Bennett

Bernadino Ghetti

Brad Hyman

Denis Evans

Eric Larson

Paul Crane

John Hardy

Ilyas Kamboh

Eric Reiman

Nilifur Taner

Julie Schneider

Steve Younkin

Denis Dickson

Charlie DeCarli

Douglas Galasko

Elaine Peskind

Neil Graff-Radford

Matthew Frosch

John Trojanowski

Vivianna Van Deelin

John Morris

NACC

Bud Kukull

Duane Beekly

NCRAD

Tatiana Foroud

Kelly Michelle Faber

University of Miami

Peggy Pericak-Vance

Adam Naj

Gary Beecher

Paul Gallins

Eden Martin

Boston University

Lindsey Farrer

Gyungah Jun

Jacqueline Buros

Case Western

Jonathan Haines

NIA/NIH, Alzheimer's Association

EADI

Philippe Amouyel
Jean-Charles Lambert

GERAD

Julie Williams
Paul Hollingworth
Denise Harold
Peter Holmes



ADGC

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Peggy Pericak-Vance
Jonathan Haines
Richard Mayeux
Lindsay Farrer
Gyungah Jun
Jacqueline Buros
Gary Beecham
Adam Naj
Eden Martin
Li-San Wang

CHARGE

Sudha Seshadri
Cornelia van Duijn
Lenore Launer
Ainta DeStefano

NIA/NIH, Alzheimer's Association

ADGC
Alzheimer's Disease Genetics Consortium

NIAGADS

ADSP Project

experimental design
power calculations – drive design
case/control selection
family selection
data flow and database planning
existing genetic data – submit to dbGap
phenotype data – submit to dbGaP
conference calls: 3-6/week, past 30 months
DNA samples to sequencing centers

ADSP Project

Gerard Schellenberg
Gary Beecham
Amanda Partch
Laura Cantwell
Adam Naj
Richard Mayeux
Lindsay Farrer
Peggy Pericak-Vance
Jonathan Haines
Li-San Wang
Wendy Raskind/Tom Bird
Tatiana Foroud
Kelley Faber
Anita DeStefano
Marilyn Miller

**ADGC
NCRAD
NACC
NIAGADS**



ADGC
Alzheimer's Disease Genetics Consortium

NIAGADS

alzheimer's association

CHGR
center for human genetics research
VANDERBILT UNIVERSITY

NCRAD
The National Cell Repository for
Alzheimer's Disease

NACC
National Alzheimer's Coordinating Center
[University of Pittsburgh](#)



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research center

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