

Emerging traits of economic importance

Feed Efficiency

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Key questions

- Is feed efficiency sufficiently important?
- Can we make progress in it?
- How do we approach it?
 - What is phenotype we want?
 - Is it different in beef and dairy cattle?
 - Could there be negative associated effects?

Definition of feed efficiency

Feed conversion efficiency =
Feed intake / weight gain

Limitations:

Selection for FCE tends to lead to bigger animals

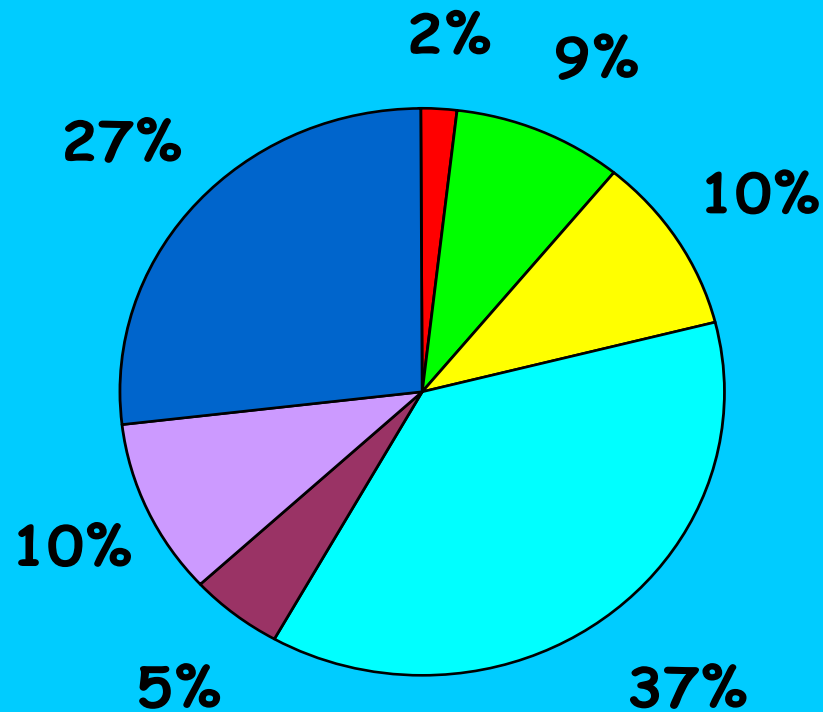
Residual feed intake

- Tries to account for both maintenance and productive use of energy
- RFI = difference between actual feed intake and the expected feed requirements for maintenance and production

Calculating RFI

No.	Weight (kg)	Weight gain (kg/d)	Total NE req (UFL/d)	Total DMI req. (kg/d)	Actual DMI (kg/d)	RFI
1	400	1.0	8.5	8.1	8.0	-0.1
2	450	0.9	8.3	7.9	9.0	1.1
3	440	1.2	9.2	8.8	8.5	-0.3

Physiological mechanisms



■ feeding pattern

■ heat increment of fermentation

■ digestibility

■ protein turnover, tissue metabolism & stress

■ body composition

■ activity

■ other

Why feed efficiency?

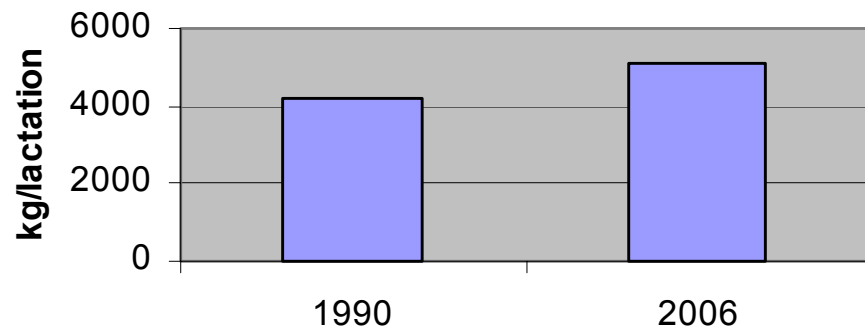
- Feed is an important cost in animal production
- Important for reducing environmental footprint
- Important for food production
 - 2 kg feed to produce 1 kg pork
 - 10 kg feed to produce 1 kg beef
 - 3 kg feed to produce 1 kg milk solids

Can we make progress?

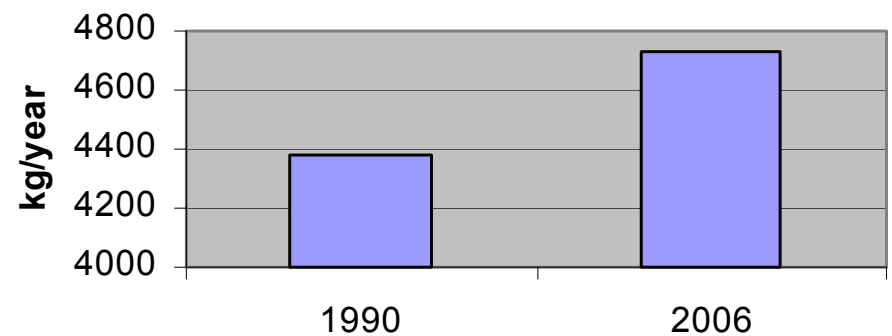
- Has been significant progress in the trait in other species – pig, poultry
- RFI is moderately heritable (0.46; Crowley et al., submitted)
- Significant effort and progress in some other countries
 - Australia, Canada, New Zealand/Australia
- Molecular genetic progress now gives us a powerful additional tool

Conventional animal breeding has delivered to date

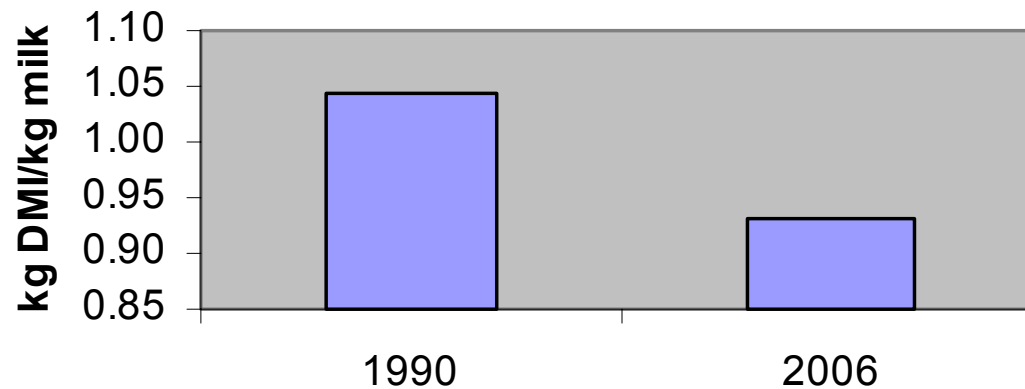
Yield



DMI



FCE



Is there additional progress possible in biological feed conversion efficiency?

- Are some animals more efficient metabolically at using nutrients?
- Are some animals more efficient digesters of feed, or loose less in methane?
- Do some animals expend more energy moving, eating, etc, than others?
- Residual feed intake tries to capture this.

Australian/Canadian beef experience

- Have made progress in selecting for RFI, especially in Australia
- Significant difficulty in measuring feed intake on a large scale, so difficult to do at a population level
- EBV's on some bulls in Australia based on own performance

Australian/NZ dairy experiment

- 2,000 heifers
- Intake measured at weaner stage in research facility
- RFI calculated on basis of intake and weight gain
- High and low RFI animals identified. Look for SNP's associated with the trait and these genetic markers then used in national breeding programme
- Watch for negative associated traits

Irish resources

- Suckler cow herd (60 cows) selected for divergent RFI at Grange
- Beef heifers (50) selected for divergent RFI at UCD Lyons
- Large database of intake and milk production of cows at Moorepark over many years
 - Could we get a feed efficiency trait from these data?

Problem

- Small numbers of animals with good data
- The measurements discussed so far all involve estimating feed intake, which is difficult - even on an experimental farm
- Not suitable for conventional breeding programme but ...
- genome wide SNP association study could unlock potential, but need more animals for this

Other options

- Look at components of feed efficiency
and/or
- Use indirect markers for feed efficiency

Component - marker approach

- Are differences in feed efficiency too multi-factorial to explain?
- Pick one component, e.g. protein or N efficiency
- Look for a marker for this that could be measured on a large number of animals
 - Ratio of $N_{14}:N_{15}$ in urine or milk could be a marker N efficiency
- Possibility to measure in individual milk samples

Feed efficiency in dairy cows

- Advantage:
 - Milk energy is easy to measure
- Difficulties:
 - Measuring feed intake
 - Calf and conceptus
 - Changes in body reserves
 - Is dry period included?
 - Is longevity considered?

Summary

- Is it worth going after?
- Can we make progress?
- Can we agree a definition of the trait?
- How do we get sufficient numbers of animals for genome wide association studies?
- Can we use a marker to increase no. of animals measured?