1.

Record Nr.	UNISA990003040430203316
Autore	SECCIA, Giorgio
Titolo	Monte Zebio : dalla Strafexpedition alla vittoria finale, 1916-1918 / Giorgio Seccia
Pubbl/distr/stampa	Chiari, : Nordpress, 2007
ISBN	978-88-88657-75-2
Descrizione fisica	430 p. : ill. ; 21 cm
Collana	Sui campi di battaglia ; 5
Disciplina	940.4272
Soggetti	Guerra mondiale 1914-1918 - Monte Zebio - 1916-1918 Guerra mondiale 1914-1918 - Altopiano di Asiago - 1916-1918 - Diari
Collocazione	X.3.B. 4573
Lingua di pubblicazione	Italiano
Formato	Materiale a stampa
Livello bibliografico	Monografia

2.

Record Nr.	UNINA9910136804103321
Autore	Philippe V. Baret
Titolo	Advances in farm animal genomic resources [[electronic resource] /] / edited by: Stéphane Joost, Michael W. Bruford, Ina Curik, Juha Kantanen, Johannes A. Lenstra, Johann Sölkner ... [and 6 others]
Pubbl/distr/stampa	Frontiers Media SA, 2016 [Lausanne, Switzerland] : , : Frontiers Media SA, , 2016 ©2016
Descrizione fisica	1 online resource (293 pages) : illustrations; digital, PDF file(s)
Collana	Frontiers Research Topics
Soggetti	Cattle - Genetics Cattle - Genome mapping Livestock - Conservation Livestock - Genetics Biodiversity
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Nota di bibliografia	Includes bibliographical references.
Sommario/riassunto	The history of livestock started with the domestication of their wild ancestors: a restricted number of species allowed to be tamed and entered a symbiotic relationship with humans. In exchange for food, shelter and protection, they provided us with meat, eggs, hides, wool and draught power, thus contributing considerably to our economic and cultural development. Depending on the species, domestication took place in different areas and periods. After domestication, livestock spread over all inhabited regions of the earth, accompanying human migrations and becoming also trade objects. This required an adaptation to different climates and varying styles of husbandry and resulted in an enormous phenotypic diversity. Approximately 200 years ago, the situation started to change with the rise of the concept of breed. Animals were selected for the same visible characteristics, and crossing with different phenotypes was reduced. This resulted in the formation of different breeds, mostly genetically isolated from other

populations. A few decades ago, selection pressure was increased again with intensive production focusing on a limited range of types and a subsequent loss of genetic diversity. For short-term economic reasons, farmers have abandoned traditional breeds. As a consequence, during the 20th century, at least 28% of farm animal breeds became extinct, rare or endangered. The situation is alarming in developing countries, where native breeds adapted to local environments and diseases are being replaced by industrial breeds. In the most marginal areas, farm animals are considered to be essential for viable land use and, in the developing world, a major pathway out of poverty. Historic documentation from the period before the breed formation is scarce. Thus, reconstruction of the history of livestock populations depends on archaeological, archeo-zoological and DNA analysis of extant populations. Scientific research into genetic diversity takes advantage of the rapid advances in molecular genetics. Studies of mitochondrial DNA, microsatellite DNA profiling and Y-chromosomes have revealed details on the process of domestication, on the diversity retained by breeds and on relationships between breeds. However, we only see a small part of the genetic information and the advent of new technologies is most timely in order to answer many essential questions. High-throughput single-nucleotide polymorphism genotyping is about to be available for all major farm animal species. The recent development of sequencing techniques calls for new methods of data management and analysis and for new ideas for the extraction of information. To make sense of this information in practical conditions, integration of geo-environmental and socio-economic data are key elements. The study and management of farm animal genomic resources (FAnGR) is indeed a major multidisciplinary issue.The goal of the present Research Topic is to collect contributions of high scientific quality relevant to biodiversity management, and applying new methods to either new genomic and bioinformatics approaches for characterization of FAnGR, to the development of FAnGR conservation methods applied ex-situ and in-situ, to socio-economic aspects of FAnGR conservation, to transfer of lessons between wildlife and livestock biodiversity conservation, and to the contribution of FAnGR to a transition in agriculture (FAnGR and agro-ecology).