Genome-wide diversity and admixture of Angler and Red-and-White dual purpose cattle

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About the breeds

Angler (RVA)

Red & White dual-purpose (RDN)

- Dual-purpose local breeds

- Have relatively small numbers

	RVA	RDN
Milk yield/lactation (kg)	7,677	7,048
Milk protein content (%)	3.60	3.58
Milk fat content (%)	4.58	4.33
Herdbook cows (2017)	12,480	3,796

(Report: BRS, 2017)

Introduction

Previous study

- Pedigree-based analysis revealed high genetic contributions of some Red Holstein (RH) sires to the RVA and RDN populations

RVA

Animal ID	Breed	Contr.
840000001842371	Red Holstein	0.045
840000001629391[a]	Red Holstein	0.029
276000102168990	Angler	0.028
276002240018965	Angler	0.027
840000001491007[b]	Red Holstein	0.026
752000000093907	Angler	0.025
840000001427381[c]	Red Holstein	0.023
000008400028756	Angler	0.021
528000775157228	Red Holstein	0.019
276000102142217	Angler	0.019

RDN

Animal ID	Breed	Contr.
840000001629391[a]	Red Holstein	0.031
840000001491007[b]	Red Holstein	0.025
528000000355040	Red &White DP	0.019
124000000267150	Red Holstein	0.018
528000000338535	Red Holstein	0.018
840000001427381[c]	Red Holstein	0.017
840000001189870	Red Holstein	0.014
000009002053500	Red Holstein	0.013
528000951276374	Red & White DP	0.011
000009002037187	Red Holstein	0.011

(Addo *et al*, 2017)

Two-fold objective

Investigation of admixture events between RVA and RDN cattle, and the influence of RH breed

&

Determination of molecular estimates of inbreeding within each breed

Data (Pre-study)

- Data obtained from *vit* in Verden, Germany

- Animals genotyped with the BovineSNP50 BeadChip

PLINK

Description of genomic data before and after
quality control

Breed/(SNPs)	Before	After
	(54,609)	(38,042)
RVA	156	147
RDN	70	68
Total	**226**	**215**

Autosomal SNPs
Individual call rate: > 95%
SNP call rate: > 99%
MAF: > 5%
HWE: $P \leq 0.0001$

Data (Main study)

Description of genomic data before and after quality control

Breed/(SNPs)	Before (51,131)	After (40,877)
RVA	169	168
RDN	69	69
RH	100	100
Total	**338**	**337**

Pedigree information for genotyped individuals

Breed	N	Records (n)
RVA	155	3,375
RDN	65	2,204

- Additional filtering
  - Restriction on genomic relatedness (Gen. rel. < 0.3)
  - Moderate linkage disequilibrium (--indep 50 5 2) ➡ 14,239 SNPs

Parameters & population structure

- Genetic diversity indices
    - Observed Heterozygosity (H_o)
    - Expected Heterozygosity (H_e)
    - Runs of Homozygosity (ROH)
        - Inbreeding coefficient based on ROH (F_{ROH})
    - Inbreeding coefficient based on pedigree (F_{PED})

- Population structure
    - Multidimensional scaling (MDS)
    - Admixture analysis (Alexander *et al*, 2009)
    - NetView analysis (Neuditschko *et al*, 2012)

Computations

- ROH definition

  - 50 SNP-window
  - 1 het. SNP
  - 2 missing genotypes
  - Density of 1 SNP per 100 kb
  - Maximum gap of 1000 kb

- $F_{ROH} = \dfrac{\sum L_{ROH}}{L_{AUTO}}$

  (McQuillan *et al*, 2008)

- F_{PED}

  (Meuwissen & Z. Luo, 1992)

Regression of F_{ROH} on F_{PED}

Consecutive runs of homozygous SNPs
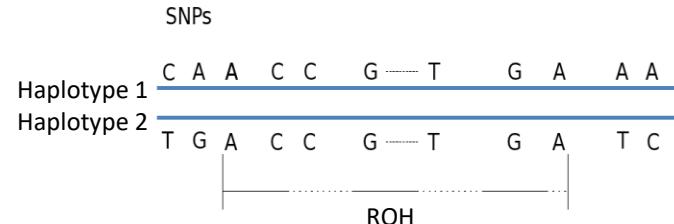
SNPs

	C A A	C C	G ---- T	G A	A A

Haplotype 1
Haplotype 2

	T G A	C C	G ---- T	G A	T C

ROH

Pedigree completeness
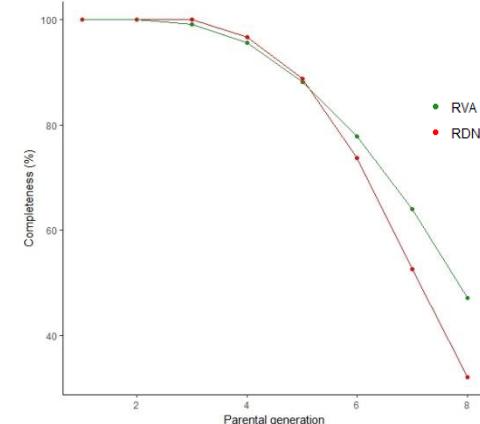
Genetic diversity

Average observed (H_o) and expected (H_e) heterozygosity for all three breeds

Breed	$H_o \pm$ SD	H_e
RVA	0.374 ± 0.008	0.369
RDN	0.356 ± 0.013	0.352
RH	0.363 ± 0.011	0.360

- H_o slightly higher in RVA

- Moderately high genetic diversity in all three breeds

- Estimates comparable to similar European breeds

Genetic diversity

Mean and range of pedigree- (F_{PED}) and ROH-based (F_{ROH}) inbreeding coefficients for the studied breeds

Breed	F_{ROH}		F_{PED}	
	Mean	Range	Mean	Range
RVA	0.021	0.000 – 0.075	0.013	0.000 – 0.065
RDN	0.045	0.002 – 0.113	0.023	0.000 – 0.080
RH	0.053	0.009 – 0.119	NA	NA

- Lower F in RVA consistent with H_O estimate

- F is highest in RH as expected

- F_{ROH} predicts trends of inbreeding

$F_{ROH} = 0.01 + 0.92\ F_{PED}$
$R^2 = 0.42$

$F_{ROH} = 0.02 + 1.07\ F_{PED}$
$R^2 = 0.45$
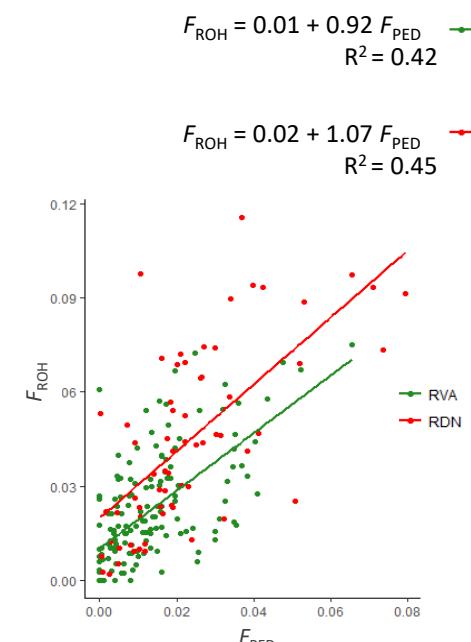
Plot of regression of F_{ROH} on F_{PED} for RVA & RDN

Pre-study

No restriction on relatedness
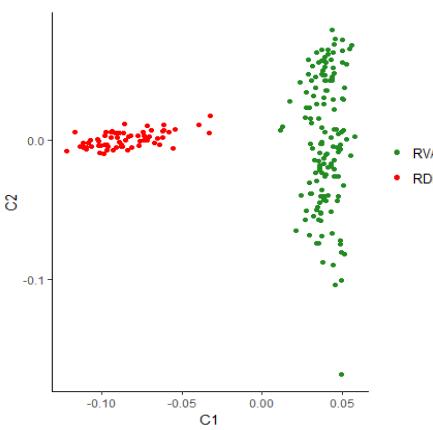
Admixture results (optimal K = 11)
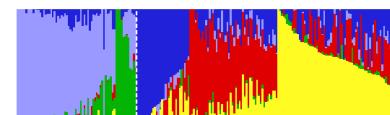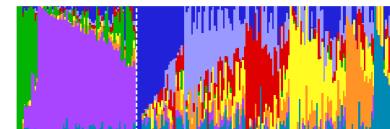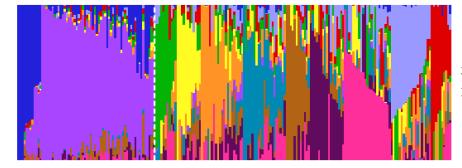
NetView results
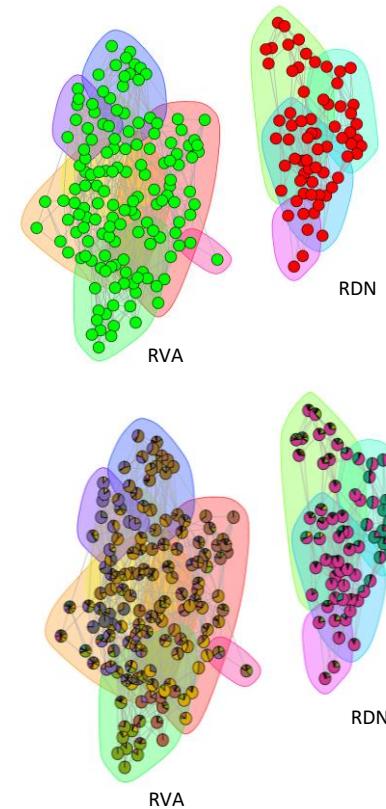
MDS-plot

Results and Discussion

## Main study

Gen. rel. < 0.3

LD pruned

MDS-plot
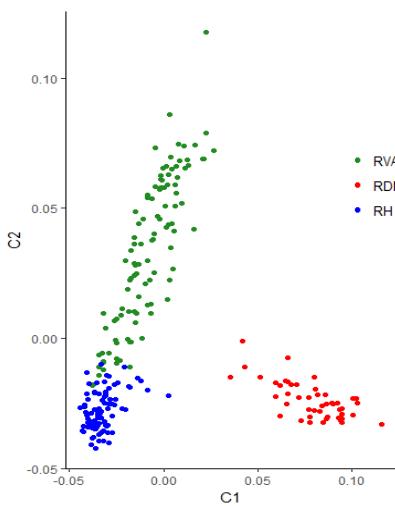
Admixture results (optimal K = 6)
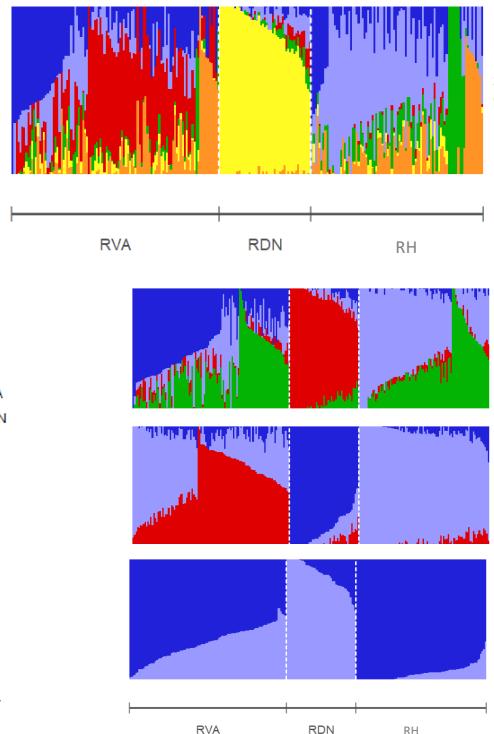
NetView results
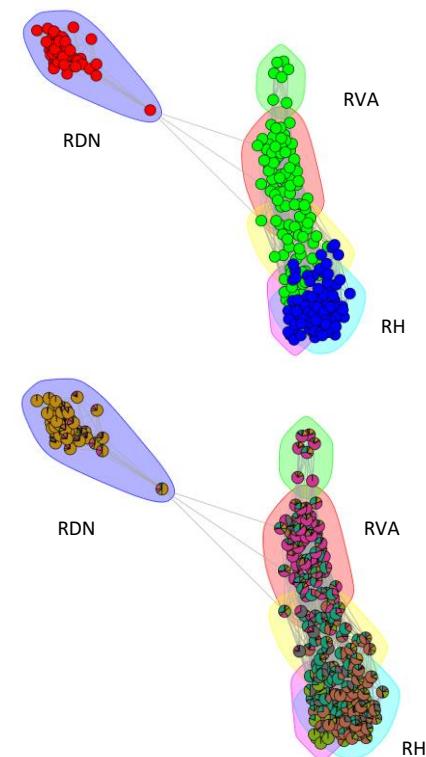
Conclusion

- The modern Angler population maintains a relatively high within-breed genetic diversity

- The study provides molecular evidence of shared ancestry by the Angler, Red-and-White dual purpose and Red Holstein cattle

- Gene flow among the breeds highlights crossbreeding schemes used for breed improvement in recent years