UNIVERSITY OF LJUBLJANA
Biotechnical Faculty

The possibilities of using genomic information in the selection of horses for meat production

M. Šimon[1], A. Kaić[2], B. Luštrek[1], K. Potočnik[1]

[1] University of Ljubljana, Biotechnical Faculty, Department of Animal Science, Groblje 3, 1230 Domžale, Slovenia

[2] University of Zagreb, Faculty of Agriculture, Department of Animal Science and Technology, Svetošimunska 25, 10000 Zagreb, Croatia

Presenter: Martin Šimon

Email: martin.simon@bf.uni-lj.si

NAČRT ZA OKREVANJE IN ODPORNOST

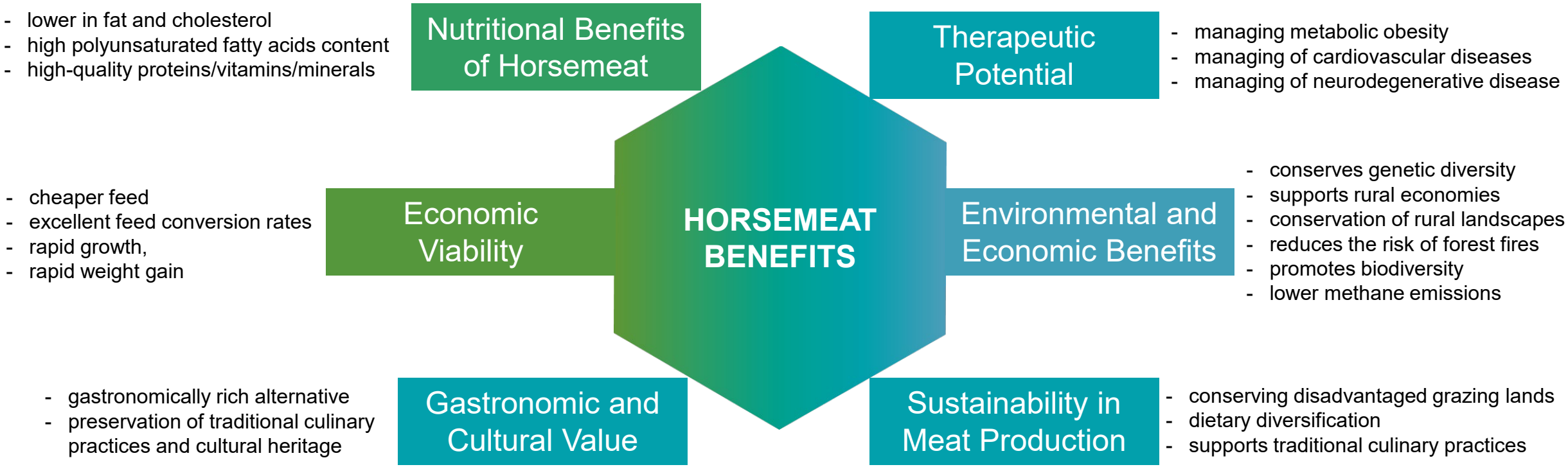
REPUBLIKA SLOVENIJA
MINISTRSTVO ZA KMETIJSTVO, GOZDARSTVO IN PREHRANO

Financira Evropska unija
NextGenerationEU

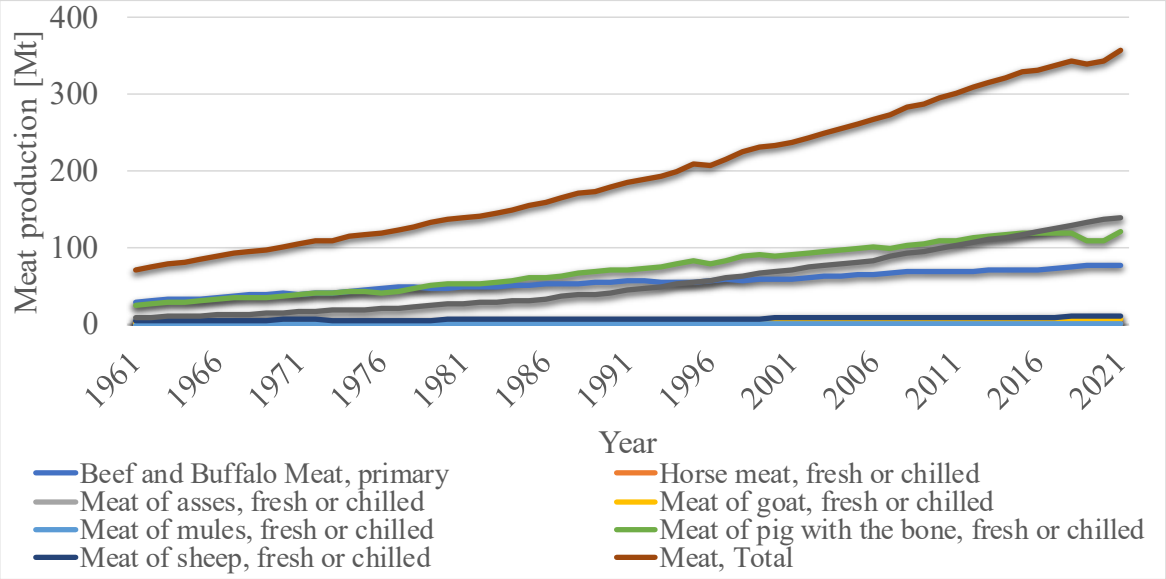
DigŽiv

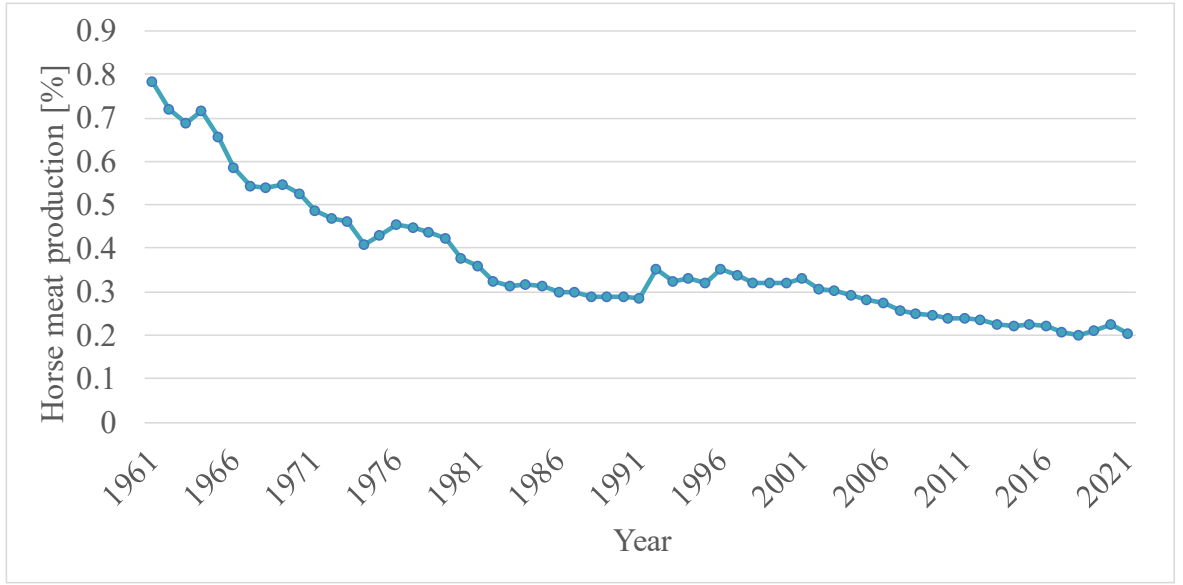
Introduction

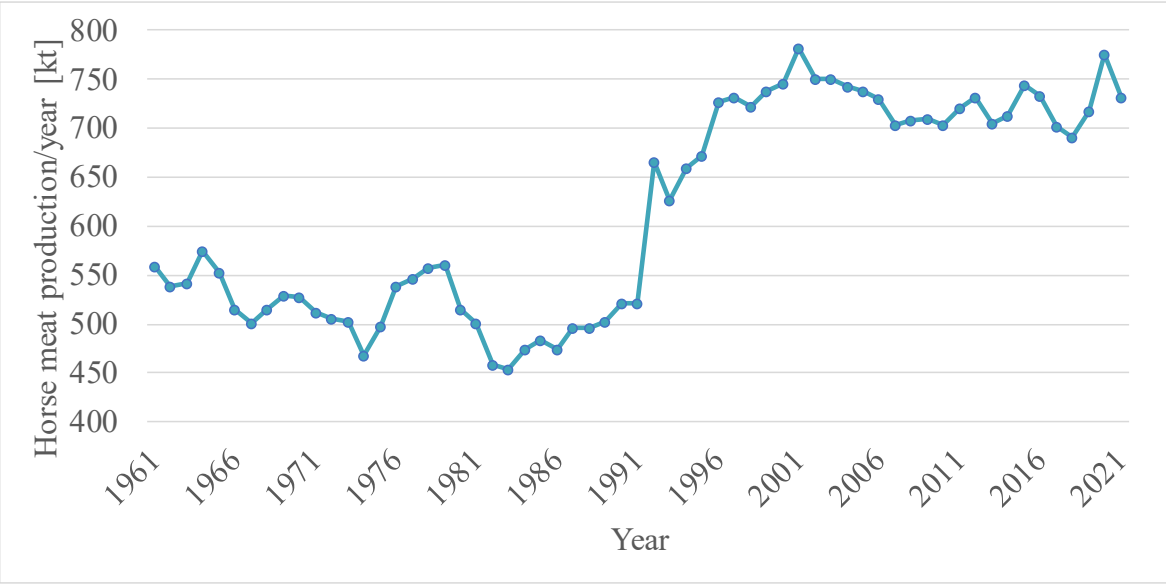
- With **global meat production** exceeding 350 million tons in 2021 and projected **to rise by 30-60% by 2050**, the urgency of finding sustainable sources of meat is clear.
- **Horsemeat represents a viable alternative**, particularly in light of high quality meat demands and the environmental challenges posed by resource-intensive meat production methods.

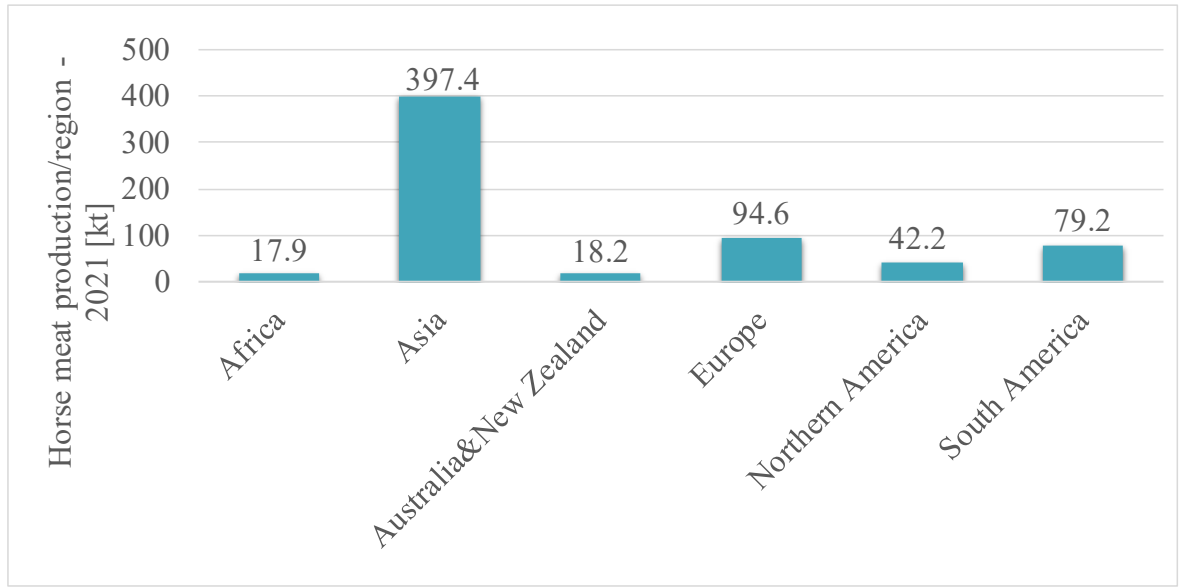


Introduction



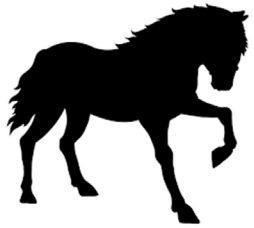






Introduction

- Efforts to **genotype horses, particularly concerning their production potential, have been neglected**. Moreover, the most comprehensive publicly available database on QTLs and single-nucleotide polymorphism/gene association data of livestock species does **not contain QTLs or associated genes/markers related to equine production traits**.



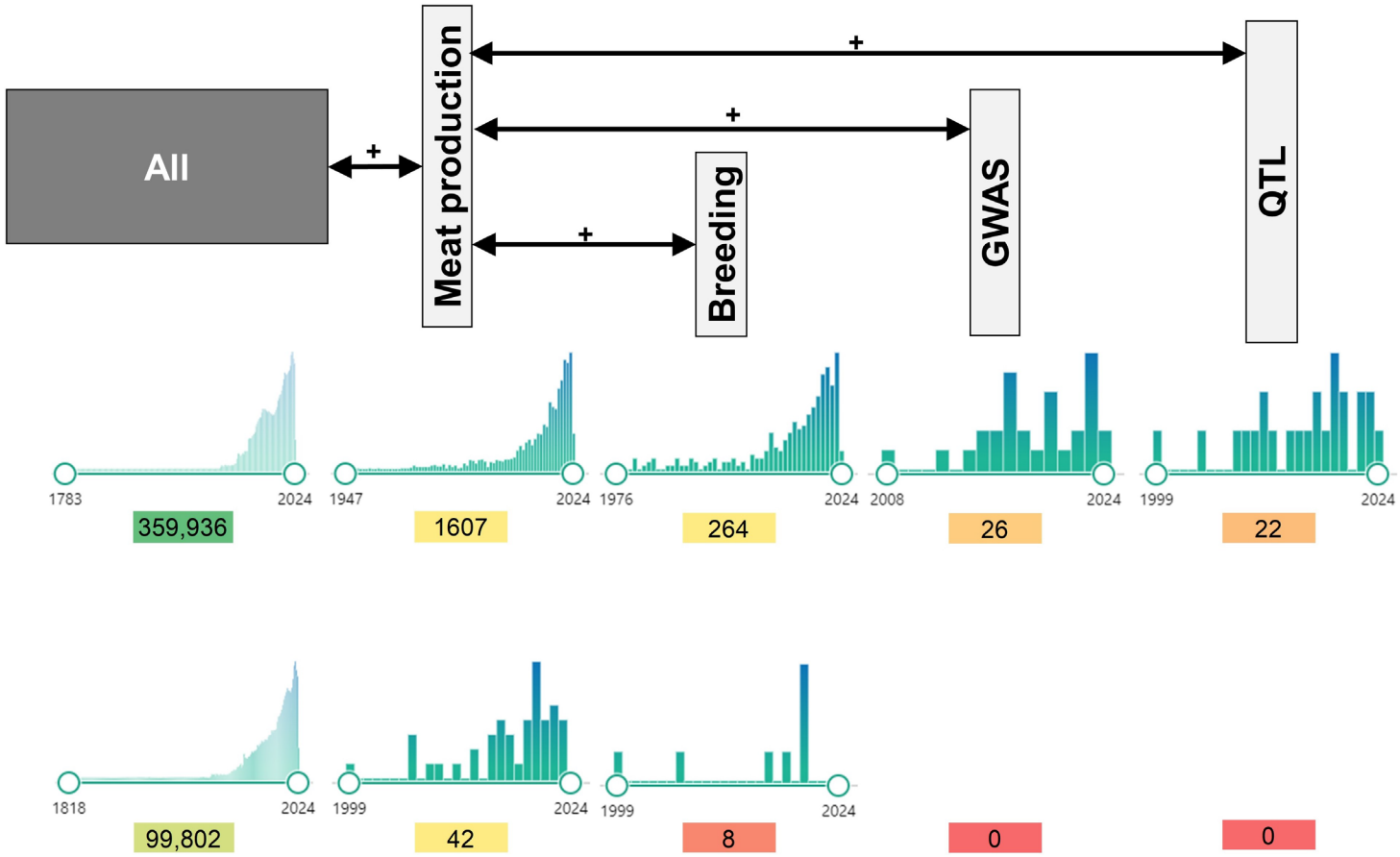


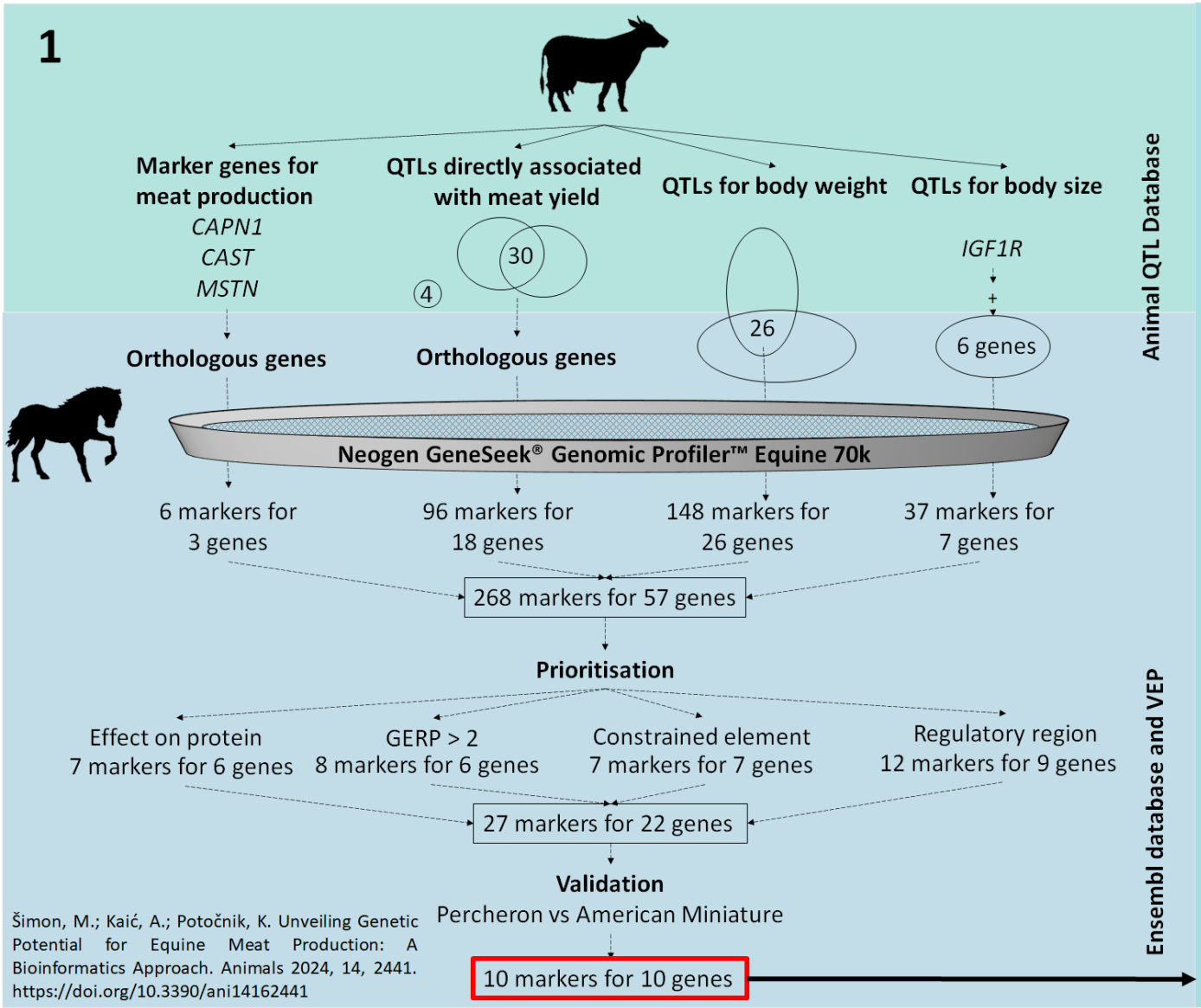
Figure: Comparative analysis of genetic research in cattle and horses for meat production (1783–2024) using keyword and searched in PubMed database.

Aims

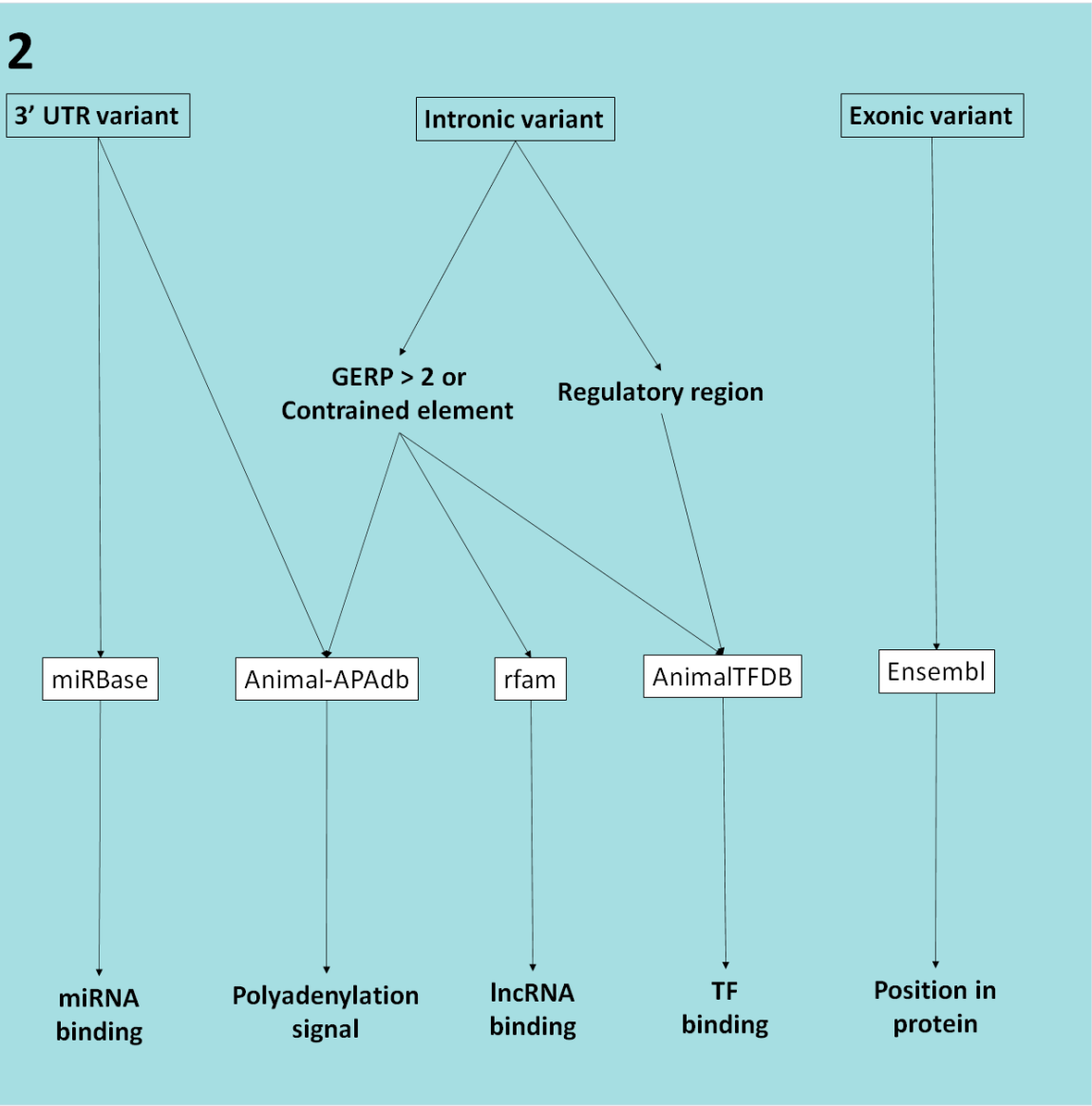
- To address this gap, we conducted a comparative genomic analysis with cattle, which have:
  - significant physiological and genetic similarities to horses,
  - extensive genomic and QTL data,
  - pigs, being omnivores in intensive systems, are less suitable as models,
  - sheep and goats share grazing behavior with horses but lack sufficient genomic research.

- Therefore, this study aims to:
  - apply cattle QTL knowledge to horses by prioritizing markers on the GGP Equine chip,
  - assist horse breeders in their decision-making processes,
  - enrich findings with GWAS and other genomic evaluations for future advancements.

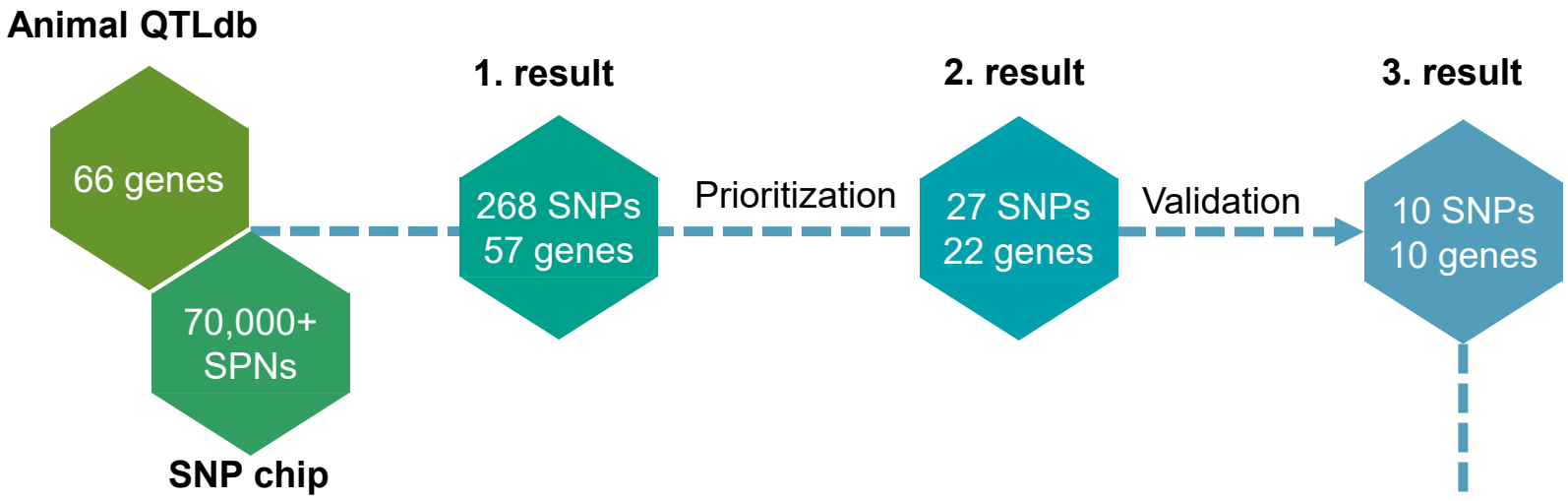
Material and Methods



Šimon, M.; Kaić, A.; Potočnik, K. Unveiling Genetic Potential for Equine Meat Production: A Bioinformatics Approach. Animals 2024, 14, 2441. https://doi.org/10.3390/ani14162441



Results



Gene symbol	Marker	SNP ID	Variant Consequence	Potential effect on protein	GERP > 2	Constrained element	Regulatory element	Percheron	American Miniature
C18H2orf88	BIEC2_417365	rs69126368	intronic variant			✓		A|G	G|G
DNAH7	Affx-102281324	rs396935555	missense variant	✓				C|T	T|T
ENSECAG00000052525	GGP_100_BODY_SIZE_ECA3	rs68603064	intronic variant				✓	C|C	T|T
FAM184B	BIEC2_808625	rs68454110	intronic variant				✓	C|C	T|T
IGF1R	BIEC2-44702	rs68514854	intronic variant				✓	G|A	A|A
LASP1	BIEC2_144152	rs68875002	intronic variant				✓	T|T	C|C
	BIEC2_144165	rs68876315	intronic variant				✓	C|C	C|T
LGI2	UKUL843	rs1147560021	3 prime UTR variant		✓			C|T	T|T
MSTN	BIEC2_417365	rs69126368	intronic variant			✓		A|G	G|G
PCDH7	UKUL834	rs68555658	intronic variant		✓			T|G	G|G
QDPR	BIEC2_808653	rs68520444	intronic variant				✓	A|A	A|G

Results

Table: For TF, lncRNA, and miRNA binding, only those present in the DNA sequence with the reference allele but not with the alternative allele, and vice versa, are shown.

Gene symbol	SNP ID	Variant Consequence	Ref. Allele	Alt. Allele	Percheron	American Miniature	TF binding		lncRNA binding		miRNA binding	
							Ref. Allele	Alt. Allele	Ref. Allele	Alt. Allele	Ref. Allele	Alt. Allele
C18H2orf88	rs69126368	intronic variant	A	G	A|G	G|G	ALX4, ARID3B, DUX4, LHX3, MIXL1, UNCX	GATA3, HDX, ONECUT1-3, PAX3, PAX7	ENSECAG00000046689.1, ENSECAG00000059506.1	ENSECAG00000052995.1, ENSECAG00000039246.2, ENSECAG00000050111.1, ENSECAG00000054519.1, ENSECAG00000031841.2, ENSECAG00000049441.1, ENSECAG00000048120.1		
*DNAH7**	rs396935555	missense variant	C	T	C|T	T|T						
ENSECAG00000052525	rs68603064**	intronic variant	T	C	C|C	T|T	MEF2A, MEF2C	TEAD1-2, ZNF254, ZNF317, ZNF85				
FAM184B	rs68454110	intronic variant	C	T	C|C	T|T	ESR1, ESRRA, KLF17, PAX2, PAX9, ZBTB3, ZNF322, ZNF8					
IGF1R	rs68514854	intronic variant	G	A	G|A	A|A	EGR1, ZNF587, ZFP202, MAZ, ZNF148, ZNF37A, GLIS1, ZNF436	CTCFL, JUN, SMAD2-4, ZNF263, ZNF529				
LASP1	rs68875002	intronic variant	T	C	T|T	C|C	ZFP12	RORA, TP73				
	rs68876315	intronic variant	C	T	C|C	C|T	ZNF33A	HDX, NR1I2, ZBTB3				
LGI2	rs1147560021	3 prime UTR variant	C	T	C|T	T|T					eca-mir-505 precursor	
MSTN	rs69126368	intronic variant	A	G	A|G	G|G	PHOX2B, ALX1, ALX4, ARX, PHOX2A, UNCX, DUX4, MIXL1, ARID3B, LHX3, ZNF419	ZNF85, GATA3, ONECUT1-3, PAX3, PAX7	ENSECAG00000048426.1, ENSECAG00000052521.1, ENSECAG00000054671.1, ENSECAG00000050523.1	ENSECAG00000056687.1, ENSECAG00000050248.1, ENSECAG00000052521.1		
PCDH7	rs68555658	intronic variant	T	G	T|G	G|G	RORA, RORB, RORC, ZFP112	CDX1, CDX4, ELK3-4, ETV4, HOXA9-13, HOXB13, HOXB9, HOXC9-13, HOXD9-12, PBX2, ZFP574, ZNF764				
QDPR	rs68520444	intronic variant	A	G	A|A	A|G	TRERF1	ZFP105				

* a missense variant rs396935555 alter amino acid in the dynein heavy chain, C-terminal domain

** *rs68603064 usually asigned to LCORL*

C18H2orf88 - chromosome 2 open reading frame 88; *DNAH7* - dynein axonemal heavy chain 7; *FAM184B* - family with sequence similarity 184 member B; *IGF1R* - insulin like growth factor 1 receptor; *LASP1* - LIM and SH3 protein 1; *LCORL* - ligand dependent nuclear receptor corepressor like; *LGI2* - Leucine rich repeat LGI family member 2; *MSTN* - myostatin; *PCDH7* - protocadherin 7; *QDPR* - quinoid dihydropteridine reductase

Discussion

- Key Findings
  - Identification of Potentially Functional SNPs:
    - The study identified SNP markers in key genes (*LCORL*, *LASP1*, *IGF1R*, *MSTN*) crucial for horsemeat production.
  - Regulatory Insights:
    - Analysis of TF binding, miRNA interactions, and other regulatory elements provides deeper insights into how these SNPs influence gene function and impact meat production traits.
- Implications:
  - Enhanced Breeding Programs:
    - The identified SNPs and their regulatory interactions can refine selective breeding strategies, supporting efficient and precise breeding programs.
    - Integration of these insights into large-scale genotyping (e.g., GWAS) will improve the accuracy of genomic breeding value predictions.
- Limitations:
  - Scope of Trait Coverage:
    - Not all meat production-related traits, such as chest circumference, body length, or quality parameters like fat deposition and marbling, were included in the analysis. This may limit the comprehensiveness of the breeding recommendations.
  - Transcript Focus:
    - The analysis was centered on canonical transcripts, which may have neglected other transcript variants that could play significant roles in meat production traits.
  - Inclusion Criteria:
    - The strict criteria for SNP inclusion may have led to the exclusion of potentially relevant markers, possibly overlooking some important genetic variations.
  - SNP Coverage:
    - The study did not include SNPs from whole genome sequencing that are in linkage disequilibrium with the identified markers. These SNPs could have provided additional insights into genetic variations affecting meat production.
- Future Directions:
  - Experimental Validation
  - Expanded Trait Analysis
  - Population-Specific Insights:
    - Assess genetic variability within populations to tailor breeding programs and refine breeder guidelines.

Conslusion

- Objective Achievement:
  - Our research successfully identified potential functional SNP markers in key genes (*LCORL*, *LASP1*, *IGF1R*, and *MSTN*) associated with meat production traits in horses using bioinformatic tools.
  - Predictive analyses of TF binding, miRNA interactions, and other regulatory elements provide insights into how these SNPs might influence gene function and impact meat production traits.
- Integration with DigŽiv Project:
  - The findings will be incorporated into the Digitization of Livestock Databases (DigŽiv) project, funded by the Recovery and Resilience Plan and the Ministry of Agriculture, Forestry, and Food.
  - This integration will help develop technical applications and databases that enhance routine selection work for breeders and professional services.
- Broader Application:
  - The principles and methodologies used in this study can be extended to other economically important traits and species, broadening the impact of this research beyond horsemeat production.

Thank you for your attention!

NAČRT ZA OKREVANJE IN ODPORNOST
REPUBLIKA SLOVENIJA
MINISTRSTVO ZA KMETIJSTVO, GOZDARSTVO IN PREHRANO
Financira Evropska unija
NextGenerationEU
DigŽiv

Acknowledgement

NAČRT ZA OKREVANJE IN ODPORNOST

REPUBLIKA SLOVENIJA
MINISTRSTVO ZA KMETIJSTVO, GOZDARSTVO IN PREHRANO

Financira Evropska unija
NextGenerationEU

DigŽiv

Digitalizacija podatkovnih zbirk v živinoreji

Kmetijski inštitut Slovenije

Univerza v Ljubljani
Biotehniška fakulteta
petinsedemdesetletnica

Univerza v Ljubljani
Veterinarska fakulteta