

Introduction to **GWAS**:

A quick overview

Christian Werner

(Quantitative geneticist and biostatistician) **EiB, CIMMYT**, Texcoco (Mexico)

Filippo Biscarini

(Biostatistician, bioinformatician and quantitative geneticist) **CNR-IBBA**, Milan (Italy)

@HerrFaloppio

Oscar González-Recio

(Computational biologist and quantitative geneticist) **INIA-UPM**, Madrid (Spain)

@OscarGenomics





Something you need to carefully look at, or that may impair your GWAS



Something to do, or that optimizes your GWAS



Don't. Discourage to use this.



Smart tip. Something that makes the trick.



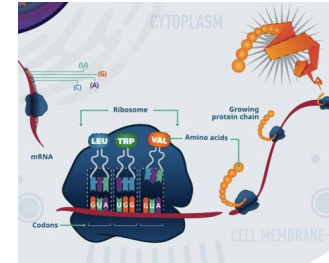
Advanced. Something to dive in.



Genetic basis of GWAS-GWP

Phenotypic variation
Genetic variants

- Allele substitution effect



- Infinitesimal model

Genetic basis of GWAS-GWP

Phenotypic variation
Genetic variants

$$P = G + E$$

- Continuous trait
- Categorical trait (threshold model)



Genetic basis of GWAS-GWP

Phenotypic variation

Genetic variants

Linkage disequilibrium

$$P = G + E$$

Genotype-Phenotype association → causal or functional link



Genetic basis of GWAS-GWP

- A study that agnostically tests hundreds of thousands of single nucleotide polymorphisms (SNPs) densely spaced across the genome for association with a given disease or trait.
- Rationale:
 - Not limited by a priori knowledge of disease process or the results of linkage studies
 - If large SNP density, each gene is expected to be in LD with at least 1 SNP
 - Preferable approach (so far) for diseases of complex etiology
 - Evidence for functional SNPs outside of coding regions

“First, our studies provide convincing evidence that the genome is pervasively transcribed, such that the majority of its bases can be found in primary transcripts, including non-protein-coding transcripts, and those that extensively overlap one another.” ENCODE, Nature June 2007



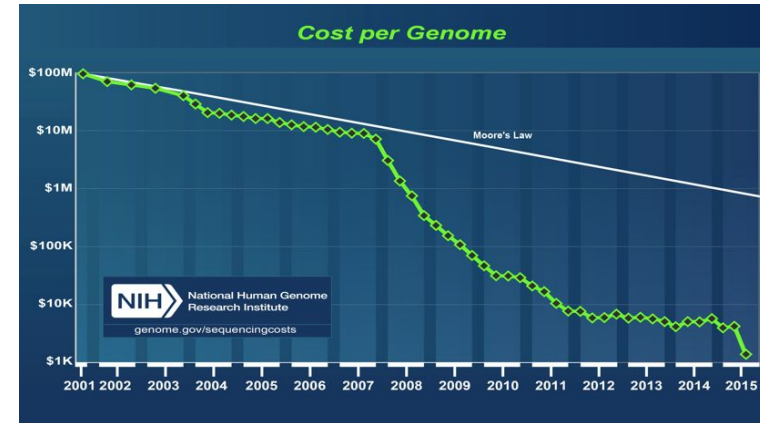
Genetic basis of GWAS-GWP

- Exposure:
 - SNPs
 - Indels
 - *Might* - copy number variants (CNV), haplotypes, other type of markers
- Outcome: easily adaptable to either dichotomous or quantitative outcomes
- Study Populations: Case-control, cross-sectional, or cohort. Family or population based.
 - Need to have large sample sizes!
- Analytic methods: logistic/linear regression
 - Flexibility for different genetic models - additive, dominant, recessive.



Genetic basis of GWAS-GWP

- Genotyping – Since early 2000 (25-100€)
 - Genome sequencing - (approx. 1000 €)
- Quantitative genetics – many genes – need many markers
- Use LD between gene and marker
- ⚠ □ We assume that all genes are in LD with at least one marker (we need a high coverage throughout the genome)



Costs matter - approximate current **SNP array prices**



Microarray



For Research Use Only



DNA

BovineHD DNA Analysis Kit

This comprehensive genome-wide bovine genotyping array kit features over 777,000 SNPs, and is compatible with any breed of beef or dairy cattle.



Microarray



For Research Use Only



DNA

BovineLD Genotyping BeadChip

Extend genomic selection to the entire herd with this expert-designed genotyping array featuring scalable content at an economical price.



Microarray



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DNA

BovineSNP50 v3 DNA Analysis BeadChip

This BeadChip microarray provides high density multi-sample bovine genotyping for genome characterization of major dairy and beef cattle breed types.



Microarray



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DNA

GGP Equine Arrays 65k

Select desired breed traits and verify animal pedigree with the GeneSeek Genomic Profiler (GGP) equine microarray.



Microarray



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DNA

CanineHD Whole-Genome Genotyping BeadChip 170k

This array enables genotyping of any domestic dog breed, and offers ample SNP density for within-breed association and CNV studies.

GGP Porcine HD Array

This genome-wide porcine genotyping array is ideal for marker-assisted selection and prediction applications. Array content includes:

- 70,000 SNPs for all major porcine breeds
- Average marker spacing of ~42 kb
- 20 key causative mutations

GGP Porcine LD Array

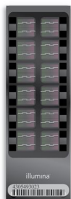
This array is designed for marker-assisted selection, Illumina PorcineSNP60 imputation, GGP Porcine HD imputation, and prediction applications. Array content includes:

- More than 10,000 SNPs for all major porcine breeds
- Average marker spacing of ~250 kb
- ~20 important causative mutations

OvineSNP50 DNA Analysis Kit

This sheep microarray features over 54,241 evenly spaced SNP probes for genome-wide association studies, genome-wide selection, and genetic merit determination.[Read More...](#)

The BeadChip was developed in collaboration with leading ovine researchers from AgResearch, Baylor UCSC, CSIRO, and the USDA as part of the International Sheep Genomics Consortium. It features over 54,241 evenly spaced probes that target single nucleotide polymorphisms (SNPs).



Costs matter - approximate current **SNP array prices**



Microarray



For Research Use Only



DNA

MaizeLD BeadChip Kit

Microarray kit for maize breeding applications and assessment of essentially derived varieties. Samples used include the Plant Variety Protection Act panel.



Microarray



For Research Use Only



DNA

MaizeSNP50 DNA Analysis Kit

This array enables genetic variation analysis across maize lines. It includes over 50,000 validated markers derived from the B73 corn reference sequence.



For Research Use Only



DNA



Microarray



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DNA

GGP Potato Arrays **12k**

Identify resistance regions with maximum coverage using the GeneSeek Genomic Profiler (GGP) potato microarray. [Read More...](#)

Select Product(s)

[What size kit do I need?](#)

0



GGP Potato-24 v4.0 (48 samples) ⓘ
20044459

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GGP Potato-24 v4.0 (288 samples) ⓘ
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20044821

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Genome-wide association studies (**GWAS**)

1. Genotyping costs have decreased dramatically over the last 10 years, in most species
2. Large number of genotyping experiments
→ explosion of GWAS experiments!

Powerful (*supposedly*) approach to the identification of genes/genomic regions involved in plant, animal and human phenotypes



Genome-wide association studies (**GWAS**)

association is one type of statistical problem

- discovery of interesting relationships among variables in large data sets (i.e., **association**);
- division of data sets into several discrete groups (i.e., **clustering**);
- assignment of observations to groups (i.e., **classification**);
- Extrapolate quantitative outputs based on attributes of observational units (i.e., **prediction**);
- etc.



Inference vs Prediction

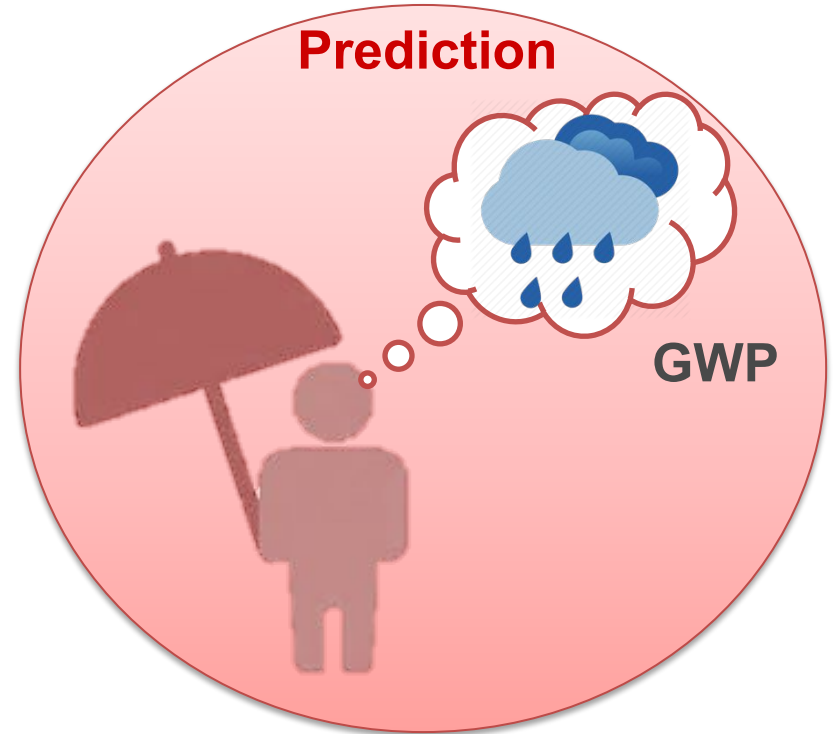
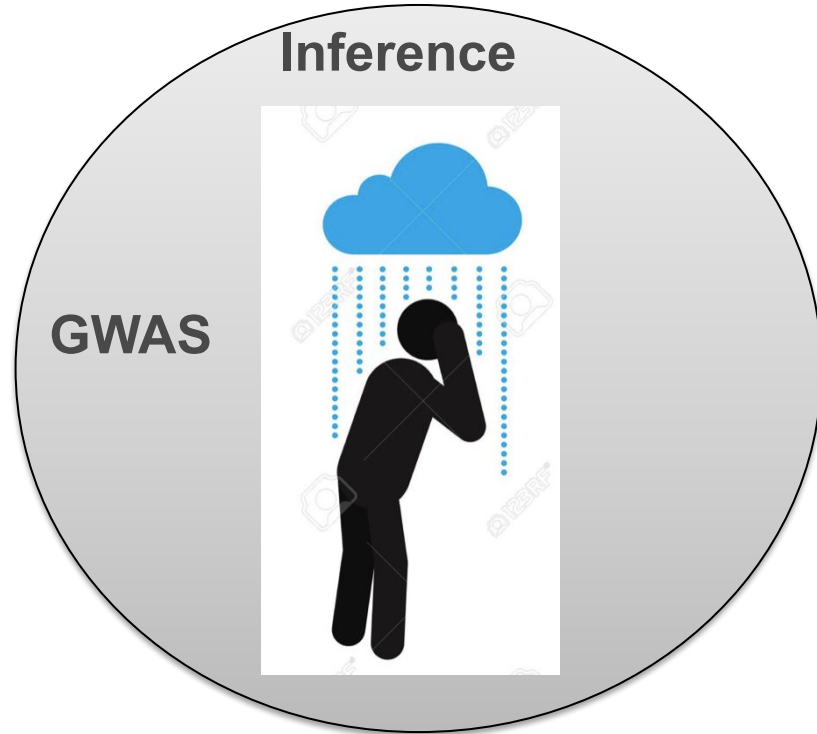
Inference

- Determine the effect of a covariate on the response
- Determine the causal relationship between a covariate and the response (Need specific experimental designs)

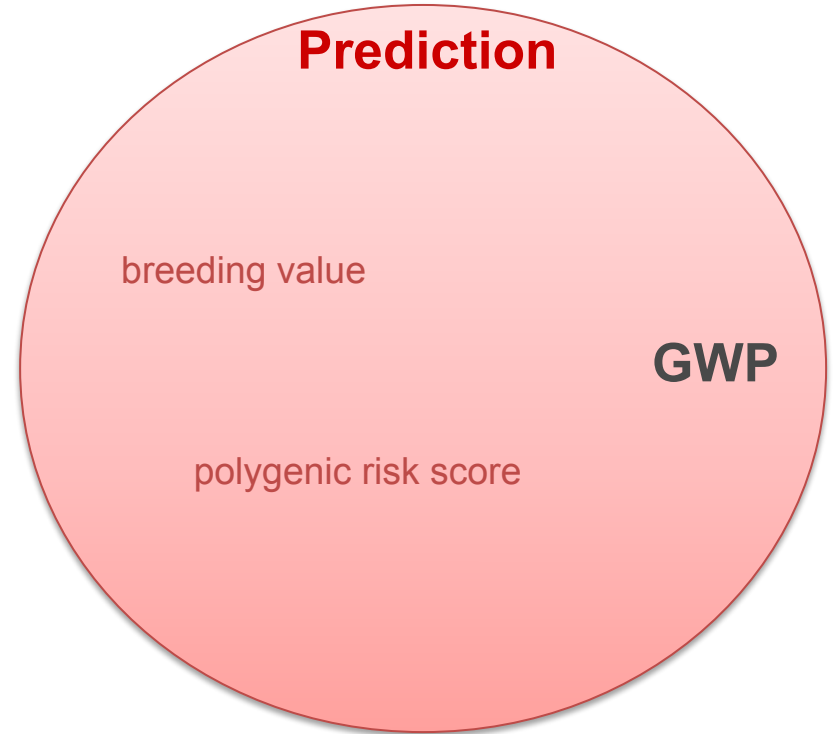
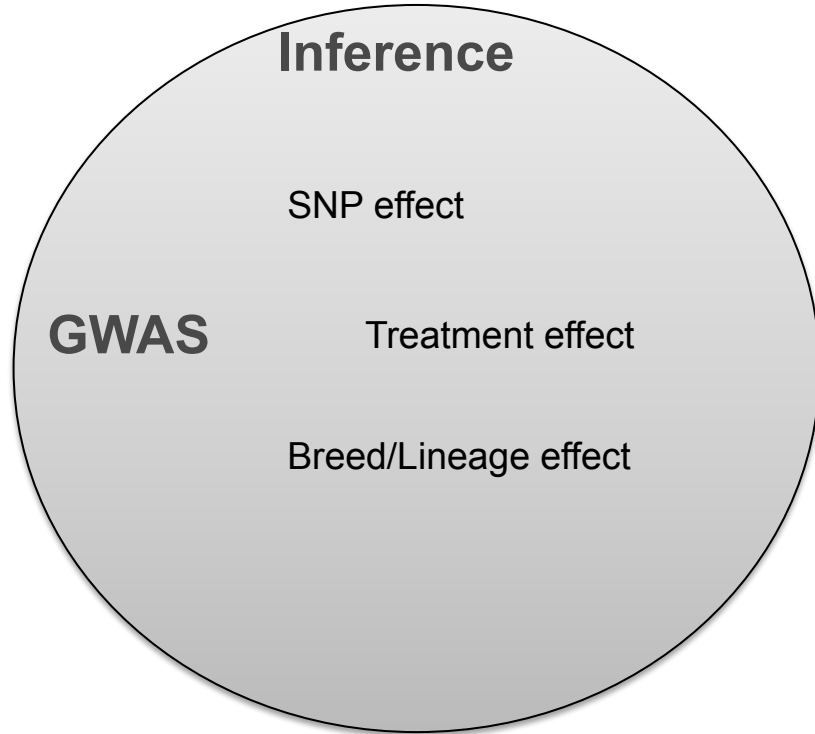
Prediction

- Educated guess of the outcome
- Expected behaviour in the future
- Based on proxies/markers

Inference vs Prediction



Inference vs **Prediction**



Inference vs Prediction



- Know the past
- Predict the future
- Act consequently

INFERENCE

Genetic basis of GWAS-GWP

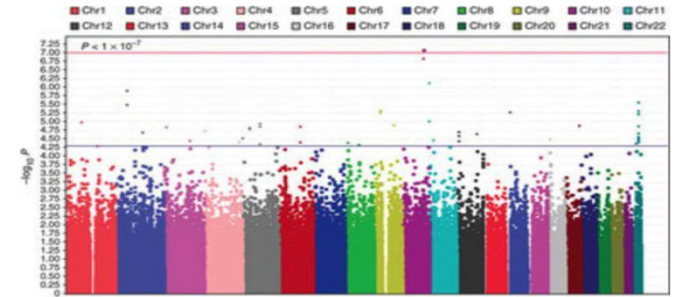
GWAS goal

- Detect genomic markers/regions associated to phenotypes (traits) of interest
- Find biological pathways of interest
- Interaction between treatments/drugs and genes

GWP goal

- Calculate the genomic risk score /predisposition of a disease or trait
- Calculate the genomic merit of individuals
- Predict future performance
- Sire/dam selection in animal breeding

Some examples



GWAS – Rheumatoid arthritis

BMC Proceedings

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Volume 3 Supplement 7

Genetic Analysis Workshop 16

Proceedings | [Open Access](#) | [Published: 15 December 2009](#)

Detecting single-nucleotide polymorphism by single-nucleotide polymorphism interactions in rheumatoid arthritis using a two-step approach with machine learning and a Bayesian threshold least absolute shrinkage and selection operator (LASSO) model

[Oscar González-Recio](#), [Evangelina López de Maturana](#), [Andrés T Vega](#), [Corinne D Engelman](#) ✉ & [Karl W Broman](#)

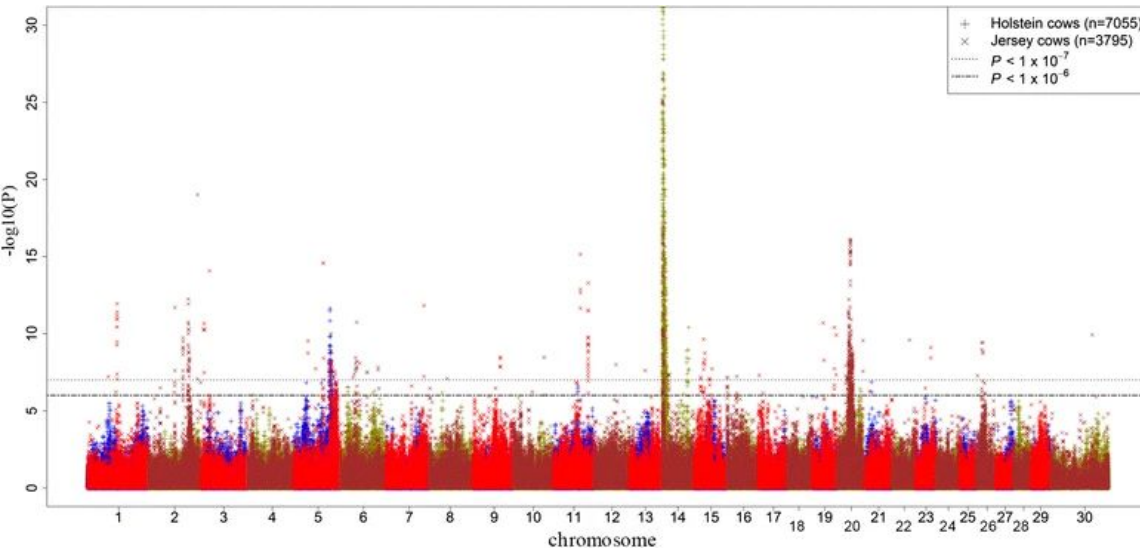
[BMC Proceedings](#) 3, Article number: S63 (2009) | [Cite this article](#)

504 Accesses | 4 Citations

Chrom:	6-HLA REGION						6	1	2	2	6	8	8	9	10	10	12	12	13	14	14	16	17	18	18	19	21
GENE	Class II	unknown	LY6SD	unknown	unknown	unknown	unknown	PTPN22	unknown	CD28	unknown	ZFPM2	PSD3	unknown	WDFY4	unknown	PDE1B	unknown	unknown	RIN3	unknown	GRIN2A	WNT3	DSC3	unknown	unknown	unknown
SNP	rs10484560	rs2395175	rs3749952	rs3763338	rs660895	rs9262632	rs9369550	rs2476601	rs2353317	rs3181096	rs10094729	rs10103119	rs1038848	rs10976357	rs2671682	rs4759005	rs1022232	rs2365675	rs26543	rs12885166	rs234592	rs1875206	rs10514911	rs12455854	rs1389969	rs8104309	rs1041778
HLA REGION	rs10484560			G-G				G-G						G-G			G-T					G-G	G-G				
	rs2395175							G-G						G-G			G-T						G-G			G-T	
	rs3749952								T-A	T-C	T-A								T-A								
	rs3763338																										
	rs660895							A-G																			
	rs9262632											A-A															
Major effect	A			G		T	A				A	A	G		A	T			T	T	C					T	
Previously associated to RA	Yes	Unknown	Yes	Unknown	Unknown	Unknown	Unknown	Yes	Unknown	Yes	Unknown	No	No	Unknown	No	Unknown	No	Unknown	Unknown	Unknown	Unknown	No	Yes	No	Unknown	Unknown	Unknown

RISK FACTOR
Protective factor

GWAS – Milk yield dairy cattle



- **DGAT1** gene on BTA 14 in dairy cows (HOL and JER)
- milk fat content

BMC Genetics

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Research article | [Open Access](#) | Published: 22 July 2015

Validation of markers with non-additive effects on milk yield and fertility in Holstein and Jersey cows

Hassan Aliloo , Jennie E. Pryce, Oscar González-Recio, Benjamin G. Cocks & Ben J. Hayes

BMC Genetics 16, Article number: 89 (2015) | [Cite this article](#)

4154 Accesses | 8 Citations | 3 Altmetric | [Metrics](#)



GWAS – Fertility dairy cattle

A number of **fertility-related** traits
(additive and dominance)

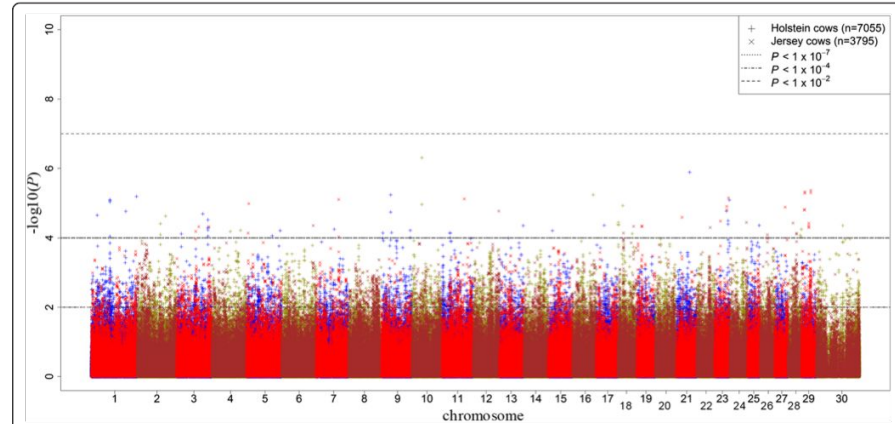


Fig. 4 Distribution of dominance SNP effects for fertility. Manhattan plot of all dominance SNP effects for calving interval in discovery and validation populations with chromosome number on horizontal axis and $-\log_{10}(P\text{-value})$ on vertical axis

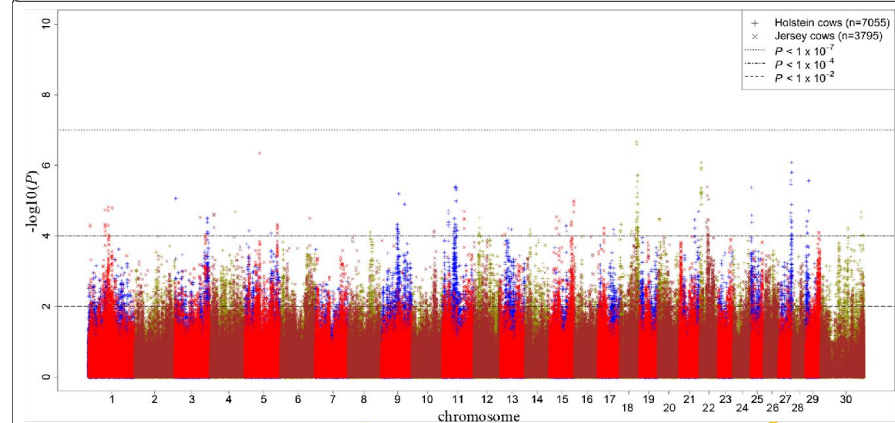


Fig. 2 Distribution of additive SNP effects for fertility. Manhattan plot of all additive SNP effects for calving interval in discovery and validation populations with chromosome number on horizontal axis and $-\log_{10}(P\text{-value})$ on vertical axis

GWAS – curly hair in cattle

naturegenetics

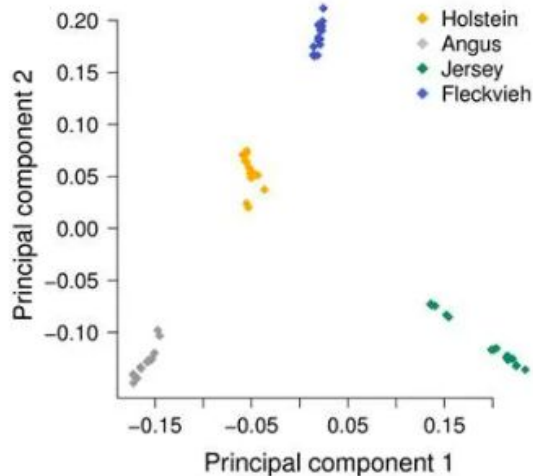
Article | Published: 13 July 2014

Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle

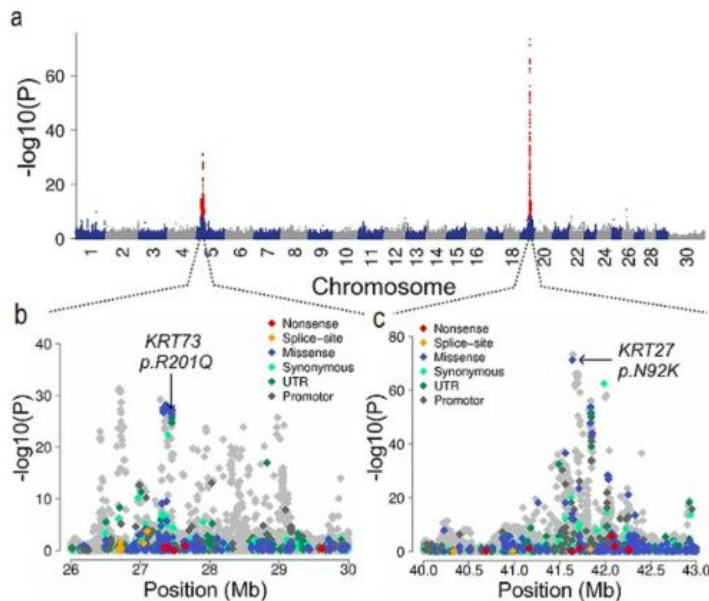
Hans D Daetwyler, Aurélien Capitan, [...] Ben J Hayes

Nature Genetics 46, 858–865(2014) | Cite this article

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From: Whole-genome sequencing of 234 bulls facilitates mapping of monogenic and complex traits in cattle



Manhattan plot showing the association of 17,640,970 imputed variants with the proportion of daughters with curly hair in 3222 Fleckvieh bulls (a). Red dots represent variants with $P < 10^{-9}$. Detailed overview of the associated regions on chromosomes 5 (b) and 19 (c). Variants in the promoter (defined to encompass 1,000 bp upstream of the transcription start), in the untranslated regions (UTR) and in the amino acid coding region are highlighted with different color. The associated region on BTA5 encompasses Krt71, which underlies curly hair in various species. Variant calling yielded four missense mutations in Krt71 (p.R133W, p.F143I, p.N177I, p.P452H); however, none of them was polymorphic in the 43 resequenced Fleckvieh animals. Functional annotation of the variants within the QTL region on BTA5 revealed that 12 closely linked missense mutations in Krt73, Krt2 and Krt76 are highly significantly associated with curly hair in Fleckvieh cattle. Among those, only the p.R201Q mutation in Krt73 (c.G602A, chr. 5: 27,445,800 bp, ss682156288) was predicted to be damaging by PolyPhen-2 and SIFT analysis.

GWAS - Schizophrenia

Molecular
Psychiatry

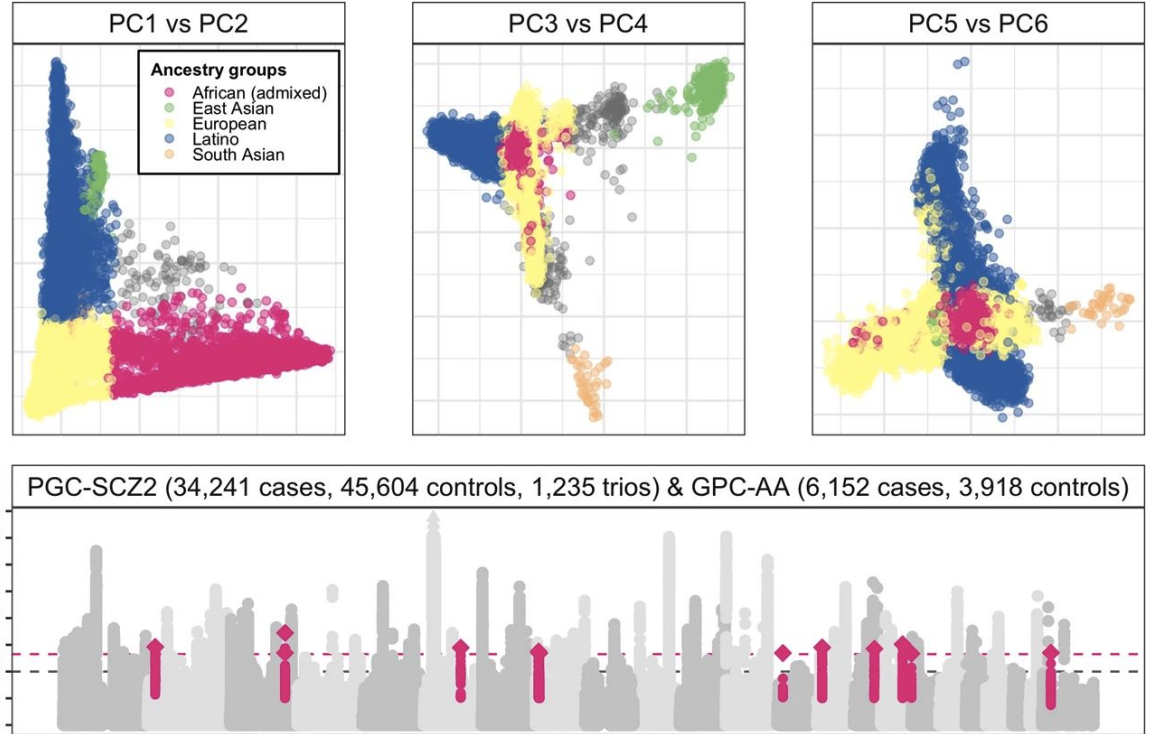
Article | [Open Access](#) | Published: 07 October 2019

Contributions of common genetic variants to risk of schizophrenia among individuals of African and Latino ancestry

Tim B. Bigdeli , Giulio Genovese, [...] Carlos N. Pato

Molecular Psychiatry (2019) | [Cite this article](#)

2537 Accesses | 1 Citations | 63 Altmetric | [Metrics](#)



GWAS - Covid-19

nature

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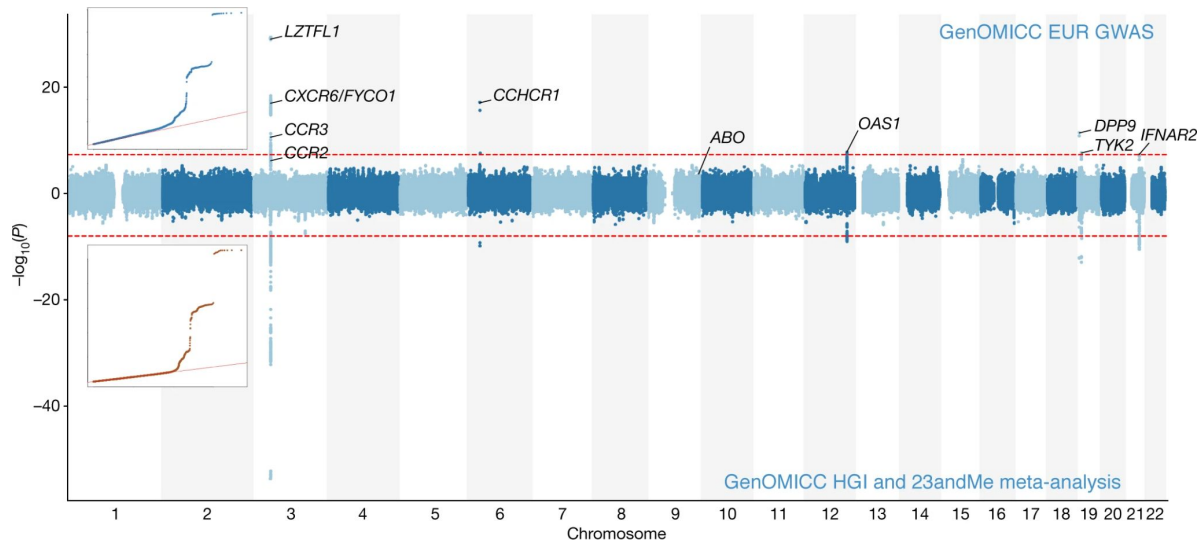
Article | Published: 11 December 2020

Genetic mechanisms of critical illness in COVID-19

Erola Pairo-Castineira, Sara Clohisey, [...] J. Kenneth Baillie [✉](#)

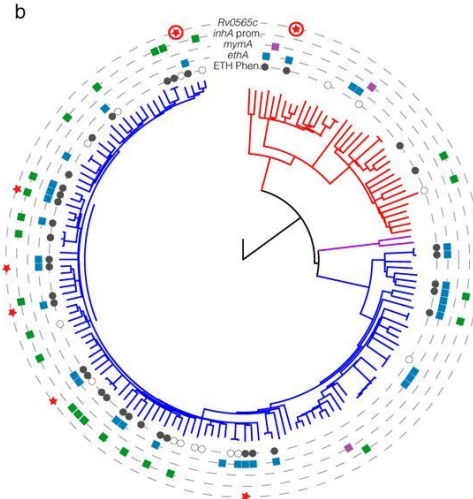
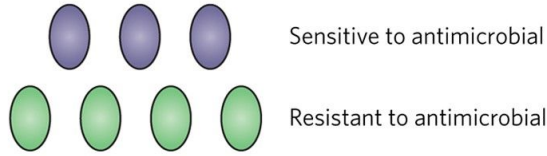
Nature **591**, 92–98 (2021) | [Cite this article](#)

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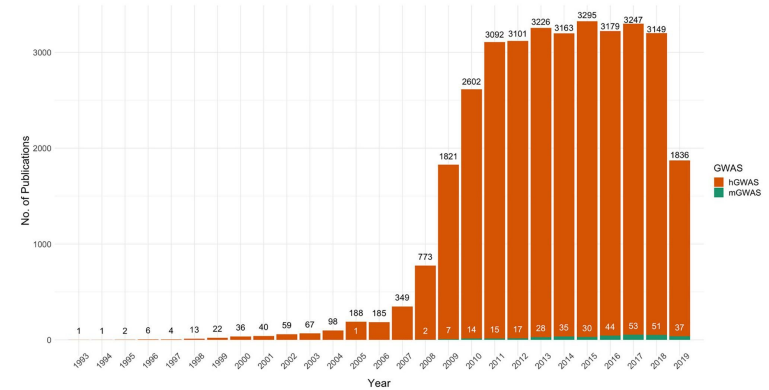


GWAS - bacterial

GWAS in bacteria



Not as popular as human GWAS (hGWAS)



Boosted by WholeGenomeSequencing of bacterial genomes along with phenotypes (e.g. antimicrobial resistance).

GWAS - **bacterial**

Particularities

- Haploid organisms
- Strong population structure (Difficult to find Causal mutation and epistatic effects)
- Great variation of the pan-genome
- Low sample sizes
- Unavailability of SNP-chips (necessary whole-genome sequencing)

Relevant in

- Antibiotic susceptibility
- Susceptibility to disinfectants
- Transmissibility
- Disease presentation/severity
- Carriage duration
- Invasiveness



Doing a GWAS is “easy”



Doing a GWAS is “easy”



Doing a GWAS CORRECTLY is not



What will you **learn**

- How GWAS work
- Use the right type of analyses
- Identify and understand the individual steps involved in a GWAS project
- Understand the limitations of GWAS
- Visualize results of GWAS
- Assemble the different steps into a reproducible pipeline



Regarding GWAS - **what we will do**

0. getting the data
1. data preprocessing (**EDA**)
2. data preprocessing (**filtering**)
3. **imputation** of missing genotype data
4. **GWAS** basic models
5. single SNP vs many SNP
6. continuous/binary traits
7. population structure
8. Manhattan plots/qq-plots (post-hoc analysis)
9. build the **pipeline**



NEXT LECTURE

Introduction to GWAS: Linkage disequilibrium and Linear Regression

