Proceedings of the Joint Meeting AGI-SIBV-SIGA
Assisi, Italy – 19/22 September, 2011
ISBN **978-88-904570-2-9**

Poster Communication Abstract – 9.51

MITOCHONDRIAL DNA HAPLOGROUP R IN MODERN CATTLE: A CONTRIBUTION OF ITALIAN AUROCHSEN?

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Bovine mitochondrial DNA, domestication, European aurochsen, Bos primigenius

The debate on the genetic contribution of European aurochsen to taurine cattle gene pool after the generally agreed Neolithic domestication that occurred in the Fertile Crescent from local *Bos primigenius*, is still open. We have sequenced the D-loop of 2032 taurine cattle from 40 European, 3 Egyptian and 7 Ethiopian breeds confirming the overall clustering within haplogroups of Near Eastern ancestry (T1, T2, T3 and T5), but also identifying 28 mtDNAs (1.4%) not clustering within haplogroup T. Complete mtDNA sequencing of non-T samples revealed 10 subjects belonging to the novel haplogroup R, which represents a very early split (~135 ky) in the mtDNA phylogeny of *B. primigenius*. The remaining 18 samples clustered within the recently discovered haplogroup Q. Phylogeographic data indicate that R mtDNAs might derive from female aurochsen of the Italian Peninsula sporadically included in domestic herds, whereas Q and T subclades were most likely involved in the same event of Neolithic domestication in the Near East.