AN EVALUATION OF EXTENDED LACTATION IN THE AUSTRALIAN DAIRY INDUSTRY

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Extended lactation

Day 0  Day 305  Day 600+?

Standard Lactation length

Extended Lactation length
Extended lactation

![Graph showing milk yield over days in milk for standard and extended lactation.]
Improved feed

Why extend lactation?

Resulted

Introduction of NA germ plasm

Australian dairy herds

NA HF
Why extend lactation?

Trend in milk production average yield by year (1930-2014)

Source: ADHIS Annual Report, 2014
Why extend lactation?

Trend in milk production average EBVs by year of birth (1980-2011)

Source: ADHIS Annual Report, 2014
Why extend lactation?

Long-term declining trends in fertility

**Daughter Pregnancy Rate (1957-2013)**

![Graph showing declining DPR from 1957 to 2013](image)

**Calving Rate (1990-2001)**

![Graph showing declining CR from 1990 to 2001](image)

Source: Council on Dairy Cattle Breeding (2014) - USA

Source: Evans et. al (2006) - IRE
Why extend lactation?

Trend in average daughter fertility EBVs by year of birth (1980-2011)

Source: ADHIS Annual Report, 2014
Why extend lactation?

**Introduction**

- Improved feed
- Introduction of NA germ plasm

**Resulted**

- Australian dairy herds
- Retain high productive cows, delay rebreeding - milk for extra 6 months (18 month calving interval)

**FERTILITY**
Why extend lactation?

![Graph showing milk yield over days in milk with an insemination point.](image-url)
Why extend lactation?

![Graph showing milk yield vs. days in milk for standard and extended lactation](image)
Advantages of extended lactation

- Protein: Fat
- Breeding and animal health costs
- Replacements
Research Aims

› Limited information on potential for genetic improvement of extended lactation (XLAC) under Australian dairy system

› Mathematical model for extended lactation curves
› Quantitative definition of extended lactation
› Quantitative genetic analysis of XLAC traits
   - Heritability
   - Genetic correlations between XLAC traits/milk traits
   - Obtain estimated breeding values (EBVs) for XLAC traits
› Consider: incorporate XLAC EBVs in selection index
Lactation Modelling

Lactation models are useful in helping to define and estimate lactation characteristics of individual cows for genetic selection.

- Wood (1967) model chosen:
  - Captures key features of lactation curve shape
  - Can be fitted with relatively few observations / lactation
  - Properties easily derived, and predictions made
Mathematical definition:

\[ W(t; k, b, c) = \exp(k + b\log_e t - ct) \]

- \( W(\cdot) \) = model-based milk yield at time (days in milk) \( t \)
- \( k \) = scale parameter
- \( b \) = parameter associated with early increase in yield
- \( c \) = exponential rate of decline of milk yield

Using \( k, b, c \):
- Time to peak yield = \( t_{\text{max}} = b / c \); Max yield = \( W(t_{\text{max}}; k, b, c) \)
- Cumulative yields evaluated using numerical integration
- Can be done for each cow-lactation data set
Need objective definition of extended lactation/persistency to derive traits

Persistency = \frac{y_{305}}{y_{\text{max}}}

Ext Lac = \frac{\text{Area}_B}{\text{Area}_A}
Why a ratio definition for XLAC?

› First definition for XLAC (?)
› Measure of capacity of cows to lactate beyond 305 days for an extended period of time, relative to the first 305 days
› Selection based on XLAC (ratio): independent of peak yield.
› By not selecting cows based on peak yield = Reduced:
  - Fewer metabolic issues
  - Less health problems
  - Fewer fertility issues
Materials and Methods - Data

Randomly split into 8 subsets

ADHIS

~1 million cows
~20 million TD

PRELIMINARY ANALYSIS

10,000 cows randomly selected - extract pure HF ~6,000 cows, 244,183 TD records

~158 million TD 1985 to 2010

Analysis small data set allow decisions of modelling techniques automated data screening to be developed \( \rightarrow \) applied to 8 large data subsets

All lactations from the one cow kept in the same subset and analysis and editing conducted on each of the 8 files
Automated data handling pipeline

Assist in analysing and editing large scale industry test day records:

› Involved a 26 step automated process:
  
  ❖ Data extraction
  ❖ Merging
  ❖ Filtering
  ❖ Calculate variables (parity, test day per cow-lactation, age at calving, calving interval)
  ❖ Identifying true/false extended lactations
  ❖ Fitting Wood model for each cow-lactation
  ❖ Pedigree editing
  ❖ Quantitative genetic analysis
Identifying true/false extended lactations:
- Fit single Wood model vs 2\textsuperscript{nd} starting at 365 DIM (\texttt{nls()} in R)
- Assess if double-curve significantly better fit

![Graphs showing milk yield (kg) vs DIM with P < 0.001 and P > 0.05 labels]
Model fitted to milk yield data using \texttt{nlme()} nonlinear mixed model package in R

Data: $Y_{it} =$ milk yield (kg) on DIM $t$ for cow-lactation $i$
Also repeated for fat yield (FY, kg) and protein yield (PY, kg)

Model: $Y_{it} = W(t; k_i, b_i, c_i) + \epsilon_{it}$

$k_i, b_i, c_i$ are random effects for cow-lactation $i$

$\epsilon_{it} =$ random error for test-day record

Estimates of $k_i, b_i, c_i$ used to derive XLAC & other measures
Variation in the fitted lactation models

Variation in shape of lactation curves of different cows with extended lactation.
Why the Wood model?

› Haile-Mariam and Goddard (2008) used random regression (RRM) for modelling extended lactation curves

› RRM limitation: cannot reliably predict when there are sparse data records (e.g. fewer test day records from 305-610 DIM)

› Wood model approach allows predictions to be obtained for cows with fewer observations in the range from 305-610 DIM.

› Simple alternative approach and fits lactation data well.
Validating the Wood model

Validation: Cumulative 305 day yields were used as a validation of the use of the Wood model against Dairy industry (ADHIS) standards

› Compare estimates between model-based 305 day yields and industry 305 day estimates (ADHIS)
  ❖ High phenotypic correlation = 0.96
  ❖ High genetic correlation = 0.99

>>> effectively the same trait
Summary Statistics from the Wood model

› Milk production during XLAC phase (305-610 d) = 40% of production of 305 d lactation
› Av. (potential) milk production = 8,887 L
› Cows are on average ~50% of peak production by day 305
Ideal vs non-ideal extended lactation curve

Persistency = 0.92
XLAC = 0.84
Rate of decline = 0.001847
Peak yield = 24 L
610Yield = 12,587 L

Persistency = 0.55
XLAC = 0.41
Rate of decline = 0.004361
Peak yield = 38.1 L
610Yield = 13,374 L
The animal model fitted to the phenotypic data was:

\[ Y = \mu + HYS + PG + A + \text{CowID} + \varepsilon \]

- \( Y = \) XLAC ratio measure (for MY, PY or FY)
- \( HYS = \) Herd-Year-Season of the cow (fixed effect)
- \( PG = \) parity group (fixed effect)
- \( A = \) animal polygenic effect (random effect)
- \( \text{CowID} = \) National Cow ID for repeatability (random effect)
- \( \varepsilon = \) random error
- Model fitted using ASReml-R
Genetic parameter estimates

**Heritability**

› XLAC  
  Milk yield: 0.087 ± 0.004
  Protein yield: 0.064 ± 0.004
  Fat yield: 0.085 ± 0.004

› Low – still respond to selection but slow genetic progress

**Repeatability**

› XLAC  
  Milk yield: 0.198 ± 0.070
  Protein yield: 0.173 ± 0.069
  Fat yield: 0.163 ± 0.079

› Moderate - early cow performance is indicator for a cow’s successive lactation performance.
### Genetic and phenotypic correlations

<table>
<thead>
<tr>
<th></th>
<th>Milk yield</th>
<th>Protein yield</th>
<th>Fat yield</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield</td>
<td></td>
<td>0.91</td>
<td>0.85</td>
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<tr>
<td>Protein yield</td>
<td>0.93</td>
<td></td>
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<tr>
<td>Fat yield</td>
<td>0.78</td>
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</tbody>
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› Genetic correlation (above diagonal)

› Phenotypic (correlation below diagonal)

› High genetic correlations: selection for any XLAC trait will have positive effect on all three XLAC traits
Genetic and phenotypic correlations: XLAC with cumulative Day 305 yield trait

<table>
<thead>
<tr>
<th></th>
<th>Genetic</th>
<th>Phenotypic</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield</td>
<td>0.06</td>
<td>0.11</td>
</tr>
<tr>
<td>Protein yield</td>
<td>0.04</td>
<td>0.09</td>
</tr>
<tr>
<td>Fat yield</td>
<td>-0.07</td>
<td>0.07</td>
</tr>
</tbody>
</table>

› Low genetic correlations: selection for increased XLAC will not adversely impact highly important economic traits

>>> Cumulative 305 day yields

>>> Australian Selection Index (ASI)
Estimated breeding values (EBVs) were generated for XLAC for milk, fat and protein yields, to assist with the selection of cows and bulls (top tails).
Steady increase in last 20 years = 1 genetic SD

› Increase despite low genetic correlation with 305-d cumulative yield traits
› However, high genetic correlation of XLAC with 305-610-d yield traits
What are the benefits?

› Provide Australian dairy industry with the breeding tools to enable selection of bulls to produce cows that are best suited to extended lactation in pasture-based systems

› Assist with managing the fertility and overall health of the dairy cow

› **Breeding program**: Incorporate XLAC in selection index with cumulative 305 day yield and persistency.

› It has also opened avenues for genomic predictions for these traits = GEBVs

› Still required: explore genetic / phenotypic correlations with other traits, particularly fertility traits
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