Table 1: Characteristics of animals with equine metabolic syndrome

	Age (years)	Breed	Sex	BCS	CNS	Glucose (mg/dl)	Insulin (µiu/ml)	MIRG
1	8	Andalusian	F	7	3	104	51.1	10.8
2	10	Andalusian	M	7	4	79	27.1	13.1
3	12	Andalusian	M	8	4	83	25.7	11.8
4	9	Andalusian	F	7	3	74	24.1	13.6
5	5	Shetland pony	M	8	5	94	‹200	OR*

* Out of range due to insulin level being too high
BCS Body condition score, CNS Cresty neck score, F Female, M Male, MIRG Modified insulin-to-glucose ratio

EQUINE MEDICINE

Genetics of equine metabolic syndrome

EQUINE metabolic syndrome (EMS) is defined as a complex disorder characterised by a phenotype of insulin dysregulation, obesity and a predisposition toward laminitis, resulting from the combination of one or more inherited genetic alleles and environmental influences.[1]

Recently, a genome-wide association study (GWAS)[2] identified two genetic markers for EMS located in the *FAM174A* gene region in Arabian horses: BIEC2-263524-C and FAM174A 3' UTR -11(G) (*Equus caballus* chromosome 14:69,276,814 and 14:69,119,991 in EquCab2.0, respectively), with a correlation of 98 per cent between the two. However, uniform fasting guidelines were not followed and the studied populations were older than the general age of onset of EMS.[3] This led to inconsistent diagnoses of EMS, since variability in non-structural carbohydrates, content of forage and age of horses influence metabolism and phenotypic measures.[1-4]

In addition, some EMS cases used for the GWAS were affected by pituitary pars intermedia dysfunction, which also produces insulin dysregulation. This element could have been solved by validating GWAS results with a second population. However, insulin and modified insulin-to-glucose (MIRG) ratio values considered elevated in this second group were not outside the reference interval[5] and only one of these horses was diagnosed with laminitis. Therefore, horses within the second population were considered not to have EMS.

We studied five horses (Table 1) with the aim of validating the presence of the FAM174A 3' UTR -11(G) allele in animals suffering from EMS, and only one of these horses (Table 1, horse 1) displayed a heterozygous genotype including one copy of the 11(G) EMS-associated allele.

The method suggested may lead to incorrect diagnoses

We believe that the method to identify EMS-affected animals suggested by the authors of the GWAS[2] may lead to incorrect diagnoses. The FAM174A 11(G) allele seems a poor indicator of EMS, as it is absent in most EMS-affected individuals. This is most likely due to a low effect of the *FAM174A* gene on the aetiology of this disease, the complexity of the resulting phenotype and the fact that several loci may be driving its genetic background. Future studies should take all intrinsic and extrinsic factors into account to establish a clear phenotype of EMS.

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