

# A novel morphotype of *Hyalosphenia papilio* from Wales

Evelyn Greeves and Richard Payne  
University of York, Environment & Geography Dept

## Introduction

- Testate amoebae are a useful bioindicator when examining past and present climate events
- A novel morphotype of *H. papilio* from **Cors Fochno** bog was observed and studied



**Figure 1.**  
A specimen of the morphotype, characterised by broad test (shell)

## Methods

- Samples collected at intervals along a transect and abiotic data recorded
- Novel morphotypes identified using light microscope and measured
- Specimens photographed using scanning electron microscopy

## Acknowledgments

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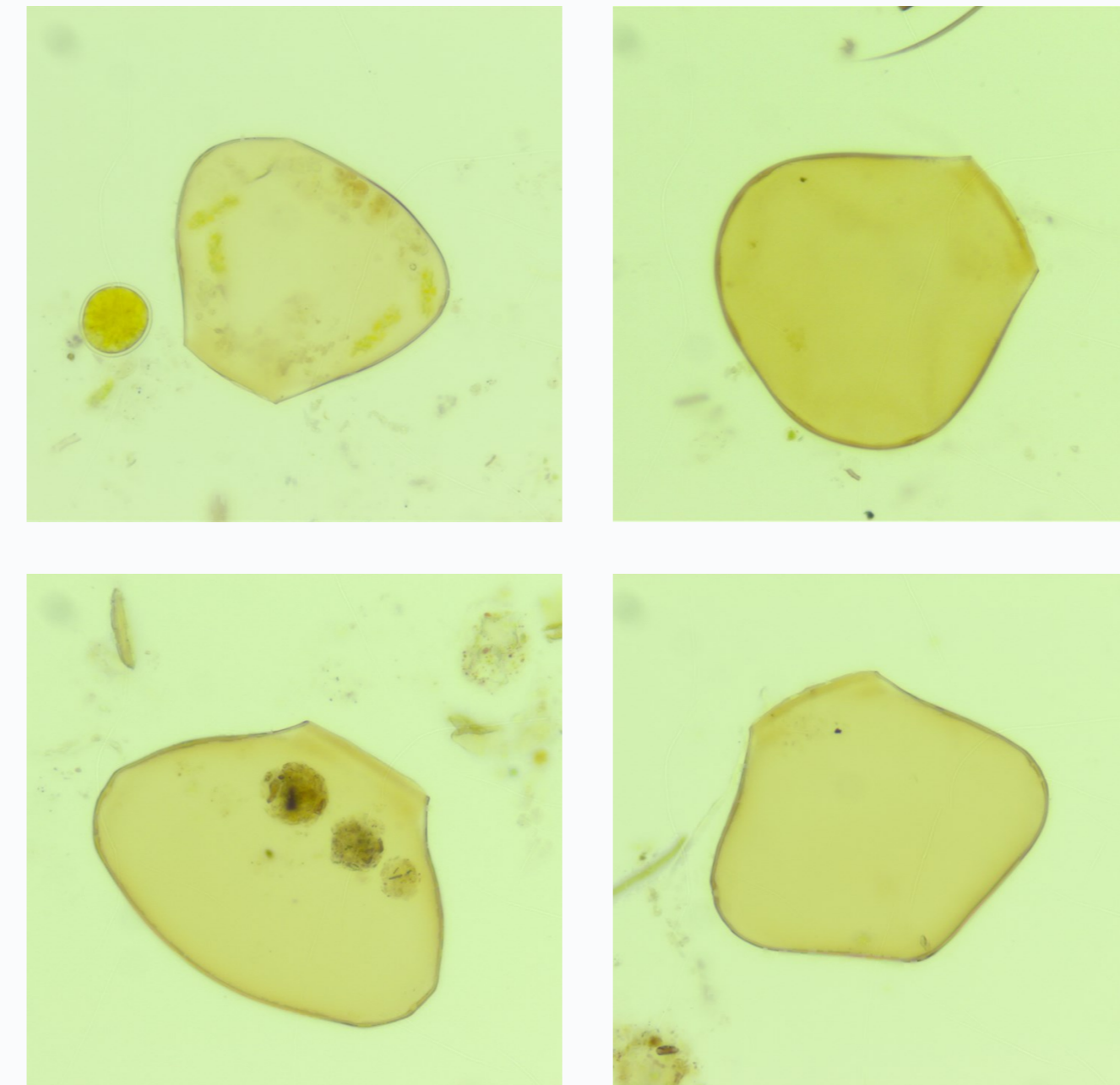
## About me

I'm a second year biologist interested in science journalism/communication and anything cell-sized or smaller!



## Results

- Found at 3 sites out of total 36
- Mean length **108µm**; mean breadth **128µm**
- Significantly **shorter and broader** (both  $p < 0.01$ ) than recorded literature values for *H. papilio*
- Between 2 and 5 pores visible
- No clear correlation between sites containing the morphotype and environmental conditions at those sites
- Several sites also had significant volume of *Nebela flabellulum*, another species with a short, broad phenotype

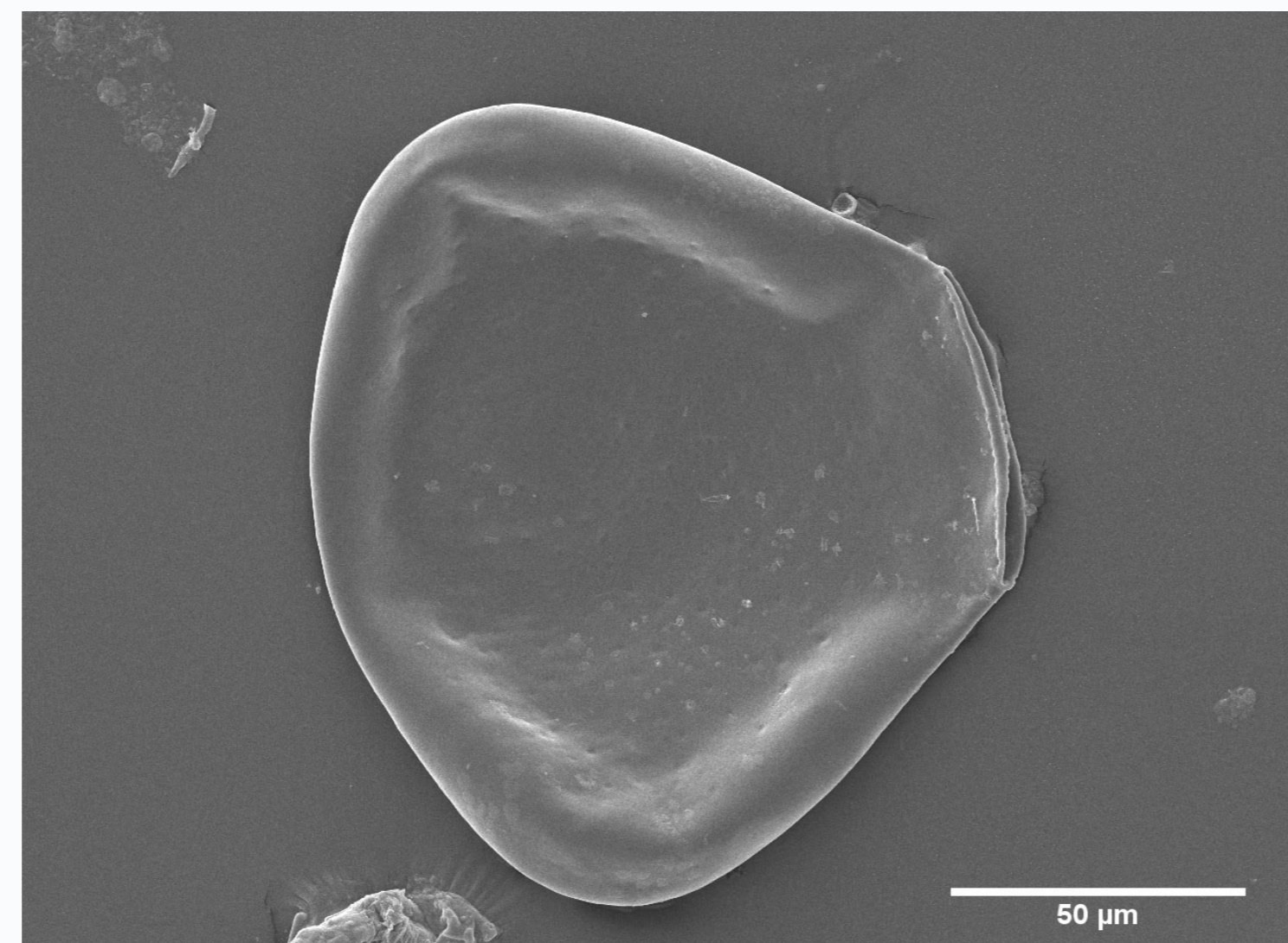


**Figure 2. (top right)**

Photomicrographs demonstrating the variability in exact shape and size of the specimens.

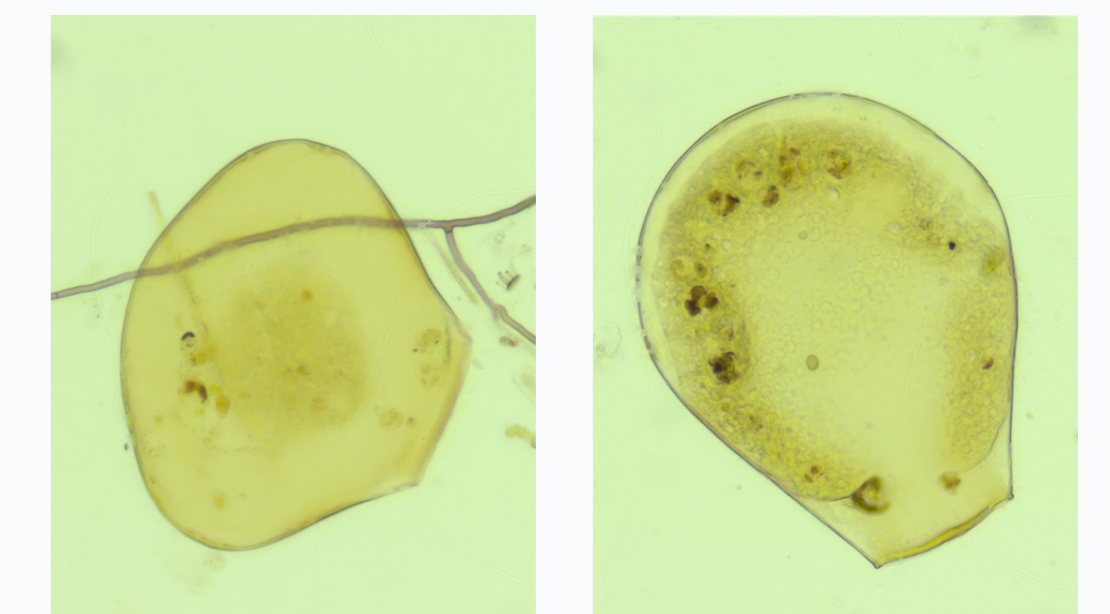
**Figure 3. (bottom left)**

An SEM photomicrograph of a specimen, clearly showing the slit-shaped aperture. Caved shell is a microscope artefact.



## Conclusions

- Very likely that morphotype has originated from *Hyalosphenia papilio* due to similar morphology and presence of up to 5 pores
- Current genetic analysis suggests not a new species as fingerprint **appears identical**



**Figure 3.** the morphotype (left) is shorter and broader than *H. papilio* (right), but is otherwise similar.

- Unique morphology may be due to **environmental factors** causing an extreme phenotype without genetic change
- Alternatively could be an evolutionary adaptation due to **genetic change**, as yet undetectable in fingerprint region
- Next steps involve looking for morphotype in similar geographic locations and a more complex genetic analysis