

New Zealand plans for sheep genetics research for GHG mitigation

JC McEwan, Ken Dodds & C Pinares

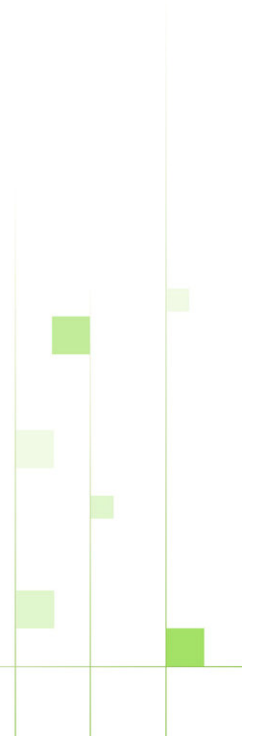
Background

Need to determine genetic parameters for NZ sheep

- Methane production
- Feed intake
- Efficiency
- Relationship with existing traits

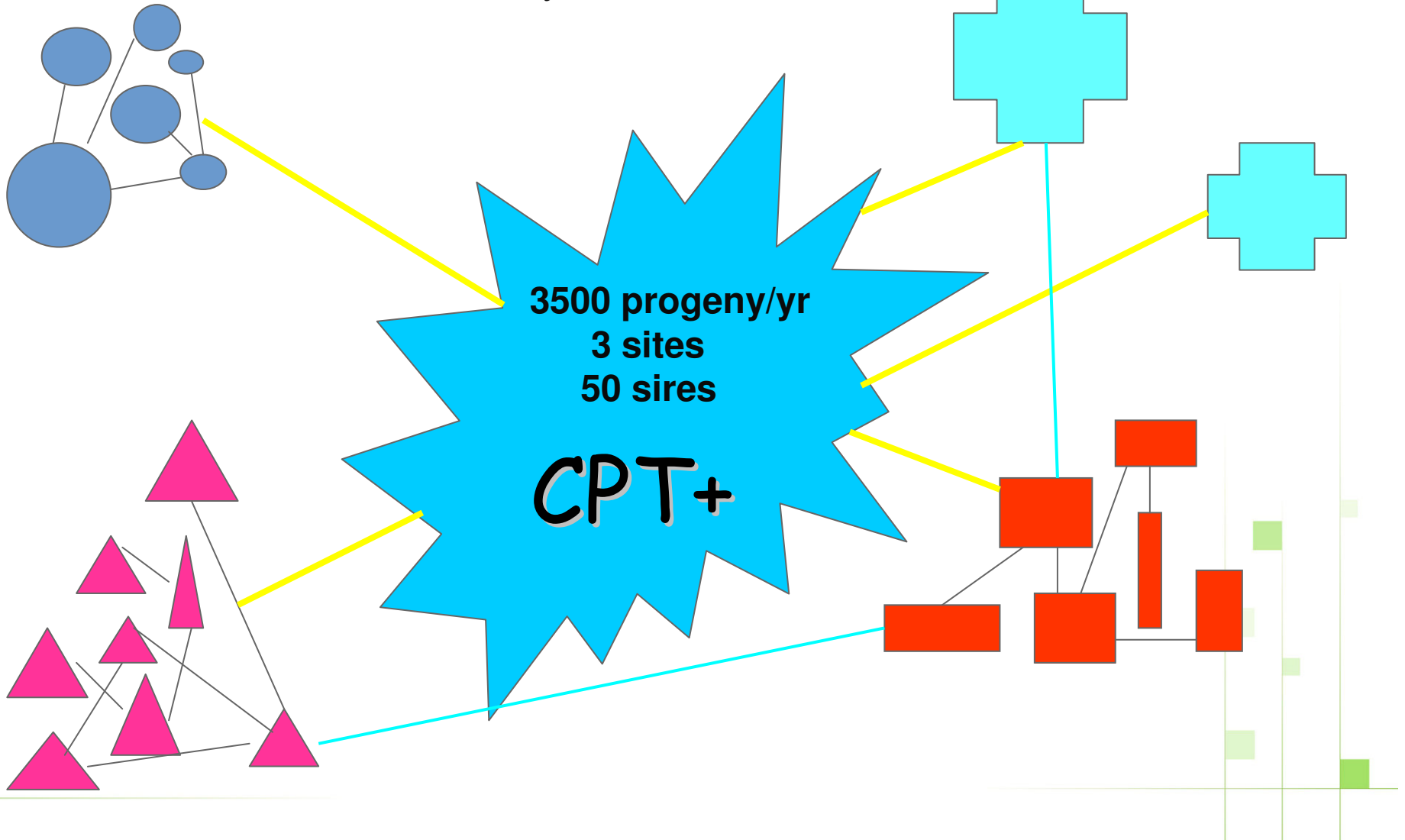
To reduce costs ... need to better use existing resources

- Central Progeny Test
- Woodlands Coopworth progeny test
- Both industry linked and largest long standing existing genetic research flocks



Across flock, breed and year analysis (genetic links/common sires)

ACE analysis >2.6M animals



Traits

Liveweights

Wool weight

NLB

Lamb survival

Parasites

FE

Ultrasound

Meat quality

Meat yield

Feed intake

GHG.....

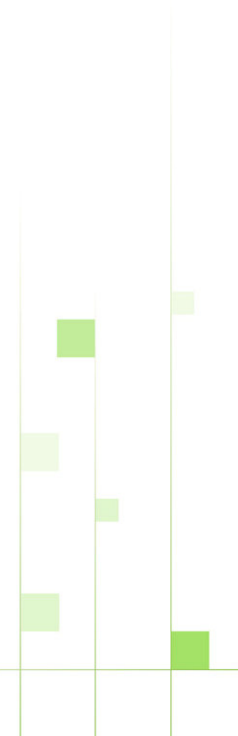
CPT ~70 prog/sire

Issues trait definition



Central Progeny Test

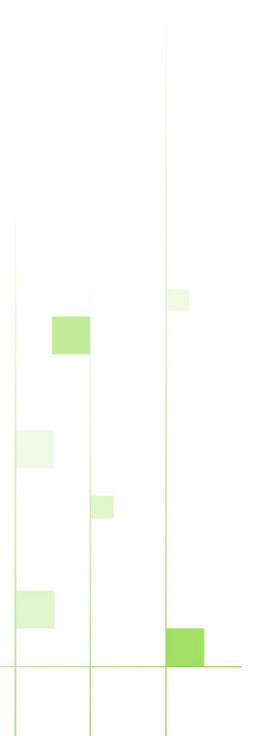
- CPT only need to add methane & feed intake measurements.
 - Several hundred to 1000 animals per year?
 - Different numbers for intake and methane?
 - How many measurements? 1 maybe 2.
- Feed intake needs added even if CH₄ cannot be
 - CH₄ still has to be monitored in some way
- Provides BVs for key sires and near relatives immediately
- Design changes in CPT? More sires and fewer progeny/sire?
- Are there other “predictor traits” or samples to be collected?



Genome Wide Selection

Whole genome selection works on the basis of “guilt by association”

- 30-300K SNPs tested across the genome of an animal
- Test on 1000-4000 animals recorded for trait(s) of interest
- Derive prediction equations of genetic worth
 - Need independent validation resource (progeny)
 - Expect $r \sim 0.4-0.6$
 - Needs updated (incrementally and annually)
- Could use CPT and WCPT results



What is a SNP and what is a SNP chip?

SNP = single nucleotide polymorphism

SNP chip = test 60,000 to 1,000,000 SNPs

WGS works by being able to:

- predict status of other SNP variants nearby
- includes variants that affect production traits

MELD	atcgcgtgtagct	agtgctagctgctagctagctgatgca
ROM1_read12667	t.....
AWA1_read00345
SBF1_read06734
TEX1_read00234	t.....
ROM1_read10385	t.....
TEX1_read39890



What GWS benefits?

$$\Delta G = h^2 * i^* \sigma_p / L$$

Can test many more animals than can measure (\$ and practicality)

- Greater accuracy & selection pressure

Often more accurate than indirect indicators aka correlated traits

- Greater accuracy

Can measure at a younger age (reduce generation interval)

- Reduce generation interval
- i.e. use rams at 1 yr of age not 2 yrs of age

Faster and more effective genetic gain



GWS Implementation

Use the CPT animals

- Progeny of leading industry sires
- Already collecting DNA

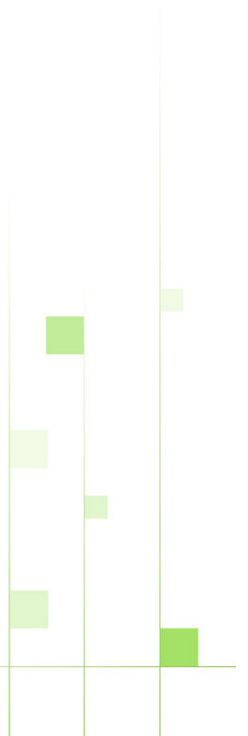
Issue of predictive ability across breeds

- May force minor design changes
- How many measurements? Costs and benefits?

Implementation via selected SNPs on stud ram progeny

Results would be BVs for new traits

Transparent implementation into existing SIL system



Implementation: possible NZ sheep system



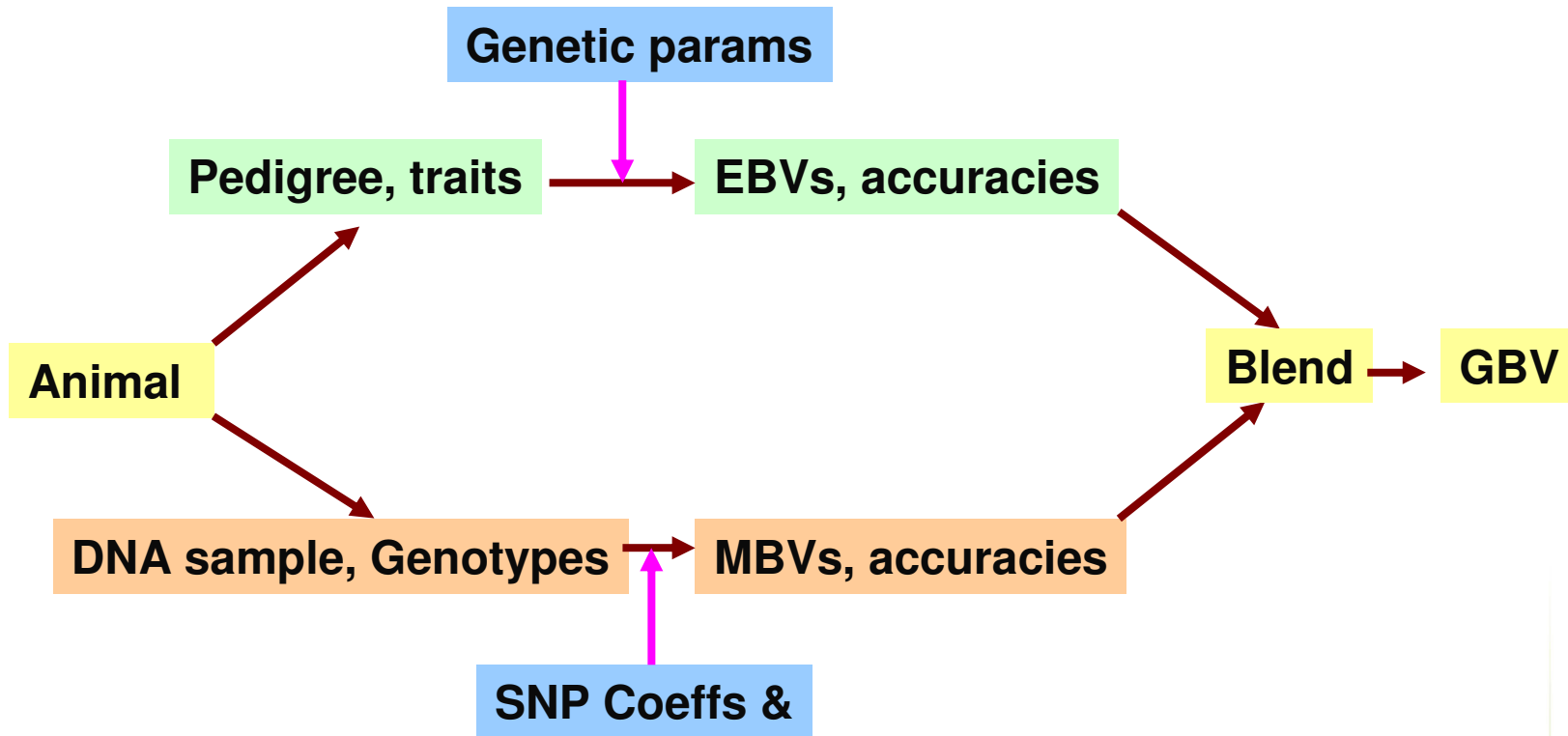
	Stud sires		Stud ewe		Commercial ewes
	2500	SNP Key	250,000		20,000,000
Select	1000	→	70,000	→	
SNPs	60K		50-1600		
Cost	\$400		\$60		
\$/ewe	\$0.02		\$0.21		

The first 2 steps process can potentially increase the genetic gain

break even is less than a 15% increase in genetic gain

Genotyping cost ↓ rapidly: same for less or more for the same price

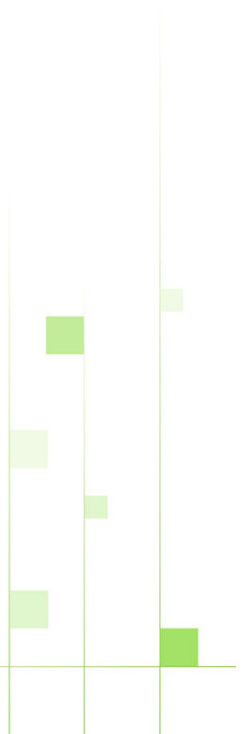
Data Flow



Other required research

Need to have mobs of high and low emitters for detailed studies

- Understanding mechanism
 - Better indirect predictors
 - Alternate methane mitigation methods
- Measuring related trait changes: economically important, but not commonly measured
- Stability across ages, feed types and metabolic status
- Examples include:
 - differences in rumen microbial populations
 - Differences in host VFA metabolism
 -
- Essential before widespread industry adoption



High and low emitter selection lines

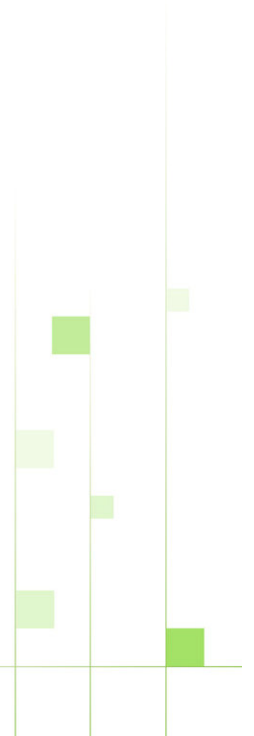
Select & retain phenotypic extremes CPT (male and female)

Breed them

Create small selection lines

Use progeny for studies while retaining and selecting lines

- ~60 males and 30 females per year/line



Selection Line Proposal

Screen 100 males and 200 females from CPT for 2 years

Retain best 5 sires and 50 ewes per year

Create divergent lines with 100 ewes and then breed and measure and select progeny.

Initial line differences =7% and then ~2%/yr

Objective obtain progeny differ genetically 20% CH₄ prod



Is it worth it?



Current genetic gain	~\$0.90/yr
Potential genetic gain	~\$1.40/yr
Potential GWS gain	>\$2.00/yr?

Potential methane reduction

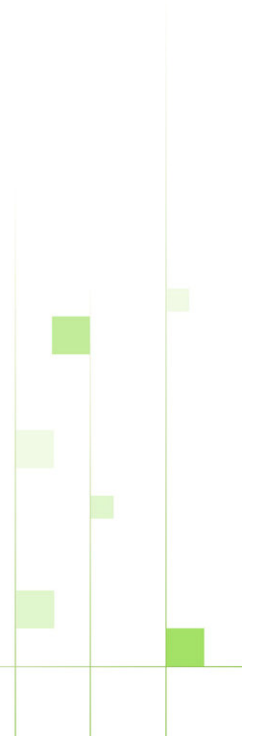
- direct ~\$0.13/yr
- via intake reduction ~\$0.20/yr
- ~70% max via Prod Index ~\$0.24/yr

Potential value intake reduction

- ~70%max via prod index ~0.63/yr

GHG could contribute significantly genetic gain

- assumed implemented via GWS
- also major indirect benefits via reduced feed costs
- actual \$ needs genetic estimates and detailed modelling



Summary

Use the CPT & WCPT for animal resource to reduce costs

- Uses leading industry animals

Direct application via WGS and SIL

Concurrently from same animals create selection lines

- detailed studies

Crude estimates adds value to existing \$ NZ genetic index

Also have indirect benefits via reduced feed costs

Needs full costing and likely benefits with detailed research plan



Assumptions

GHG \$/tonne CO2	25	Lf	3.5
Kg CH4/kg intake	0.019	Lm	2.0
Intake kg/ewe wintered	970	LW%	150
GHG \$/ewe/yr	10.60	Mate ratio	1/100
		Male select (p)	0.013
CH4/kgDMI		<i>im</i>	2.377
CV%	10	Fem select (p)	0.333
h2	0.2	<i>f</i>	1.097
r	0.25		
RFI			
CV%	7.8		
h2	0.39		
\$/kg DM intake	0.048		

