

The EpiTwin Project

<http://www.epitwin.eu/>

DNA methylation profiles in 5,000 UK Twins

Jordana T. Bell

Department of Twin Research and Genetic Epidemiology, King's College London

Wellcome Trust Centre for Human Genetics, University of Oxford

EpiTwin Aims

DNA methylation whole blood profiles in 5,000 UK Twins using MeDIP-sequencing and Illumina 450K arrays.

1. DNA methylation changes in common complex disease
2. Heritability of DNA methylation, methylation QTLs
3. Environmental effects on DNA methylation

Collaborative projects[§]:

4. Methylation patterns in different tissues
5. Integration of multi-level functional genomic data

[§] Partly in collaboration with the MuTHER (<http://www.muther.ac.uk>) and the EU Eurobats projects (<http://www.twin-research.ac.uk/projects/eurobats.html>)

Advantages of the study design

- **TWINS**

- Disease-discordant MZ twins & combined analyses of unrelated and related individuals.
- **MZ twins**: no cohort/age- & maternal effects, similar environments, identical genetic influences on latent epigenetic factors.
- Twin- and family-based epigenetic heritability estimate

- **Phenotype & genotype data resources**

- Deeply **phenotyped** cohort, where the majority of sample will have **DNA sequence** data available as well.

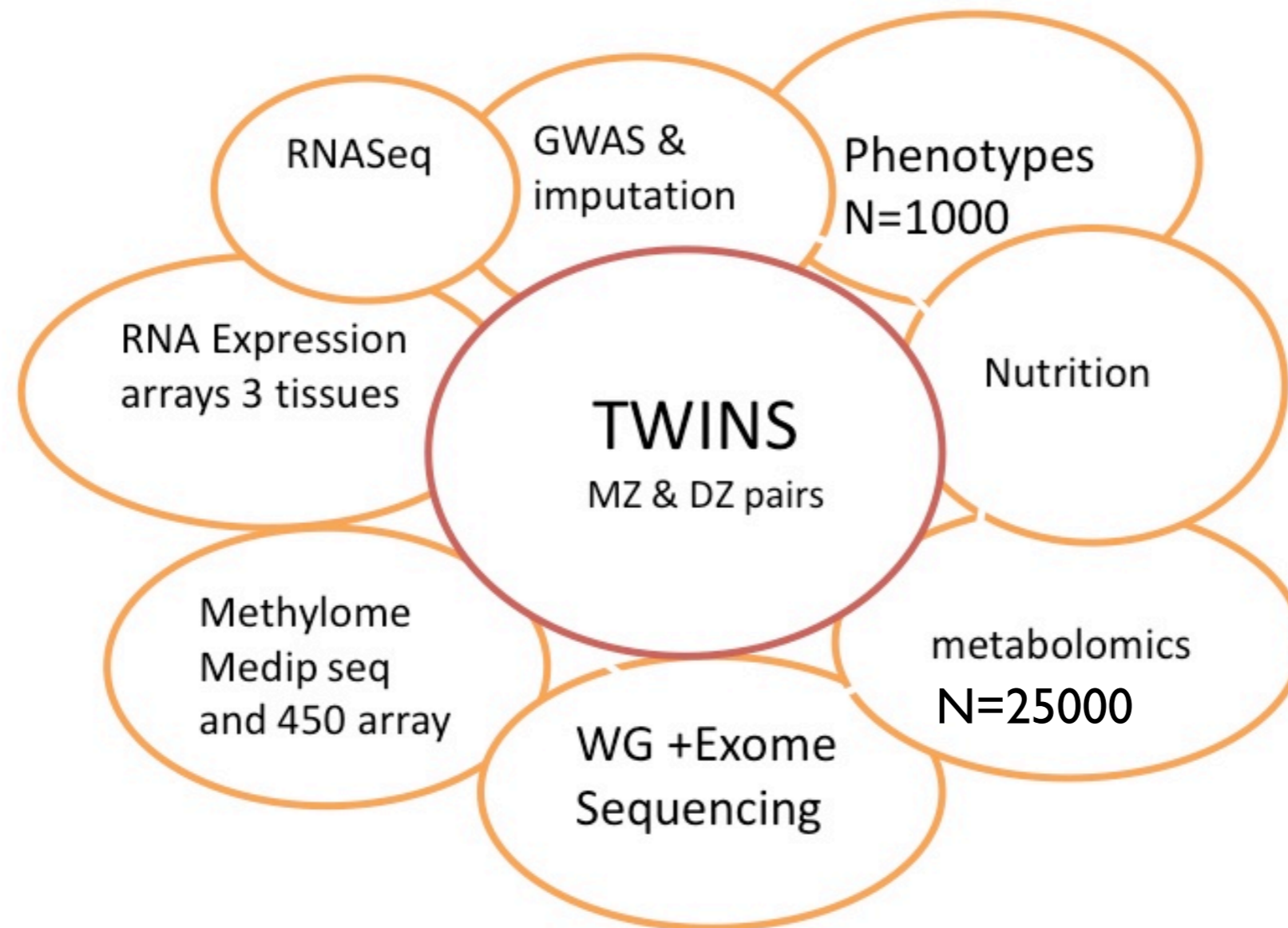
- **Longitudinal** data and samples available

Challenges

- Sample availability / storage for multiple functional genomic assays
- Computational burden of storing and processing MeDIP-sequencing data
- Tissue source
- Trade-off between cost, coverage, & precision of methylation assays

Future plans:

Integrating EpiTwin + On-going projects = A complete 'omics' resource



EpiTwin project

Partners and Collaborators

Dept Twin Research, KCL, UK

Tim Spector (PI)

Jordana Bell

Kirsten Ward

Pei-Chien Tsai



BGI, China

Jun Wang

Ning Li, Ryan Liu, Yunjie Wang, Pingbo Zhang



Wellcome Trust Sanger Institute, UK

Panos Deloukas



Murdoch Childrens Research Institute, Australia

Jeff Craig & Richard Saffery

