

# The DNA revolution - can amateurs help with the fungi

Tony Leech, Norfolk County Fungus  
Recorder



## TO BE CONSIDERED

- Data flow for fungus records
- Why fungi are difficult to identify
- How DNA sequencing is helping
- Possible contributions by amateurs

## IDEALISED DATAFLOW

RECORDERS



COUNTY RECORDER



LOCAL BIOLOGICAL RECORD CENTRE (eg NBIS)

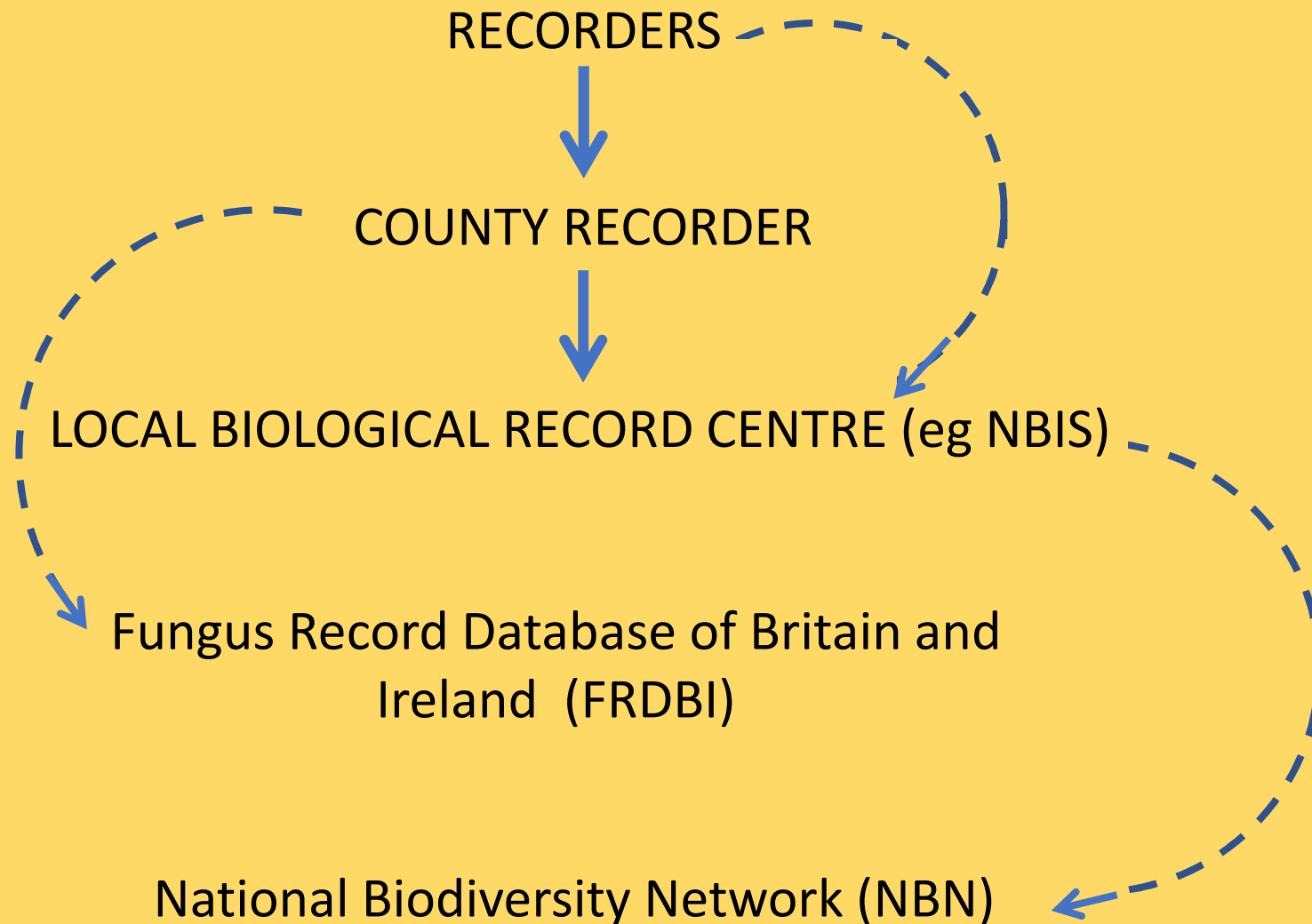


Fungus Record Database of Britain and  
Ireland (FRDBI)



National Biodiversity Network (NBN)

## ADDITIONAL/ALTERNATIVE DATAFLOW PATHS



## PROBLEMS WITH DATA

- 1 Lack of verification because fungi are difficult to identify. Conflict between data quality and number of records offered.
- 2 Duplication. Can usually be eliminated 'by eye' but not usually recognised in searches.
- 3 Over-representation of scarce species or unusual hosts.
- 4 Under-representation of species which are difficult to record.

# WHY FUNGI ARE DIFFICULT TO IDENTIFY

- There are very many of them
- Variation between individuals
- Comparison with images is only a start
- Need for a microscope and technical literature
- Taxonomic uncertainty

## HOW CAN DNA HELP?

Sequencing of ITS region may allow confirmation, or discrimination between similar species

BUT

- Many incorrect sequences in databases – ideally only sequences of type specimens should be used
- Many of these have not been sequenced

# FALSE CHANTERELLE

an example of use of DNA



*Hygrophoropsis aurantiaca*



*Hygrophoropsis aurantiaca* var. *pallida*



*Hygrophoropsis rufa*



# *Cortinarius pratensis*

forming ectomycorrhiza  
with Sand Sedge *Carex  
arenaria* (arrowed)



Species identified  
by reference to  
type collection

Relationship  
established by  
finding fungus DNA  
in sedge

## STEPS

- 1 Extraction and isolation of DNA by use of primers and PCR - currently carried out by at least one non-professional group in UK – more getting ready
- 2 Sequencing - done by commercial firm
- 3 Interpretation of data - databases and free software available to non-professionals)