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## **Low allelic diversity in vaccine candidates genes from different locations sustain hope for *Fasciola hepatica* immunization**

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1 **Low allelic diversity in vaccine candidates genes from different locations sustain hope for**  
2 ***Fasciola hepatica* immunization**

3

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15

16 **Abstract**

17 *Fasciola hepatica* is a trematode parasite that causes fasciolosis in animals and humans. Fasciolosis  
18 is usually treated with triclabendazole, although drug-resistant parasites have been described in  
19 several geographical locations. An alternative to drug treatment would be the use of a vaccine,  
20 although vaccination studies that have been performed mainly in ruminants over the last 30 years,  
21 show high variability in the achieved protection and are not yet ready for commercialisation. Since  
22 *F. hepatica* exhibits a high degree of genomic polymorphism, variation in vaccine efficacy could be  
23 attributed, at least partially, to phenotypic differences in vaccine candidate sequences amongst  
24 parasites used in the challenge infections. To begin to address this issue, a collection of *F. hepatica*  
25 isolates from geographically dispersed regions, as well as parasites obtained from vaccination trials  
26 performed against a field isolate from Uruguay and the experimentally maintained South Gloucester  
27 isolate (Ridgeway Research, UK), were compiled to establish a *F. hepatica* Biobank. These  
28 collected isolates were used for the genetic analysis of several vaccine candidates that are important  
29 in host-parasite interactions and are the focus of the H2020 PARAGONE vaccine project  
30 (<https://www.paragoneh2020.eu/>), namely FhCL1, FhCL2, FhPrx, FhLAP and FhHDM. Our results  
31 show that *F. hepatica* exhibits a high level of conservation in the sequences encoding each of these  
32 proteins. The consequential low variability in these vaccine candidates amongst parasites from  
33 different geographical regions reinforces the idea that they would be suitable immunogens against  
34 liver fluke isolates worldwide.

35 **Keywords:** *Fasciola hepatica*; Genetic variation; Phenotypic variation; Vaccines

36

## 37 **1. Introduction**

38 *Fasciola hepatica* is the causative agent of fasciolosis, a parasitic disease of ruminants that  
39 seriously affects farm productivity worldwide as a result of livestock morbidity and mortality, as  
40 well as being an important zoonotic parasite of man (Cwiklinski et al., 2016; Carmona and Tort,  
41 2017; Mehmood et al., 2017). The annual losses related to pathologies caused by fasciolosis have  
42 been reported to be 3 billion USD (Spithill et al., 2012). While triclabendazole is the most effective  
43 drug treatment, *F. hepatica* has rapidly developed drug resistance resulting in the widespread threat  
44 to livestock production systems (Kelley et al., 2016). Therefore, the development of an effective  
45 vaccine is paramount and would represent the most appropriate and sustainable way forward in the  
46 control of fasciolosis (Dalton et al., 2013).

47 Since the early 1990s, a growing number of vaccine trials in livestock have evaluated the  
48 efficacy of candidate antigens from *F. hepatica*. Among them, different parasite secreted antigens  
49 such as cathepsin L peptidases 1 and 2 (FhCL1, FhCL2), the antioxidant peroxiredoxin (FhPrx) and  
50 the gut-associated exopeptidase leucine aminopeptidase (FhLAP) have been selected as vaccine  
51 candidates due to their importance in host-parasite interactions (Dalton et al., 2013; Toet et al.,  
52 2014). These studies highlighted that high levels of variability in vaccine efficacy occur between  
53 trials which likely results from differences between the antigen source, the adjuvants used and the  
54 host species vaccinated. Variation between animals from the same or different breeds was also  
55 observed. In general, native antigens were more effective than recombinant vaccines, and with the  
56 exception of FhLAP combination of antigens perform better than single antigen formulations (see  
57 an overview of vaccine data in Table 1).

58 Following the sequencing of the *F. hepatica* genome, high levels of genetic polymorphism  
59 were observed, particularly in the chemosensory and neurodevelopmental pathways which might  
60 account for adaptations to the host environment and the capacity for rapid evolution (Cwiklinski et  
61 al., 2015). Further genome sequencing of liver flukes from two American locations also found  
62 polymorphisms between the *F. hepatica* isolates (McNulty et al., 2017). Both studies were based on

63 sequencing several individual parasites but opened the path to population genetic approaches, a  
64 much needed follow-up of the helminth genomic era (Wit and Gilleard, 2017). Analysis of UK  
65 isolates based on neutral markers (microsatellites) confirmed substantial variation within *F.*  
66 *hepatica* populations (Beesley et al., 2017), which complements the population genetics studies of  
67 liver fluke populations carried out using ribosomal and mitochondrial markers to unravel  
68 geographical variations (reviewed by Teofanova et al., 2012). Although marked genetic  
69 heterogeneity between liver fluke populations is now well recognised, an association between *F.*  
70 *hepatica* haplotypes and specific phenotypic traits has yet to be made (reviewed in Zintl et al.,  
71 2015).

72 To further the development of vaccines against a range of economically important parasitic  
73 pathogens of livestock, the EU H2020 funded consortium PARAGONE  
74 (<https://www.paragoneh2020.eu/>) has brought together liver fluke researchers with an aim to  
75 develop a multi-valent vaccine against *F. hepatica*. Our current vaccine candidates include those  
76 molecules that have shown potential in previous studies, including cathepsin L proteases (FhCL1),  
77 leucine aminopeptidase (FhLAP) and peroxiredoxin (FhPrx), in addition to assessing the *F.*  
78 *hepatica* helminth defence molecule (FhHDM) as a vaccine candidate. Specifically, this study  
79 evaluates FhHDM as a recombinantly expressed protein, which complements recent sheep  
80 vaccination trials by the Prof. Ubeira group using native and synthetically synthesised FhHDM  
81 (Martínez-Sernández et al., 2017; Orbegozo-Medina et al., 2018).

82 An important task of the project is to investigate the potential genetic variability of these  
83 vaccine targets within different *F. hepatica* isolates that may be a cause of variability in efficacy  
84 results between vaccine trials. Accordingly, we sourced *F. hepatica* from geographically dispersed  
85 liver fluke populations for genetic analysis and compared these results with an analysis of the liver  
86 fluke isolates that we used in our vaccine trials, namely a field isolate from Uruguay and the  
87 laboratory-maintained South Gloucester isolate from Ridgeway Research, UK. The collection of *F.*

88 *hepatica* isolates sourced as part of this study is now housed in a *F. hepatica* Biobank and is  
89 publically available.

## 90 **2. Materials and methods**

### 91 **2.1. Parasite material and sample processing**

92 A comprehensive biobank for *F. hepatica* was established at the Institute of Natural  
93 Resources and Agrobiology of Salamanca (IRNASA-CSIC) (Salamanca, Spain), with the aim of  
94 collecting representative samples of *F.hepatica* from different geographical locations, hosts and  
95 variable drug susceptibility/resistance. Samples were sourced from geographically dispersed regions  
96 collected at local abattoirs and stored individually in RNAlater (Sigma Aldrich). Samples from the  
97 PARAGONE *F. hepatica* vaccine trials were also included in the biobank from cattle  
98 experimentally infected with a field isolate from Uruguay and sheep experimentally infected with  
99 the laboratory maintained South Gloucester isolate (Ridgeway Research). The samples used for this  
100 study are detailed in Table 2.

101 All samples were processed upon arrival to the biobank following the European rules for  
102 handling and traceability of biological samples. In brief, adult liver flukes stored in RNAlater were  
103 transversally sliced in half and used for (a) extraction of genomic DNA (Nucleospin Tissue,  
104 Magerey Nagel), and (b) extraction of RNA and subsequent cDNA synthesis (PureLink RNA  
105 Minikit, Thermo Fischer Scientific; Kit First Strand cDNA Synthesis, Roche), according to the  
106 manufacturer's instructions. The extracted genomic DNA and RNA were assessed for quality and  
107 quantity by OD at 260/280 nm and by gel electrophoresis. The nucleic acids from each sample were  
108 stored at -80°C in 2D-coded tubes of 500 µl volume (Wilmut, Spain). The code on each tube was  
109 automatically associated with a submission form (Supplementary file 1) containing the sample  
110 information, including isolate number, origin (country and locality), animal host, date of isolation,  
111 and type of isolate. The unique code given to each sample includes the Nomenclature of Territorial

112 Units for Statistics (NUTs) country code, and two successive ordinal numbers identifying the  
113 country region and the sample number.

## 114 **2.2. PCR Amplification and sequencing**

115 Primers were designed to amplify the whole coding sequence of each gene, including the  
116 start and stop codons (Table 3), based on the following *F. hepatica* sequences publicly available in  
117 GenBank: FhCL1 (U62288), FhCL2 (U62289), FhPrx (FJ168037) and FhLAP (AY644459). Due to  
118 the small size of the FhHDM (FR848429) gene transcript, this gene was directly amplified from  
119 genomic DNA of samples from Uruguay and Argentina, resulting in a 490 bp product that included  
120 the coding sequence and the corresponding introns. PCR reactions were performed in 25 µl volume  
121 containing 0.1 µl Taq Platinum (5 U/µl; Thermo Fischer Scientific, Spain), 2.5 µl 10x Taq Platinum  
122 buffer, 1 µl 25 mM MgSO<sub>4</sub>, 1 µl each dNTP (10 mM), 0.5 µl of each primer (10 µM) and 1 µl  
123 cDNA. The PCR cycling conditions consisted of an initial denaturation at 94°C for 30s, followed by  
124 35 cycles at 94°C for 30s, 48°C (or 60°C for FhHDM) for 1min and 72°C for 2 min, followed by a  
125 final extension at 72°C for 5 min. PCR products were analysed by gel electrophoresis (1% agarose  
126 gel) and the bands of the expected molecular weight were excised and the DNA extracted according  
127 to the manufacturer's instructions (GeneJET Gel Extraction and DNA Cleanup Kit, ThermoFisher  
128 Scientific, Spain). The purified products were added to the corresponding forward and reverse  
129 primers used in the PCR reaction in a 96 well plate and sent for automatic sequencing (Standard-  
130 Seq; Macrogen, The Netherlands) by traditional sequencing in a 96-capillary 3730xl DNA Analyzer  
131 (Thermo Fischer Scientific).

## 132 **2.3. Data analysis and variant calling**

133 Chromatogram files were processed with CLC Main Workbench (Qiagen). All sequences  
134 were imported and trimmed by quality, removing regions and/or sequences with poor quality, and  
135 aligned to the reference consisting of the complete coding sequences (CDS) for each vaccine target  
136 gene. All variant sites compared with the reference sequence were automatically detected and

137 termed “conflicts”, which were manually inspected to confirm whether or not these differences  
138 represented true variants. For each target gene the coverage was determined for all positions (the  
139 number of times a good quality read was found for this particular position), and a global variation  
140 list generated. Finally a short representation of each sample was generated keeping only those  
141 positions that show variation in at least one sample or each target gene (Supplementaryfile 2).

142 Specific analysis was carried out where non-synonymous substitutions resulted in a change  
143 of amino acid residues critical for protein structure and/or function, as determined by previous  
144 biochemical analysis of our target molecules and analysis using Conserved Domain Database  
145 (<https://www.ncbi.nlm.nih.gov/cdd/>).

146

### 147 **3. Results and Discussion**

148 In order to examine the sequence variability in our *F. hepatica* vaccine candidate genes  
149 (FhLAP, FhPrx, FhHDM and FhCL1), we analysed samples included in the *F. hepatica* BioBank  
150 from 87 individual adult parasites obtained from naturally and experimentally infected cattle and  
151 sheep isolated in Uruguay, Argentina, Belgium, Ireland and UK (laboratory; from sheep infected in  
152 Spain).

153 We detected low levels of variation for all the target genes. Almost half of the variations  
154 detected were homozygous sites found in all the samples analysed. The conservation at these  
155 positions, despite the diverse geographical origins of the samples and the fact that they are shared  
156 also by the two available genome drafts, strongly suggest that they represent errors from invalid  
157 base calling in the reference sequences available in GenBank rather than true variable sites.

158 Analysis of the 1,575bp of the FhLAP coding sequence identified 14 variable sites. Four  
159 homozygous variants were observed compared with the reference sequence (Acosta et al., 2008) in  
160 all the individuals sequenced showing good quality sequences (see Supplementary file 2) and in the  
161 corresponding sequence in both genomic drafts; namely three non-synonymous changes – at base



162 pairs C1210G (Pro to Ala), C1337T (Thr to Ile), A1489G (Thr to Ala), and one synonymous  
163 variation at position 78 (C78A, Table 4, Figure 1). Several geographical differences were observed  
164 for the remaining 10 variable sites. In particular, three fluke samples from Uruguay were  
165 heterozygous at position 93 (G/A) in contrast to the sequences amplified from the rest of the  
166 samples and the corresponding genome sequences, where a synonymous change (G to A) was  
167 observed (Table 4). A change at position 1464 was detected in a single adult parasite from Uruguay.  
168 Interestingly, we observed 3 heterozygous variants at positions A1039C, G1057T, A1166T in one  
169 of the Belgian field isolates. Specifically the variation at nucleotide position 1057 results in an  
170 amino acid change from Ala to Ser situated between 2 metal co-ordination residues adjacent to the  
171 active site that may subsequently have an effect on protein function (Acosta et al. 2008).

172         Only 6 variants were observed throughout the FhPrx sequence (Table 5, Supplementary file  
173 3). Three of them correspond to non-synonymous variations observed in one individual fluke from  
174 Ireland (T227A and A234C, resulting in Phe to Ile and Asp to Ala changes, respectively) and in one  
175 Belgian fluke that has a Val to Glu change due to the substitution T498A. These variable sites were  
176 not at positions expected to affect the active site residues important for peroxiredoxin function  
177 (McGonigle et al 1997). The remaining three changes were synonymous and showed variable  
178 amounts of homozygous and heterozygous individuals in samples from different locations.  
179 Interestingly, geographical differences can be detected at some positions; for example nucleotides at  
180 position 82 are predominantly homozygous in the Irish samples with thymine being more frequent  
181 (82T; 23/33), while the UK samples preferably display a homozygous cytosine (82C; 9/12  
182 samples). Samples from Belgium show a predominance of heterozygotes in this position, while in  
183 Uruguay three possible genotypes at this site are detected (Table 5 and Supplementary file 2).

184         A more complex scenario pertains for FhCL1 as six genes in the *F. hepatica* genome encode  
185 isoforms of this protease (Cwiklinski et al., 2015, McNulty et al 2017). The similarity between  
186 these six genes does not allow for the design of PCR primers that can differentiate between them.  
187 As such, the FhCL1 primers used in this study amplify at least three of the FhCL1 genes, which

188 makes defining SNPs in the sequences challenging (Table 6, Supplementary file 4). Consequently,  
189 the variants that might exist in each of them are confounded by the different FhCL1 sequences.  
190 Clear evidence of this is the lower quality of the FhCL1 sequences, since they represent a pool of  
191 highly similar but divergent molecules from each individual. In addition, 45 potential variants were  
192 observed, interspersed throughout the gene sequence. This number of variants is in contrast to the  
193 variation observed in genes of similar size analyzed as part of this study, namely FhLAP and  
194 FhCL2, that show lower levels of variation. Nine positions (495, 602, 624, 663, 666, 697, 715, 804,  
195 911) differ from the FhCL1 originally described (Roche et al., 1997) but are homozygous in all the  
196 samples analyzed despite their geographical origin and the available genomic sequences, suggesting  
197 base call errors in the original sequences. The remaining 36 variations might correspond to either  
198 true heterozygous sites or variant sites between FhCL1 sequences. While changes at 13 of these  
199 positions do not alter the resulting amino acid, non-synonymous substitutions occur at the  
200 remaining 23 variable positions. Only one of the non-synonymous changes (V267L) corresponds to  
201 an amino acid position potentially important for the CL1 functionality (the S2 pocket). In fact while  
202 Val is present in FhCL1 at this position, the presence of Leu is characteristic of FhCL2. However, a  
203 recent study demonstrates that a single change in this position generated by site directed  
204 mutagenesis does not affect the specificity of the enzyme (Corvo et al, 2018). These observations  
205 reinforce the idea that a diversity of FhCL1 isoforms with subtle differences might be produced  
206 simultaneously by the parasite. The only experimental methods to further explore the complexity  
207 and diversity of this *Fasciola* cathepsin L subfamily would be to consider digital PCR sequencing  
208 or next generation sequencing.

209         Since assessing the variability of the FhCL1 vaccine candidate was challenging due to the  
210 presence of several genes, we evaluated the potential for variation within the complex *F. hepatica*  
211 cathepsin gene family by analyzing a related protease of the same family, FhCL2, which is encoded  
212 by a single copy gene. In contrast to that found for FhCL1, 12 changes were observed throughout  
213 the FhCL2 sequence in comparison to the reference sequence (Table 7, Supplementary file 5). Four

214 variants, comprised of non-synonymous changes at positions 41, 302, 490 and 501, were found in  
215 both of the *F. hepatica* genome sequences and in all the individuals analysed showing good quality  
216 sequences (see Supplementary file 2), indicating only variation compared with the reference  
217 sequence. The remaining variants were represented by six non-synonymous changes and two silent  
218 mutations at positions 273 and 378 (G273A, Ser; G378A, Gln) (Table 7). The synonymous change  
219 at position 378 within four adult parasites obtained in Ireland is of particular note, as this position  
220 corresponds to the amino acid residue that is part of the active site S1 binding subsite and therefore  
221 a non-synonymous change at this position may have affected the enzymatic activity of the protein.  
222 A predominance of the heterozygote state (A/G) at two base pair positions (273 and 373) was also  
223 observed in most of individuals analysed, which in the case of position 373 that corresponds to the  
224 first position of the codon resulted in two amino acid variants, namely Asn and Asp. In addition, we  
225 observed variations that were specific to geographical locations. Specifically, variations at positions  
226 649 and 670 were only been found in the Irish and UK (Ridgeway) isolates, indicating this may be a  
227 variation restricted to European fluke isolates. In contrast, variability at position 259 was only  
228 observed in the samples from Uruguay and Argentina suggesting a distribution restricted to South  
229 America.

230 To date our analysis of the FhHDM gene in samples from South America has detected six  
231 variations within the intron sequences and two synonymous substitutions in the coding sequence  
232 that consequently do not affect the protein sequence (Table 8, Supplementary file 6). Further  
233 analysis of other isolates is required to determine whether this high level of conservation is  
234 observed across all *F. hepatica* isolates. As the molecular function of FhHDM relies on its distinct  
235 secondary protein structure that includes an amphipathic  $\alpha$ -helix (Robinson et al., 2011), and is  
236 encoded by a single copy gene, the lack of variation we observe indicates that the function of this  
237 molecule needs to be maintained by maintaining the secondary structure of this molecule.

238 Antigenic polymorphism is considered an important mechanism of immune evasion used by  
239 a large number of pathogens, including helminths (Maizels and Kurniawan-Atmadja, 2002). In

240 addition, when allelic diversity affects immune targets, it might pose a challenge for vaccine  
241 approaches. As a result, the development of multivalent vaccines may require the incorporation of  
242 allelic variants in order to cover most of the isolates/strains responsible for an infection. This type  
243 of approach has recently been used for the development of a vaccine against malaria (Terheggen et  
244 al., 2014). Similarly, *Haemonchus contortus* vaccination studies using cathepsin B-like cysteine  
245 proteases have identified parasite populations with defined allelic profiles suggesting that  
246 immunisation imposes a genetic selection on these genes and that specific alleles may play a  
247 immunoprotective role (Martin et al., 2015).

248 Our study highlights a low level of allelic variability within prime vaccine candidate gene  
249 targets (FhCL1, FhPrx, FhHDM and FhLAP) in geographically dispersed *F. hepatica* isolates as  
250 well as the laboratory maintained isolate used in our sheep vaccine trials. These results suggest that  
251 the variability among vaccine studies (see Table 1) are not related to heterogeneity in these genes.  
252 As such host-related effects and the level of animal susceptibility status to *F. hepatica* infection  
253 should be investigated in the future that may provide a more plausible explanation for the variability  
254 observed in *F. hepatica* vaccine trials. Adjuvant selection is also an important issue for liver fluke  
255 vaccine trials. There is a need to find an adjuvant as potent as Freund's Complete Adjuvant, without  
256 the side effects, that will elicit appropriate potent immune responses in a broad range of hosts to  
257 overcome animal variability. Furthermore, to date native fluke antigens have been more effective  
258 than recombinant vaccines, which may imply that post-translational modifications such as  
259 glycosylation may be important in eliciting protective immune responses, which needs to be taken  
260 into consideration.

261 To date, investigation of vaccine candidate antigen variability in trematodes has only been  
262 previously examined in schistosomes (Gleichsner et al., 2015). Consistent with our study of *F.*  
263 *hepatica*, analysis of the cathepsin B sequence in *Schistosoma mansoni* also identified low levels of  
264 that most probably will not impact on protein-antibody interaction and binding (Simões et al.,  
265 2007). Studies of candidate antigens tetraspanins both in *S.mansoni* and *S.japonicum* show more

266 variability, however it should be taken into account that these membrane proteins constitute a large  
267 gene family, so it is not clear if the variability is allelic or due to multiple genes, similarly to what  
268 we found in FhCL1 (Cupit et al., 2011; Young et al., 2015; Zhang et al., 2011). Taken together  
269 these data suggest that in spite of the variability that might be detected at the genomic level,  
270 trematodes show conservation in the sequence of antigens important for key biological functions.  
271 This limited variability reinforces the idea that the selected proteins could be good immunogens for  
272 liver fluke worldwide. In addition to our study of antigen variability, we have sourced 87 *F.*  
273 *hepatica* isolates that are now housed in a publically available *F. hepatica* biobank that provides the  
274 liver fluke research community with access to a variety of isolates, which in particular are suitable  
275 for ongoing population genetic studies of this parasite. This biobank can be accessed upon request  
276 to M. Siles-Lucas at IRNASA-CSIC and is open to new submissions.

277

278

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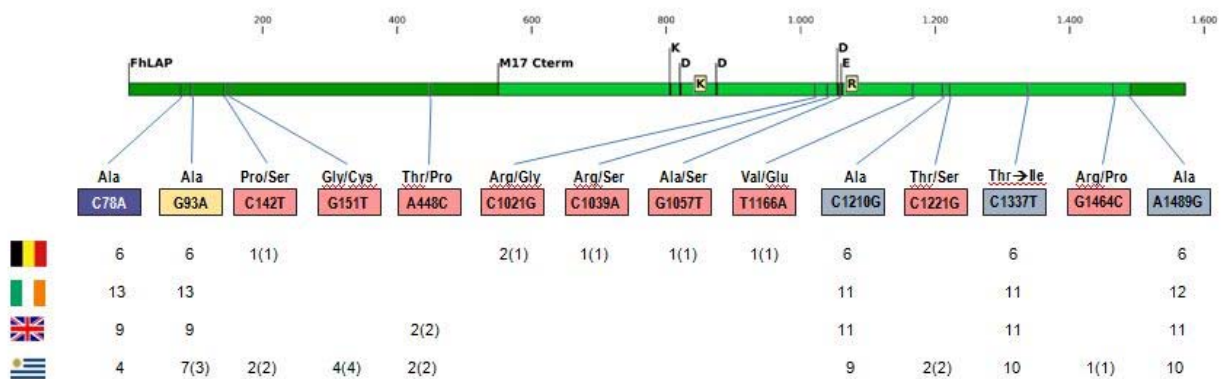
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## Figure legends

**Figure 1.** SNPs variants detected along the region amplified of the FhLAP gene. The C-terminal catalytic domain (Interpro IPR000819) is highlighted in light green. The active site residues are shown in the boxes and the residues involved in metal binding are shown above the schematic, indicated by the lines. The variable positions in different geographical populations of liver fluke are shown at the bottom of the figure. The numbers in brackets indicate number of heterozygote individuals.



**Table 1.** Efficacy of single or combination vaccines against *Fasciola hepatica*.

Antigen	Source	Host	Schedule <sup>1</sup>	Adjuvant	Efficacy <sup>2</sup>	Reference
FhCL1	Adult E/S	Cattle	10-500 µg X 3	FCA/FIA	38.2-69.5%	Dalton et al., 1996
			200 µg X 3		42.5%	
		Sheep	100 µg X 2		33%	Piacenza et al., 1999
	Recombinant	Cattle	200 µg X 2	Montanide <sup>3</sup>	47.2%	Golden et al., 2010
				Montanide <sup>4</sup>	49.2%	
		Goat	100 µg X 2	Quil A	0%	Pérez-Ecija et al., 2010
					38.7%	Buffoni et al., 2012
					0%	Zafra et al., 2013
				Montanide <sup>3</sup>	0%	Pacheco et al., 2017
	Mimotope	Goat	1×10 <sup>13</sup> pp	Quil A	46.9-79.5 %	Villa-Mancera et al., 2014
FhCL1+Hb		Cattle	200 µg X 3	FCA/FIA	51.9%	Dalton et al., 1996
FhCL2		Sheep	100 µg X 2	FCA/FIA	34%	Piacenza et al., 1999
FhCL2+Hb	Adult E/S	Cattle	200 µg X 3	FCA/FIA	72.4%	Dalton et al., 1996
				FCA/FIA	72.4%	Mulcahy et al., 1998
				FIA	11.2%	
				FCA/FIA	29%	Mulcahy et al., 1999
FhCL1+CL2		Sheep	100 µg X 2	FCA/FIA	60%	Piacenza et al., 1999
		Cattle	200 µg X 3	FCA/FIA	55%	Mulcahy et al., 1999
FhCL1+CL2 +LAP	Adult E/S, SOM	Sheep	100 µg X 2	FCA/FIA	79%	Piacenza et al., 1999
FhCL1+Prx +Sm14	Recombinant	Goat	100 µg X 2	Quil A	10.1%	Buffoni et al., 2012
FhLAP	Adult SOM	Sheep	100 µg X 2	FCA/FIA	89.6%	Piacenza et al., 1999
	Recombinant	Rabbit	100 µg X 2	FCA/FIA	78%	Acosta et al., 2008
		Sheep	100 µg X 2	FCA/FIA	83.8%	Maggioli et al., 2011
				Alum	86.7%	
				Adyuvac 50	74.4%	
				DEAE-D	49.8%	
Ribi	49.5%					
FhPrx	Recombinant	Goat	100 µg X 2	Quil A	33.1%	Mendes et al., 2010
					33.1%	Buffoni et al., 2012

Adult E/S or SOM, *F. hepatica* adult worm excreted/secreted or somatic products. FCA/FIA, Freund's complete/incomplete adjuvant. <sup>1</sup>Vaccination dose (µg, micrograms; pp, phage particles number) and boosts number; <sup>2</sup>Only referred to the reduction of worm numbers in vaccinated and infected animals, compared with infected and non-vaccinated animals. <sup>3</sup>Montanide ISA70VG. <sup>4</sup>Montanide ISA206VG.

**Table 2.** *Fasciola hepatica* isolates from the Biobank used in this study.

Country	Region	Isolate type	Host	Nb. of samples
Uruguay	Colonia	Field	Cattle	2
Uruguay	Florida	Field	Cattle	3
Uruguay	Montevideo	Field	Cattle	14 <sup>1</sup>
Argentina	Córdoba	Field	Cattle	1
Ireland	East Ireland	Field	Cattle	34
	Lendeledede			
	Lapscheure			
Belgium	Zuierenkerke	Field	Cattle	6
	Nieuwmunster			
	Aartrijke			
Uruguay	Canelones	Experimental infection	Cattle	15 <sup>2</sup>
UK	Laboratory	Experimental infection	Sheep	12 <sup>3</sup>

<sup>1</sup>Samples used only for FhHDM amplification and sequencing. <sup>2</sup> Field isolate from Uruguay used to infect Polled Hereford-breed cattle as part of the PARAGONE vaccine trial using FhCL1, FhLAP, FhPRX and FhHDM in Montanide 61VG. <sup>3</sup> Laboratory maintained South Gloucester isolate (Ridgeway Research) used to infect Merino sheep-breed in Cordoba, Spain as part of the PARAGONE vaccine trial using FhCL1, FhLAP, FhPRX and FhHDM in Montanide 61VG.

**Table 3.** Primers used for amplification.

<b>Primer</b>	<b>Sequence</b>
<b>FhCL1Fwd</b>	5'-ATGCGATTATTCGTATTAGCCG-3'
<b>FhCL1Rev</b>	5'-TCACGGATATTGTGCCACC-3'
<b>FhCL2Fwd</b>	5'-ATGCGGTGCTTCGTATTAGC-3'
<b>FhCL2Rev</b>	5'-TCACGGAAATCGTGCCACC-3'
<b>FhPrxFwd</b>	5'-ATGTGTGATCGCGATCAGTGCTC-3'
<b>FhPrxRev</b>	5'-CTAGTTGGCTGAGGAGAAATATG-3'
<b>FhLAPFwd</b>	5'-ATGGCGGCGTTGGCTGTGGG-3'
<b>FhLAPRev</b>	5'-CTATTTGAATCCCAGTCGTGG-3'
<b>FhHDMFwd</b>	5'-GTCTTGCTGTGGTCCTTCTT-3'
<b>FhHDMRev</b>	5'-TTTCCCGCGTATTTCTCAA-3'

**Table 4.** Sequence changes detected in the FhLAP coding sequence of the analysed *Fasciola hepatica* isolates, showing the number of heterozygote individuals in brackets.

FhLAP			Geographical origin –NUTs code- and number of flukes				
Nucleotide change	Amino acid change	Change type*	BE, 6	IE, 30	UK, 12	UY, 11	AR, 1
<b>C78A</b>	26A	Synonymous	6	13	9	4	
<b>G93A</b>	31A	Synonymous	6	13	9	7 (3)	
<b>C142T</b>	P46S	Non-synonymous	1 (1)			2 (2)	
<b>G151T</b>	G51C	Non-synonymous				4 (4)	
<b>A448C</b>	T150P	Non-synonymous			2 (2)	2 (2)	
<b>C1021G</b>	R341G	Non-synonymous	2 (1)				
<b>C1039A</b>	R347S	Non-synonymous	1 (1)				
<b>G1057T</b>	A353S	Non-synonymous	1 (1)				
<b>T1166A</b>	V389E	Non-synonymous	1 (1)				
<b>C1210G</b>	P404A	Non-synonymous	6	11	11	9	
<b>C1221G</b>	T407S	Non-synonymous				2 (2)	
<b>C1337T</b>	T446I	Non-synonymous	6	11	11	10	
<b>G1464C</b>	R488P	Non-synonymous				1 (1)	
<b>A1489G</b>	T497A	Non-synonymous	6	12	11	10	



**Table 5.** Sequence changes detected in the FhPrx coding sequence of the analysed *Fasciola hepatica* isolates, showing the number of heterozygote individuals in brackets.

FhPrx			Geographical origin –NUTs code- and number of flukes				
Nucleotide change	Amino acid change	Change type	BE, 6	IE,33	UK, 12	UY, 11	AR, 1
<b>C82T</b>	30N	Synonymous	5 (4)	30 (7)	3 (3)	8 (5)	
<b>T227A</b>	F79I	Non-synonymous		1			
<b>A234C</b>	D81A	Non-synonymous		1			
<b>A418G</b>	142E	Synonymous	4 (4)	9 (8)	12 (3)	7 (7)	1 (1)
<b>T498A</b>	V169E	Non-synonymous	1				
<b>A514G</b>	174E	Synonymous	2 (2)	1 (1)		4 (3)	1 (1)

**Table 6.** Sequence changes detected in the FhCL1 coding sequence of the analysed *Fasciola hepatica* isolates, showing the number of heterozygote individuals in brackets.

FhCL1		Geographical origin –NUTs code- and number of flukes					
Nucleotide change	Amino acid change	Change type	BE, 6	IE, 34	UK, 12	UY, 11	AR, 1
A30G	10T	Synonymous	2 (2)	3 (1)			
A69G	23Q	Synonymous	5 (3)	23 (10)	12 (2)	9	
C87T	29N	Synonymous	6 (6)	24 (21)	11 (11)	8 (8)	1 (1)
C104A	A35D	Non-synonymous	1 (1)	10 (10)	3 (3)		
C112G	Q38E	Non-synonymous	5 (5)	20 (20)	5 (5)		
A136G	K46E	Non-synonymous	6 (5)	21 (17)	12	11 (11)	1 (1)
T153C	51I	Synonymous	6 (5)	27 (17)	12	11	1
T162C	54H	Synonymous	5 (5)	11 (11)	12 (12)	3 (3)	1 (1)
C257T	T86I	Non-synonymous		3 (3)	4 (4)	1 (1)	
T265C	S89P	Non-synonymous	5 (5)	20 (19)	6 (6)	5 (5)	1 (1)
G295A	V99I	Non-synonymous	5 (5)	25 (24)	12 (12)	8 (8)	1 (1)
T315C	105N	Synonymous	5 (5)	19 (19)		3 (3)	
A365G	E122G	Non-synonymous	5 (5)	14 (14)	2 (2)	4 (4)	
C390T	130G	Synonymous	6 (2)	27 (7)	12 (3)	11 (8)	1
G449A	R150K	Non-synonymous	2 (2)	7 (7)			
C492T	164S	Synonymous	6 (6)	18 (17)	12 (12)	11 (11)	1 (1)
C493G	R165G	Non-synonymous	6 (5)	21 (7)	12 (6)	11 (9)	1
A495T	R165G	Non-synonymous	6	24	12	11	1
G517A	G173S	Non-synonymous	6 (6)	21 (11)	12 (12)	11 (11)	1 (1)
G602A	G202E	Non-synonymous	6	19	12	11	1
A623G	K208R	Non-synonymous	5 (5)	11 (8)	12 (12)	7 (7)	1 (1)
A624G	K208R	Non-synonymous	6	19	12	11	1
A630G	210L	Synonymous	4 (4)	17 (14)	12 (12)	9	1 (1)
T657C	219Y	Synonymous	6 (6)	18 (16)	12 (12)	11 (11)	1 (1)
T663G	221V	Synonymous	6	18	12	11	1
A666T	Q222H	Non-synonymous	6	17	12	11	1
G670T	G224T	Non-synonymous	3 (3)	4 (4)	5 (5)		
C694T	232L	Synonymous		6 (6)	11 (11)	1 (1)	
A697G	I233V	Non-synonymous	6	17	12	11	1
T703G	S235A	Non-synonymous	6 (6)	17 (15)	12 (5)	11 (11)	1 (1)
T715G	S239A	Non-synonymous	6	17	12	11	1
G721A	V241I	Non-synonymous	6 (5)	8 (8)		5 (5)	1 (1)
G760A	S254G	Non-synonymous	2 (2)	10 (10)	12 (12)	11 (11)	1 (1)
C788T	S263L	Non-synonymous	4 (4)	12 (12)	10 (10)	11 (11)	1 (1)
C793T	L265F	Non-synonymous	3 (3)	8 (6)	5 (5)	5 (5)	1 (1)
C796G	R266G	Non-synonymous	6 (5)	17 (13)	12 (12)	11 (11)	1 (1)
G799T	V267L	Non-synonymous	6 (5)	17 (16)	12 (12)	11 (11)	1 (1)
C804T	268N	Synonymous	6	17	12	11	1

<b>T828C</b>	276Y	Synonymous	3 (3)	14 (14)	12 (12)	11 (11)	1 (1)
<b>G839A</b>	G280D	Non-synonymous	5 (5)	15 (15)	12 (12)	11 (11)	1 (1)
<b>T878C</b>	L293S	Non-synonymous	4 (4)	11 (9)	12 (12)	11 (11)	1 (1)
<b>C881A</b>	S294Y	Non-synonymous	4 (4)	2 (2)	11 (11)	10 (10)	1 (1)
<b>G882C</b>	S294Y	Non-synonymous	3 (3)	1 (1)	11 (10)	11 (10)	
<b>T911C</b>	V304A	Non-synonymous	6	17	12	11	
<b>C918T</b>	366N	Synonymous	5 (3)	17 (17)	12 (7)	7	

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**Table 7.** Sequence changes detected in the FhCL2 coding sequence of the analysed *Fasciola hepatica* isolates, showing the number of heterozygote individuals in brackets.

FhCL2			Geographical origin –NUTs code- and number of flukes				
Nucleotide change	Amino acid change	Change type	BE, 6	IE, 34	UK, 12	UY,11	AR, 1
A41T	Y14F	Non-synonymous	5	15	10	8	
G259A	E87K	Non-synonymous				3 (3)	1 (1)
G273A	91S	Synonymous	3 (3)	29 (29)	9 (9)	6 (5)	
T302A	F101Y	Non-synonymous	6	29	11	11	
T352G	Y118D	Non-synonymous		4 (4)			
A373G	N125D	Non-synonymous	6 (6)	28 (27)	11 (11)	8 (8)	
G378A	126Q	Synonymous		4			
C490A	P164T	Non-synonymous	6	29	11	11	1
G501T	L167F	Non-synonymous	6	29	11	11	1
G649T	G217C	Non-synonymous		5 (5)	4 (4)		
G670T	G224C	Non-synonymous		5 (5)	5 (5)		
G750C	M250I	Non-synonymous		1 (1)			

**Table 8.** Sequence changes detected in the FhHDM coding sequence of the analysed *Fasciola hepatica* isolates, showing the number of heterozygote individuals in brackets.

FhHDM			Geographical origin – NUTs code- and number of flukes	
Nucleotide change	Amino acid change	Change type	UY (34)	AR(1)
<b>G13T</b>		Intron 1	6 (4)	
<b>C26T</b>		Intron 1	2 (2)	
<b>T35C</b>		Intron 1	14 (11)	
<b>A66G</b>	51A	Synonymous	4 (4)	
<b>A105C</b>	63L	Synonymous	12 (9)	
<b>A25G</b>		Intron 4	11 (10)	
<b>A37G</b>		Intron 4	11 (8)	
<b>T47C</b>		Intron 4	6 (4)	