

Provisional Book of Abstract

ASPA 26th Congress Turin (ITALY), June 17–20, 2025

#ASPA2025

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The 26th congress of the Animal Science and Production Association

“Innovations in animal sciences: shaping the way for a sustainable future is under patronage of

***Turin (ITALY),
June 17–20, 2025***

Venue

***Campus SAMEV (Scuola di Agraria e medicina Veterinaria)
Largo Braccini 2, Grugliasco (TO)– ITALY***

Robertsonian translocation 1-29: a focus on Sicilian breeds

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Robertsonian translocation 1;29 (rob(1;29)) is the most widespread chromosomal aberration in meat cattle, known to cause fertility impairment in heterozygous carriers. While karyological screening programs exist for some breeds, SNP data analysis has proven to be a faster and more cost-effective method to identify carriers. We analysed SNP data from 1,938 individuals across 11 Italian cattle breeds, routinely collected by breeders' associations. Principal component and haplotype analyses on the first 6Mb of BTA29 allowed us to screen for rob(1;29), and partitioning methods to identify the smallest subset of SNPs that could reliably detect carriers. The frequency of rob(1;29) carriers in 5 beef breeds of Podolian origin aligned with previous reports, while no carriers were identified in Piedmontese or Pezzata Rossa Italiana breeds. 2% of Modicana and Bruna Italiana, and 1% of Pezzata Rossa d'Oropa were carriers. A striking 40% of Cinisara individuals carried rob(1;29), with 4% being homozygous. Genomic inbreeding (F_{ROH}) analysis revealed that the Cinisara breed exhibited relatively low values, implying that its high frequency of rob(1;29) cannot be justified by high levels of inbreeding. One to three SNPs from this region were sufficient to distinguish between carriers and wild-type individuals. While no hotspots of high linkage disequilibrium (LD) were observed between BTA1 and BTA29 in heterozygous rob(1;29) individuals, the average LD was significantly higher in carriers compared to wild-type individuals. Pedigree analyses were performed in Modicana and Cinisara breeds to identify potential fertility-related issues associated with rob(1;29), not previously reported by breeders. After data cleaning, no differences were observed in the number of offspring, inter-calving intervals, or in longevity between carriers and wild-type individuals. Nevertheless, the data currently collected may not be reliable or comprehensive enough to allow a thorough and satisfactory evaluation of this issue. Our findings confirm the feasibility of using a small SNP set for rob(1;29) carrier detection, advocating its inclusion in routine genotyping panels. Particularly for breeds with a high prevalence of the translocation, like the Cinisara, systematic data collection, genotyping, and fertility monitoring programs are crucial to effectively study and manage rob(1;29).

Acknowledgements: ANARB, ANABIC, ANAPRI, and ANABORAPI associations.

Research supported by Agritech National Research Center and received funding from the European Union Next-GenerationEU (PIANO NAZIONALE DI RIPRESA E RESILIENZA (PNRR) – MISSIONE 4 COMPONENTE 2, INVESTIMENTO 1.4 – D.D. 1032 17/06/2022, CN00000022).