



Genome-wide characterization of local cattle breeds from central and western Mediterranean

Journal:	<i>Italian Journal of Animal Science</i>
Manuscript ID	TJAS-2017-0356
Manuscript Type:	Abstract Submission
Date Submitted by the Author:	28-Feb-2017
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Abstract:	Following-up on previous studies that investigated genetic relationships among several world-wide cattle breeds using genome-wide SNP data, we focus here on the central and western part of the Mediterranean. Notably,

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	<p>50K genotypes from 30 Marismeña (Spain); 24 Guelmoise (Algeria); 46 Brune de l'Atlas Fauve, 15 Brune de l'Atlas Grise, and 15 Blonde du Cap (Tunisia); 29 Modicana and 30 Cinisara (Sicily); 24 Podolica Italiana (Southern continental Italy); 34 Chianina and 24 Romagnola (Central Italy); 23 Modenese, 24 Reggiana, 23 Alpine Grey and 50 Pezzata Rossa Italiana (Northern Italy); 50 Bruna Italiana and 50 Frisona Italiana were considered. When included in a world-wide dataset, the three Tunisian, the Algerian, the two Sicilian, the Podolica, the Chianina and the Romagnola were the taurine breeds showing the highest closeness to the Indian zebu group in the MDS plot of the IBS distance. These results were also confirmed by ADMIXTURE analysis ($K = 2$). This relatively lower influence of zebu material into cattle breeds from Northern Italy suggests a major maritime-mediated route of dispersal of zebu material into Southern Europe and Northern Africa. Interestingly, breeds from the Iberian peninsula showed lower evidence of zebu introgression, suggesting that zebu introgression was likely not mediated by Moors, and possibly occurred at earlier times. Clear evidence of more recent introgression of material from improved dairy cattle breeds (Bruna Italiana and Brown Swiss) into the two Brune de l'Atlas populations from Tunisia highlights the need for urgent conservation of this cross-border cattle.</p>
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Genome-wide characterization of local cattle breeds from central and western Mediterranean

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Following-up on previous studies that investigated genetic relationships among several world-wide cattle breeds using genome-wide SNP data, we focus here on the central and western part of the Mediterranean. Notably, 50K genotypes from 30 Marismeña (Spain); 24 Guelmoise (Algeria); 46 Brune de l'Atlas Fauve, 15 Brune de l'Atlas Grise, and 15 Blonde du Cap (Tunisia); 29 Modicana and 30 Cinisara (Sicily); 24 Podolica Italiana (Southern continental Italy); 34 Chianina and 24 Romagnola (Central Italy); 23 Modenese, 24 Reggiana, 23 Alpine Grey and 50 Pezzata Rossa Italiana (Northern Italy); 50 Bruna Italiana and 50 Frisona Italiana were considered. When included in a world-wide dataset, the three Tunisian, the Algerian, the two Sicilian, the Podolica, the Chianina and the Romagnola were the taurine breeds showing the highest closeness to the Indian zebu group in the MDS plot of the IBS distance. These results were also confirmed by ADMIXTURE analysis (K = 2). This relatively lower influence of zebu material into cattle breeds from Northern Italy suggests a major maritime-mediated route of dispersal of zebu material into Southern Europe and Northern Africa. Interestingly, breeds from the Iberian peninsula showed lower evidence of zebu introgression, suggesting that zebu introgression was likely not mediated by Moors, and possibly occurred at earlier times. Clear evidence of more recent introgression of material from improved dairy cattle breeds (Bruna Italiana and Brown Swiss) into the two Brune de l'Atlas populations from Tunisia highlights the need for urgent conservation of this cross-border cattle.