

# Phenotype Curation in PomBase

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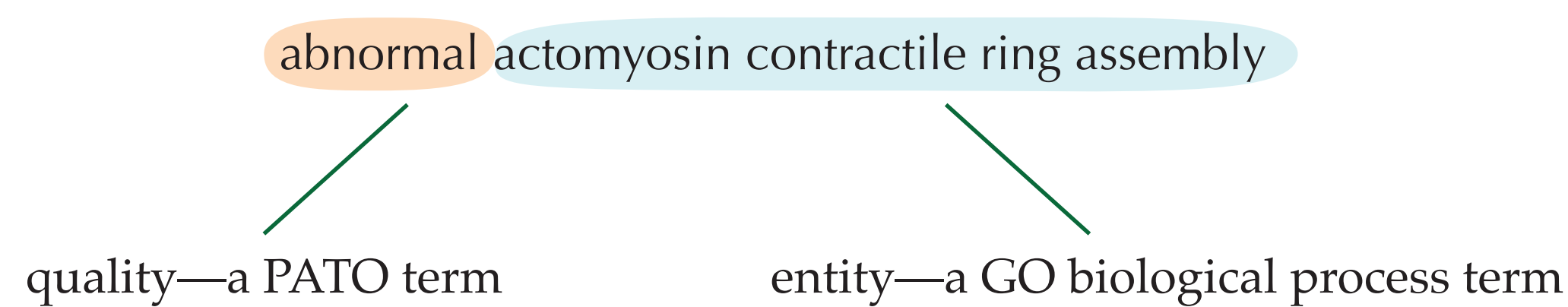
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# Introduction

PomBase, the recently established online fission yeast resource, has made the comprehensive and detailed representation of phenotypes a high priority. To support highly specific phenotype annotation, we are actively developing the FissionYeast Phenotype Ontology (FYPO), a modular ontology that uses terms from several OBO Foundry ontologies in logical phenotype definitions. Phenotype curation is featured in Canto, the PomBase community curation tool. Phenotype annotations are displayed on PomBase gene pages, and can be queried in the PomBase advanced search.

## FYPO: Fission Yeast Phenotype Ontology

## The basics: Entity–quality (EQ) definitions

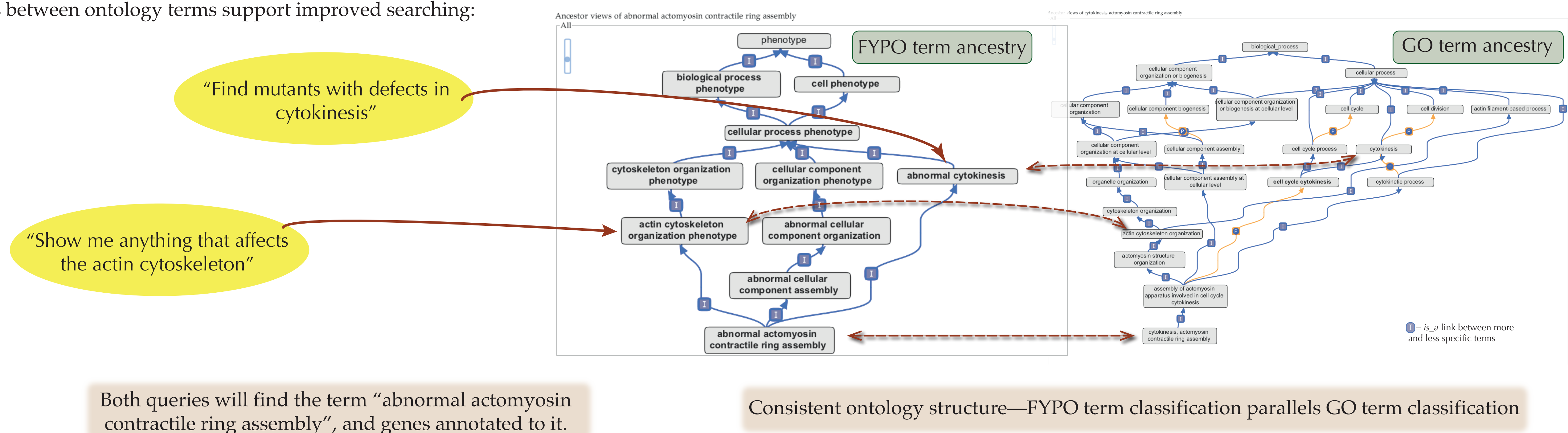


A phenotype ontology describes phenotypes based on the affected *entity*—a structure or process—and the *quality* that specifies how the entity is affected. FYPO uses terms from several ontologies, including ChEBI and all three branches of GO, and the Phenotypic Quality Ontology (PATO) for qualities.

### Using FYPO's logical structure

EQ definitions and links to other ontologies confer several benefits. Reasoning software uses EQ definitions to help maintain internal consistency, and ensure that FYPO's structure is consistent with GO, PATO and ChEBI

Links between ontology terms support improved searching:



## PomBase Phenotype Annotation

## Phenotypes in Canto

[Home page](#) - [PMD173940](#)  
[>Enter rmg2](#)  
[>Search](#)

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### Search for phenotype term

A phenotype is any observable characteristic or trait of an organism; such as development, biochemical or physiological processes, behavior, and products more.

Starting typing a phenotype in the search box. If you do not find the term you are your initial search, bring with a broad term (multinucleate, abnormal spindle, etc.)

abnormal **contractile ring** localization (**FYPO:0000033**)

abnormal **contractile ring assembly** (**FYPO:0000163**) (synonym)

cytokinesis defects, **contractile ring actin absent** (**FYPO:0000230**)

cytokinesis defects, **contractile ring myosin distribution defective** (**FYPO:**

cytokineses

Select a new old term or "abnormal astromyosin contractile ring assembly".

Detection:

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**Questions?** Contact curators ...

<Home page - PMD173940  
>Enter rmg2

Choose curation type for rmg2:

- ☒ GO molecular function
- ☐ GO biological process
- ☐ GO cellular component
- ☐ Phenotype
- ☐ Post-translational modification
- ☐ Chemical reaction
- ☐ Physical interaction

[View details](#)

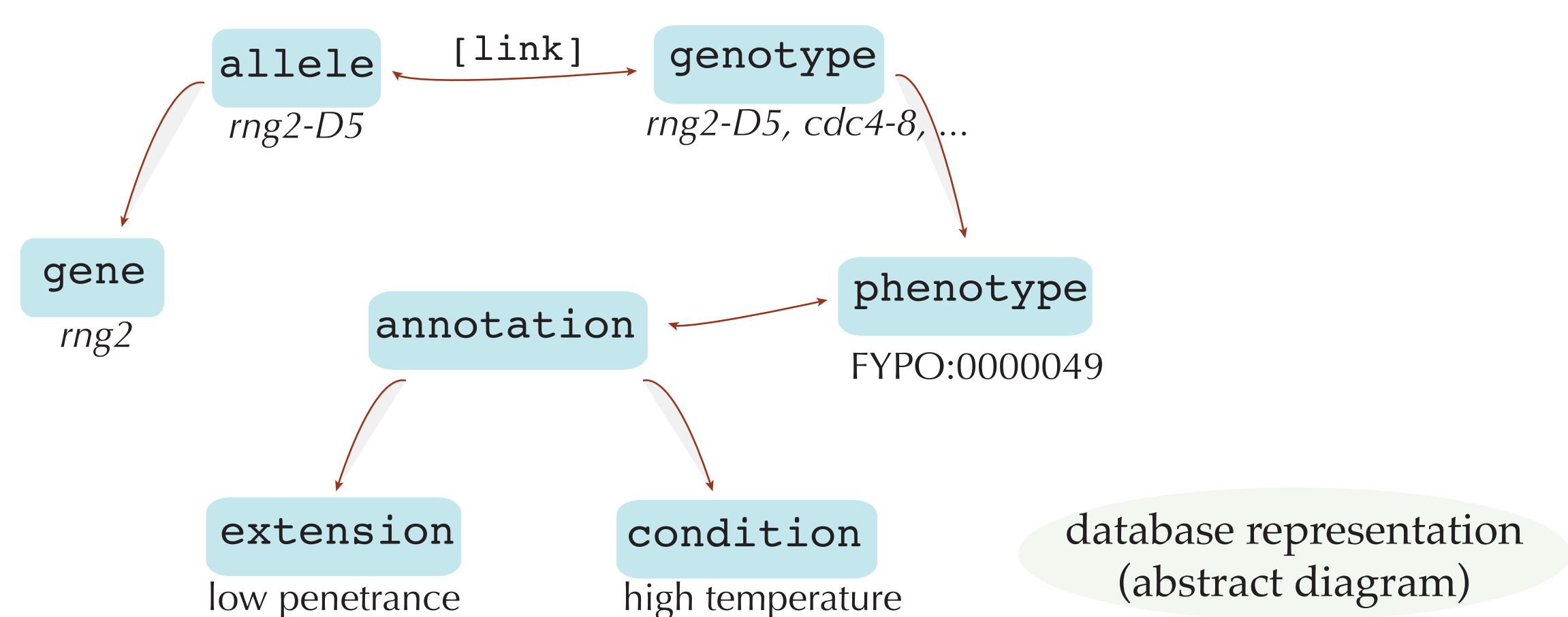
Identifier	Name	Product
SPACAF8.13c	rmg2	IGAPG

[Download DDB](#) [AnnotGO DDB](#)

[Change gene](#)

Phenotype annotation is featured in the Canto annotation tool, allowing researchers to annotate specific phenotypes using FYPO terms, based on publications. The system allows users to curate new alleles and recommend new phenotype terms for addition to FYPO.

## Alleles & genotypes



Canto and the Chado database underlying PomBase support associating phenotypes with genotypes, to capture

- different phenotypes for different alleles of a single gene
- double, triple, etc. mutant phenotypes
- annotation extensions such as penetrance or expressivity

## PomBase gene page

Phenotype annotation details are shown on PomBase gene pages. Each FYPO ID links to a page with term details and a list of annotated genes.

FYPO:000544	protein modification abolished <b>assayed_using</b> <i>pk1</i> <b>assayed_using</b> <i>pk1</i>	Other direct assay	sam5 (G441E)	amino_acid	<div><div><div>GO: PRK1 267 SPBC9A.153 SPBC13.13 4041 SPBC9A.154 (View in UniProt browser)</div><div>Fission Yeast Phenotype Ontology</div></div><div><table><thead><tr><th>Term ID</th><th>Term Name</th><th>Evidence</th><th>Amino Acid</th><th>Amino Type</th><th>Expression</th><th>Condition</th><th>Reference</th></tr></thead><tbody><tr><td>FYPO:000544</td><td>amino acid modification</td><td>MONOCOPY</td><td>amino acid</td><td>amino acid</td><td></td><td></td><td>Gupta DR et al. (2011)</td></tr><tr><td>FYPO:000547</td><td>amino acid deletion</td><td>MONOCOPY</td><td>amino acid</td><td>amino acid</td><td></td><td></td><td>Gupta DR et al. (2011)</td></tr></tbody></table></div></div>	Term ID	Term Name	Evidence	Amino Acid	Amino Type	Expression	Condition	Reference	FYPO:000544	amino acid modification	MONOCOPY	amino acid	amino acid			Gupta DR et al. (2011)	FYPO:000547	amino acid deletion	MONOCOPY	amino acid	amino acid			Gupta DR et al. (2011)	al. (2011)
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	<b>assayed_using</b> <i>pk1</i>	Other direct assay	sam7 (G441R)	amino_acid_mutation		Gupta DR et al. (2011)																								
FYPO:000553	increased pseudohyphal growth during cellular hyperosmotic response	Microscopy	not recorded (wild type)	wild_type	Overexpression standard glucose minimal medium	Gupta DR et al. (2011)																								
FYPO:000584	decreased sporulation	Cell growth assay	T356D (T356D)	amino_acid_mutation	standard glucose rich medium	Gupta DR et al. (2011)																								

## Acknowledgements

PomBase is funded by the Wellcome Trust, and is run by a consortium comprising the University of Cambridge, the European Bioinformatics Institute and University College London. PomBase consortium members: Kim Rutherford (Cambridge); Mark McDowall, Dan Staines, Paul Kersey (EBI). We thank Heiko Dietze, George Gkoutos, Jacky Hayles, Robert Hohendorf, and Chris Mungall for helpful discussions on various topics.

## Querying in PomBase

Filter

Please select the required filter(s)

Select Filter:

Name:

- [FYPO:0000549] normal protein modification
- [FYPO:0000546] delayed protein modification
- [FYPO:0000329] abnormal protein modification
- [FYPO:0000544] protein modification abolished
- [FYPO:0000547] increased protein modification
- [FYPO:0000545] decreased protein modification
- [FYPO:0000548] increased duration of protein modification

Submit

FYPO terms can be queried by name or ID in the PomBase advanced search. A list of annotated genes is returned, and can be used in further queries. Allele querying will be supported in the future.