

# Isolating the Isolate: Proteomic Profiling of Triclabendazole-Susceptible and Resistant *Fasciola hepatica*



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# **Background**

Fascioliasis is a disease caused by *Fasciola hepatica*, which infects livestock and humans and thus poses a substantial threat to food security and human health <sup>[1]</sup>. The overdependence on triclabendazole (TCBZ) for the control and management of fascioliasis has led to the establishment of TCBZ-resistant *F. hepatica* <sup>[2]</sup>. Recent work has identified a major locus and the gene content likely conferring TCBZ resistance <sup>[3]</sup>. Hence, there is a need to further confirm potential TCBZ resistance targets, particularly at the protein level.

# <u>Aim</u>

The current study aims to utilize an in-depth proteomic approach to confirm the protein profiles from isolates of *F. hepatica* varying in their TCBZ susceptibility.





#### **Approach**



## **Results (Somatic Analysis)**

A total of 1236 proteins of high confidence were identified across the four isolates of *F. hepatica*. **Table 1** demonstrates the number of unique proteins within the isolates and between TCBZ status. Notably, this analysis revealed the two TCBZ-Resistant isolates share a commonality in possessing the **Microtubule-actin cross-linking factor 1 isoforms 1/2/3/5.** 

### Table 1: Quantitative Comparison of Proteins in Different F. hepatica Isolate

| Fasciola hepatica Isolate   | <b>Unique Proteins</b> |
|-----------------------------|------------------------|
| Aberystwyth (S)             | 14                     |
| Italian (S)                 | 17                     |
| Kilmarnock (R)              | 33                     |
| Penrith (R)                 | 6                      |
| Aberystwyth and Italian (S) | 20                     |
| Kilmarnock and Penrith (R)  | 4                      |



The PCA graph in **Figure 3** demonstrates the grouping patterns seen across different *F. hepatica* isolates. A notable observation is the close clustering of susceptible isolates, with the Kilmarnock isolate standing out as the most distant from this group.

Figure 3: PCA of F. hepatica Somatic cells proteomic data

The heatmap shows the abundance levels of proteins in the different *F. hepatica* isolates (**Figure 2**). Notably, the susceptible isolates cluster together with Kilmarnock most distant.



This study identified seven proteins from the 30 proteins Beesley *et al*. <sup>[3]</sup> noted within the locus likely conferring TCBZ resistance (Table 2).

 Table 2: Proteins that confers TCBZ resistance in Fasciola hepatica according to

 Beesley et al. [3]

| S/N | SeqName   | Description                                  | Isolate |
|-----|---|--|---------|
| 1.  | maker-scaffold10x_157_pilon-snap-gene-0.197-mRNA-1    | ADP-ribosylation factor                      | ALL     |
| 2.  | maker-scaffold10x_157_pilon-snap-gene-0.187-mRNA-1    | Fatty acid binding protein V                 | ALL     |
| 3.  | maker-scaffold10x_1853_pilon-snap-gene-0.14-mRNA-1    | 26S proteasome non-ATPase regulatory subunit | ALL     |
| 4.  | maker-scaffold10x_157_pilon-snap-gene-0.190-mRNA-1    | Ubiquitin carboxyl-terminal hydrolase        | A & I   |
| 5.  | maker-scaffold10x_157_pilon-snap-gene-0.207-mRNA-1    | Ubiquitin carboxyl-terminal hydrolase        | A, I &K |
| 6.  | maker-scaffold10x_157_pilon-augustus-gene-0.89-mRNA-1 | Ubiquitin carboxyl-terminal hydrolase        | All     |
| 7.  | maker-scaffold10x_157_pilon-snap-gene-0.182-mRNA-1    | Ras-related protein Rap-1                    | Α       |

## **Ongoing Direction**

- 1. Isolation of *F. hepatica* EVs from ES products using size exclusion chromatography (SEC).
- 2. Confirmation of EVs by using GeLC proteomics searching against the *F. hepatica* genome, EVs marker identification and





### Figure 2: Heatmap of *F. hepatica* Somatic cells proteomic data

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TEM.

3. GELC proteomics on *F. hepatica* membrane-bound proteins.

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