



A novel family-based
sequencing approach
and dissection of
regulatory networks
underlying a colour
polymorphism

Project Team



University of Jyväskylä

- **Johanna Mappes**
- **Juan Galarza**
- **Melanie Brien**
- Elisa Salmivirta
- Sari Viinikainen
- Kaisa Suisto



UNIVERSITY OF JYVÄSKYLÄ



University of Cambridge

- **Chris Jiggins**
- **Anna Orteu**
- Charley Yen



UNIVERSITY OF
CAMBRIDGE

Wellcome Sanger Institute

- Richard Durbin



Genomics in non-model organisms

We need genome assemblies to answer evolutionary questions

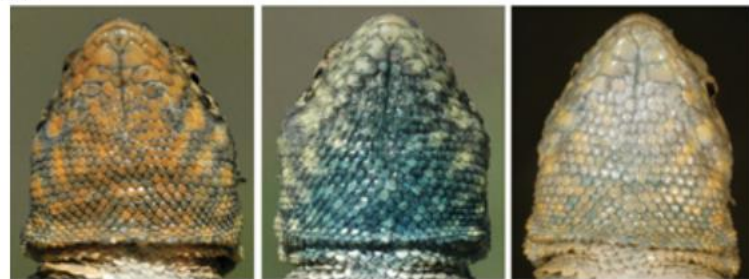
Around 80 Lepidoptera genomes currently available



Colour polymorphism



A



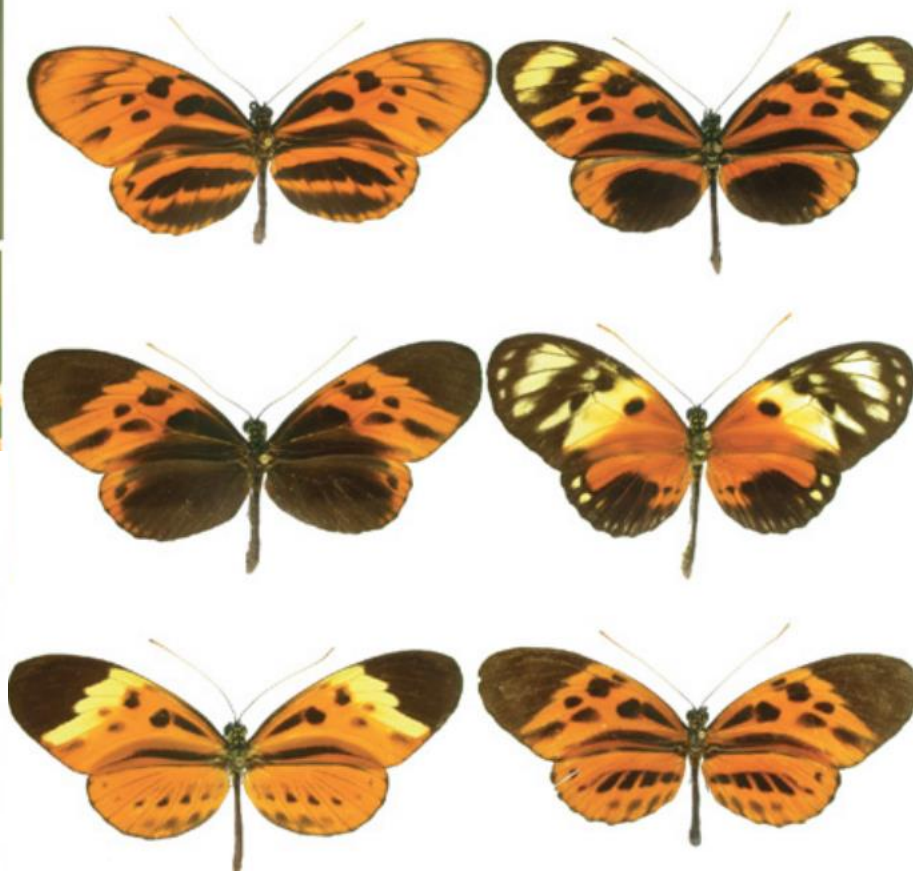
B



D



E



A



B



C



D



Wood tiger moth, *Arctia plantaginis*



WW or WY

White and Yellow colour morphs

Three genotypes



YY

Male hindwing colour correlated with behaviour and life history traits

Aims

Develop

Develop methods for
genome assembly

Determine

Determine the genetic basis
of the colour polymorphism

Identify

Identify gene regulatory
elements underlying the
polymorphism

Aims

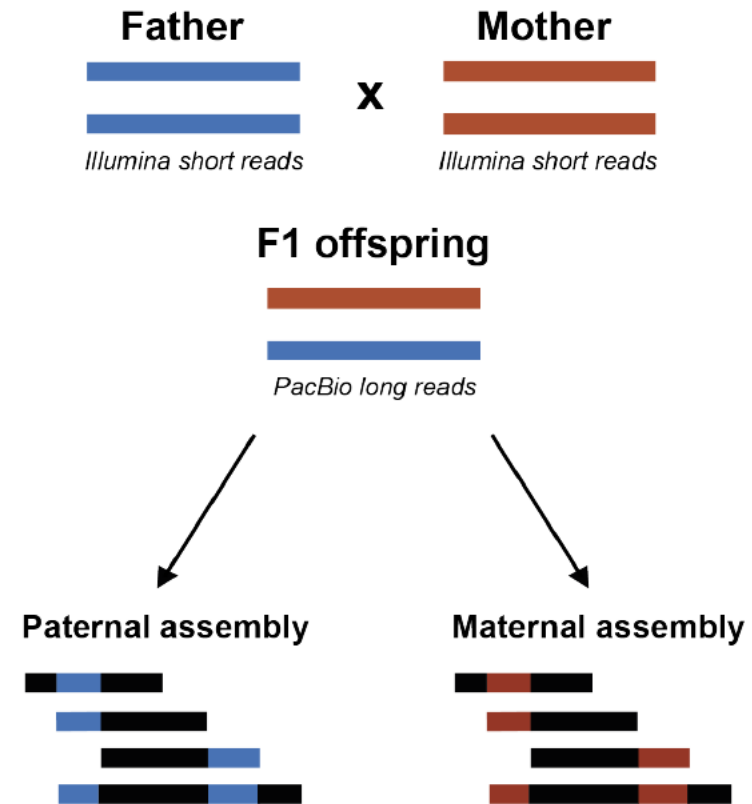


Develop

Develop methods for genome
assembly

Genome assembly

Trio Binning method
produced two reference
genomes, one for White and
one for Yellow



Genome quality

Measure of assembly
quality



	Assembly size (Mb)	Scaffold Count	Longest Scaffold (Mb)	N50 (Mb)	BUSCO
<i>Bombyx mori</i>	482	696	21.5	16.8	98.4 %
<i>Heliconius melpomene</i>	275	332	18.1	14.3	98.7%
Tiger moth White	585	1071	21.5	6.7	98.1%
Tiger moth Yellow	578	1052	24.2	9.8	96.4%

Genes expected to be present at >90%



Aims

Develop

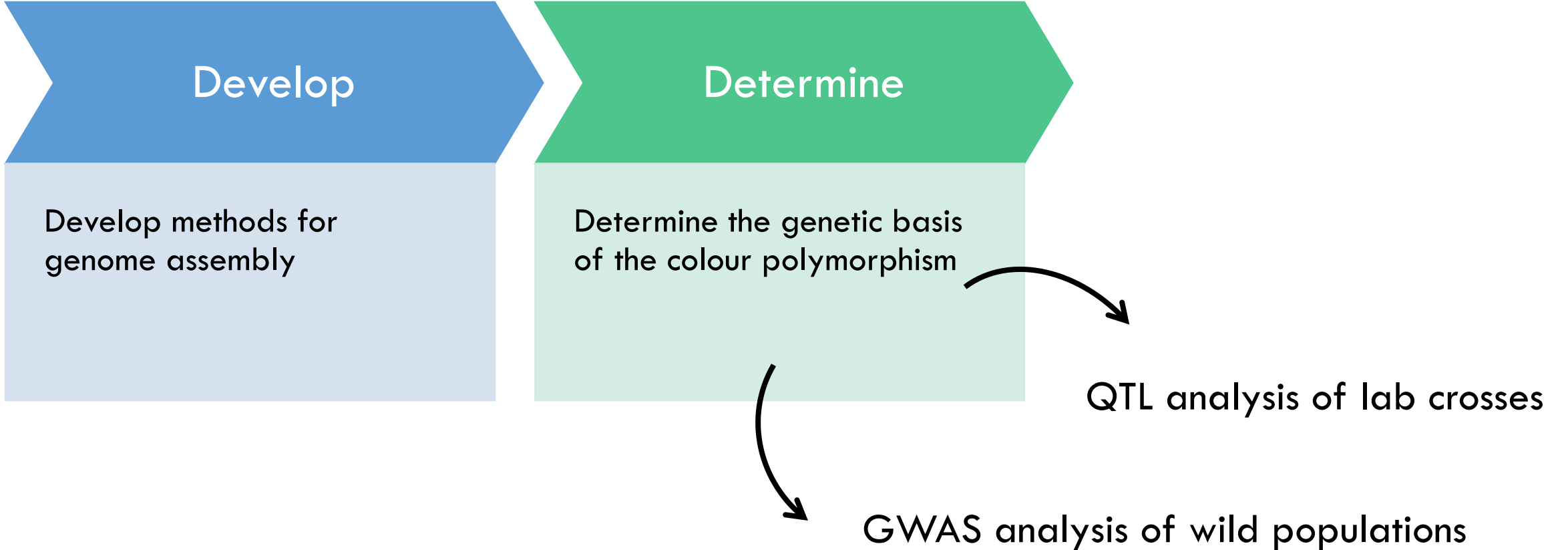
Develop methods for
genome assembly

Determine

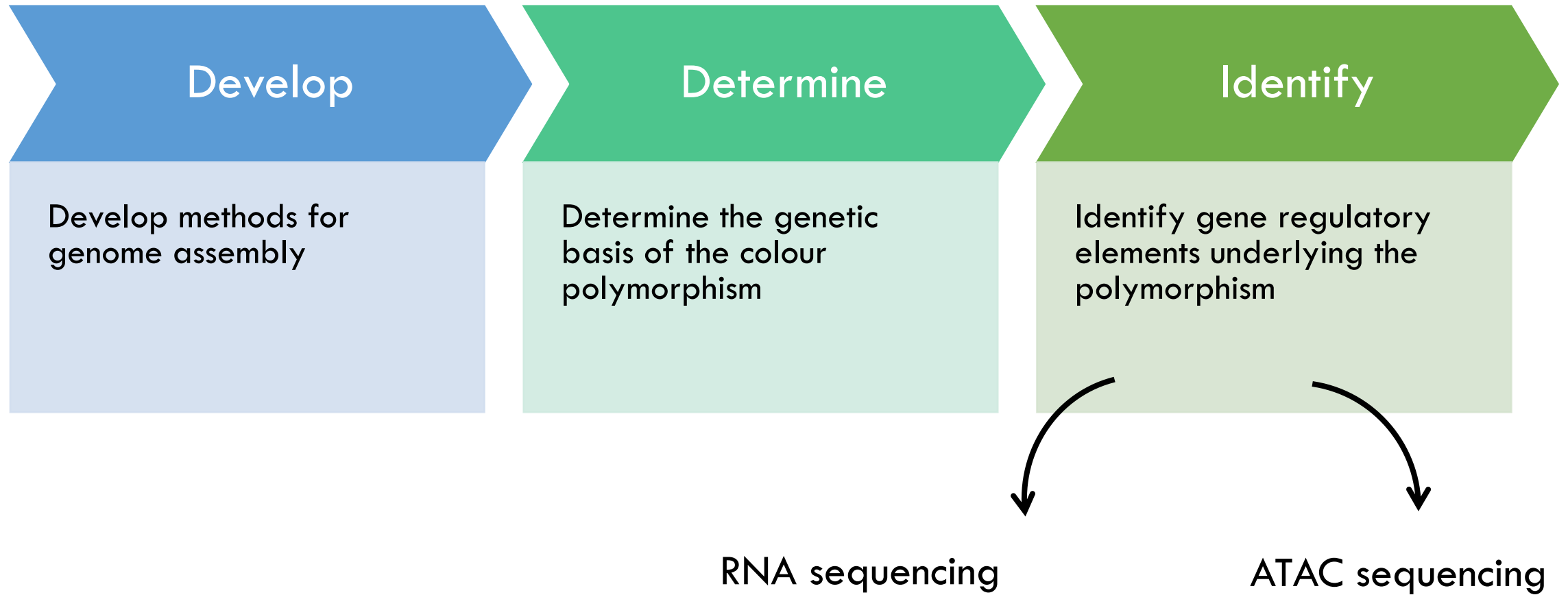
Determine the genetic basis
of the colour polymorphism

QTL analysis of lab crosses

GWAS analysis of wild populations



Aims





Summary

High quality genome assembly produced
using novel approach

Used to uncover the genetic basis of a
colour polymorphism

Thank you!