Sheep breeding in South Africa: New challenges, and how we should react to it

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Elsenburg and University of Stellenbosch
Outline of talk

Background:
- The environment
- Small stock in South Africa
- Sheep breeding in South Africa

Research and Development
- Initiation and expansion of small stock recording

New challenges
- Genomics
- Resistance
- Climate change and greenhouse gasses
- Local capacity

Bottom line
Background: The environment - global humidity index
The environment

South Africa pastoral country, with large areas of low potential

Large areas primarily designated to extensive small stock farming

Provide sustenance for labourers and farming households

The very livelihood of rural communities
Background: Sheep production in South Africa
Large parts of SA arid and not suitable for cropping, totaling ~72 M ha

Only fit for the extensive production of meat and fibre

Small stock is predominant in the central and western regions

Replaced by beef cattle as we move eastwards and northwards
Agriculture in South Africa

Gross value ~ 3% of GDP

Total monetary value R 140.4 billion

Animal products about half at R 67.7 billion
## Animal production in SA - value of small stock

<table>
<thead>
<tr>
<th>Product</th>
<th>Gross value (R 1 000 000)</th>
<th>% of total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wool</td>
<td>1 675</td>
<td>2.37</td>
</tr>
<tr>
<td>Mohair</td>
<td>218</td>
<td>0.32</td>
</tr>
<tr>
<td>Karakul pelts</td>
<td>8</td>
<td>0.00</td>
</tr>
<tr>
<td>Ostrich products</td>
<td>399</td>
<td>0.58</td>
</tr>
<tr>
<td>Poultry</td>
<td>25 069</td>
<td>37.04</td>
</tr>
<tr>
<td>Eggs</td>
<td>6 676</td>
<td>9.96</td>
</tr>
<tr>
<td>Beef and veal</td>
<td>15 037</td>
<td>22.22</td>
</tr>
<tr>
<td>Pork</td>
<td>3 027</td>
<td>4.47</td>
</tr>
<tr>
<td>Fresh milk</td>
<td>9 114</td>
<td>13.47</td>
</tr>
<tr>
<td>Other animal products</td>
<td>2 904</td>
<td>4.29</td>
</tr>
<tr>
<td>Total</td>
<td>67 686</td>
<td>100.00</td>
</tr>
</tbody>
</table>
Thus….

Animal products important for the economy at nearly 50% of gross Agricultural GDP.

Small stock relatively small at ~8% of animal GDP.

Mostly sheep (~21 M) and goats (~3 M).

Of major regional importance despite modest monetary output.

Shown to be sustainable under adverse conditions.
Sheep numbers and products

[Graph showing sheep numbers and various products over the years from 1980 to 2008]
Thus...

Sheep numbers and production declined markedly to early 90’s

Wool productions since relatively stable on lower levels

Meat production inclined

Sheep meat readily imported if in short supply locally
Sheep breeding in South Africa

Research and development:

• Preceded formal animal recording

• Several well-documented flocks as resource material

• Reviewed by Schoeman et al. (2010)
Sheep breeding in South Africa

Initiation and expansion of sheep recording:
• Wool testing since 1934
• NSIS formally launched in 1964
• Linkages between flocks exploited in 1990’s
• First across-flock analysis on Merinos in 1998
• Since been done on a routine basis:
  • Supplied to farmers for decision support
  • Formed the basis of many studies
Distribution of breeds in SA

- Dohne Merino 23.9
- Dorper 24.2
- Merino 31.4
- Merino Landsheep 1.6
- Ile de France 2.9
- Other 2.4
- SA Mutton Merino 6.1
- Afrino 1.6
- Dormer 6.0
Genetic trends for production in mainstream breeds - Dohne Merino (Olivier, unpublished)
Genetic trends in reproduction (NLW as %) of mainstream breeds - Dohne Merino (Olivier, unpublished)
### Differences in genetic progress (Merinos; Olivier and Cloete, 2007)

<table>
<thead>
<tr>
<th>Trait</th>
<th>Worst flock</th>
<th>Breed</th>
<th>Best flock</th>
</tr>
</thead>
<tbody>
<tr>
<td>Live weight (kg)</td>
<td>0.01 ± 0.06 (0.02)</td>
<td>0.24 ± 0.01 (0.52)</td>
<td>0.50 ± 0.07 (2.09)</td>
</tr>
<tr>
<td>Fleece weight (kg)</td>
<td>-002 ± 0.01 (-0.54)</td>
<td>-0.01 ± 0.00 (-0.24)</td>
<td>0.03 ± 0.01 (0.73)</td>
</tr>
<tr>
<td>Staple length (mm)</td>
<td>0.18 ± 0.07 (0.17)</td>
<td>0.20 ± 0.02 (0.19)</td>
<td>0.77 ± 0.21 (0.74)</td>
</tr>
<tr>
<td>Fibre diameter (μm)</td>
<td>-0.06 ± 0.01 (-0.32)</td>
<td>-0.08 ± 0.01 (-0.42)</td>
<td>-0.09 ± 0.03 (-0.48)</td>
</tr>
<tr>
<td>TWW (kg)</td>
<td>-0.08 ± 0.05 (-0.27)</td>
<td>0.04 ± 0.01 (0.14)</td>
<td>0.22 ± 0.08 (0.73)</td>
</tr>
<tr>
<td>REV(R)</td>
<td>0.31 ± 0.15</td>
<td>1.17 ± 0.05</td>
<td>2.80 ± 0.31</td>
</tr>
</tbody>
</table>
Thus ….

Generally speaking, genetic progress of 1-2% p.a. should be attainable when focused on a single trait. The NSIS provide a vehicle for sheep producers to achieve such gains. Taken up by some, but not all. Not widely adopted (~81,392 live weights recorded in 2006). Uptake range from as low as 4.5% of breeders to as high as 73% of breeders (depending on breed). Substantial gains are feasible if all animals are selected purposefully.
New challenges: Advances in broader genetics field

Whole genome sequencing of several organisms

The underlying genetics of complex traits better understood

• “Missing heritability” explained by deeper sequencing
• Infinitesimal model thus supported

Epistatic interactions among genes the next great debate
Human genetics

Many subjects already sequenced
Allow a better understanding of
many diseases and disorders
Amazing breakthroughs on personal
medication
Good funding opportunities
Advances likely to spill over in
livestock breeding
SNP’s

- Single Nucleotide Polymorphisms
  - DNA sequence variation
  - Single nucleotide (A,T,C,G) difference between individuals or chromosomes
- SNP chip technology
  - Genotype thousands of SNPs
  - Genome-wide association, quantitative trait loci mapping (QTL)
Back to livestock

High density SNP chips for major species (>50 K) available
Powerful tool for genome-wide association studies
Sometimes (mostly) population specific
Training or reference population thus needed
Predicting genomic breeding values less accurate as the distance from the reference population increases
Dairy cattle leaders in genomics

High density SNP chips for major species (700 K)
Cattle genome sequenced
First whole genome sequenced dairy bulls available (n = 133) (Hayes et al., 2012)
Consists of:
• Holstein (n = 90)
• Simmental (n = 43)
Dairy cattle leaders in genomics

Numbers still too low for reliable predictions using different computing strategies
Will improve as numbers increase
Likely to play a substantial role as the number of sequenced animals increase
Likely to spill over in the beef industry
Sheep also catching up

Fairly dense (50 K) SNP chip available (Illumina)
Used for studies on population structure
Led to studies on estimating genomic breeding values in Australia and New Zealand
Excellent resources with many animals genotyped
Figure 2. Population structure within the global sheep diversity panel. Principal component (PC) analysis of genetic distance was performed using a subset of 20,279 SNP identified by LD-based SNP pruning. Heat strips for each of the first 10 PCs are shown for 74 breeds (top panel). The PC value for each animal was normalised to range from 0 to 1 and visualised as a colour spectrum from green (0) to red (1). Plots for PC1 and 2 (bottom left) and PC1 and 3 (bottom right) each revealed the clustering of 1,612 animals selected to balance the number of animals across breeds. Individuals are colour coded to represent their geographical origin. doi:10.1371/journal.pbio.1001258.g002
Genomic breeding value prediction in Australia (Van der Werf et al., 2011)

Additional rates of genetic gain predicted at:
• 30% in wool sheep (meat and lambs)
• 20% in meat sheep (carcass and meat quality)

Augmented with information from the Information nucleus flock
• 7000 genotyped animals with phenotypes for many traits
• Combine experimental and industry genetic material, different breeds
South Africa: Lines selected divergently for reproduction

Two distinct genetic groups for all 6 chromosomes
Thus ...

Progress at all levels impressive

Important prerequisites:

• Animals need to be phenotyped
• A suitable training population needs to be genotyped
• Phenotyping is a major task if all the traits of economic importance is considered

What is needed?
The road ahead ....

Phenotype, phenotype, phenotype ......
Formally include measures of resistance/tolerance in official schemes
Ensure DNA collection from “valuable” phenotyped animals:
• Experimental flocks/herds
• National flocks/herds participating in animal recording
• Animals from resource poor farmers
Will ensure that reference populations are representative of the national genetic resource
Challenges: Research in South Africa

Research under pressure worldwide!
South Africa no exception
South Africa an emerging economy
Many other priorities:
  • Health
  • Social welfare
  • Education

Agricultural research not as important
Global trends - Researchers per 1000 community members
Thus …

• Funding and number of researchers limited in SA
• Agricultural research probably under-funded
• More pressure on project teams
• Lots of challenges
• More outputs required with less resources
**Bottom line**

Producers have a valuable tool for small stock breeding in NSIS
Could possibly be enhanced by adopting new technology
Research funding for Agriculture remains a challenge
Capacity needs to be developed and retained in the system
Possibly in collaboration with overseas institutes and international scientists
Share resources

The Bovine HapMap Consortium

Overall project leadership: Richard A. Gibbs,‡,1,4 Jeremy F. Taylor,‡,4 Curtis P. Van Tassel†,4

HapMap project group leaders: William Barendse,5,6 Kelly A. Eversole,‡ Richard A. Gibbs,1,J Clare A. Gill,6 Ronnie D. Green,7 Debora L. Hamann,10 Steven M. Kappes,1,9 Sigríður Lien,11 Lakshmi K. Matakumnal,12,14 John C. McEwan,13 Lynne V. Nazareth,1,2,15 Robert D. Schnabel,3 Jeremy F. Taylor,3 Curtis P. Van Tassel,4 George M. Weinstock,5,6 David A. Wheeler,J Breed champions: Paolo Ajmone-Marsan,2† William Barendse,5,6 Paul J. Boettcher,6 Alexandre R. Caetano,6 Jose Fernando Garcia,13,17 Clare A. Gill,6 Ronnie D. Green† (leader), Olivier Hanotte,3 Sigríður Lien,11 Paola Mariani,15 John C. McEwan,13 Loren C. Skow,10 Tad S. Sonsteberg,1 Curtis P. Van Tassel,4 John L. Williams15,21

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SNP discovery: Chuan Gao,8 Robert St. Clair,6 Xu Yue Jiang,1,2 Yue Liu,1,2 Stephen S. Moore,22 Lynne V. Nazareth,1,2 Yanru Ren,1,2 Xing-Zhi Song,2,2 David A. Wheeler,J2 (leader), Kim C. Worley,J

ENCOD resequencing: Carlos D. Bustamante,29 Ryan D. Hernandez,29 Donna M. Muzny,2,2 Lynne V. Nazareth,1,2 Shobha

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References and Notes

7. B. Grisart et al., Genome Res. 12, 222 (2002).
10. Materials and methods are available as supporting materials on Science Online.
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