Genetics response of small ruminants to heat stress

Plant and Animal Genomes Conference: Animal Genomics and Adaptation to Climate Change Workshop

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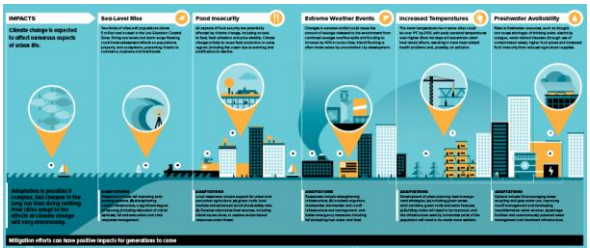
The Global Facts and Challenges – Human population

- By 2050, the world's population is projected to increase by a third, to more than 9.6 billion people.
- Most of that increase will occur in the developing world, where hunger and malnutrition are already chronic problems.
- Food production will have to increase by over 70% by 2050* if we wish to leave the future generations a less hungry and more stable world. (*FAO)

The Sustainability Fact and Challenge – Climate Change



The Technical Facts and Challenges

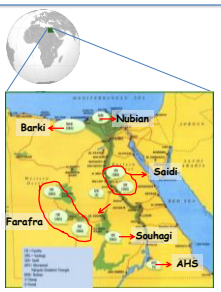
- **Adaptation traits:**
  - Have low heritability ($h^2 \leq 0.25$)
  - Difficult to improve using conventional animal breeding strategies
  - Are difficult and expensive to measure
  - Cannot be accurately measured until maturity
- **Genomics:**
  - Offers the most promising alternative strategy to improve adaptation traits.

The Genomics of adaptation

- **Livestock species adapted to hot and dry environments (constant heat and feed stress)**
  - Camels (*Camelus dromedarius*)
  - Donkeys (*Equus africanus asinus*)
  - Indigenous sheep and goats

Increasing

Study Approach…



Sheep:

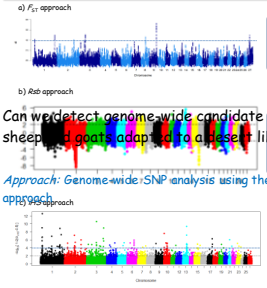
Barki	= 181
Saidi	= 72
Farafra	= 62
Souhagi	= 49
AHS	= 30
Total	= 394

Goats:

Barki	= 150
Saidi	= 60
Nubian	= 84
Farafra	= 72
Total	= 366

- Genotyped with the Ovine and Caprine SNP 50K Chip
- Various breeds of sheep and goats from temperate in Northern Europe

Signatures of selection - Sheep



- Seven candidate regions, 6 xsomes:
  - Chromosomes 1, 2, 3, 8, 9 and 27
- The most significant region:
  - Chromosome 9

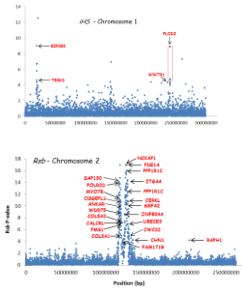
- Thirteen candidate regions, 8 xsomes:
  - Chromosomes 1, 2, 3, 7, 8, 13, 15, 20, 26
- The most significant region:
  - Chromosome 2

- Thirteen candidate regions, 8 xsomes:
  - Chromosomes 1, 2, 3, 6, 10, 13, 15, 17
- The most significant region:
  - Chromosomes 1 & 13

Can we detect genome-wide candidate signatures of selection in sheep and goats adapted to a desert like environment?

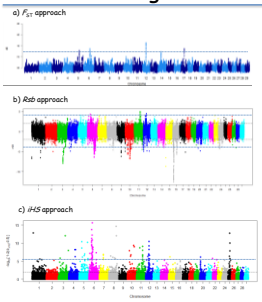
Approach: Genome-wide SNP analysis using the Fst variant, Rsb and iHS approach

Signatures of selection - Sheep



- The 31 candidate regions spanned 140 genes
- 68 SNPs found within 43 genes in the three most significant regions

Signatures of selection - Goats



- Five candidate regions, 5 xsomes:
  - Chromosomes 5, 6, 12, 14 and 17
- The most significant region:
  - Chromosome 12

- Sixteen candidate regions, 7 xsomes:
  - Chromosomes 3, 6, 9, 10, 11, 12, 16
- The most significant region:
  - Chromosome 16

- Eleven candidate regions, 7 xsomes:
  - Chromosomes 5, 6, 7, 11, 12, 20, 25
- The most significant region:
  - Chromosomes 6 and 25

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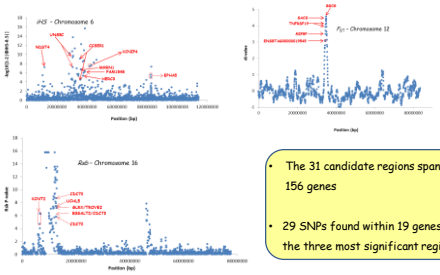
Signatures of selection - Goats



- The 31 candidate regions spanned 156 genes
- 29 SNPs found within 19 genes in the three most significant regions

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Functions of the candidate genes - Sheep

Function	Genes
Growth and development/morphology	ITGA4, NCKAP1, FRZB, COL5A2, PPP1R1C, LIMS2, PRDX1
Reproduction physiology	FRZB, WDR33, TESK2
Response to oxidative stress	TP53INP1, ERCC3, PRDX1
Skin morphogenesis/pigmentation	ITGA4, COL5A2, FRZB, NAB1, ERCC3, UROD
Response to nutrient levels/starvation	COL5A2, AKR1A1, MMACHC
Response to temperature/UV radiation	TP53INP1, ERCC3, POLR2D, EIF2B3
Regulation of stress-activated protein kinase signaling and MAPK cascade	PRDX1
Cellular respiration/energy homeostasis	NDUFAF6, DNAJC10, ERCC3, PMS1
Immune response	NCKAP1, PRDX1, PLSCR4
Regulation of translation in response to stress/DNA repair	EIF2B3, RAD54B, ERCC3, POLR2D, PMS1, WDR33, PMS1
Response to hypoxia/oxygen levels	ERCC3, PLOD2,

detected


SCIENTIFIC REPORTS

OPEN Genomic footprints of dryland stress adaptation in Egyptian fat-tail sheep and their divergence from East African and western Asia cohorts

Functions of the candidate genes - Goats

Function	Genes
Growth and development/morphology	SGCG, SPP1, SLIT2, EPHA5, MEPE, PKD2, ATOH1, PALB2
Reproduction physiology	SLIT2, BMPR1B, SLC34A2, ABCG2, SPP1, ZP2, RBBP6, RGS2
Response to oxidative stress	PKD2, PPARGC1A, SOD3, SNCA, PARK7, GLRX2
Skin morphogenesis/pigmentation	ATOH1, TNFRSF19, ERRFI1, SLIT2, PKD2, PPARGC1A, PALB2
Response to nutrient levels/starvation	PPARGC1A, ABCG2, SPP1, PKD2, CRYM, TNRC6A, RGS2
Response to temperature/UV radiation	PPARGC1A, DCUN1D3, TROVE2, GLRX2
Water homeostasis/Kidney development	SLIT2, PKD2, SCNN1G, SCNN1B, AQP8, PPARGC1A, RGS2
Cellular respiration/energy homeostasis	PARK7, PPARGC1A, DHX15, UQCRC2, NDUFAB1
Innate and adaptive immune response	HERC5, SNCA, SLIT2, TNFRSF19, SPP1, PRKCB, PRKCB, TNRC6A, POLR3E, CDC73
Response to hypoxia	PPARGC1A, SOD3,

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Common signatures of selection in goats and sheep

- We found one candidate region on chromosome

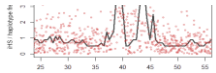
➢ Genes found in the common candidate region

Can we detect genomic regions under selection in a common environment in two

Breed	Barki		
	Goats	Sheep	Common
Number of genes	29	29	8

genes to investigate common candidate regions of conserved synteny in sheep, goats, and cattle.

E-S Kim[1,5], AR Elbeltagy[2,5], AM Aboul-Naga[2], B Rischkowsky[3], B Sayre[4], JM Mwacharo[3] and MF Rothschild[1]



- The region was however too broad (>5 mb) to be resolved adequately

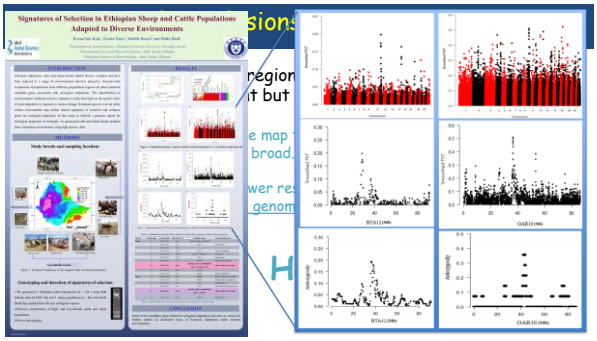
General Conclusions – Sheep and Goats

1. Can we detect genomic signatures of selection in African indigenous goats and sheep?

Yes - Adaptation to a hot arid environment

2. What is the genetic basis behind these candidate signatures?

Multiple functions related to various cellular signaling, thermo-tolerance, reproduction and development, digestive metabolism and immunity



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