Testing the 'parasite-mediated domestication' hypothesis: a comparative approach to the wild boar and domestic pig as model species (#100752)

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Testing the 'parasite-mediated domestication' hypothesis: a comparative approach to the wild boar and domestic pig as model species

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The mechanisms underlying the domestication process have already been well explained. Starting with Belyaev's pioneering experiment on silver foxes, which showed that selection for tameness leads to destabilisation of the regulatory systems that control morphological and behavioural development, resulting in the changes characteristic of the domestication syndrome. Later, the thyroid rhythm hypothesis and the neural crest cell hypothesis provided additional explanations. Recently, the parasite-mediated domestication hypothesis (PMD) has been proposed, suggesting an important role of endoparasites in the domestication process. PMD proposes that the frequency of domesticated syndrome traits is associated with a higher susceptibility to parasites. PMD can be tested either experimentally or comparatively. We followed a systematic comparative approach by analysing the parasite load in wild boar (WB) and free-ranging domestic pig (DP) populations from a comparable environment in a geographically close area. Fresh faeces from WB and DP populations, one each from Slovenia (SI) and Croatia (HR), were sampled. A total of 59 individual faecal samples were collected (SI: 12 WB, 20 DP; HR: 14 WB, 13 DP). Parasitological diagnostics were carried out using the sedimentation and floatation method. Five different taxa were found in WB and seven in DP. Three parasite taxa were found exclusively in DP (*Cystoisospora suis*, *Trichuris* sp., *Balantidium coli*), and one (*Strongyloides* sp.) only in WB. Of the parasites found in both cohorts, Strongyles/*Oesophagostomum* sp. were significantly more abundant in DP, while *Eimeria* sp. was found in equal amounts in both (but in HR only in WB). According to the preliminary study presented here, there is evidence to support the PMD baselines in the wild boar – domestic pig association. However, we cannot draw a definitive conclusion as there are many aspects that may bias the interpretation based on parasite load alone, which are also discussed here. Therefore, comparative studies should be supported by a more focussed methodology, including an experimental approach.

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Abstract

The mechanisms underlying the domestication process have already been well explained. Starting with Belyaev's pioneering experiment on silver foxes, which showed that selection for tameness leads to destabilisation of the regulatory systems that control morphological and behavioural development, resulting in the changes characteristic of the domestication syndrome. Later, the thyroid rhythm hypothesis and the neural crest cell hypothesis provided additional explanations. Recently, the parasite-mediated domestication hypothesis (PMD) has been proposed, suggesting an important role of endoparasites in the domestication process. PMD proposes that the frequency of domesticated syndrome traits is associated with a higher susceptibility to parasites. PMD can be tested either experimentally or comparatively. We followed a systematic comparative approach by analysing the parasite load in wild boar (WB) and free-ranging domestic pig (DP) populations from a comparable environment in a geographically close area. Fresh faeces from WB and DP populations, one each from Slovenia (SI) and Croatia (HR), were sampled. A total of 59 individual faecal samples were collected (SI:

12 WB, 20 DP; HR: 14 WB, 13 DP). Parasitological diagnostics were carried out using the sedimentation and floatation method. Five different taxa were found in WB and seven in DP. Three parasite taxa were found exclusively in DP (*Cystoisospora suis*, *Trichuris* sp., *Balantidium coli*), and one (*Strongyloides* sp.) only in WB. Of the parasites found in both cohorts, strongyles/*Oesophagostomum* sp. were significantly more abundant in DP, while *Eimeria* sp. was found in equal amounts in both (but in HR only in WB). According to the preliminary study presented here, there is evidence to support the PMD baselines in the wild boar – domestic pig association. However, we cannot draw a definitive conclusion as there are many aspects that may bias the interpretation based on parasite load alone, which are also discussed here. Therefore, comparative studies should be supported by a more focussed methodology, including an experimental approach.

Introduction

Domesticated animals are characterised by a set of phenotypic traits that are either behavioural or morphological and are referred to as the domestication syndrome. When considering the beginning of the domestication process in animals, tameness is an essential prerequisite, followed by floppy ears, a short and curled tail, piebaldism, depigmentation, short and wide skull, reduced size of the adrenal gland, and others. Many of the mechanisms behind the domestication/domestication syndrome have already been well explained. Starting with the pioneering studies on domestication by Dmitry Belyaev, who proposed that the domestication syndrome is genetically linked to genes associated with tameness. His experiment on domestication of silver foxes, which is among the most influential work in this field, showed that selection for tameness (impaired stress response, changes in the ‘hypothalamic-pituitary-adrenal system' - HPA axis) leads to significant destabilisation of regulatory systems controlling morphological and behavioural development, resulting in changes that are otherwise characteristic of domestication syndrome ~~(Belyaev, 1979).~~ Much later, some other findings and hypotheses were added (Wilkins, 2017). In the thyroid rhythm hypothesis, Crockford (2004) proposed that domestication is also driven by genetically controlled changes in the activity rhythm of the thyroid gland, which have a crucial effect on heterochronic changes and thus play an important role in the domestication syndrome (e.g. paedomorphism). Furthermore, Wilkins, Wrangham & Fitch (2014) proposed that the main phenotypic components of domestication syndrome are neural crest cells (NCC) derivatives, i.e. a result of a developmental reduction in NCC input for the affected phenotypic traits. Recently, the parasite-mediated domestication hypothesis (PMD) has been proposed (Skok, 2023). Parasites affect literally all the major mechanisms that otherwise underlie the domestication syndrome (HPA, thyroid, NCC –e.g. neuroendocrine regulation, hormonal modulation, changes in the host miRNA profile, etc.), and in this way could mediate the domestication process, both directly through manipulation of host behavioural traits (~~e.g.~~ Poulin, 1994, 2013; Adamo, 2013) and indirectly via genes related to resistance/tolerance to parasites, the role of miRNA in the process of epigenetic inheritance or the transgenerational inheritance of stress pathology (~~see~~ Skok, 2023). Therefore, the PMD assumes an important role of endoparasites in the process of domestication, especially in the initial phase (proto-domestication). It predicts that the frequency of domestication syndrome traits in the wild population increases with decreasing genetic resistance to parasites and/or with increasing parasite load. PMD can be tested in different ways, either experimentally (experimentally parasitised wild population) or comparatively (on the existing wild and domestic populations). Although comparative studies can be problematic for a variety of reasons, they are relatively easy to conduct and are therefore suitable for an initial test of hypothesised PMD baselines. It can be assumed that, under comparable conditions, the parasite load in the domestic population will be higher than in the wild population. Therefore, we tested the PMD in *Sus scrofa* with a systematic comparative approach by analysing the parasite load in wild boar and free-ranging domestic pigs from a comparable environment. We selected animals from two regions, one in Slovenia and the other in Croatia. In each region, samples were collected from wild and domestic cohort in a relatively narrow geographical area. According to PMD, we proposed a higher parasite load in the domestic pig compared to its wild counterpart, both in terms of diversity of parasite taxa and quantitatively (severity of infection).

Materials & Methods

Study sites and sampling period

The study took place in Croatia and Slovenia. The samples in both countries consisted of two cohorts, wild boar and domestic pigs. In both countries, the wild boar and domestic pig populations were located about 15-20 km apart, so they had similar chances of being exposed to the local parasitofauna. In Croatia, the wild boar samples were collected on 3-4 November 2023 in the Prolom hunting ground (village of Buzeta, Glina municipality, Sisak-Moslavina County) and the domestic pigs on 10 November 2023 in the free-range enclosure of the autochthonous Banija spotted pig (Banijska šara) in the village of Srednje Mokrice (Petrinja municipality, Sisak-Moslavina County). In Slovenia, wild boar samples were collected on 10 December 2023 in the Stoperce hunting ground (village of Stoperce, municipality of Majšperk, Štajerska region) and domestic pigs on 11 December 2023 in the free-range enclosure of the autochthonous Krškopolje pig or black-belted pig (Krškopoljski prašič) in the village of Zgornje Laže (municipality of Slovenjske Konjice, Štajerska region).

Animals and faeces collection

Wild boar populations and free-ranging (grazing) domestic pig populations, one each from Slovenia (SI) and Croatia (HR), were included in the study. Fresh faeces were collected from the rectum of hunted wild boar or immediately after the defecation of domestic pigs. Each individual sample was collected in plastic cups with lids - the rubber gloves were changed before each faecal collection. The samples were then stored in a refrigerator at a temperature of 4°C and analysed up to 48 hours after sampling. A total of 59 individual faecal samples (SI: 12 wild boar, 20 domestic pig; HR: 14 wild boar, 13 domestic pig) were examined for endoparasites. Domestic pigs were not threated against parasites.

Diagnosis of parasitic infections

Due to the occurrence of African swine fever (ASF) in Croatia (the first occurrence of the virus was confirmed in domestic pigs on June 26, 2023), which also hindered the sampling process in general, all samples remained in the country of origin and were analysed there. The Croatian samples were analysed in the Laboratory for Parasitology of the Croatian Veterinary Institute in Zagreb. Slovenian samples were analysed in the Unit for Parasitology of the Institute of Microbiology and Parasitology at the Veterinary Faculty of the University of Ljubljana. The faecal samples were examined for the presence of endoparasites using the flotation or McMaster method and the sedimentation method according to Thienpont, Rochette & Vanparijs (2003). A saturated salt solution (density 1.20 at 20°C) was used to float nematode and cestode eggs, while tap water was used for sedimentation. Taxon determination under the microscope was based on the different morphotypes of the eggs/(oo)cysts. The assessment of parasite load differs between national laboratories, but this was irrelevant for the reliability of the PMD testing, as we primarily aimed to compare wild and domestic populations within the selected area (country) and not between countries. In its standard methodology, the Slovenian laboratory uses 5 classes for the intensity of parasite load, defined by the number of eggs/(oo)cysts present in the sample/smear. The classes were defined as follows: Negative = 0; Individual egg/oocyte = 3-5; + = 5-10; ++ = 10-20; +++ ≥21. In the Croatian laboratory, the total number of eggs/(oo)cysts per gram in the sample of a given quantity (approx. 2-5 g) was defined. For this reason, the results are presented here separately for each country and with a different scale for the figures.

Data analyses

Due to the restriction with regard to ASF and the separate diagnostics within the country from which the samples originate, the estimates of the parasite load differ between the two data sets and were therefore also statistically analysed differently. For the Slovenian data, where the parasite load estimators were reported as classes, the non-parametric Mann-Whitney U-test (also known as Wilcoxon rank sum test) was used to compare the parasite load between the domestic and wild cohorts. The Croatian estimator was a continuous variable. However, as it was not normally distributed, the non-parametric Independent-Samples Wald-Wolfowitz Run test was used to compare the parasite load between the domestic and wild cohorts.

Results

As shown in Table 1, a total of five different parasite taxa were found in the HR samples. Wild and domestic populations were each infected with three different parasite taxa (wild boar: *Eimeria* sp., Strongyle type eggs, and *Strongyloides* sp.; domestic pig: *Cystoisospora suis*, strongyle type eggs, and *Trichuris* sp.). A total of four different parasite taxa were found in SI samples. Only two of them were found in wild boar, *Eimeria* sp., and *Oesophagostomum* sp. (strongyle), but all four (*Eimeria* sp., *Balantidium coli*, *Oesophagostomum* sp. (strongyle), and *Trichuris* sp.) were found in domestic pig. *Strongyloides* sp. was the only parasite taxon found only in wild boar but not in domestic pigs, all others were found either exclusively in domestic pigs or in both cohorts.

In the Croatian samples, the only taxon present in both cohorts were strongyles, the eggs of which were significantly more abundant in domestic pigs than in wild boar. Of the others, *Cystoisospora suis* and *Trichuris* sp. were found exclusively in domestic pigs, while *Eimeria* sp. and *Strongyloides* sp. were only found in wild boar (Figure 1).

In the Slovenian samples there were two parasite taxa, *Trichuris* sp. and *Balantidium coli*, which were found exclusively in domestic pigs, while the other two were found in both cohorts. For two matching parasites, the load of *Oesophagostomum* sp. (strongyle) was significantly higher in domestic pig than in wild boar, while *Eimeria* sp. was present to the same extent in both cohorts (Figure 2).

Discussion

Our results are in favour of PMD, as domestic pigs generally had a significantly higher parasite load (taxon richness) than their wild counterparts from the same area. According to PMD baselines, domestic pigs descend from parasite-susceptible ancestors, with susceptibility to parasites, which presumably trigger the domestication syndrome, being passed on/inherited through generations of progeny after the domestication process. Rare earlier comparative studies on parasite load in *Sus scrofa* have shown mixed results, some of which contradict ours – although it should be emphasised that the sampling in previous comparative studies was not as systematically targeted as ours. For example, Ineson (1954) found differences in parasite load depending on parasite species, with domestic pigs in New Zealand having a higher overall parasite load (richness) than wild boar. In contrast, Alwin et al. (2015) found that parasite loads were higher in the wild boar than in domestic pig in semi-free range and on farms in India. Based on our results, we cannot draw a definitive conclusion because, apart from the fact that this is only a very preliminary attempt at a systematic comparison to test PMD, there are many aspects that could confound interpretation.

The first aspect concerns the possible artificial (either intentional or spontaneous) selection of resistant/tolerant animals aimed at increasing resistance (McManus et al., 2014) and possibly leading to a deceptively high resistance/tolerance to parasites in the domestic population, which was certainly not the case in our study. In fact, none of the breeds included in our study had been historically subjected to methodical selection for parasite resistance. Furthermore, selection for parasite resistance/tolerance in pigs has generally not received much attention in contrast to sheep, although the heritability of host resistance to certain parasites is so high that breeding for resistant pigs could be a possibility (Roepstorff et al., 2011).

The second aspect, which can lead to the opposite conclusion, concerns relaxed selection, in which the source of selection that was previously important for the maintenance of a particular trait is weakened or even eliminated (Lahti et al., 2009). Indeed, selection pressure from parasites may have been reduced during the domestication process. Since domestication, animals have been confined, at least to a certain extent, which prevents them from being exposed to the full spectrum of parasites that could infect/infest them in their natural environment. This, together with "stringent" artificial selection for desirable traits, could influence (jeopardise) the evolution of genetic resistance in (parasite-naïve) domestic animals (Eizaguirre et al., 2012; Smallbone et al., 2021).

With regard to genetic parasite resistance, the major histocompatibility complex (MHC) and its variability is often considered one of the functionally most important loci associated with parasite resistance (Sommer, 2005; Axtner & Sommer, 2012; Arbanasić et al. 2019). MHC is a large locus of genes responsible for the adaptive immune system, helping to activate not only appropriate T cells that help the organism to eliminate intracellular pathogens (e.g. viruses), but also B cells involved in the elimination or neutralisation of extracellular pathogens, including parasites (Janeway et al., 2001; McManus et al., 2014). It is assumed that animals with limited MHC gene diversity also have low resistance to parasites.

Indeed, constant selection pressure by various parasites leads to rapid adaptive evolutionary changes that result in an adaptive shift in allele frequency, implying that parasite-mediated selection directly contributes to the maintenance of MHC polymorphism (Eizaguirre et al., 2012). Accordingly, Smallbone et al. (2021) found a significantly lower number of MHC alleles and MHC supertypes per individual in domesticated guppies (*Poecilia reticulata*) compared to the wild ones. They pointed out that artificial selection for desirable, economically important traits may lead to the loss of key immune functional alleles and thus reduce the immunogenetic diversity that protects populations from the risk of parasite infection/infestation, which could significantly impair host resistance to parasites. Similar results have been shown for the red junglefowl (*Gallus gallus*) compared to the domestic chicken (Nguyen-Phuc, Fulton, Berres, 2016). In contrast, studies on the pig did not follow the same premise and showed that domestication does not appear to act as a bottleneck limiting MHC diversity (Moutou et al., 2013), and the same was found in the zebra finch (*Taeniopygia guttata*), for example (Newhouse & Balakrishnan, 2015).

However, MHC diversity does not necessarily imply higher functional resistance, but may simply be the signature of the pathogens and parasites that the animal has been confronted with during evolution (Mikko et al., 1999; ~~see also~~ Portanier et al., 2019, showing that MHC diversity in mouflons (*Ovis gmelini musimon*) is associated with resistance to nematodes but not to coccidia). In addition to MHC, there are other quantitative trait loci for parasite resistance (McManus et al., 2014), which makes this aspect of PMD testing even more challenging.

Testing PMD based on parasite load/resistance/tolerance in existing populations of wild or domestic animals and simply comparing these populations is therefore interpretatively quite complex, although relatively easy to perform. Comparative studies, such as the present one, should be supported by a more focussed methodology. Either to examine the frequency of domestication syndrome traits in the wild population in relation to their parasite resistance/load, or to examine the parasite resistance/load of wild animals showing signs of domestication syndrome (e.g. tameness) in comparison to completely wild animals of the same population, as originally proposed (Skok, 2023). The other and probably most reliable way to test PMD would be an experimental approach, i.e. experimental proto-domestication, such as the Belyaev fox experiment (Belyaev, 1979). However, instead of selecting animals for tameness, an experimental population of the wild counterpart of domestic animals would be experimentally exposed to parasites, selected against parasite resistance (whereby more infected/infested, less resistant individuals would be selected), and analysed over generations for the frequency of domestication syndrome traits in the population. It is predicted that the frequency of typical domestication syndrome traits (tameness, depigmentation, floppy ears, etc.) would increase in a parasite-susceptible population.

It should also be considered that the influence of parasites on the domestication process cannot simply be generalised to the entire parasite load in the host, as it is also possible that only certain parasites play a mediating role in the domestication process.

To mediate domestication, direct (i.e., without an intermediate host) interspecific transmission including a possible zoonotic potential of the parasite seems to be a necessary criterion. Of the parasite taxa found in our study, all parasites found exclusively or predominantly in domestic pig (*Balantidium coli*, Strongyle/ *Oesophagostomum* sp. and *Trichuris* sp.) fulfil both criteria, but not *Cystoisospora suis*, which was only found in domestic pig and is species-specific. In addition, the only parasite taxa found exclusively in wild boar was *Strongyloides* sp. of which none of the known species infecting pigs were found to be zoonotic. Furthermore, *Strongyloides* sp. have been shown to be both parthenogenetic and autoinfectious (Moore, 2002), making them less reliant on intensive transmission between hosts.

Further, the PMD predicts that parasites should increase the occurrence of domestication syndrome traits. For the parasites found in our study, there is a significant lack of specific information on their potential effects on phenotypic traits of interest in the context of PMD. However, of the target traits, mainly behavioural changes/correlates of the host have been investigated so far.

Studies on the impact of the endoparasites taxa relevant (found) in our study on host behaviour usually deal with either parasite load in relation to a specific personality type or social behaviour (~~e.g.~~ Côté & Poulin, 1995; Ezenwa, 2004; Melfi & Poyser, 2007; Müller-Klein et al., 2019; Santicchia et al., 2019), avoidance/sickness behaviour within a social group (~~e.g.~~ Ghai et al., 2015; Chapman et al., 2016; Friant, Ziegler & Goldberg, 2016; Wren et al., 2021), changes in the complexity and dynamics of a social group (Burgunder et al., 2017) and the fear response to predators (Moore, 2002; Barber & Dingemanse, 2010; Kaushik, Lamberton & Webster, 2012). Indeed, behaviours that are (in)directly indicative of the animals' degree of tameness, which is otherwise a pivotal trait of the domestication syndrome, are primarily of PMD interest.

Tameness in the context of domestication can be defined as reduced fear of humans, as well as increased boldness and reduced aggression, which have been shown to cause the development of many aspects of the domestication syndrome (Belyaev, 1979; Agnvall et al., 2015). With regard to PMD, the influence of parasites on behaviours such as reduced fear of novelty or of other species, including humans, is therefore of particular interest. However, such studies are relatively rare, and the results are often inconclusive.

Fear of predators or novelty (neophobia) as well as boldness and exploratory behaviour appear to be suitable candidates as indicators of tameability. Of the parasites found in the present study, some (*Eimeria* sp., Strongyles, *Strongyloides* sp., *Trichuris* sp.) were associated with host behaviour, but the results are not conclusive. *Eimeria* sp., for example, has generally been shown to reduce fear of predators (~~reviewed in~~ Moore, 2002; Kaushik, Lamberton & Webster, 2012). However, when looking at neophobia/boldness, for example, it was found that rural and urban rats, the latter being considered less neophobic (bolder), did not differ in *Eimeria* sp. load, but were more infected with *Trichuris* sp. (Battersby Parsons & Webster, 2002). In addition, bolder and more exploratory individuals of grey squirrels (*Sciurus carolinensis*) were shown to be more heavily infected with *Strongyloides* sp. (*S. robustus*), but this was considered to be a cause rather than a consequence of infection severity (~~e.g.~~ Santicchia et al., 2019). Given the apparent species specificity, potential studies in our model species (*Sus scrofa*) are of particular importance, but they are scarce. In wild boar, a study was recently conducted on parasite load in relation to the degree of urbanisation of the area in which they forage. No general difference in endoparasite load (including one strongyle species, *Oesophagostomum dentatum*) was found between wild boar foraging in suburban areas and those foraging in urban areas – except for *Eimeria* sp., the prevalence of which was significantly higher in individuals foraging in urban areas, i.e. those that were less afraid of the anthropogenic environment/humans (Pilarczyk et al., 2024). Therefore, *Eimeria* sp. appear to be associated with tame-like behaviour in pigs and could therefore also be one of the candidate parasites associated with PMD.

Although not of paramount importance in the context of PMD, intraspecific interactions among members of the same social group have also been frequently studied and should therefore be considered. Indeed, literally all domesticated animals except the cat are social, with the dominant status of an individual indirectly indicating the degree of tameness. In general, subordinate animals are considered less aggressive/tameable (e.g. Blanchard et al., 1988; Holekamp & Strauss, 2016) and (with some exceptions) less neophobic, i.e. they are bolder and tend to explore new environments and objects (King, 1973; Robertson, 1982; Johnson & Balph, 1990; Darrow & Shivik, 2009; ~~but see also~~ Mettler & Shivik, 2007; Schaffer et al., 2021). Among the parasites found in our study, susceptibility to infection with some of them was also found to be related to individual social status (dominant vs. subordinate). In plain zebras (*Equus quagga*), for example, it was found that subordinate individuals, which could also be considered tamer, were more susceptible to infection with strongyles as well as *Strongyloides* sp. (Fugazzola & Stancampiano, 2012; Joly et al., 2023). In contrast, in bovids (several species of gazelles), territorial males, which can be considered dominant, have been found to have a higher strongyle and coccidia (including *Eimeria* sp.) load (Ezenwa, 2004).

However, our results do not fit easily into this picture of previous findings on the relationship between specific parasite and tameness, as we found *Eimeria* sp. to the same extent in the domestic and wild cohort; moreover, in the Croatian sample it was found only in the wild cohort, while strongyle/*Oesophagostomum* sp. and *Trichuris* sp. were found in domestic pig to a significantly higher extent or exclusively in the domestic cohort, and *Strongyloides* sp. was found only in wild boar.

Conclusions

The main findings of the present study are consistent with the PMD in terms of overall parasite load/richness, as more parasite taxa were found in the domestic pig, whereby of the parasites found in both cohorts strongyle/*Oesophagostomum* sp., but not *Eimeria* sp. (the same), was significantly higher in the domestic pig. However, when considering the influence of a particular parasite on the traits of the domestication syndrome, no clear conclusions can be drawn as the relevant studies are limited to (indirect) behavioural traits only and some of the parasites found have not been studied at all in this regard. In addition, the studies to date suggest that the influence of a particular parasite may even be species-specific, but the studies on pig (*Sus scrofa*) are sparse (and only indirect). Therefore, we can only infer partial and indirect correlations, which are ultimately inconclusive. Nevertheless, the present study provides some indices in favour of PMD, but no definitive answers. This was neither possible nor expected given the nature of the study, as it was a preliminary test of the hypothesised baselines of PMD – indeed, no other than an experimental approach can provide a definitive answer.

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Table 1(on next page)

Description of the parasites found in the study.

Parasite taxa found in the study with summarised taxa richness (S) for each cohort. † – only domestic cohort infected, †† – only wild cohort infected, HR – Croatia, SI – Slovenia.

Table 1: Description of the parasites found in the study.

Parasite taxa found in the study with summarised taxa richness (S) for each cohort. † – only domestic cohort infected, †† – only wild cohort infected, HR – Croatia, SI – Slovenia.

	Domestic pig	**Wild boar**	S
HR	*Cystoisospora suis* † Strongyle type eggs *Trichuris* sp. †	*Eimeria* sp. Strongyle type eggs *Strongyloides* sp. ††	5
SI	*Eimeria* sp. *Oesophagostomum* sp. (strongyle) *Trichuris* sp. † *Balantidium coli* †	*Eimeria* sp. *Oesophagostomum* sp. (strongyle)	4
S	7	5	

Figure 1

Figure 1: Parasite load in the HR wild boar – domestic pig association.

Comparison of the intensity of infection with certain parasite taxa between wild boar and domestic pig cohorts in Croatia. The centre lines of the boxplots indicate the medians, the edges of the boxes represent the 25th and 75th percentiles. [1] indicates that only one cohort was infected, TS - test statistics, r - effect size.

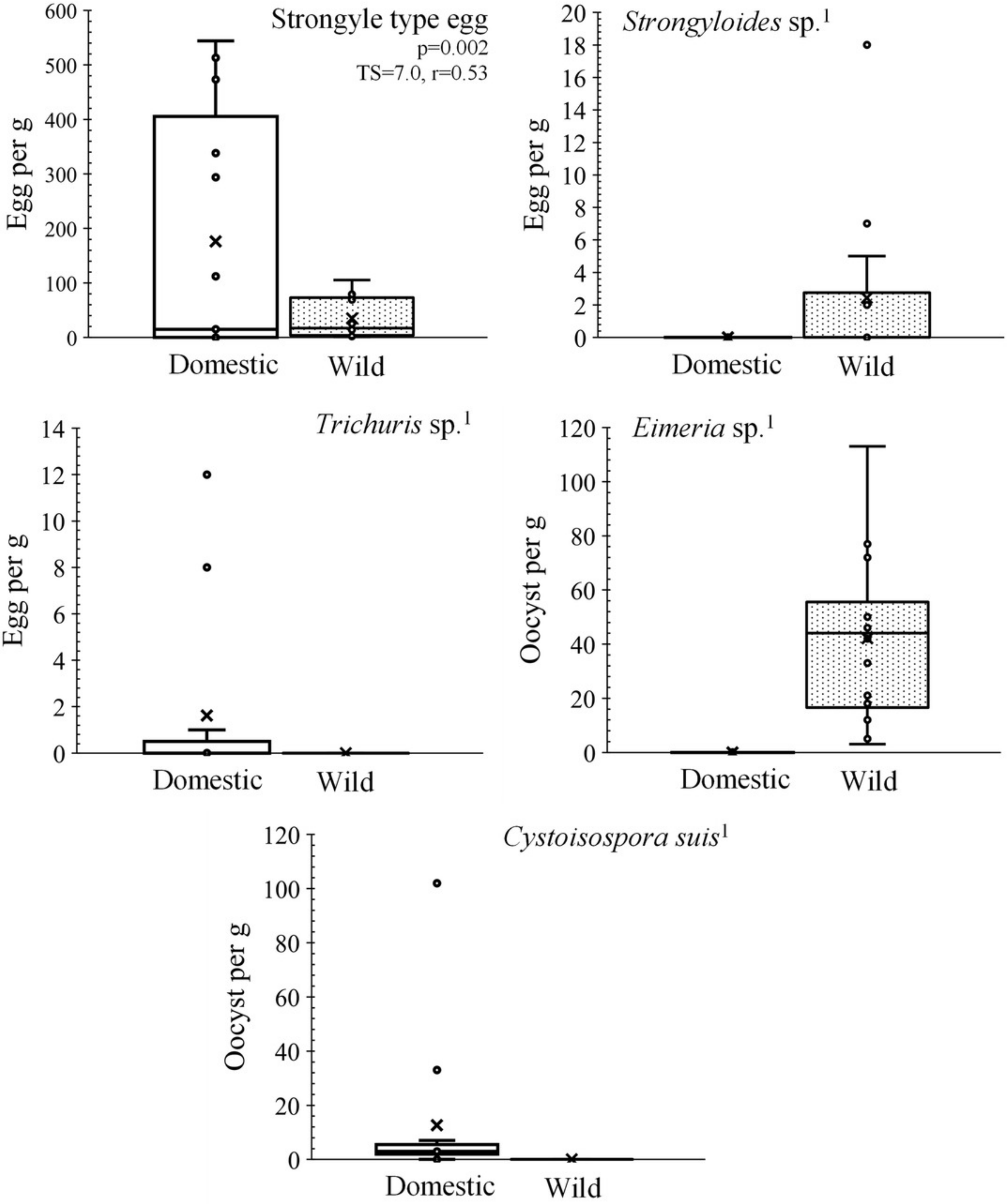
Strongyle type egg
p=0.002
TS=7.0, r=0.53
Egg per g
0
100
200
300
400
500
600
Domestic
Wild
Strongyloides sp.1
Egg per g
0
2
4
6
8
10
12
14
16
18
20
Domestic
Wild
Trichuris sp.1
Egg per g
0
2
4
6
8
10
12
14
Domestic
Wild
Eimeria sp.1
Oocyst per g
0
20
40
60
80
100
120
Domestic
Wild
Cystoisospora suis1
Oocyst per g
0
20
40
60
80
100
120
Domestic
Wild

Figure 2

Figure 2: Parasite load in the SI wild boar – domestic pig association.

Comparison of the intensity of infection with certain parasite taxa between wild boar and domestic pig cohorts in Slovenia. The centre lines of the boxplots indicate the medians, the edges of the boxes represent the 25th and 75th percentiles. [1] indicates that only one cohort was infected, U - test statistics, r - effect size.