

8. ANEXO

Tabla S1: Características de los 17 marcadores microsatélites estandarizados y recomendados por la ISAG en equino.

| Locus | Localización en cromosoma | Cebadores (Directo y Reverso) | Longitud amplicón (pb) |
|---------------------------------|---------------------------|---|------------------------|
| <i>AHT4</i> | 24q14 | D: AACCGCCTGAGCAAGGAAGT R: CCCAGAGAGTTTACCCT | 144–164 |
| <i>AHT5</i> | 8 | D: ACGGACACATCCCTGCCTGC R: GCAGGCTAAGGAGGCTCAGC | 126–144 |
| <i>ASB2</i> | 15q21.3–q23 | D: CCACTAAGTGTCGTTTCAGAAGG R: CACAACCTGAGTTCTCTGATAGG | 216–250 |
| <i>ASB17</i> | 2p14–p15 | F: ACCATTTCAGGATCTCCACCG R: GAGGGCGGTACCTTTGTACC | 87–129 |
| <i>ASB23</i> | 3q22.1–q22.3 | F: GAGGGCAGCAGGTTGGGAAGG R: ACATCCTGGTCAAATCACAGTCC | 175–211 |
| <i>CA425</i> <i>UCDEQ425</i> | 28q18 | F: AGCTGCCTCGTTAATTCA R: CTCATGTCCGCTTGTCTC | 226–246 |
| <i>HMS1</i> | 15 | F: CATCACTCTTCATGTCTGCTTGG R: TTGACATAAATGCTTATCCTATGGC | 170–186 |
| <i>HMS2</i> | 10 | F: CTTGCAGTCGAATGTGTATTAAATG R: ACGGTGGCAACTGCCAAGGAAG | 222–248 |
| <i>HMS3</i> | 9 | F: CCATCCTCACTTTTTCACTTTGTT R: CCAACTCTTTGTACATAACAAGA | 148–170 |
| <i>HMS6</i> | 4 | F: GAAGCTGCCAGTATTCAACCATTG R: CTCCATCTTGTGAAGTGTAACCTCA | 151–169 |
| <i>HMS7</i> | 1q25 | F: TGTGTGTGAAACATACCTTGACTGT R: CAGGAAACTCATGTTGATACCATC | 165–185 |
| <i>HTG4</i> | 9 | F: CTATCTCAGTCTTGATTGCAGGAC R: CTCCCTCCCTCCCTCTGTTCTC | 127–139 |
| <i>HTG6</i> | 15q26–q27 | F: GTTCACTGAATGTCAAATTCTGCT R: CCTGCTTGAGGCTGTGATAAGAT | 84–102 |
| <i>HTG7</i> | 4 | F: CCTGAAGCAGAACATCCCTCCTTG R: ATAAAGTGTCTGGGCAGAGCTGCT | 118–128 |
| <i>HTG10</i> | 21 | F: TTTTATTCTGATCTGTCACATTT R: CAATTCCC GCCCACC CCGGCA | 95–115 |
| <i>LEX3</i> | Xq | F: ACATCTAACCAGTGCTGAGACT R: GAAGGAAAAAAGGAGGAAGAC | 142–164 |
| <i>VHL20</i> | 30 | F: CAAGTCCTCTTACTTGAAGACTAG R: AACTCAGGGAGAATCTTCCTCAG | 87–105 |

Tabla S2: Componentes de la reacción de amplificación, PCR multiplex, M1

| Componentes | Volumen (μl) | Características |
|----------------------------------|--------------|---|
| Quiagen Multiplex PCR Buffer, 2X | 3 | Contiene iones MgCl ₂ , KCl, (NH ₄) ₂ SO ₄ dNTPs, y tampón para PCR multiplex. |
| Q-Solution, 5X | 0.6 | Contiene HotStartTaq DNA polimerasa |
| Mezcla de oligos M1 | 0.675 | Microsatélites: AHT 4, HMS3, HMS6, HMS7, HTG4 y VHL20 |
| H2O miliQ | 0.725 | Agua purificada |
| DNA | 1 | DNA purificado del apartado 4.1 |
| Volumen final | 6 | |

Tabla S3: Componentes de la reacción de amplificación, PCR multiplex, M2

| Componentes | Volumen (μl) | Características |
|----------------------------------|--------------|--|
| Quiagen Multiplex PCR Buffer, X2 | 3 | Contiene iones MgCl ₂ , KCl, (NH ₄) ₂ SO ₄ dNTPs, y tampón para PCR multiplex |
| Q-Solution, 5X | 0.6 | Contiene HotStartTaq DNA polimerasa |
| Mezcla de oligos M2 | 0.34 | Microsatélites: ASB2, AHT5, HTG10 y HMS2 |
| H2O miliQ | 1.06 | Agua purificada |
| DNA | 1 | DNA purificado del apartado 4.1 |
| Volumen final | 6 | |

Tabla S4: Componentes de la reacción de amplificación, PCR multiplex, M3

| Componentes | Volumen (μl) | Características |
|----------------------------------|--------------|--|
| Quiagen Multiplex PCR Buffer, X2 | 3 | Contiene iones MgCl ₂ , KCl, (NH ₄) ₂ SO ₄ dNTPs, y tampón para PCR multiplex |
| Q-Solution, 5X | 0.6 | Contiene HotStartTaq DNA polimerasa |
| Mezcla de oligos M3 | 0.12 | Microsatélites: ASB17 y ASB23 |
| H2O miliQ | 1.28 | Agua purificada |
| DNA | 1 | DNA purificado del apartado 4.1 |
| Volumen final | 6 | |

Tabla S5: Concentración y calidad del DNA obtenido en los Apartados 4.1.1 y 4.1.2.

| Sample ID | Concentración (ng/μl) | Ratio (A _{260nm} /A _{280nm}) | Ratio (A _{260nm} /A _{230nm}) |
|------------------------|-----------------------|---|---|
| Sec. referencia | 155.42 | 1.75 | 1.02 |
| Potro afectado | 117.94 | 1.56 | 1.19 |
| Madre Juna | 41.22 | 1.41 | 1.19 |
| Abuela | 36.11 | 1.43 | 1.85 |
| Padre nas | 25.44 | 1.35 | 1.33 |
| Hermana madre | 27.74 | 1.40 | 1.62 |
| Potro hermano | 30.26 | 1.48 | 2.25 |
| Q-758 | 10.87 | 1.03 | 0.51 |
| Q-759 | 23.65 | 1.47 | 1.17 |
| Q-760 | 27.44 | 1.41 | 0.80 |
| Q-761 | 23.32 | 1.44 | 1.19 |
| Q-762 | 15.15 | 1.73 | 1.73 |
| Q-763 | 17.62 | 1.24 | 0.72 |
| Q-763 | 11.47 | 1.11 | 0.68 |
| Q-764 | 14.44 | 1.36 | 0.68 |
| Q-765 | 5.88 | 1.14 | 0.42 |
| Q-766 | 16.00 | 1.39 | 0.78 |
| Q-767 | 6.66 | 1.33 | 1.11 |
| Q-768 | 12.02 | 1.39 | 1.50 |
| Q-769 | 11.26 | 1.88 | 2.14 |
| Q-770 | 8.14 | 0.96 | 0.30 |
| Q-771 | 13.23 | 1.31 | 0.64 |
| Q-772 | 12.64 | 1.29 | 0.60 |
| Q-773 | 17.05 | 1.50 | 0.88 |
| Q-774 | 12.45 | 1.23 | 0.68 |
| Q-775 | 13.79 | 1.51 | 0.69 |
| Q-776 | 12.84 | 1.58 | 0.98 |
| Q-777 | 9.41 | 1.18 | 0.48 |
| Q-778 | 11.26 | 1.31 | 0.40 |
| Q-779 | 9.54 | 1.36 | 1.03 |
| Q-780 | 2.66 | 1.13 | 1.54 |
| Q-781 | 5.81 | 1.31 | 1.32 |
| Q-782 | 11.84 | 1.15 | 0.49 |
| Q-783 | 18.34 | 1.43 | 1.80 |
| Q-784 | 25.95 | 1.12 | 1.32 |
| Q-785 | 19.46 | 1.41 | 1.44 |
| Q-786 | 13.37 | 1.44 | 1.68 |
| Q-787 | 19.02 | 1.50 | 1.17 |
| Q-788 | 14.53 | 1.37 | 0.93 |
| Q-789 | 17.75 | 1.32 | 0.74 |
| Q-790 | 79.98 | 1.76 | 2.31 |
| Q-791 | 7.01 | 1.21 | 0.93 |
| Q-792 | 82.37 | 1.67 | 1.57 |
| Q-793 | 17.87 | 1.46 | 1.02 |
| Q-795 | 16.19 | 1.48 | 1.26 |
| Q-796 | 17.15 | 1.25 | 0.75 |
| Q-797 | 8.81 | 1.17 | 0.51 |
| Q-798 | 11.15 | 1.24 | 0.99 |

Congenital Liver Fibrosis in a Purebred Spanish Horse Foal

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Introduction

Congenital Liver Fibrosis (CLF) is a monogenic autosomal recessive inherited lethal disease described mainly in the Franches-Montagnes Horse (FMH), characterized by marked porto-portal bridging fibrosis and abundant dilated bile ducts often surrounded by inflammatory cells within the fibrotic tissue. CLF has been associated with two mutations in the Polycystic Kidney and Hepatic Disease 1 (*PKHD1*) gene^{1,2}. Here we describe the first case of CLF in a Purebred Spanish Horse (PSH) foal and present the results of the genetic studies performed in this animal and others PSH horses.

Material and methods

A one-month-old PSH foal showed a clinical history of diarrhea with acholic faeces from birth and developed neurological signs and constipation leading to death.

Pathologic studies

Only the liver, kidney, spleen and a portion of small intestine were submitted for pathologic examination. Tissues were assessed grossly and fixed in 10 % formalin for histopathologic evaluation. Samples were stained with HE and Masson's trichrome. Immunohistochemistry for cytokeratin (AE1/AE3) was performed.

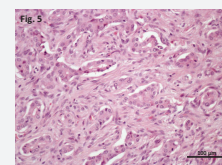
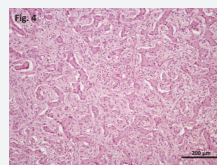
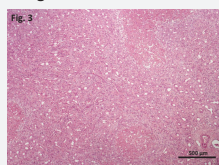
Results



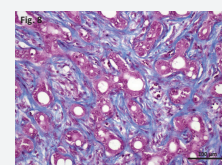
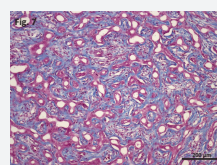
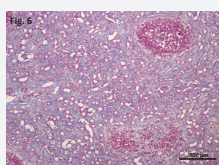
Fig. 1. Liver. Enlargement and gray discoloration. Increased consistency and weight.



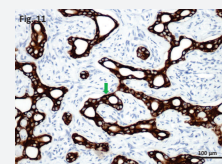
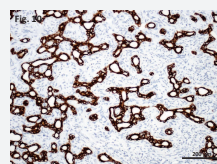
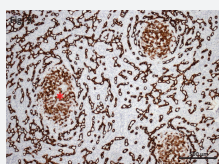
Fig. 2. Liver, cut surface. Diffuse reticular fibrosis. **Insert:** Presence of a small cyst.



Figs. 3-5. Liver. HE stain. Diffuse porto-portal bridging fibrosis. Multiple small and irregular bile ducts, often dilated. The remaining hepatocytes show necrotic changes.



Figs. 6-8. Liver. Masson's trichrome stain. Note the severely increased amount of fibrous tissue.



Figs. 9-11. Liver. Immunohistochemistry for cytokeratin (AE1/AE3). Note the remaining hepatocytes (*) and the positive cuboidal epithelial cells that line the bile ducts (†).

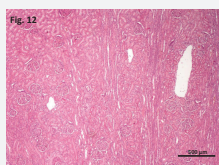


Fig. 12. Kidney, HE stain. Multifocal interstitial cysts in the cortex.

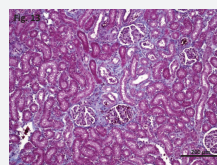


Fig. 13. Kidney, Masson's trichrome stain. Moderate and multifocal interstitial fibrosis.

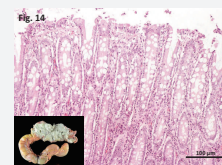


Fig. 14. Small intestine, HE stain. Goblet cell hyperplasia. **Insert:** Steatorrheic intestinal content

Genetic studies

1st The two mutations in the *PKHD1* were analyzed in the affected animal

-**Reference sequence:** NCBI Reference Sequence: NW_001867389.1 *Equus caballus* isolate Twilight breed thoroughbred chromosome 20 genomic scaffold, EquCab2.0 scaffold_7, whole genome shotgun sequence.

-**Two SNPs** were analysed by automatic sequencing in ABI *Prism* 3130: g,49,630,834G>A (*PKHD1*, exon 37: SNP c.6112C>T) and g,49,597,760A>T (*PKHD1*, exon 43: SNP c.6845T>A) predicted to cause the non-conservative changes p.H2038Y and p.I2282N on the *PKHD1* protein¹.

Table 1. Details of the used primers (*Software Primer Express 2.0; Applied Biosystems*)

| Primer name | Forward | Reverse | Tm (°C) |
|-------------|-----------------------|------------------------|---------|
| c.6112C>T | CTCTGCCACGGGAATTACAAC | TCCATCTTGTTCCTCATGG | 59 |
| c.6845T>A | CACTGAAGCCTCACTCCAAA | GGCTGACAGCAGATGTATAGAT | 59 |

2nd A pedigree evaluation was performed

-5 relatives (**maternal grandmother, maternal aunt, mother, father and brother**) were analyzed for the two former SNPs.

-Relationship was established by the analysis of the standardized microsatellites recommended by the ISAG (International Society of Animal Genetics): AHT4, ASB2, ASB17, ASB23, HMS2, HMS3, HMS6, HMS7, HTG4 y VHL20.

3rd Both mutations were analyzed in a population of PSH horses

-**40 adult (5-10 years old) animals**, with no familiar relationship, were selected for these studies.

-Genotypic and genic frequencies were calculated and compared with a population of FMH¹.

Results

1st The foal was heterozygote for the two analyzed mutations (**CT; TA**)

2nd Pedigree of the affected foal

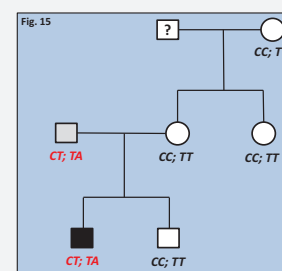


Fig. 15. Males are represented by squares and females by circles. Black square represents the case and the grey square the father with the same genotypes for the two variants *PKHD1*:c.6112C>T and *PKHD1*:c.6845T>A predicted to cause the non-conservative changes p.H2038Y and p.I2282N on the *PKHD1* protein.

3rd Genotypic / genic frequencies of the mutations in a population of PSH and comparison with those obtained in a population of FMH¹.

Table 2. In the studied PSH population there are approximately a 40% of heterozygotes and a 10 % of homozygotes for both mutations (circles).

| Analyzed SNP | SNP c.6112C>T g,49,630,834G>A (<i>PKHD1</i> , exon 37) | | SNP c.6845T>A g,49,597,760A>T (<i>PKHD1</i> , exon 43) | |
|---------------------|--|------------------------|--|------------------------|
| | Franches-Montagnes Horse | Purebred Spanish Horse | Franches-Montagnes Horse | Purebred Spanish Horse |
| Genotype 1 | CC | CC | TT | TT |
| Genotypic frequency | 0,843 | 0,500 | 0,834 | 0,500 |
| Genotype 2 | CT | CT | TA | TA |
| Genotypic frequency | 0,145 | 0,406 | 0,166 | 0,395 |
| Genotype 3 | TT | TT | AA | AA |
| Genotypic frequency | 0,012 | 0,094 | 3,93x10 ⁻⁴ | 0,105 |
| Allele 1 | C | C | T | T |
| Genic frequency | 0,916 | 0,703 | 0,917 | 0,697 |
| Allele 2 | T | T | A | A |
| Genic frequency | 0,084 | 0,296 | 0,083 | 0,303 |

Conclusions

- These findings are consistent with Congenital Liver Fibrosis. To the best of our knowledge this is the first report of this disease in the Purebred Spanish Horse.
- The affected animal is heterozygote for the two mutations that were strongly associated with the disease in the Franches-Montagnes Horse.
- The frequencies of heterozygotes and homozygotes in the Purebred Spanish Horse are higher than those found previously in the Franches-Montagnes Horse.
- This is the first study of the genic and genotypic frequencies for these two mutations in a Purebred Spanish Horse population.

References:

1. Drögemüller et al., Congenital hepatic fibrosis in the Franches-Montagnes Horse is associated with the Polycystic Kidney and Hepatic Disease 1 (*PKHD1*) gene. *Plos One*, PLoS One. 2014 Oct 8;9(10):e110125
2. Haechler S et al., Congenital hepatic fibrosis and cystic bile duct formation in Swiss Freiburger horses. *Vet Pathol*. 2000 Nov;37(6):669-71

CONGENITAL LIVER FIBROSIS IN A PUREBRED SPANISH FOAL

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Introduction: Congenital liver fibrosis (CLF) is a monogenic autosomal recessive inherited lethal disease described in Swiss Freiberger breed horses, linked to a mutation in PKHD1 gene. We report the first case of CLF in a Purebred Spanish Horse (PSH) foal.

Materials and Methods: a 1-month-old PSH foal presented with a clinical history of diarrhea since birth followed by neurological signs. Due to bad prognosis, the animal was killed and samples from liver, kidney, small intestine and spleen were submitted for histopathological examination. Tissues were evaluated using HE, Masson's trichrome and PAS stains and also by IHC for cytokeratin. Genomic analyses are in progress to confirm both, the genetic etiology of the disorder and the defect in the PKHD1 gene.

Results: Gross examination showed an enlarged, pale and firm liver with marked reticular pattern on cut surface and an acholic intestinal content. Microscopically, the liver showed a severe diffuse porto-portal bridging fibrosis associated with intense multifocal irregular bile ducts proliferations, with occasional cyst formation. Remaining hepatic tissue was only observed around central veins. The kidney showed multifocal small cysts in the cortex. There was pronounced hyperplasia of goblet cells in the small intestine. The spleen showed follicular depletion and multifocal histiocytosis.

Conclusions: Histopathological lesions are consistent with CLF, the first case in a PSH foal and underline the importance of including this entity as a differential diagnosis in foals with clinical signs of progressive liver disease, independently of their breed.




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