VARIANT DISCOVERY IN GENES IDENTIFIED AS DIFFERENTIALLY EXPRESSED GENES BETWEEN THE ABOMASAL LYMPH NODE TRANSCRIPTOME OF RESISTANT AND SUSCEPTIBLE ADULT SHEEP TO *TELADORSAGIA CIRCUMCINCTA* INFECTION

Chitneedi[1], P.K., Suárez-Vega[1], A., Martínez Valladares[2,3], M., Arranz[1] J.J. y Gutiérrez-Gil[1], B.

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INTRODUCTION

Gastrointestinal nematode infections are one of the major health issues facing grazing sheep populations and it incurs on major economic losses for sheep breeders. The resistance/susceptibility trait appears to be a highly complex trait (Behnke et al. 2003; Dominik 2005). In sheep resistance to nematode infection shows a moderate level of heritability (range 0.3-0.6) (Stear et al. 2001). Several QTL mapping studies have tried to identify genomic regions and mutations that influence resistance to nematode infection (Atlija et al. 2016; Coltman et al. 2001; Gutiérrez-Gil et al. 2009; Sayers et al. 2005), although the detection of causal mutations for this trait is still a challenge for the research community. The recently available RNA-seq technology provides the opportunity to extract high-throughput transcriptome data from a specific tissue to perform gene quantification, differential gene expression and detection of variants (SNPs and indels), which could be assessed as potential causal mutations (Hudson, Dalrymple, and Reverter 2012). A previous study of our research group has identified a list of 106 differential expression genes (DEGs) based on RNA-Seq dataset obtained from the abomasal lymph nodes of 12 adult sheep, previously classified as resistant or susceptible to GIN infection based on an artificial infection with *T. circumcincta* larvae Chitneedi et al. (2018). In the present study we present a detailed study of the variants mapping within the list of DEGs previously reported in that study. Thus, the present study provides a list of functionally relevant variants that could underlie the genetic control of resistance/susceptibility to *T. circumcincta* in adult sheep.

MATERIALS AND METHODS

Experimental infection: The animals included in the present study were 12 adult ewes of Churra sheep from a commercial flock of Churra dairy breed reared under a semi-intensive management and belonging to the National Association of Spanish Churra sheep breeders (ANCHE). These animals were subjected to two experimental infections with *T. circumcincta* larvae, as described in detail by Chitneedi et al. (2018).

RNA sequencing: From the six resistant and the six susceptible sheep included in this study, mRNA was extracted from abomasal lymph nodes, using the Absolutely RNA miRNA Kit from Agilent (La Jolla, CA, USA). RNA integrity (RIN value) was analyzed using the Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA). The average RIN values of the RNA samples was 7.2 ranging between 6.7 and 7.5. After library preparation, the subsequent sequencing was performed with an Illumina HiSeq sequencer 2000, generating stranded paired-end reads of 75 base pairs with a depth of 30 million reads.

Bioinformatics analysis: The read quality of the 12 abomasal lymph node samples was determined using FastQC_v0.11.5 (Bioinformatics 2011). All the samples were aligned against the ovine genome assembly v.3.1 (Oar_v3.1) using the STAR_v2.5.3a aligner (Dobin et al. 2013). After alignment, editing read groups and marking duplicate reads were carried out with Picard_v2.9.0 (Broad Institute 2016). Then, the pre-processing of aligned reads, including read trimming, realignment and recalibration was performed with GATK_v3.7 (Van der Auwera et al. 2013). The variant calling analysis was individually performed using two different software, GATK_v3.7 and SAMTOOLS_v1.4 (Wysoker et al. 2009). Later, quality filters were applied independently to each of the resulting VCF files. The variants detected by Samtools were filtered with SnpSift (QUAL > 30) whereas for the GATK-detected variants the GATK specific filtering recommendations were followed (DP > 5 & QUAL > 30 & MQ > 40.0 & QD > 5.0 & FS < 60.0). After that, variants commonly identified by the two independent software were extracted with BCFtools_v1.4 ("isec" option) (Wysoker et al. 2009) and were considered as high-quality variants.

With the aim of characterizing transcriptome variants that may underlie sheep resistance to GIN, we used SnpEff ("–fi" option) followed by a bed file with the coordinates of the 106 DEGs reported by Chitneedi et al. (2018) to select the variants included in the studied genes. The variants extracted from the DEG coordinates were individually annotated for functional consequences with the software VEP_v90 (McLaren et al. 2016) and SnpEff_v4.3 (Cingolani et al. 2012). Later, we selected, for each subset, those predicted by the two annotation analyses to have relevant functional consequences (classified as HIGH or MODERATE impact). The selected variants were annotated with the online web tool VEP (https://www.ensembl.org/Tools/VEP) and the amino acid substitution effects on protein function were predicted using the SIFT algorithm (Kumar, Henikoff, and Ng 2009).

RESULTS AND DISCUSSION

The pipeline followed for variant discovery with the transcriptome data of abomasal lymph node is shown in Figure 1. Based on the FastQC estimates, all the 12 samples analyzed were of high quality; thus, no trimming was performed. After aligning against the ovine reference genome (Oar_v3.1) around 80.27% paired reads per sample were uniquely mapped against the reference genome and around 8.5 % paired reads were mapped to multiple loci. After performing the variant calling and variant filtering, we found 1,326,960 common variants considered as high quality variants across the whole genome. From these high-quality variants, we extracted 6,168 variants (6,104 SNPs, 30 insertions and 34 deletions) mapping within the 106 DEGs. Among these, 332 variants (329 SNPs, 3 insertions and 2 deletions) were predicted to be of relevant functional impact ("High" and "Moderate"). The functional annotation of these variants with the VEP, which included 109 novel variants revealed a total of 471 functional consequences distributed across 60 genes. From these, the SIFT algorithm detected 50 deleterious variants most were missense consequence and two were splice region variants. These deleterious variants were included in a total of 15 genes. Four of these genes, *BPIFB1* (Zhou et al. 2017), *KRT20* (Sen et al. 2012), *SLC38A2* (Carter 2012) and FNDC1 (Sigdel et al. 2015) have been found to be associated with the immune response. Another gene harboring a missense deleterious variant was *MMP28*, which has been reported as responsible for cell proliferation in response to skin injury (Saarialho-Kere et al. 2002). Other genes harboring "High" impact variants were *LGALS4* (splice acceptor variant), *SLC38A2* (stop lost), *ASIC3* (stop gained and splice acceptor variant), and *SULF1* (frameshift variant). Future studies focusing on the

variations in these gene regions and pathway analysis combining these genes may provide information about potential causal mutations related to resistance against GIN infection in sheep. In addition, the deleterious variants which are located in the non-annotated gene regions were equally important for further investigation.

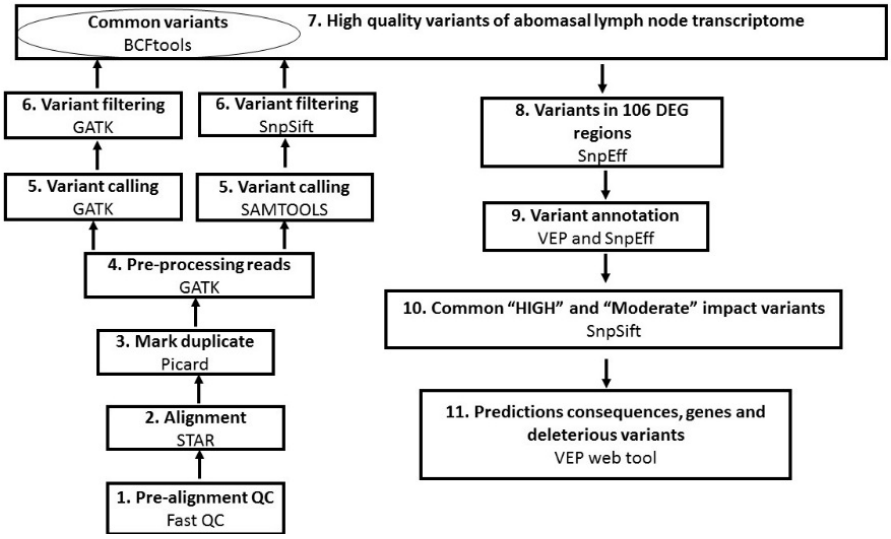

Figure 1. *The pipeline shows the steps followed and tools used to detect variants and the consequences related to nematode infection in sheep found in DEG regions.*

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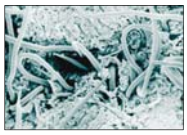
VARIANT DISCOVERY IN GENES IDENTIFIED AS DIFFERENTIALLY EXPRESSED GENES BETWEEN THE ABOMASAL LYMPH NODE TRANSCRIPTOME OF RESISTANT AND SUSCEPTIBLE ADULT SHEEP TO *Teladorsagia circumcincta* INFECTION

Chitneedi, P.K[1]., Suárez-Vega, A[1]., Martínez Valladares, M[2,3]., Arranz J.J[1]. y Gutiérrez-Gil, B[1].
1 Departamento de Producción Animal, Facultad de Veterinaria, Universidad de León, 24071 León.
2 Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad de León, Campus de Vegazana s/n, 24071 León, Spain 3 Instituto de Ganadería de Montaña, CSIC-Universidad de León, 24346, Grulleros, León, Spain. pchi@unileon.es

XIX REUNIÓN NACIONAL DE MEJORA GENÉTICA ANIMAL
León, 14 y 15 de junio de 2018
Paraninfo de la Facultad de Veterinaria, Universidad de León

Introduction

Churra sheep



Teladorsagia circumcincta (Robin et al. 2007)

- Gastrointestinal nematode (GIN) infections are one of the major health issues facing grazing sheep populations. The resistance/susceptibility trait appears to be a highly complex trait.
- Several QTL mapping studies have tried to identify genomic regions and mutations[1,2] but the detection of causal mutations for this trait is still a challenge for the research community.
- The RNA-Seq technology provides the opportunity to perform gene quantification, differential gene expression and detection of variants with high-throughput transcriptome data from a specific tissue.
- In a previous study, we identified a list of 106 differential expression genes (DEGs) based on RNA-Seq dataset obtained from the abomasal lymph nodes of 12 adult sheep[3].

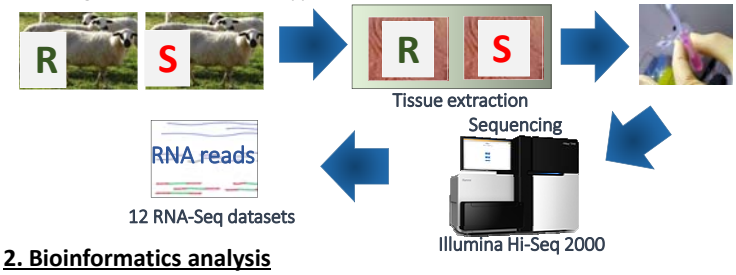
Objective: In the present study, we have performed a variant calling analysis on the same RNA-Seq dataset with a focus on the list of the reported 106 DEGs.

We present a list of functionally relevant variants that could underlie the genetic control of resistance/susceptibility to *T. circumcincta* in adult sheep.

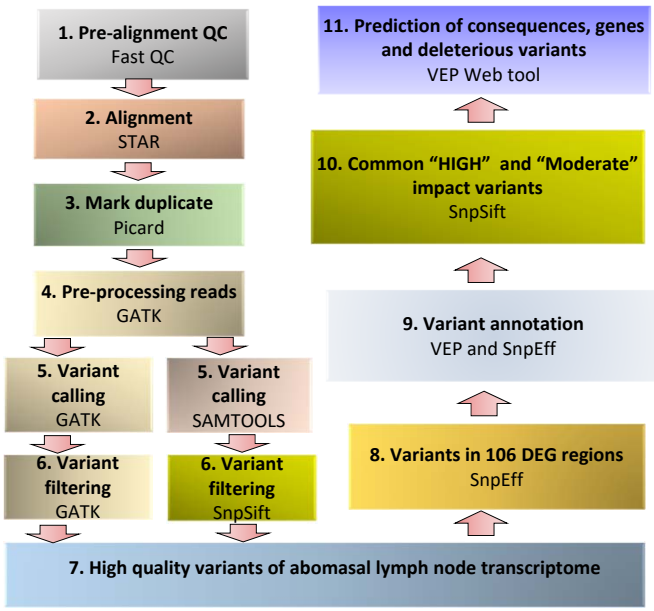
Materials and methods

1. Experimental infection, RNA extraction and RNA-Seq

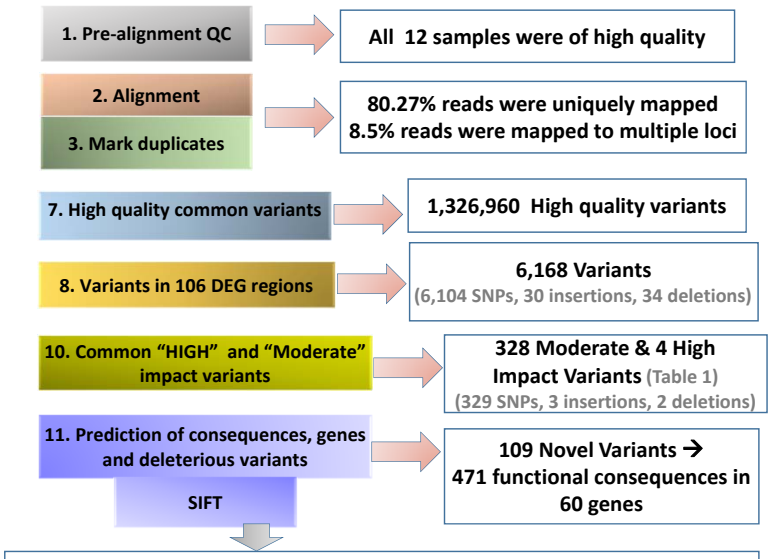
- 12 adult Churra ewes previously classified as 6 resistant (R) and 6 susceptible (S) to *T. circumcincta* were subjected to an experimental infection (EI). After seven days after, animals were humanitarian sacrificed.
- RNA samples were extracted from abomasal lymph node tissue, sequenced through an Illumina RNA-Seq protocol.



2. Bioinformatics analysis



Results and Discussion



- **We found 50 deleterious missense consequences, 25 of them located in 15 genes with known symbol ID.**
- **Some of these genes harboring missense were related to the immune response according the literature review.**

Immune response

BPIFB1[4], KRT20[5], *SLC38A2*[6], *FNDC1*[7].

Cell proliferation in response to skin injury

MMP28[8]

Table 1: "High" Impact variants identified by both VEP and SnpEff.

S. No	Gene	Location	Consequence
1	*LGALS4*	OAR14:47718975-47718975	splice acceptor variant
2	*SLC38A2*	OAR3:139947003-139947003	stop lost
3	*ASIC3*	OAR4:113023157-113023157	stop gained and splice acceptor variant
4	*SULF1*	OAR9:46254552-46254553	frameshift variant

Conclusion

- ✓ This study has identified genetic variants in genes previously identified as differentially expressed in relation to GIN resistance/susceptibility in adult sheep.
- ✓ The variants predicted to have a potential functional impact should be assessed through future studies as potential relevant variation underlying the genetic architecture of sheep GIN resistance in adult sheep.

References

1. Coltman et al. 2001. Parasitology, 122: 571–82.
2. Atlija et al. 2016. Genet Sel Evol, 48: 4.
3. Chitneedi et al. 2018. Vet Res 49.1: 39.
4. Zhou et al. 2017. Open Med (Wars) 12: 299–307.
5. Sen et al. 2012. Proc Natl Acad Sci U S A, 109: 20667–72.
6. Carter 2012. Physiol Rev, 92: 1543–76.
7. Sigdel et al. 2015. J Immunol Res, 2015: 848790.
8. Saarialho-Kere et al. 2002 J Invest Dermatol, 119:14-21.

Acknowledgements

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PROGRAMA

XIX REUNIÓN NACIONAL DE MEJORA GENÉTICA ANIMAL
León, 14 y 15 de junio de 2018

http://xixrnmga.unileon.es/

Organiza: Grupo de Mejora Genética Animal de la Universidad de León.

@VetGeneULE

Lugar: Paraninfo de la Facultad de Veterinaria de la Universidad de León.

Jueves 14 de junio

8:15 – 9:00: Recogida de documentación.

9:00 – 9:15: Presentación de la XIX Reunión Nacional de Mejora Genética Animal.

JUAN JOSÉ ARRANZ. Coordinador de la Jornada. Universidad de León.

9:15 – 10:00: PONENCIA INVITADA 1

"Domestication of salmon and sheep: contrasting patterns of genomic diversity and signatures of selection"

JAMES KIJAS. CSIRO, Australia

10:00 – 11:30: Sesión 1.
Moderadora: Romi Pena (U. de Lleida).

10.00: Experimento de mejora de la resiliencia en cerdos**. Joan Estany. Universidad de Lleida.**
Fraile L., Abella G., Novell E., Tarancón V, Pena R.N., y Estany J.

10.15: Programa de evaluación genética de verracos de distintos orígenes ganaderos para caracteres de calidad. **Juan Mª García Casco, Centro de I+D en Cerdo Ibérico, INIA Badajoz**.
Duarte J.L., Ureta P., Diéguez E., Moreno B., Moreno P., Navarro S., Fernández Barroso M.A., Caraballo C., López García A., Muñoz M., y García Casco J.M.

10.30: Identificación de regiones genómicas asociadas con fertilidad e indicadores de la capacidad de fertilización de toros Holstein. **Gabriel Molina. Universidad Politécnica de Valencia; INIA, Madrid**.
Molina, G., Carabaño, M.J., Karoui, S., y Díaz, C.

10.45: Genetic analyses of fertility traits in Italian Brown Swiss and Simmental breeds. **María Martínez Castillero. University of Padova, Italia.**
Castillero, M.M., Varona, L., y Cecchinato, A.

11.00: Evaluación genética en espacios paramétricos circulares: el caso de la estacionalidad en ovinos. **Quim Casellas. Universitat Autònoma de Barcelona**.
Casellas, J., Martín de Hijas Villalba, M., Id-Lahoucine, S.

11.15: Distorsión de la segregación mendeliana en el genoma bovino: patrones de naturaleza alélica y genotípica. **Samir Id-Lahoucine. University of Guelph, Canadá**.
Id-Lahoucine S., Casellas, J., Suárez-Vega, A., Miglior, F., Fonseca, P.A.S., Sargolzaei, M., Miller, S., Schenkel, F., Medrano, J.F., y Cánovas, A.

11.30: Evaluación funcional de las regiones con distorsión de la segregación mendeliana especifica de sexo en ganado vacuno lechero. **Aroa Suarez-Vega. University of Guelph, Canadá**.
Suárez-Vega, A., Id-Lahoucine, S., Miglior, F., Casellas, J., Fonseca P.A.S., Sargolzaei, M., Miller, S., Schenkel, F., Medrano, J. F., y Cánovas, A.

11:45 – 12:05. Café

12:05 – 13:45: Sesión 2.
Moderador: María Saura (INIA, Madrid).

12.05: The metagenome can predict feed efficiency: a validation study. **Óscar González Recio. INIA, Madrid.**
González-Recio,O., Delgado, B., Guasch, I., González, C., Elcoso, G., Pryce, J.E., y Bach, A.

12.20: Estudio preliminar sobre la caracterización del microbioma de la glándula mamaria en ovejas Assaf en lactación**. Cristina Esteban. Universidad de León.**
Esteban-Blanco, C., Gutiérrez-Gil, B., Marina, H., Linaje, B., Acedo A. y Arranz, J.J.

12.35: The bovine other genome: a catalog of genes of the bovine rumen microbiome. **Yuliaxis Ramayo Caldas. IRTA, Barcelona.**
Li, J., Zhong, H., Ramayo-Caldas, Y., Terrapon, N., Lombard, V., Potocki-Veronese, G., Estellé, J., et al.

12.50: Determinismo genético de la microbiota intestinal del conejo. **María Velasco-Galilea. IRTA, Barcelona.**
Velasco-Galilea, M., Piles, M., Viñas, M., Rafel, O., Gónzalez-Rodríguez, O., Guivernau, M., y Sánchez, J.P

13.05: Comparación de dos herramientas bioinformáticas para análisis de amplicones 16S en rumen de vacuno lechero. **Adrián López García. INIA, Madrid.**
López-García, A., García-Rodríguez, A., Pineda-Quiroga, C., Atxaerandio, R., y González-Recio, Ó.

13.20: Predicting complex traits using microbiome information: a comparison of metagenome distance matrices. **Alejandro Saborío. Universidad Politécnica de Valencia.**
Saborío-Montero, A., Bach, A., y González-Recio, O.

13.35: Taxonomic and functional analysis of metagenome data from bovine rumen samples and its association with feed efficiency. **Beatriz Delgado. INIA, Madrid.**
Delgado, B., Bach, A., Guasch, I., Elcoso, G., González, C., y Gonzalez-Recio, O.

13:50 – 15:15. Comida: Restaurante Universitario.

15:15 – 16:00: PONENCIA INVITADA 2

"En el centenario del artículo de Fisher R.A. (1918): The correlation between relatives on the supposition of Mendelian inheritance".

MIGUEL ANGEL TORO. Universidad Politécnica de Madrid.

16:00 – 17:30: Sesión 3.

Moderador: Marcel Amills (UAB, Barcelona).

16.00: Can deep learning improve genomic prediction of complex traits? **Miguel Pérez Enciso. CRAG, CSIC-IRTA-UAB-UB, Barcelona.**
Bellot, P., de los Campos, G., y Pérez-Enciso, M.

16.15: Estrategias para reducir costes en evaluación genómica en programas de selección de acuicultura **Silvia Garcia Ballesteros. INIA, Madrid.**
García-Ballesteros, S., Fernández, J. y Villanueva, B.

16.30: Diseño de apareamientos óptimo para aprovechar la dominancia en esquemas de selección genómica en especies de acuicultura. **Jesús Fernández. Dpto. Mejora Genética Animal, INIA. Madrid.**
Fernández, J., Villanueva, B., y Toro, M.A.

16.45: Selección genómica en la raza ovina de leche Latxa cara rubia. **Itsasne Granado Tajada. NEIKER-Tecnalia, Instituto Vasco de Investigación y Desarrollo Agrario.**
Granado-Tajada, I., y Ugarte, E.

17.00: Selección para la homogeneidad del rendimiento deportivo de equinos en competiciones de raid. Análisis preliminar. **Isabel Cervantes. Universidad Complutense de Madrid.**
Cervantes, I., Bodin, L., y Gutiérrez, J.P.

17.15: Distribución de los tamaños de camada de ovinos. Resultados de una encuesta sencilla en Francia y España que pone en evidencia la presencia de genes mayores. **Luis Bodin. INRA GenPhySE, Castanet-Tolosan, Francia**
Bodin, L., Raoul, J., Alabart, J.L., Folch, J., Lahoz, B., Fantova, E., de la Fuente, L. F., Molina, A., Perez Guzman, M.D., y Mintegi, L.

18:15 – 19:00. Visita guiada al Museo Panteón de la Basílica de San Isidoro de León

20:15: Autobús a Valdevimbre para la cena en el restaurante "Cueva del Tunel". Recogida en la Plaza de Santo Domingo (Junto al BBVA).

21:00 – 23:00: Cena.

Viernes 15 de junio

9:00 – 9:45: PONENCIA INVITADA 3.

"Epistasis against background: a source for future genetic variation and a refuge for selection sweeps".

TONI REVERTER. CSIRO, Australia.

9:45 – 11:15: Sesión 4.
Moderador: Jesús Fernández (INIA, Madrid).

9.45: Efecto de la ingestión de alimento sobre la expresión de genes circadianos en cinco tejidos porcinos. **Marcel Amills. UAB.**
Cardoso, T.F., Quintanilla, R., Castelló, A., Mármol-Sánchez, E., Ballester, M., Jordana, J., y Amills, M.

10.00: Diferencias de expresión de transcriptoma de hígado y testículo entre cerdos machos ibéricos enteros e inmunocastrados. **María Muñoz. Centro de I+D en Cerdo Ibérico, Badajoz.**
Muñoz, M., Izquierdo, M., Caraballo, C., García Casco, J.M., Garrido, N., y Hernández-García, F.

10.15: Potenciales reguladores de la eficiencia alimentaria en porcino identificados mediante genética de sistemas. **Yuliaxis Ramayo Caldas. IRTA, Barcelona.**
Ramayo-Caldas, Y., Ballester, M., Sánchez, J.P., González-Prendes, R., Amills, M., y Quintanilla, R.

10.30: Análisis de marcadores de resiliencia en relación con la tasa de abortos en cerdas. **Romi Pena. Universidad de Lleida.**
Pena, R.N., Fernández, C., Blasco-Felip, M., Fraile L., y Estany, J.

10.45: Predicción de la respuesta correlacionada en íncide de conversión usando modelos de interacción social: evaluación por simulación en cerdos Duroc. **William Herrera. IRTA, Barcelona.**
Herrera, W., y Sánchez, J. P.

11.00: Mitigation of greenhouse gases in livestock via genetic selection: incorporation of methane emissions into the breeding goal in dairy cattle under different scenarios. **Latifa Ouatahar. Universidad Politécnica de Valencia.**
Ouatahar, L., Lopez-Paredes, J., Charfeddine, N., y González-Recio O.

11.15: Efectos de la suplementación de la dieta con ácido oleico sobre el transcriptoma de tejido adiposo en cerdos Ibéricos y Duroc en crecimiento. **Rita Benítez. INIA, Madrid.**
Benítez, R., Isabel, B., Núñez, Y., De Mercado, E., Gómez Izquierdo, E., García-Casco, J., López-Bote, C. y Óvilo, C.

11:30 – 12:00. Café

12.00 – 13:30: Sesión 5.
Moderador: Quim Casellas (UAB, Barcelona).

12.00: Estimación de la variabilidad genética en ovino lechero francés. **Silvia Rodriguez-Ramilo. INRA, Castanet-Tolosan, Francia.**
Rodríguez-Ramilo, S. T., y Legarra, A.

12.15: Evaluation of different genomic coancestry matrices to maintain genetic variability in a turbot selected population. **Elisabet Morales Gonzalez. INIA, Madrid. Universidad Politécnica de Valencia.**
Morales-González, E., Saura, M., Fernández, A., Fernández, J., Cabaleiro, S., Martinez, P., y Villanueva, B.

12.30: The importance of ensuring genetic variability when establishing selection programmes in aquaculture. **María Saura. INIA, Madrid.**
Saura, M., Caballero, A., Santiago, E., Morales, E., Fernández, A., Fernández, J., Cabaleiro, S., Martínez, P., Millán, A., Palaiokostas, C., Kocour, M., Houston, R., Prchal, M., Bargelloni, L., Kostas, T., y Villanueva, B.

13.00: Una mirada a la depresión endogámica en el tamaño de camada porcina. **Luis Varona. Universidad de Zaragoza.**
Varona, L., Legarra, A., Herring, W., y Vitezica, Z. G.

13.15: Pérdidas productivas asociadas al estrés por calor en pequeños rumiantes: Indicadores de termo-tolerancia. **Manuel Ramón. IRIAF-Cersyra, Valdepeñas**
Ramón, M., Díaz, C., Serrano, M., Pérez-Guzmán, M.D., y Carabaño M.J.

13:30– 15.00. Comida: Restaurante Universitario.

15:00 – 16:30: Sesión 6.
Moderador: Isabel Cervantes (UCM, Madrid).

15.00: Estudio de asociación genómico de la grasa intramuscular en conejo. **Samuel Sosa Madrid. Universidad Politécnica de Valencia.**
Sosa-Madrid, B.S., Ibañez-Escriche, N., Navarro, P., Blasco, A., Haley, C.S., Fontanesi, L., Pena, R.N., y Hernández, P.

15.15: Análisis genético de la ruta metabólica del ácido linoleico en porcino. **Sofía Gol. Universidad de Lleida.**
Gol, S., González-Prendes, R., Tor, M., Reixach, J., Pena R.N., y Estany, J.

15.30: Detección de regiones genómicas asociadas a la fertilidad por *inseminación artificial* en carneros de raza Assaf: comparación de frecuencias con otras razas ovinas españolas. **Malena Serrano. INIA, Madrid.**
Serrano, M., Ramón, M., Jiménez, M.A., Freire, F., Granado-Tajada, I., González C., y Calvo, J.H.

15.45: Análisis de asociación de genes candidatos para fenotipos lipídicos en una población comercial Duroc. **Emilio Mármol Sánchez. CRAG, CSIC-IRTA-UAB-UB, Barcelona.**
Mármol-Sánchez, E., Quintanilla, R., Tibau, J., Figueiredo Cardoso, T., y Amills, M.

16.00: Estudio de regiones genómicas asociadas a la varianza ambiental en el tamaño de camada en conejos. **Cristina Casto Rebollo.**
Casto-Rebollo, C., Argente, M.J., García, M.L., Pena, R.N., Fontanesi, L., Blasco A., y Ibáñez-Escriche, N.

16:15– Planes sobre la XX RNMGA y Clausura de la Reunión.

Jueves y viernes Sesión 7. POSTERS.

1. SNP+: programa para calcular la probabilidad de dropout en SNPs. **Natalia Sastre Alaiz. Universidad Autónoma de Barcelona.**
   Sastre, N., Mercadé, A., Ramírez, O., Sánchez, A., Francino, O., y Casellas, J.
2. Análisis preliminar sobre las posibilidades del uso de la selección genómica en el programa de mejora genética para la producción de leche en la raza Churra. **Milagros Sánchez Mayor. Universidad de León.**
   Sánchez-Mayor, M., Pong-Wong, R., Navarro, P., de la Fuente, L.F., y Arranz, J.J.
3. Ponderación de paneles de SNP para predicción genómica por simulated annealing. **Melani Martín de Hijas Villalba. Universidad Autónoma de Barcelona.**
   Martín de Hijas Villalba, M., Varona, L., Noguera, J.L., Ibáñez-Escriche, N., Rosas, J.P., y Casellas, J.
4. Respuesta a la selección divergente para variabilidad del peso al nacimiento en ratón respecto a una población control. **Nora Formoso Rafferty. Universidad Complutense de Madrid.**
   Formoso-Rafferty, N., Chávez, K.N., Gutiérrez, J.P., Cervantes, I.
5. Utilización de la secuenciación genómica para la identificación de variantes en genes de las proteínas de la leche en el ganado ovino. **Héctor Marina. Universidad de León.**
   Marina, H., Gutiérrez-Gil, B., Esteban-Blanco, C., y Arranz, JJ.
6. Variant discovery in genes identified as differentially expressed genes between the abomasal lymph node transcriptome of resistant and susceptible adult sheep to *Teladorsagia circumcincta* infection. **Praveen Chitneedi. Universidad de León.**
   Chitneedi, P.K., Suárez-Vega, A., Martínez Valladares, M., Arranz J.J. y Gutiérrez-Gil, B.
7. Detección de huellas de selección en el cromosoma X de las poblaciones de vacuno de carne autóctono español. **Alonso López. Instituto Agroalimentario de Aragón.**
   López, A., González-Rodríguez, A., Cañas-Álvarez, J. J., Díaz, C., Molina, A., Altarriba, J., Baro, J. A., Piedrafita, J., Varona, L.
8. Diferenciación genómica entre tres variedades de porcino ibérico. **Inés Alonso. Universidad de Zaragoza.**
   Alonso I., Ibáñez-Escriche N., Noguera J. L., Casellas J., García-Santana M. J., Varona L.

9. Estudio de la composición bacteriana en cerdos expuestos a dietas con diferentes niveles de proteína y carotenos. **Rayner González Prendes. Universitat de Lleida–Agrotecnio Center, Lleida.**
   González-Prendes, R., Pena, R.N., Solé, E., Seradj, A.R., Estany, J., y Ramayo-Caldas, Y.

10. Identificación de regiones comunes de homocigosidad en cabras y ovejas. **María Grazia Luigi. CRAG, Barcelona.**
    Luigi, M.G., Cardoso, T.F., Martínez, A., Pons, A., Bermejo, L.A., Jordana, J., Delgado, J.V., Adán, S., Ugarte, E., Arranz, J. J., Calvo, J. H., Casellas. J., y Amills M.

11. Análisis de asociación y expresión de genes candidatos para caracteres de calidad en una línea comercial de cerdos ibéricos. **Carmen Caraballo González. Centro de I+D en Cerdo Ibérico, INIA, Zafra.**
    Fernández-Barroso, M.A., Caraballo, C., Silió, L, Rodríguez, M.C., Pariente, J.M., Sánchez- Esquilache, F., Gómez-Carballar, F., García-Casco, J.M., y Muñoz, M.

12. Nivel energético de la dieta de precebo en cerdos ibéricos: efectos sobre el transcriptoma muscular. **Adrián López García. INIA, Madrid.**
    López-García, A., Núñez, Y., Calvo, L., Benítez, R., Ballesteros, J., Segura, J., López-Bote, C., y Óvilo, C.

13. ¿Es posible certificar la leche producida en ecológico utilizando microARN?. **Luis J. Royo. SERIDA, Asturias.**
    Abou el Qassim, L., Vicente, F., de la Torre, S., Jiménez-Calderón, J.D., Baizán, S., Soldado A., Martínez-Fernández, A., Royo, L.J.

14. Detección de genes candidatos relacionados con la composición de ácidos grasos en cerdos Duroc según el nivel de vitamina A y el genotipo SCD. **Emma Solé. Universitat de Lleida–Agrotecnio Center, Lleida**
    Solé, E., González-Prendes, R., Tor, M., Estany, J. y Pena, R.N.

15. Una perspectiva genómica sobre el origen de la variación genética de las caseínas caprinas. **Dailu Guan. Centre de Recerca Agrigenòmica (CRAG)- CSIC-IRTA-UAB-UB, Barcelona.**
    Guan, D., Mármol-Sánchez, E., Such, X., Landi, V., Amills M.