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A Genomic association study of gastrointestinal parasites in Ghezel sheep breed of East-Azerbaijan

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Sheep husbandry plays a prominent role for the economy of Iran, with 45 million sheep currently reared in the country. The present study – part of the International Atomic Energy Agency CRP projects on 'Genetic Variation on the Control of Resistance to Infectious Diseases in Small Ruminants for Improving Animal Productivity genetic resistance to nematodes in small ruminants' – aims to investigate the association between a selected panel of SNPs (n=157) in candidate genes and gastrointestinal nematode (GIN) infections. A total of 211 weaned lambs from ten flocks in East Azerbaijan province, Iran, were included in the study. Nematode eggs were counted in lamb's faeces (faecal egg count EPGG) and further classified into four groups: (1) EPGO: Strongyles, (2) EPGN: *Nematodirus* spp., (3) EPGT: *Trichuris* spp., and (4) EPGM: *Marshallagia marshalli*. Lambs were measured for body weight, FAMACHA test, and Packed Cell Volume (PCV). Genomic association analysis was performed using the 'RepeatABEL' R package. The model applied was Yijklm= BW + Si + Tj+ Fk+ SNPl + eijklm. We identified 118 SNPs in 39 genes located on 19 chromosomes significantly associated with either EPGO (72), EPGG (16), EPGN (14), EPGM (9), EPGT (5) and PCV (2). SNPs in CLEC1B and NLRC4 genes were significantly associated with PCV and EPGG. Our results improve the current understanding of gastrointestinal nematodes resistance at the genomic level and will be of aid in defining better breeding plans for lambs within extensive-sheep farming systems.

Phenotypic characterization of the parasite resistance in Morada Nova sheep

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Gastrointestinal nematodes (GIN) are a major constraint in small ruminant production, in particular *Haemonchus contortus*, due to parasitic resistance spread worldwide. Morada Nova, a Brazilian hair-sheep breed adapted to tropical conditions, is considered more resistant to GINs. This study aimed to characterize a Morada Nova flock in relation to its resistance against *H. contortus* through phenotypic tools. A total of 151 lambs (divided into 2 groups according to the order of birth) were dewormed (monepantel) after weaning and 15 days later were submitted to the first parasitic challenge by oral artificial infection of 4,000 L_3 of *H. contortus*, isolate Embrapa2010 (day zero; D0). Faecal samples were collected individually for eggs per gram counts (EPG) on days 0, 21, 28, 35 and 42, when the body weight (BW) was also measured. Blood collections for packed cell volume (PCV) were performed each 14 days. After D42, the animals were dewormed again and submitted to the 2nd parasitic challenge, followed by the same collection scheme. The 151 animals were categorized as resistant/R (20%), intermediate/I (60%) and susceptible/S (20%) to *H. contortus* by means of the ranking obtained using the formula = (BW×0.4) – (EPG×0.4) + (PCV×0.2). There was statistical difference ($P<0.05$) for BW, and EPG between the challenge groups (G1 and G2). ANOVA ($P<0.05$) indicated for BW: R(a) = I(a) ≠ S(b) (G1) and I(a) ≠ R(b) ≠ S(c) (G2). For EPG: R(a) ≠ I(b) ≠ S(c) in both groups. The averages for PCV were R(a) = I(b) ≠ S(c). The strongest negative Pearson correlation was between LogEPG and PCV (r=-0.68) and strongest positive one between final weight and weaning weight (r=0.86). The ranking scheme allowed the differentiation between the animals categorized as R, I and S. High EPGs were related to lower PCVs and the period between birth and weaning had an impact on the final live weight.