Genetic heritage of the Eastern Belgium Red and White breed, an endangered local breed

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Under the holsteinization pressure and in the absence of a commitment of the Red and White Herdbook to the dual-purpose breed type, the Eastern Belgium Red and White (EBRW) was considered extinct in the 1990s. Nevertheless, several farmers still kept these cattle because they were perfectly adapted to their more extensive, grazing based production system on less productive medium-altitude (Ardenne-Eiffel) meadows.

Framework
- Safeguarding and conservation of EBRW
- Public Service of Wallonia project funded

Aim
- Positioning of the EBRW breed in relation with 12 bovine breeds based on SNP data

Data
- 50K genotypes (572 animals, 39 903 SNP after editing)
  - 12 breeds: British Friesian (BRF), Dual-Purpose Belgian Blue (DPBB), Dutch Friesian (DFR), Eastern Belgium Red and White (EBRW), French Red Pied Lowland (PRP), Holstein (KEM), Meuse-Rhin-Yssel (MRY), Norwegian Red Cattle (NRC), Red Holstein (RED), Rouge des Prés (Maine-Anjou, RDP), Roodbunte DN (RBDN)

Results
- Unrooted neighbor-joining consensus tree constructed using Nei’s genetic distance of 12 breeds
  - The 5 red-pied dual-purpose breeds of North-Western Europe grouped together
  - Plot of individuals from 8 breeds according to the coordinates on the first two principal components

Conclusions
- EBRW is different from Red Holstein.
- EBRW belongs to red-pied dual-purpose breeds group in North-Western Europe.
- Based on breed standards, EBRW is still distinct from MRY and Kempen breed.

Achievements
- Set up of a dedicated breeding commission
- Creation of a dedicated Herdbook
- April 2015, official recognition of EBRW by Government of Walloon Region
- Meat valorization in short distribution channels

Analysis
- Nei’s genetic distance
  - Computed with R package STAMP (Pemberton, 2014)
  - Neighbor-joining tree built with R package ape (Paradis et al., 2014)
- Principal Component Analysis with PreGSF90 (Aguilar et al., 2014)
- Genetic structure
  - Inferred with STRUCTURE 2.3.4 (Pritchard et al., 2000)
  - Number of clusters (value K) ranging from 2 to 12
  - 10 independent runs for each value K
  - Burn-in 10 000 repeats followed by 20 000 MCMC repeats
  - Results analyzed with Structure Harvester (Earl et al., 2012), CLUMPP (Jakobsson, 2007) and DISTRACT (Rosenberg et al., 2007)

STRUCTURE based clustering at the level of individuals from 8 bovine breeds

- 6 is the most likely number of clusters based on the method proposed by Evanno et al. (2005).
- Clear separation of MRY, RED, NRC and RDP breeds
- EBRW, KEM, PRP and RBDN are distinct from:
  - HOL and RED, and also BRF and DFR
  - NRC, RDP and DPBB (breeds with a strong influence of Shorthorn breed in their ancestry)