The European Chicken Commitment challenge: toward the use of novel genotypes with slower-growth rate for meat production

EU - Meat Changes
The European Chicken Commitment challenge: toward the use of novel genotypes with slower-growth rate for meat production

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Ministero dell'Università e della Ricerca
Italiadomani PIANO NAZIONALE DI RIPRESA E RESILIENZA

FROM MARKET INITIATIVES TO LEGISLATION

To whom?

How?

When?

What ?

Who?

The European Chicken Commitment (ECC) and the Better Chicken Commitment (BCC) are science-based chicken welfare policies that are approved and supported by animal welfare organizations all over the world.

The decision-making process for additional breeds to be accepted by the ECC involves:

The company working with the ECC organizations to test the genotype at an independent research center according to the RSPCA* Broiler Breed Welfare Assessment Protocol

The results have to be submitted to the Technical Working Group of the ECC

The company and the research institute conclude that the genotype meets the thresholds set by the protocol, then it can be accepted as an ECC-approved genotype.

The genotype has to go through additional stages of review and consultation, before the committee reviews, discusses, and then votes to make a decision.

*file:///C:/Users/Admin/Dropbox/Il%20mio%20PC%20(DESKTOP-PCLEOHS)/Downloads/RSPCA%20Broiler%20Welfare%20Assessment%20Protocol%20May17.pdf

AIM OF THE PROJECT

The **aim** of the project is to characterize ECC-approved chicken strains in terms of productive performance, metabolic traits, animal welfare indicators and product quality, according to

- **genotype-related factors**

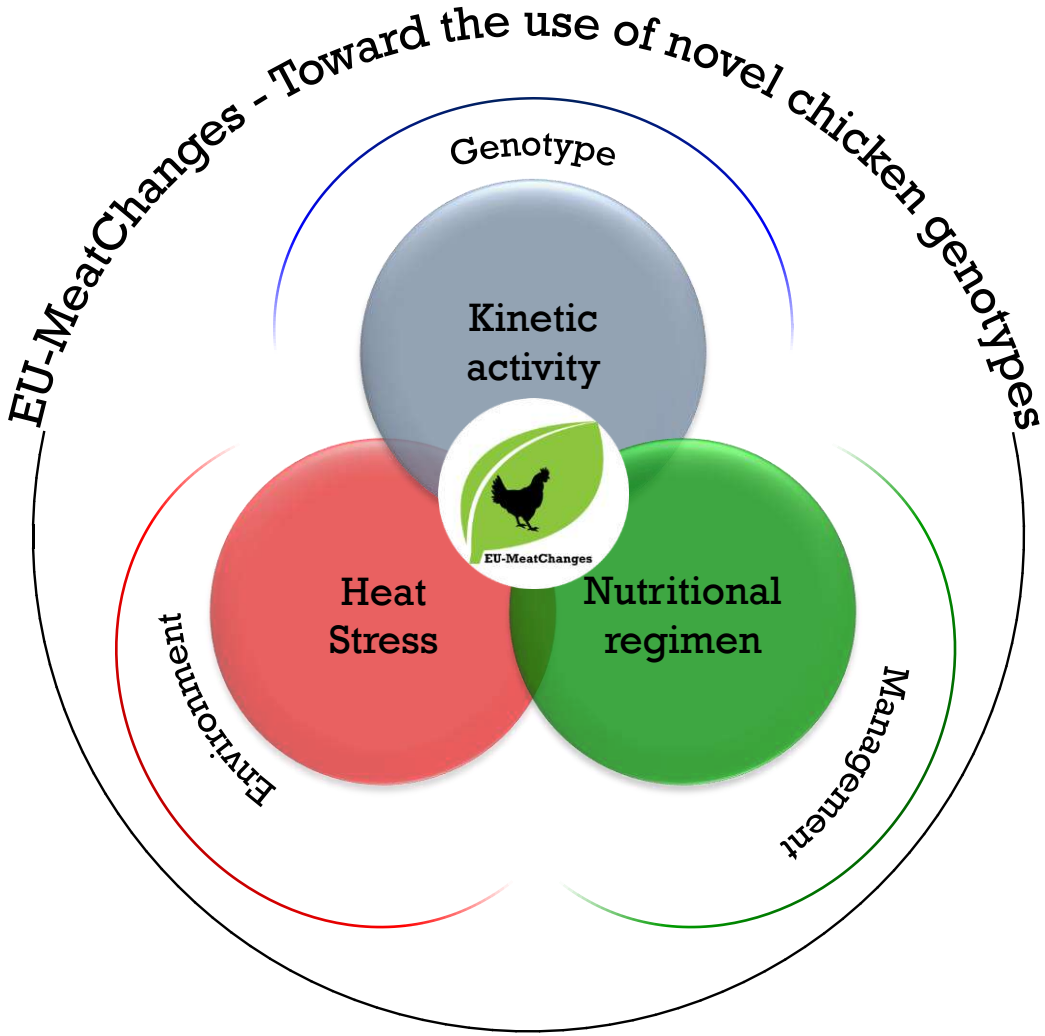
kinetic activity

- **environmental conditions**

heat stress exposure

- **nutritional regimens**

lysine-to-metabolizable energy ratio



ACTIVITIES

- WP1 whole project management (UNIPG)

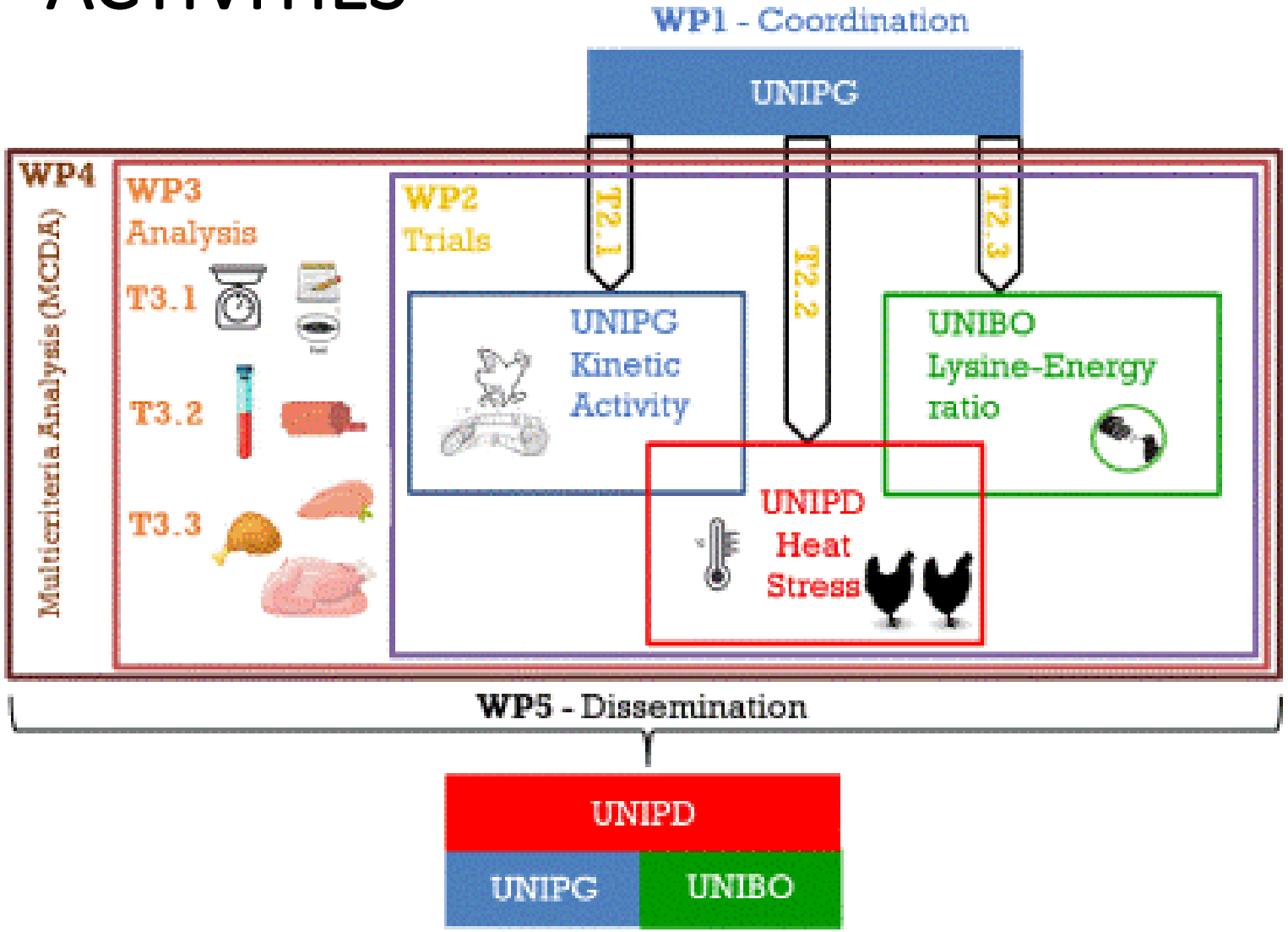
- WP2 animal trials (UNIPD):

T2.1 kinetic activity
T2.2 heat stress
T2.3 lysine-to-metabolizable energy ratio

- WP3 data acquisition and elaboration (UNIBO):

T3.1 Performance, health and welfare
T3.2 Metabolic traits
T3.3 Meat quality evaluation

- WP4 MCDA (UNIPG)



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Thanks for the attention

Preliminary results are coming….

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UNIPG team involved in the project

Prof. Simona Mattioli, Prof. Alessandro Dal Bosco, Prof. Cesare Castellini, Dr. Francesca Di Federico, Dr. Luigia Bosa, Dr. Lorenzo Nompleggio, Mr. Giovanni Migni, Mrs. Cinzia Boldrini

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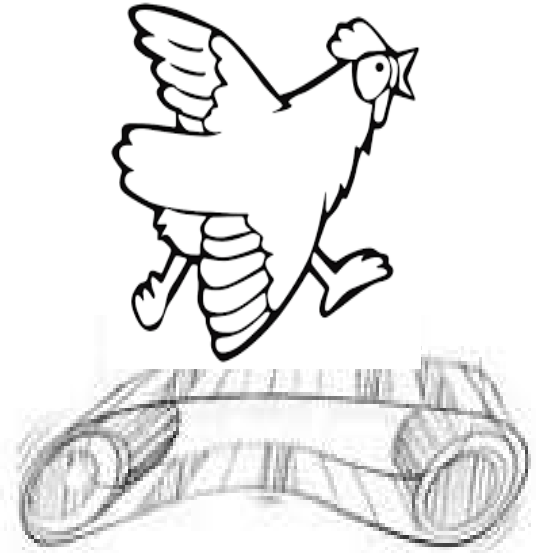

UNIPG
Kinetic
Activity

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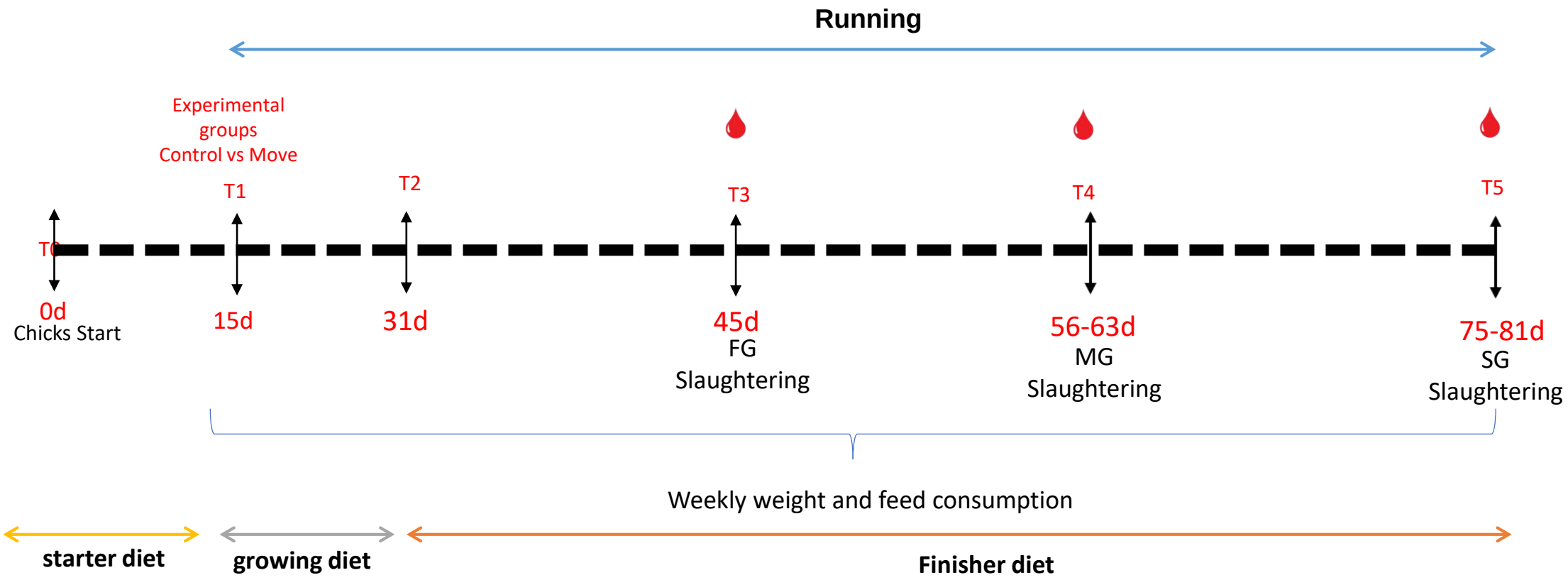
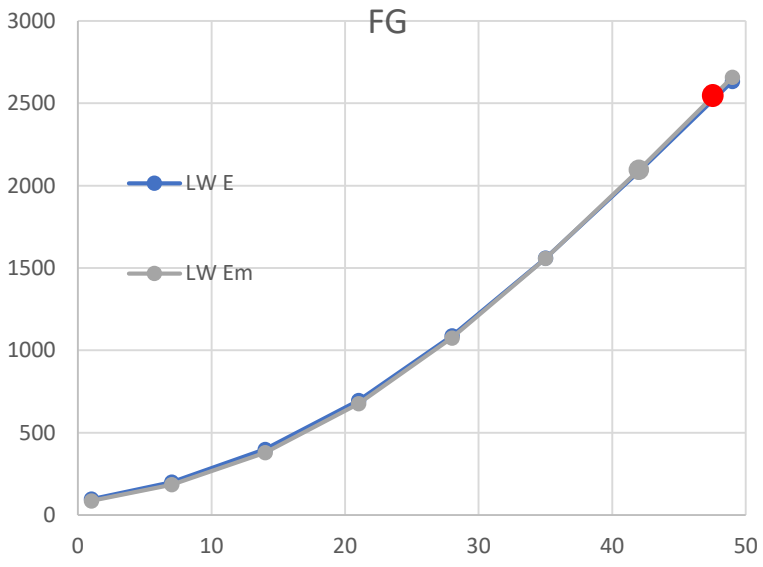
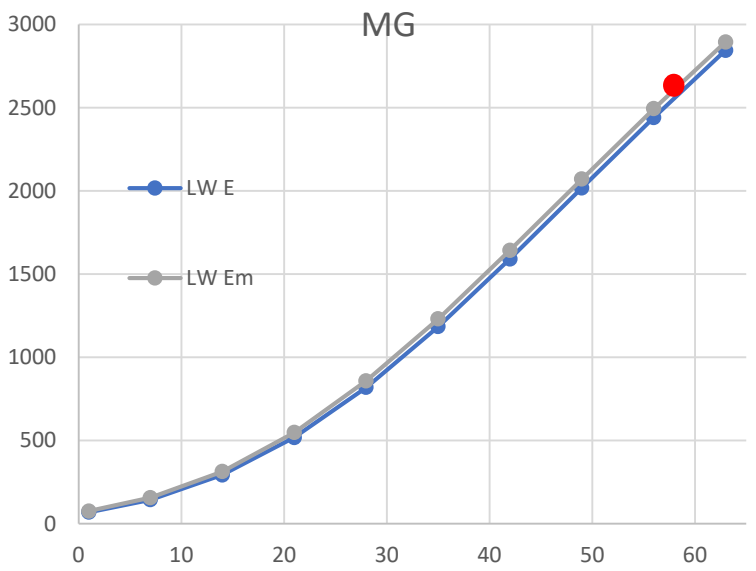
Experimental Plan

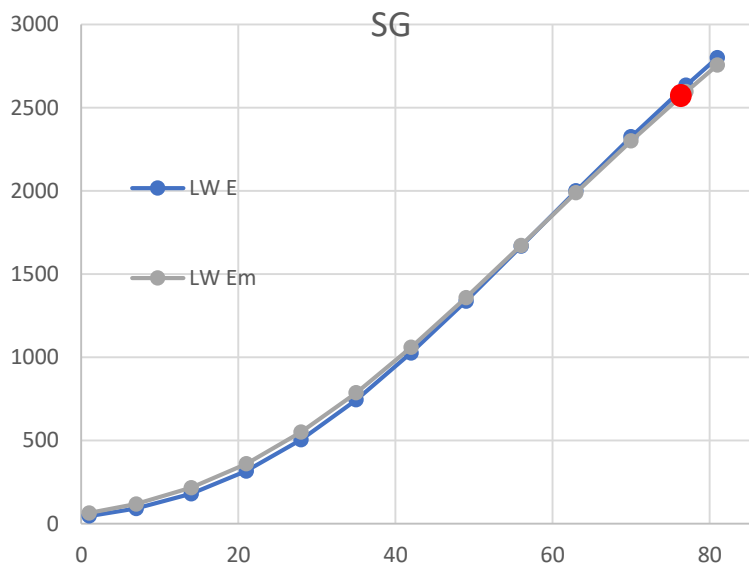


FG: 110 Ross= 50 C/ 50 M ->50 g/d
MG: 110 Ranger=50 C/ 50 M -> 40-45 g/d
SG: 110 Kabir=50 C/ 50 m -> 30-35 g/d

Performance *on farm – DWG (Gompertz)*







Muscle ^{1}H-NMR metabolomic analysis

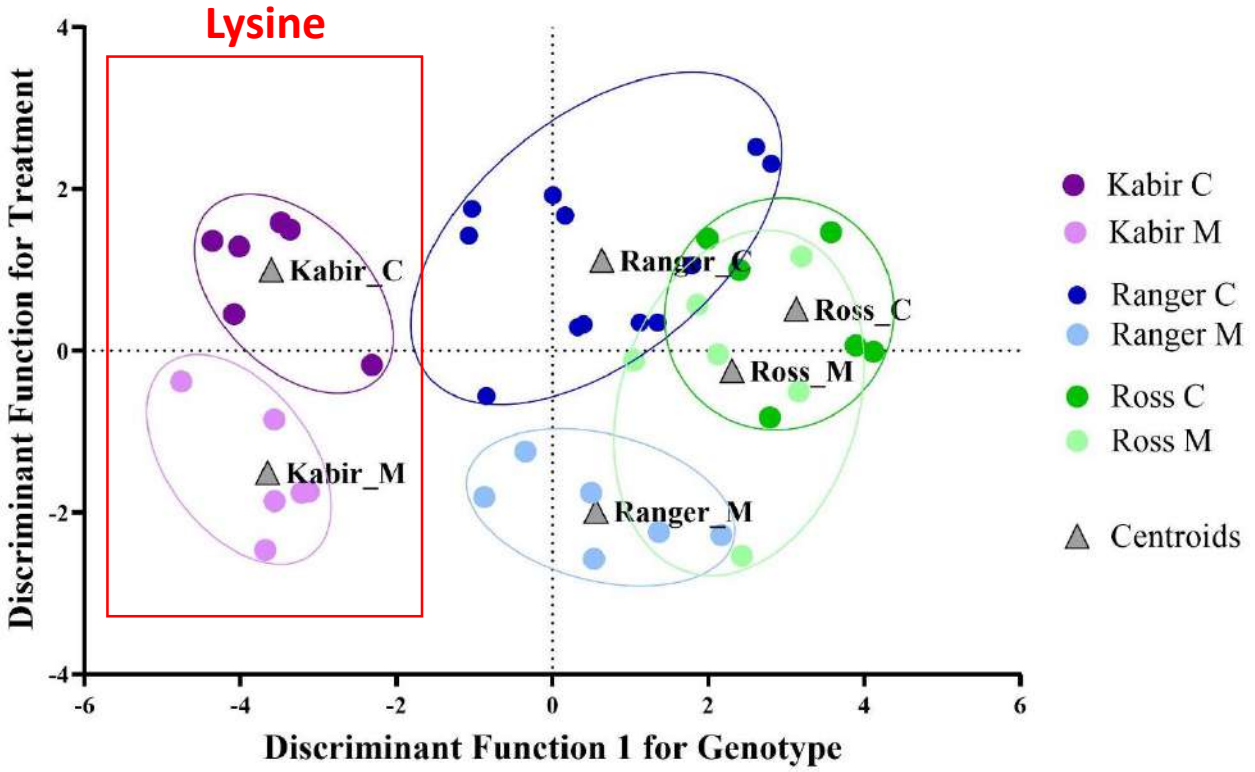
65 variables -> 38 variables -> 5 metabolism -> 10 PCs -> MANOVA 3x2 (genotype x treatment)

Energetic (EM)				Proteic (AAM)					Lipidic (LM)		Glucidic (GM)		Antioxidant (AM)	
Variable	PC			Variable	PC				Variable	PC	Variable	PC	Variable	PC
	1 EN	2 EN	3 EN		1 AA	2 AA	3 AA	4 AA		1 LIP		1 GLU		1 ANTIOX
IMP	.825			Tyrosine	.898				Acetate	.850	Glucose	.987	Beta-Alanine	.808
Fumarate	-.762			Asparagine	.776				Malonate	-.850	Mannose	.879	Glutathione	.808
NAD	.716		-.525	Alanine	.750						Lactate	.759		
Aspartate		.815		**Lysine**	**-.701**									
Creatine		.801		Serine	.645									
ADP		.750		Taurine		-.789								
AMP			.936	Methionine		.754								
				Pyruvate		.740								
				Isoleucine			.861							
				Leucine			.759							
				Phenylalanine			.701							
				Glycine				.857						
				2-Oxoglutarate				-.714						
% of variance	34.00	25.45	17.23	% of variance	39.75	13.15	12.81	7.76	-	-	-	-	-	-
Total variance (%)	76.68			Total variance (%)	73.46				Total variance (%)	72.20	Total variance (%)	77.39	Total variance (%)	65.25

-> Discriminant analysis (DAs) where PCs are indipendent variables

Standardized Canonical Discriminant Function Coefficients and centroids						
Genotype				Treatment		
Variable	Wilks' lambda	Df 1	Df 2	Variable	Wilks' lambda	Df 1
PC 1 LIP#	**.387*** **	**-.472**	**.431**	**PC 3 EN#**	**.734*** **	-1.038
PC 1 AA#	**.543*** **	**.916**	.079	PC 1 GLUC	.938^{ns}	-.744
PC 2 EN#	.585***	-.206	.500	PC 2 EN	.961^{ns}	.035
PC 1 EN	.596***	.104	.117	PC 2 AA	.976^{ns}	-.810
PC 1 GLUC#	.608***	-.448	-.591	PC 1 AA	.981^{ns}	.799
PC 3 AA	.625***	.471	.855	PC 1 LIP	.984^{ns}	1.243
PC 1 ANTIOX	.751**	-.194	-.737	PC 3 AA	.991^{ns}	.306
PC 4 for AA#	**.777** **	**1.017**	.305	PC 1 for ANTIOX	.996^{ns}	-.471
PC 2 for AA#	.804*	-.472	-.339	PC 4 for AA	.998^{ns}	.506
PC 3 for EN	.885^{ns}	-.007	.168	PC 1 for EN	1.000^{ns}	.937
Functions at Group Centroids				Functions at Group Centroids		
Kabir		-3.628	.837	C		.936
Ranger		.609	-1.682	M		-1.248
Ross		2.715	1.685			

Results



Take home message

- ✓ GEN: The variables analysed determine a clear separation between FG and SG, implying notable differences in their proteic and lipidic/energetic metabolism.
- ✓ TRT: The treatment affects energetic metabolism mostly in SG (Kabir) and MG (Ranger).

EACH GENOTYPE SHOWS A DIFFERENT METABOLISM

Thank you for the attention

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