Wildlife Industry

THE FUTURE LIES IN THE QUALITY OF THE PROGENY

Paul Lubout
History of animal breeding in livestock

CONCEPTS
Pedigrees
Linebreeding
Pure breeding

1700

Die Britse wetenskaplike Robert Bakewell sê genetiese vordering sal plaasvind as een superieure manlike dier by 'n groep vroulike diere gebruik word, as stambome gehou word en as boere van 'n "ploegdier" na 'n meer vleis beweeg (soos die Shorthorn-ras waarvan hy die teelwyse beïnvloed het).
History of animal breeding in livestock

CONCEPTS
Single genes – colour
Pedigree
Pure breeding approach
History of animal breeding in livestock

CONCEPTS
- Economic important traits
- Adaption
- Crossbreeding
- Weight of animals
History of animal breeding in livestock

CONCEPTS

- Growth tests
- Indexes
- Phase C
- Feed conversion
Laat twintigste eeu

Die volgende ommekeer was in die melkbedryf toe prof. Chuck Henderson uitgewerk het dat die gebruik van KI-vaars oor verskillende kuddes in die melkbedryf, saam met slim wiskunde en statistiektegnieke, dit moontlik kan maak om bulle en koeie regverdig met mekaar te vergelyk oor verskeie kuddes, kalfs- en-seisoene heen. Dié BLUP-technologie gee beraamde teelwaardes (EBV’s) wat nou in alle vee- en verwante bedrywe gebruik word. Namate teelmateriaal in verskillende lande gebruik word, sal internasionale vergelykings die norm word. Die EBV’s van ’n bul wat byvoorbeeld in 2012 in Namibië geteel is, is al regstreeks vergelykbaar met Suid-Afrikaans geteelde bulle wat in 2013 gebore is. EBV’s het ou indeksie in die laaste deel van die twintigste eeu grootliks vervang.

CONCEPTS

WHOLE POPULATION

BREEDING APPROACH

EBV’s

GROWTH

FERTILITY

CARCASS
History of application of genomics in US dairy cattle

- Dec. 2007  BovineSNP50 BeadChip available
- Apr. 2008  First unofficial evaluation released
- Jan. 2009  Genomic evaluations official for Holstein and Jersey
- Aug. 2009  Official for Brown Swiss
- Sept. 2010 Unofficial evaluations from 3K chip released
- Dec. 2010 3K genomic evaluations become official
History of genomics in SA

- Currently genomic research in progress
- SA livestock have the databases and calculate EBVs
- Why is SA behind
  - Lack of ancestral DNA samples
  - Non-DNA-verified pedigrees
  - Lack of sufficient data in smaller and especially indigenous breeds
  - Lack of data on difficult to measure traits such as reproduction, meat tenderness, etc.
- No national research support for initiative as in other countries
Livestock breeding Industry

- 100 years of records:
  - Phenotypes
  - Pedigree
- DNA samples for 30 years
- Domesticated animals
- Controlled management systems

Wildlife breeding industry

- No records:
  - Phenotypes
  - Pedigree
- No DNA samples
- Wild animals
- Marginal land & Uncontrolled management systems
- No national research into wildlife production
Requirements for SA Wildlife industry to utilize genomics

- It is a chicken & egg situation: ARC has sequenced the Buffalo “Horizon” but we do have phenotypic data to link.
- SO SA needs:
  - Pedigrees (DNA verified)
  - Phenotypic records (DATABASES)
  - DNA samples of animals
    (+8000 records per species over number of years and generations)

WE NEED ALL THE ABOVE, NOT ONE OR TWO ITEMS TO BE ABLE TO UTILIZE GENOMICS

- This will take more than +10 years to collect the data but, if we do not start we will never get there.

WE NEED MASS PARTICIPATION OF ALL WILDLIFE BREEDERS IF WE WANT TO GET THERE !!!!!
Problems identified

- Lack of accurate records and DNA of animals
- Misperceptions of Wildlife breeders about genetic principles
  - Extremely high levels of inbreeding (low reproduction & adaption)
High levels of inbreeding

- **Inbreeding**
  - Father daughter - 25%
  - Brother sister – 25%
  - Niece nephew – 6.25

- **Line breeding less than 3.125% inbreeding**

- **Negative effects of inbreeding**
  - Low disease resistance (High mortality Dr Johan Kriek, W &J)
  - Low reproduction
  - Low adaption
  - Low growth
Problems identified

- Lack of accurate records and DNA of animals
- Misperceptions of Wildlife breeders about genetic principles
  - Extremely high levels of inbreeding (low reproduction & adaption)
  - Value of pedigrees in diversity management and selective breeding
  - Selection for multiple gene traits (horn length, weight, etc.)
Bell-shaped curve (Normal distribution)
Problems identified

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- Misperceptions of Wildlife breeders about genetic principles
  - Extremely high levels of inbreeding (low reproduction & adaption)
  - Value of pedigrees in diversity management and selective breeding
- Selection for multiple gene traits (horn length, weight, etc.)
- Effect of crossbreeding / heterosis on horn length
Heterosis in Sable

- Number small inbred Sable populations:
  - Letaba
  - Matetsi
  - Zambian
  - West-Zambian
  - Tanzania

- In South Africa we cross the different populations: Matetsi X West Zambian
  Progeny will have longer horns than both parents due to heterosis

- Back-cross (Matetsi X WZ) ♀ X West Zambian bull – 50% heterosis lost and horns will thus be shorter, many examples, Long horn cross bulls produce shorter horned progeny
Problems identified

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  - Effect of crossbreeding / heterosis on horn length
- Mitochondrial DNA (origin) vs Nuclear DNA
DNA: Mitochondrial DNA

- **Mitochondrial DNA:**
  - Mitochondria's role is energy metabolism. It's DNA encodes genes required for this role.
  - Useful for evolutionary studies and subspecies testing.
  - m-DNA is ONLY inherited from the mother
  - Although the DNA molecules are similar, mtDNA is extra-nuclear and is only transferred from mother to offspring (father's mtDNA is lost during fertilization).
Sub Species (m-DNA)

Calf(Z)

Sire(M)

Dam(Z)

Sire(M)

Dam(M)

Sire(M)

Dam(Z)
Problems identified

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  - Effect of crossbreeding / heterosis on horn length
- Mitochondrial DNA (origin) vs Nuclear DNA
- Non-standard DNA tests over labs (WRSA initiative)
- Misunderstanding of potential uses of genomics in Wildlife
What has been done to date

- Wildlife recording database established for:
  - Pedigrees
  - Phenotypes (colour, horn length weight, etc.)
  - DNA profiles
What has been done to date

- Wildlife recording database established for:
  - Pedigrees
  - Phenotypes (colour, horn length weight, etc.)
  - DNA profiles
- Standardised DNA profiles for forensics & parentage (in process)
Validation of Breeding

REMEMBER:

Parentage is validated ONLY when 18 out of 18 markers fit.

17/18 or 16/18 is not good enough.

Preferably both dam and sire should be tested for an accurate result.
What has been done to date

- Wildlife recording database established for:
  - Pedigrees
  - Phenotypes (colour, horn length weight, etc.)
  - DNA profiles
- Standardised DNA profiles for forensics & parentage (in process)
- Standardised recording procedures and measurements (Recording manuals for most species on WS² website)
- First single gene traits have been identified – black gene DNA test in Impala (UP)
Traits affected by few genes

- Qualitative traits – small number genes e.g. Colour
- Black Impala gene identified (UP)
- Golden Wildebeest and Saddled Impala next
- The rest will follow
Black Lamb (50% chance)

Parents

Black Ram (bb)
Split Ewe (Bb)

Black Calf (bb)

Grandparents

Black Ram (bb)
Split Ewe (Bb)
Black Ram (bb)
Red Ewe (BB)
How to breed black Impala without inbreeding

**PHASE 1 – BREEDING SPLITS**
YEARS 1-4

**Camp 1**
- 30 normal impala ewes
- 1 Black ram (eg Lumarie)
- Produce split lambs
- Split female EWE LAMBS
- Cull normal ewes over time

**Camp 2**
- 30 normal impala ewes
- 1 Black ram (eg Leopard rock)
- Produce split lambs
- Split female EWE LAMBS
- Cull normal ewes over time
How to breed black Impala without inbreeding

**PHASE 2 – BREEDING BLACK**
YEARS + 6

**Camp 1**
Black ewe lambs

**Camp 2**
Black ewe lambs

**Camp 3**
Black ewe lambs
1 Black or saddled ram (e.g. LBG holdings)

PRODUCE BLACK PROGENY

NOTE: Black ram lambs sold to buy new black ram for camp 3
What has been done to date

- Wildlife recording database established for:
  - Pedigrees
  - Phenotypes (colour, horn length weight, etc.)
  - DNA profiles
- Standardised DNA profiles for forensics & parentage (in process)
- Standardised recording procedures and measurements (Recording manuals for most species on WS² website)
- First single gene traits have been identified – black gene DNA test in Impala (UP)
- Wildlife on-farm recording PC programmes (HerdMaster & BenguFarm)
- DNA testing of wildlife has increased dramatically (± 9000@ Unistel last 24 months, 5 other labs ?)
- Recording database (WS²) + 70 breeders and + 6000 animals on since 15 March 2013
WS2 Registration Certificate

REGISTRATION CERTIFICATE
Sable - Matetsi

PIET WARREN BISMARK C17

Identification: 1106
Sex: Male
Date of Birth: 11/09/2010 (age: 3 years 3 months)
Computer Number: 3702692541
Colour: NATURAL
Registration Status: Registered
Roland Ward: 35.6
SCI: 100.0
Breeder: PIET WARREN PLACE (1017)
Owner: PIET WARREN PLACE (1017)
PO Box 1 GRAVELOTTE 095
DNA Profile Animal: S3215.10 C17
DNA Profile Site: S3624.07 MD1
DNA Profile Dam: S3624.07 P4

PEDIGREE
PIET WARREN MADALA MD00
SIRE: 1107 PIET WARREN CHARLIE C00
PIET WARREN OUABOK
PIET WARREN P10
DAM: 1108 PIET WARREN P4
PIET WARREN MJ4

Dr Paul C Lubofo - Ph Sci Nat (40018470)
Director 2019

Independent Wildlife Registering Authority & Stud Services
Mobile 082 926 3967, Fax 061 522 8112 | P/O Box 20693 | Langebergpark 111 | Bloemfontein | Free State
Reg No: 2012/000944/07
Directors: DC Crook, MP Noor, PC Lubofo
we@ws2.co.za
South African Wildlife Stud Services
Signon

Authorisation Required

Please provide a Member I.D. and Password. Fields marked with an asterisk(*) are required, others are optional.

* Member I.D.: [Enter]
* Password: [Enter]

To change your password, enter your Member I.D. and current password above and your new password below:

New Password: [Enter]
New Password Validation: [Enter]

Clear  Signon
Animal view on WS² system

South African Wildlife Stud Services Animal Details
L'ORMARINS THIRD FORCE

Identification: 1169
Sex: Male
Colour: Natural
Status: Active
Registration Status: Active
Species: African Buffalo
Date of Birth (age): 2006 (age: 7)
Sire: Unavailable
Dam: Unavailable
Breeder: L'ORMARINS (PTY) LTD
Current Owner: L'ORMARINS (PTY) LTD
Progeny: None
Pedigree: Unknown
EBV Graph: [View]

View Larger Image: 250 kb View Other Images
Pedigree:

- Registration Status: Active
- Species: Sable - Matetsi
- DNA case ID: S3215.10 C17
- Sire DNA Case ID: S3624.07 MD1
- Dam DNA Case ID: S3624.07 P4
- Date of Birth (age): 08/11/2010 (age: 2.91)
- Sire: PIET WARREN CHARLIE
- Dam: PIET WARREN P4
- Breeder: PIET WARREN
- Current Owner: PIET WARREN
- Progeny: None
- Pedigree: [View]
- EBV Graph: [View]

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**PIET WARREN MADALA**

- Sire: PIET WARREN CHARLIE
  - PIET WARREN OUMABOK

**Animal: PIET WARREN BISMARK**

- Dam: PIET WARREN P4
  - PIET WARREN J2
What are we recording

- Pedigree information (Sire & dam, DNA verified)
- Phenotypes:
  - Single gene traits (colour, colour patterns, genetic defects)
  - Photographs of animals during lifetime (also teeth)
  - Reproduction traits (AFC, ICP, DLA, Scrotal circumference, etc.)
Reproduction traits

- Age at first calving/lambing
- Inter calving/lambing period
- Days last calved/lambed
- Scrotal circumference

Priorities within the industry Populating Game Data Base
What are we recording

- Pedigree information (Sire & dam, DNA verified)
- Phenotypes:
  - Single gene traits (colour, colour patterns, genetic defects)
  - Photographs of animals during lifetime (also teeth)
  - Reproduction traits (AFC, ICP, DLA, Scrotal circumference, etc.)
  - Horn traits (length, circumference, boss, etc.)
Horn measurement traits

- Length
- Circumference
- Tip to tip
- Boss (BUF)
- Diameter
  (Front and Side)
- Etc.
What are we recording

- Pedigree information (Sire & dam, DNA verified)
- Phenotypes:
  - Single gene traits (colour, colour patterns, genetic defects)
  - Photographs of animals during lifetime (also teeth)
  - Reproduction traits (AFC, ICP, DLA, Scrotal circumference, etc.)
  - Horn traits (length, circumference, boss, etc.)
  - Weights (birth, wean, year, 2 yrs., etc.)
Weight traits

- Birth weight (optional)
- Weaning
- Year
- 2 year
- Mature cow weight
What are we recording

- Pedigree information (Sire & dam, DNA verified)
- Phenotypes:
  - Single gene traits (colour, colour patterns, genetic defects)
  - Photographs of animals during lifetime (also teeth)
  - Reproduction traits (AFC, ICP, DLA, Scrotal circumference, etc.)
  - Horn traits (length, circumference, boss, etc.)
  - Weights (birth, wean, year, 2 yrs., etc.)
  - Type traits (Functional traits)
- DNA sample numbers and complete profiles
SELECTION INDEX (SA)

- You measure all the animals on a specific date born within 45 days
- You calculate the average of all animals
- You then calculate the selection index
  \[(\text{animals own value} - \text{average value}) \times 100\]
  \[
  \frac{\text{average value}}{
  \]
- Animals above 100 above average
- Animals below average below 100
- Work out average for different bulls
- Accuracy 45 -50%

THIS WILL BE AN INTERM MEASURE UNTIL THERE IS SUFFICIENT DATA FOR ESTIMATING EBV’s
What is an EBV

- Prediction of genetic value of an animal for e.g. Horn Length
- Based on:
  - Animals own performance
  - Animals relatives performance
  - Relationship between traits

“Is the best prediction of an animals genetic value” (80% accuracy)
Estimated Breeding Value (EBV)

Own Records
- Weights
- Scans
- Scores
- Measurements

Pedigrees
- Parents (sibs etc.)
- Progeny
  - Measurements
  - Daughters

Correlated Traits
- Other measurements
- Other Traits

Genomic Values
- DNA Sample
TAKE HOME MESSAGE

- Responsible game breeders will:
  - Do DNA profiles
  - Use verified pedigrees
  - Measure accurately: “man must measure”
  - Will use all the breeding tools available:
    - Stockmanship - experience
    - Pedigrees
    - Visual evaluation
    - Performance evaluation

*If you do not apply the above you are only a wildlife multiplier and not a wildlife breeder!!!!!*
THANK YOU!!! BAIE DANKIE!!!

unistel

Wildlife Stud Services

the key to a prosperous future for SA’s Wildlife industry