

POMBASE COMMUNITY LITERATURE CURATION

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PomBase obtains its highest-quality data by manual curation of the fission yeast literature, which provides experimentally supported annotations representing gene structure, function, expression and more. Approximately 5000 papers suitable for manual curation published on the model organism *Schizosaccharomyces pombe* to date, of which about 2200 have been fully curated.

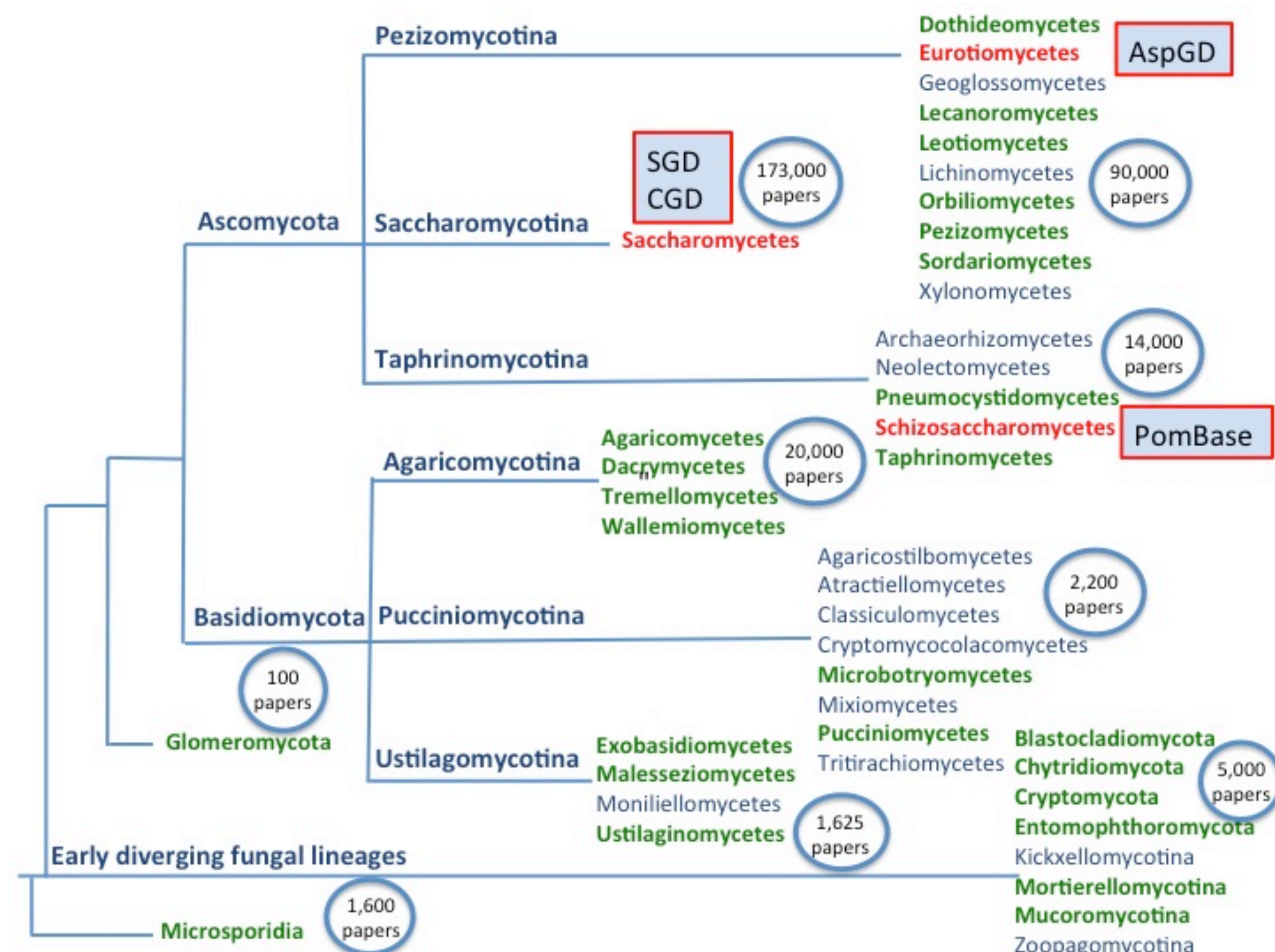
To supplement the work of its small staff of professional curators, PomBase has developed a community curation model that enables fission yeast researchers to participate directly in curating data from new publications. As of August 2015, the community has contributed annotations for 300 *S. pombe* publications. Community curation improves the visibility of recent publications, and enables researchers and professional curators to work together to ensure that PomBase presents comprehensive, up-to-date and accurate representation of published fission yeast experiments.

Furthermore, because PomBase is one of only three databases that provide manual literature curation for fungal species, electronic data transfer of high-confidence *S. pombe* annotations to other fungal species is an essential source of function-related data for the latter. Community contributions to PomBase therefore support research not only within the fission yeast community, but also throughout the broader community studying all fungi.

WHY COMMUNITY CURATION?

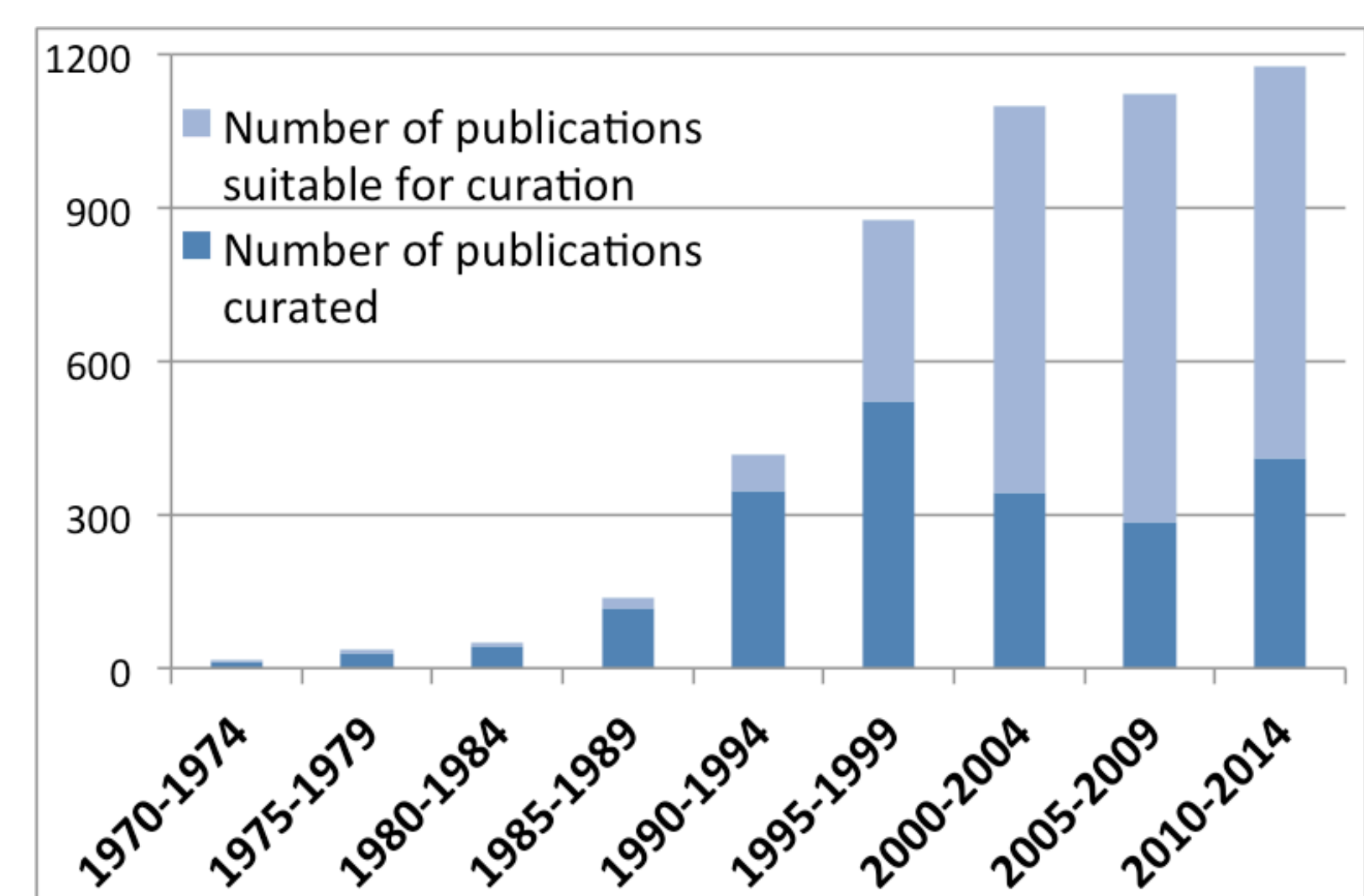
Data transfer

- An estimated >1.5M fungal species exist. Of these ~500 have been genome sequenced
- Only 4 fungal species – all Ascomycota – have dedicated databases
- Annotations can be transferred from one species to another -> Existing resources benefit the whole fungal research community



Many papers lack curation

- For *S. pombe*, many papers lack curation
- Lack of curation means that ‘known biology’ is not captured



Researcher benefits of community curation

- Community curation familiarizes authors with the types of data we represent
- Annotations facilitates locating data from different publications
- Formal language makes data from different sources comparable
- Formal data representation supports analysis of large gene sets
- Participants’ data are propagated to other databases, making it more accessible to researchers outside of the *S. pombe* community

COMMUNITY CURATION USING THE ONLINE TOOL CANTO

Users can create all major types of annotations

Intuitive search interface provides term definitions

Choose curation type for clp1:

- GO molecular function
- GO biological process
- GO cellular component
- Protein modification
- Genetic interaction
- Physical interaction
- Phenotypes:
- Single allele (add allele details and phenotype)
- Multiple allele (specify a genotype, and then add a phenotype)

Search for GO biological process term

A biological process is series of events accomplished by one or more ordered assemblies of molecular functions, such as cell cycle, transport, or signal transduction. [more ...](#)

Start typing a biological process in the search box. If you do not find the term you are looking for with your initial search, begin with a broad term (cell cycle, transport) [more ...](#)

cytokinesis

cytokinesis (GO:0000910)
meiotic cytokinesis (GO:0033206)
mitotic cytokinesis (GO:0000281)
cytokinesis checkpoint (GO:0044878)
regulation of cytokinesis (GO:0032465)
negative regulation of cytokinesis (GO:0032466)
positive regulation of cytokinesis (GO:0032467)

Term name
mitotic cytokinesis

Definition
A cell cycle process that results in the division of the cytoplasm of a cell after mitosis, resulting in the separation of the original cell into two daughter cells.

If possible, please refine your term selection. Clicking on a child term from the list below selects it and shows its definition (and children, if any):

- assembly of actomyosin apparatus involved in mitotic cytokinesis
- barrier septum assembly
- cellular bud neck septin ring organization
- cellular bud site selection
- medial membrane band assembly
- mitotic actomyosin contractile ring assembly
- mitotic actomyosin contractile ring contraction

GO biological process

New annotations from this session for PMID:499806

| Gene | Term ID | Term name | Evidence code | Curator |
|------|------------|---------------------|---------------|---------------------------------|
| clp1 | GO:0000281 | mitotic cytokinesis | IMP | Antonia Lock <a.lock@ucl.ac.uk> |

phenotype

New multi allele annotations for PMID:499806

| Genes | Genotype | Term ID | Term name | Evidence code | Conditions | Curator |
|-------|----------|--------------|----------------------------|-------------------|------------|---------------------------------|
| bir1 | bir1Δ | FYPO:0002061 | inviable | Cell growth assay | | Antonia Lock <a.lock@ucl.ac.uk> |
| clp1 | clp1Δ | | vegetative cell population | | | |

physical interaction

New annotations from this session for PMID:499806

| Interactor A | Taxon Id A | Interactor B | Taxon Id B | Evidence code | Curator |
|--------------|------------|--------------|------------|--------------------------|---------------------------------|
| cdc25 | 4896 | clp1 | 4896 | Affinity Capture-Western | Antonia Lock <a.lock@ucl.ac.uk> |

New annotations are shown in a table

More specific terms are suggested