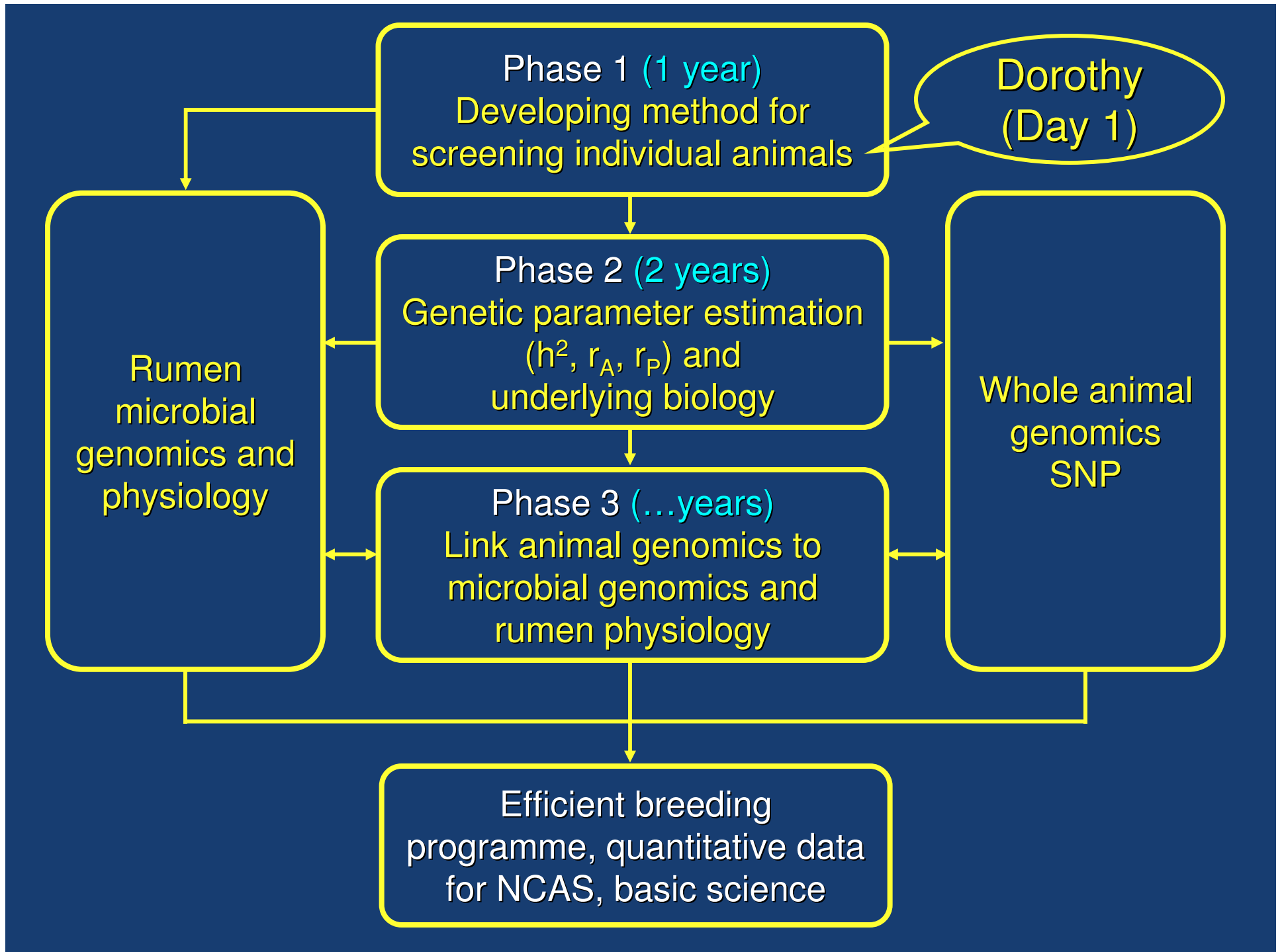


# MLA\_DAFF (Sheep CRC)

“Breeding low methane sheep and understanding the biology behind how they do it”

# DAFF\_MLA (Sheep CRC)

- 3 Phases - overview
- Phase 2 - current MLA\_DAFF project
  - Specific objectives
  - Key resources and approach
- Phase 3



Phase 1 (1 year)  
Developing method for  
screening individual animals

Phase 2 (2 years)  
Genetic parameter estimation  
( $h^2$ ,  $r_A$ ,  $r_P$ ) and  
underlying biology

Phase 3 (...years)  
Link animal genomics to  
microbial genomics and  
rumen physiology

Rumen  
microbial  
genomics and  
physiology

Whole animal  
genomics  
SNP

Efficient breeding  
programme, quantitative data  
for NCAS, basic science

# MLA\_DAFF Breeding

## Objectives (Phase 2)

- Estimate genetic parameters ( $h^2$ ,  $r_P$ ,  $r_A$ )
- Preliminary understanding of the biology behind the genetic differences

# Estimating genetic parameters

- Measurements on individuals - highly variable
- Difficulty ranking animals
- Similar to faecal worm egg count (Greeff)
  - low repeatability
  - sires progeny tested
  - heritability estimate (0.25)
  - selecting using EBV successful
- Use family averages

# Estimating genetic parameters

Using family averages

Need large progeny groups from individual sires

Year 1 - Central Test Sire Evaluation Scheme

Year 2 - Sheep CRC Information Nucleus Flock

# Central Test Sire Evaluation - Year 1

- Industry sires progeny tested for a range of production traits (emphasis on wool)
- 14 different test sites across the country (different environments)
- Sires mated to 60 ewes, 40 progeny per sire
- Managed in one group

# Central Test Sire Evaluation - Year 1

- Screen 3 sites
  - 500 animals per site
  - 10-20 sires, 30-40 progeny per sire
- Validate in chambers and NFI
  - Top and bottom 2 families at each site
  - 12 animals per family (chambers, NFI)
  - Rumen samples taken (blood)

# Central Test Sire Evaluation - Year 1

## Outcomes - Year 1

- Heritability estimate for methane production
- Phenotypic and genetic correlations with other production traits
- Validation and comparison of NFI and microbial profiles
- Quantitative information for modelling/NCAS

# Information Nucleus Flock - Year 2

- 8 flocks of ewes (5 sub-flocks)
- Different environments
- Total 5000 ewes, 100 sires annually for 5 years
- Maternal and terminal breeds
- Sheep Genetics
- Objectives
  - Diverse range of phenotypes and genetic information
  - Develop new and improved breeding values
  - Validation of molecular markers

# Information Nucleus Flock - Year 2

## What's measured?

- growth, carcass, meat, wool, reproduction and parasite-related traits
  - Xbred lambs grown out and slaughtered
  - MxM evaluated wool traits and wethers slaughtered for carcass and meat evaluation
  - MxM and BLxM ewes retained, mated naturally to evaluate reproduction traits
- Blood and tissue samples for genotyping and molecular genetic studies

# Information Nucleus Flock - Year 2

## Year 2

- Screen INF - 3 sites (NSW, Vic, WA)
  - Potentially 5000 animals (2007-2010)
  - NFI on 2010 (1500 animals)
- Validation in chambers and NFI
  - Animals at the extremes validated in chambers and rumen samples taken
- Blood/tissue samples taken routinely (INF)

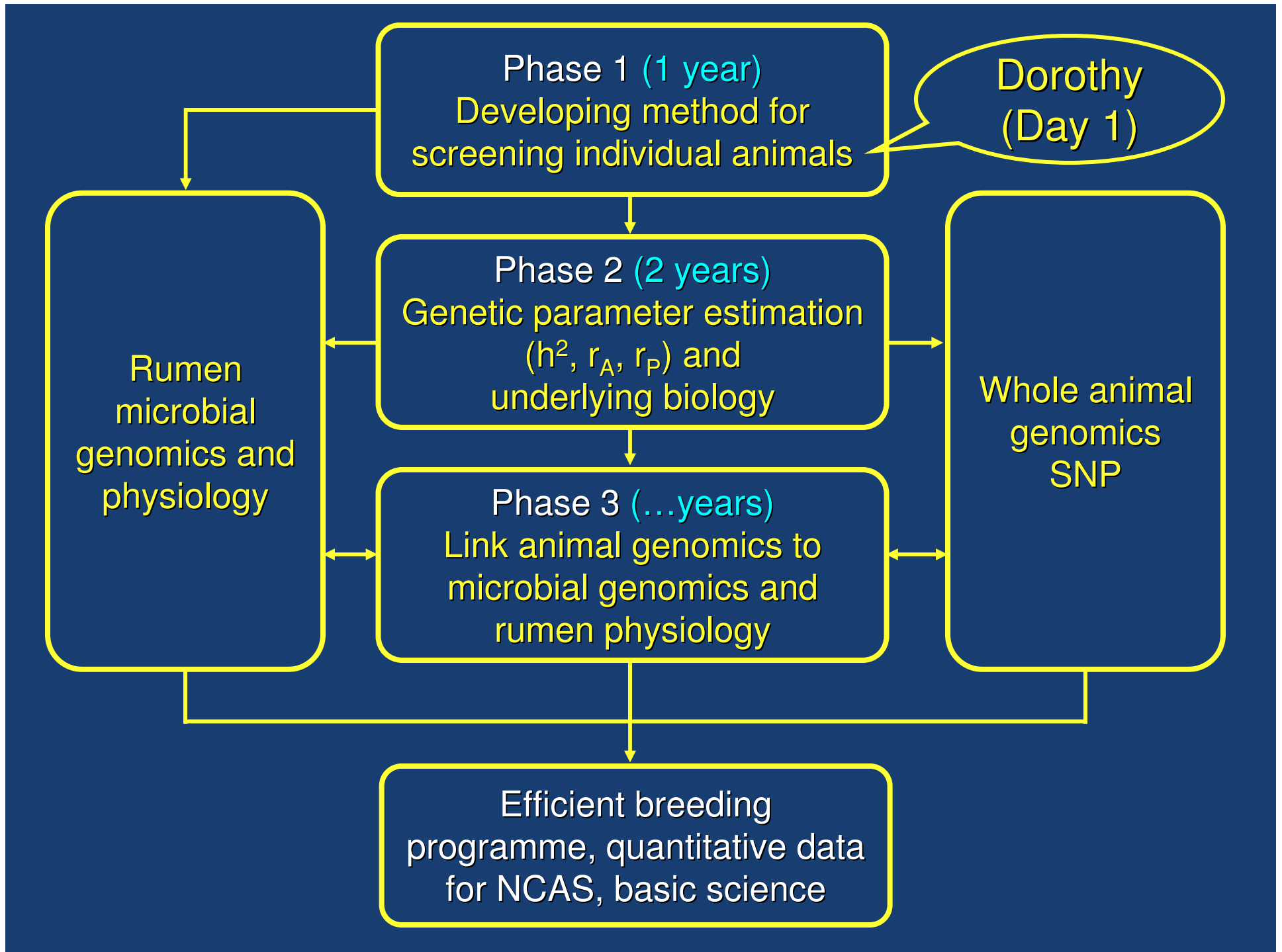
# Information Nucleus Flock - Year 2

## Outcomes - Year 2

- Initial ASBV for methane production
- $r_A$  and  $r_P$  correlations estimated for broader production and fitness traits
- Microbial profiles (fermentation patterns) compared and associated with other traits
- Quantitative information for modelling/NCAS activities
- Plan for Phase 3

# Planning for Phase 3

- Decide on best way to tackle underlying biology
  - Microbial profiling
  - Molecular genetics/SNP analysis
  - Linking the two
- Selection lines or INF resource?
- In-field monitoring - are we making a difference at the flock/paddock scale



# Objective 1

Estimate genetic parameters for methane production from sheep

- Heritability
- Correlations with other production traits

Identify the most practical/cost effective way to reduce methane/output