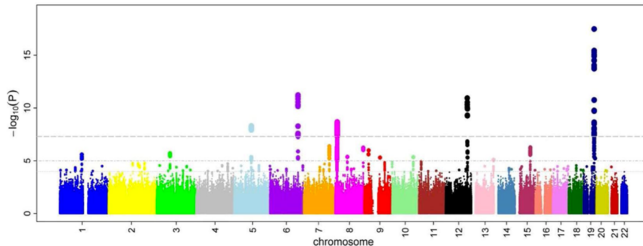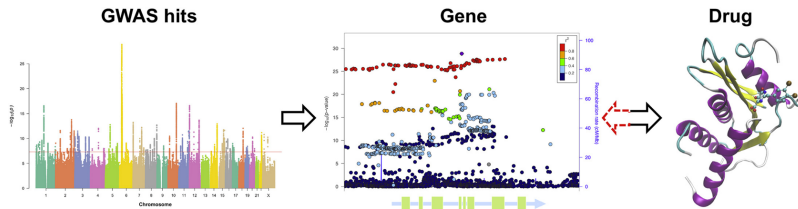# Genome-wide association studies in natural populations: managing expectations and avoiding error

Susan E. Johnston & **Lewis G. Spurgin**

Genome **W**ide **A**ssociation **S**tudy (GWAS)

Experimental design used to detect associations between genetic variants and traits in population samples

Trait	Gene with GWAS hits	Known or candidate drug
Type 2 Diabetes	*SLC30A8/KCNJ11*	ZnT-8 antagonists/Glyburide
Rheumatoid Arthritis	*PADI4/IL6R*	BB-Cl-amidine/Tocilizumab
Ankylosing Spondylitis(AS)	*TNFR1/PTGER4/TYK2*	TNF-inhibitors/NSAIDs/fostamatinib
Psoriasis(Ps)	*IL23A*	Risankizumab
Osteoporosis	*RANKL/ESR1*	Denosumab/Raloxifene and HRT
Schizophrenia	*DRD2*	Anti-psychotics
LDL cholesterol	*HMGCR*	Pravastatin
AS, Ps, Psoriatic Arthritis	*IL12B*	Ustekinumab

1. Geospiza magnirostris.
2. Geospiza parvula.
3. Geospiza fortis.
4. Certhidea olivacea.
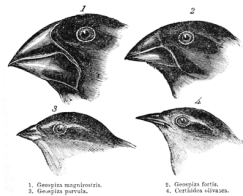
GWAS in natural populations

Example studies (finches, peppered moths etc)

Key factors to consider in GWAS

- Architecture of the trait
- Number of individuals sampled
- Number of genetic markers sampled
- Extent of linkage disequilibrium between sampled markers and causal variants

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Linkage disequilibrium (LD) and GWAS

Why LD is important for GWAS

Linkage disequilibrium (LD) and GWAS

Factors affecting LD

Linkage disequilibrium (LD) and GWAS

LD in natural populations