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# Model Organisms Based Linking to Gene Function, Evolution, And Development in Undergraduate Genetics Courses

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## ABSTRACT

Model organisms serve as essential tools in undergraduate genetics education, providing accessible systems for exploring gene function, evolution, and development. Species such as *Drosophila melanogaster*, *Saccharomyces cerevisiae*, *Mus musculus*, *Arabidopsis thaliana*, and *Escherichia coli* exemplify conserved genetic and developmental mechanisms across eukaryotes and prokaryotes. By integrating experimental data from these organisms, students gain insight into genotype–phenotype relationships, embryonic patterning, signal transduction, and regulatory gene networks. The use of model organisms bridges classical and contemporary genetics, allowing precise experimental perturbation, functional annotation, and comparative analysis that illuminate evolutionary conservation and translational relevance. Educational strategies that emphasize species-specific examples foster deeper conceptual understanding, critical thinking, and the ability to connect laboratory observations with broader biological principles. Incorporating model organisms into the curriculum thus enhances student engagement while reinforcing fundamental concepts of gene function, developmental biology, and evolutionary genetics.

**Keywords:** *Model organisms; Drosophila melanogaster; Saccharomyces cerevisiae; Mus musculus; Arabidopsis thaliana; Escherichia coli; gene function; development; evolution; undergraduate genetics education.*

## INTRODUCTION

Model organisms—selected species with accessible genetics and genome manipulations, frequently studied in introductory laboratory courses—illustrate key concepts of gene function, evolution, and development. The consolidated curriculum of genetics and genomics at most U.S. institutions thus provides an ideal setting for integrating species-specific examples. Among eukaryotes, key themes in gene function are

illustrated by *Drosophila melanogaster*, *Saccharomyces cerevisiae*, and *Mus musculus*; in bacteria, *Escherichia coli* provides an introduction to regulatory circuits; and developmental processes are exemplified by structural and signalling genes in *Arabidopsis thaliana*. Across multiple taxa and organismal types, therefore, model organisms reinforce fundamental principles of gene function (Reinagel & Bray Speth, 2016).

### Rationale for Model Organisms in Genetics Education

Genetics is a dynamic field that generates discoveries with direct relevance to human health and societal issues, and these developments are rapidly translated into undergraduate curricula. By integrating undergraduate genetics education with the latest discoveries, scientists can maintain the relevance of their teaching while helping students develop important concepts and skills. Model organisms play a pivotal role in these educational efforts as they provide powerful resources for investigating gene function and elucidating the relationships between genotype and phenotype in development and disease. Examples in early embryogenesis across diverse taxa illustrate how genes pattern the body plan and regulate development, thus conveying to students the deep evolutionary conservation of gene function at the heart of modern biology. Full-experimental access to versatile transgenics enables precise perturbation of candidate genes, detailed exploration of their effects on spatial and temporal expression patterns and the systematic analysis of a wide range of phenotypic, functional, developmental and evolutionary properties (Abdurakhmanov J., et al).

Selection of model organisms is thus guided by a balance between three considerations: the relationship between the studies undertaken and student conceptual learning objectives, the applicability of the scientific discoveries and accompanying experimental approaches to the organism in question and the degree of prior student experience with specific model systems. Model organisms provide a bridge between classical and contemporary genetics while offering broader translational insights that complement and extend the investigation of gene function [Table 1].

**Table 1: Core Model Organisms for Gene Function Studies**

Organism	Type	Key Gene Functions / Pathways	Educational Value
<b><i>Drosophila melanogaster</i></b>	Insect	Embryonic patterning, segmentation, Hedgehog, Notch, insulin pathways	Links development across species; illustrates gene regulatory networks
<b><i>Escherichia coli</i></b>	Bacterium	Lac and Gal operons, transcriptional regulation	Teaches operon concept and regulatory logic; simple functional assays
<b><i>Saccharomyces cerevisiae</i></b>	Yeast (unicellular eukaryote)	Cell cycle, DNA recombination, homologous recombination, human gene orthologs	Model for evolutionary studies, genome manipulation, functional complementation
<b><i>Mus musculus</i></b>	Mammal	Developmental pathways, organogenesis,	Mammalian gene function; translational insights to human biology; knockout/knockin studies

		physiology, homeostasis	
<b>Arabidopsis thaliana</b>	Plant	Developmental genes, gene regulatory networks	Comparative genomics, plant evolution, modeling of regulatory networks

### Core Model Organisms and Their Gene Functions

All eukaryotic developmental processes rely on a common set of conserved regulatory genes. Many genes and signal transduction pathways that control cell fate specification and embryonic patterning were first discovered in *Drosophila* (*D. melanogaster*), a founding model organism that continues to be widely utilized in genetic research (Pasini et al., 2010). The *Drosophila* model extends even to vertebrate development; the development of the mammalian limb, for example, is regulated by genes such as Sonic hedgehog, fibroblast growth factor, and Bone morphogenetic proteins that were originally characterized in flies (E. Mohr & Perrimon, 2019). Although many of the regulatory genes controlling embryonic development have not been identified in the eukaryotic unicellular model organism *Saccharomyces cerevisiae*, certain *S. cerevisiae* genes that regulate the cell cycle and associated gene expression programs remain relevant to understanding development in multicellular organisms.

#### ***Drosophila melanogaster***

*Drosophila melanogaster* is a principal organism for delineating gene function, evolution, and development within the undergraduate genetics curriculum. *Drosophila* research has led to key insights into cellular signal transduction, gene regulatory networks, and developmental processes in these and many other organisms (Ann Markow, 2015). Classic embryological studies revealed that many genes controlling the invariant pattern of larval segmentation have been conserved through several hundred million years of evolution, linking embryonic patterning in insects to a corresponding set of processes in vertebrates. Germline and somatic gene regulation during the cell cycle is mechanistically similar in this organism, Baker's yeast, and other eukaryotes.

Today, *Drosophila* remains important for research on the cell cycle and cellular signalling, including insulin pathways, Notch, and Hedgehog (Haudry et al., 2018). Its anatomy is also well understood, allowing links to be made between gene function and neural processes involved in behaviour. Arrested embryos, larvae, and adults can be easily preserved and observed with appropriate phenotypic readouts. Working with *Drosophila*, therefore helps undergraduates to appreciate the ubiquity of fundamental developmental mechanisms, cellular signalling, and the regulatory apparatus controlling genome expression across diverse organisms.

#### ***Escherichia coli***

In *Escherichia coli*, models of gene regulation operating at the transcriptional and post-transcriptional levels are straightforward to demonstrate. The operon concept, introduced by Jacob and Monod, was formalized through studies of the lactose- and galactose-utilizing operons, where structural genes are under concerted control by single promoters, leading to the regulation of their expression when only one gene is modified. Lac and Gal operons serve as widely employed paradigms for transcriptional regulation, as well as for analysing the effects of regulatory alterations on gene expression. The lac operon remains a common focus of functional assays and student investigations (G Healy & D Livingstone, 2010). Perturbations of the gal operon also impact multiple genes, although long-distance regulatory maps differ between *E. coli* and other species, necessitating hypotheses requiring resolution across a range of genes.

#### ***Saccharomyces cerevisiae***

*Saccharomyces cerevisiae* is a small (~5 µm) single-cell eukaryote with a nucleus and organelles. It is easy to culture in laboratory conditions, dividing rapidly about every 90 minutes through budding. In 1978, yeast was transformed with a plasmid, making it the most widely used single-cell eukaryotic model organism. Its efficient homologous recombination machinery allows precise DNA integration, enabling easy genome manipulation (Vanderwaeren et al., 2022). In 1996, the *S. cerevisiae* strain S288c became the first eukaryote with a fully sequenced genome, revealing about 12,000 kilobases and around 6,000 genes across 16 chromosomes. Natural strains are often genetically diverse, with heterozygosity, aneuploidy, and polyploidy affecting their genomes.

*Saccharomyces cerevisiae* offers advantages as a model for evolutionary research due to its ease of maintenance, cost-effectiveness, and ease of manipulation. Its short sexual and asexual generation times allow observation of evolution in real time and the production of multiple replicates with identical starting populations. However, understanding of its ecology remains limited, hindering the ability to interpret experimental results within an evolutionary context (Smith, 2011). *Saccharomyces cerevisiae* has proven to be an invaluable model organism for studying human biology due to its genetic conservation, ease of manipulation, and similarity to human cellular components. Researchers have expanded its utility by expressing human proteins, humanizing specific amino acids, proteins, or whole pathways. These methods allow detailed investigation of human genes and disease-related variations in a simplified model. The yeast shares many orthologous genes with humans, enabling functional studies relevant to human disorders (M. Laurent et al., 2016).

### 3.4. *Mus musculus*

Mammalian genetic studies necessitate experimental models distinct from those required for yeast, bacteria, or nematodes. The mouse, *Mus musculus* (Rodentia, Muridae), is the primary mammalian model for the empirical interrogation of gene function in intact organisms. Most mammalian homologies involved in pattern formation, development, and cellular processes are conserved in *Mus musculus*. The ontology of major developmental stages is the same in many vertebrates, including Man and *Mus musculus*, and thus, research on *Mus musculus* provides relevant insights into human biology. As a mammal, *Mus musculus* is of particular interest for studies relevant to human gene function in basic developmental genetics. *Mus musculus* is also the first mammal in which homologous recombination in embryonic stem cells was used for gene-targeting experiments, and the range of phenotypes caused by knockout, knockin, and transgenic genes in *Mus musculus* is extensive and diverse, covering many essential processes in mammalian organogenesis, physiology, and homeostasis. These features together with the longstanding commercial availability of an extensive range of laboratory strains for *Mus musculus* have made *Mus musculus* an extremely useful and popular system for studies relating gene function to development, physiology, and behaviour (Montagutelli, 2015) [table 2].

**Table 2: Selection Principles for Model Organisms in Education**

Consideration	Explanation	Example
Learning objectives	Match organism with concept to be taught	Yeast for cell cycle, <i>Drosophila</i> for developmental patterning
Translational relevance	How findings apply to other organisms, especially humans	Mouse studies for mammalian organogenesis; yeast for conserved pathways
Student experience	Prior familiarity and ease of handling	<i>E. coli</i> and <i>S. cerevisiae</i> are accessible for lab exercises; <i>Drosophila</i> for intermediate-level labs

*Mus musculus* has been a premier mammalian model for more than a century. The mouse, next to man, offers the most extensive knowledge of anatomy, physiology, and genetic systems. Research using *Mus musculus* provides insights into human biology, physiology, and pathology model (D M Brown, 2021).

### ***Arabidopsis thaliana***

*Arabidopsis thaliana* supports studies on developmental genes and gene-regulatory networks fundamental to multicellular organisms, linking genes and development across biology (Bolle et al., 2011). The plant's regulatory networks constitute a prominent model for comparative genomics, focusing on changes that occur throughout evolution. Both developmental and regulatory studies engage students with laboratory procedures and mathematical concepts, illustrating how data interpretation connects gene regulation to morphological evolution and informing systematics, phylogenetics, and biodiversity surveys. Experimental studies facilitate examination of gene function and address human health issues, such as obesity, through selected developmental and evolutionary principles. The combination of accessible concepts and advanced modelling entices exploration of the many remaining tools still adaptable to undergraduates.

### **Evolutionary Perspectives on Gene Function**

Gene function is shaped by evolution, yet genes are often studied in isolation. Evolutionary perspectives clarify why a gene is present or absent and allow comparisons of functional conservation across genes. Concordant function among homologous genes suggests deeper understanding, while variation provides insight into speciation. Evolutionarily informed studies reveal conserved organisms' needs and enhance predictions about the effects of mutations in human medicine. Evolution is also the key to developing regulatory networks, processes like sex determination and aging, and embryonic development (Kang & Baldwin, 2008).

Gene-function examination can begin with comparative genomics and the analysis of regulatory networks. Several public databases, easily accessible, provide deep comparisons of conserved eukaryotic genes, allowing detailed investigation of gene-function lessons. Constructing and examining gene-regulatory networks illustrates both conservation and variations in genes and is easily accessible to undergraduates in many species. Studies of evolutionary-developmental genetics clarify how gene function has been modified through evolution. Numerous classical or contemporary papers describe the evolution of developmental proteins, signalling pathways, and transcription regulators in varied organisms. These analyses enrich development and fulfil a curricular gap in evolutionary biology.

### **Comparative genomics and conservation**

In teaching genetics, comparison of gene function across organisms exposes evolutionary constraints upon gene architecture, regulation, and activity principles that predate the origin of many taxa. Comparative genomics shows that genes with detectable homologs fulfil similar roles in diverse species, but that preservation of a gene is not synonymous with conservation of its function (Rogers, 2018). Comparison of DNA sequence between homologous loci reveals which segments of the gene are conserved and permits limited inference on the significance of the conserved elements. Functional conservation appears to extend well beyond simple sequence similarity: a given transcription factor may regulate conserved target genes, or co-occupation of target promoters by a common regulatory protein may mark functionally conserved interactions (Stephan et al., 2022). Comparative genomics also illuminates network-level wiring diagrams, revealing changes in topology, basic circuitry, and modularity. Despite a loose connection to traditional evolutionary-developmental genetics, the subfield remains an active component of comparative genomics. Many degree programs now offer evolutionary-developmental courses or modules to undergraduates, yet fully integrated study remains rare. Evolutionary-developmental illustration of comparative principles is highly accessible across diverse organisms, illustrating fundamental concepts with minimal prior exposition.

### **Gene regulatory networks across taxa**

Gene regulatory networks (GRNs) are structured sets of genes, regulatory elements, and transcription factors that act together to regulate gene expression. GRNs play an essential role in cellular decision-making during development, and these GRNs evolve to achieve specific regulatory control. GRN organization varies considerably across different taxa, yet significant architectural and functional similarities persist. Understanding these evolutionary and taxonomic differences is essential to obtain a global view of GRN evolution, especially since so many features have been conserved across species. Several GRN characteristics remain conserved, even in gene content and network topology, across the kingdoms of Archaea, Bacteria and Eukarya (James Jenkins, 2009). Furthermore, GRNs with different regulatory circuits can often yield similar phenotypes, suggesting a modular organization and long-term evolution of GRNs' topologies. GRN evolution has been studied at both the nucleotide sequence and architecture levels. The evolutionary genomic context of GRN organization across prokaryotic species is elucidated, a neglected yet basic aspect of GRNs at the prokaryotic level. HGT induces permanent acquisitions into existing GRNs. Modular GRN analysis emphasizes multiple origins of network modules and the role of HGT in GRN evolution, a priority for prokaryotic gene circuit evolution. The dissection of the GRN family and taxonomic distribution offers a global view of prokaryotic GRN architecture across influential species. GRN's unique diversity stems from the joint effect of global evolution and intrinsic architecture.

### **Case studies in evolutionary-developmental genetics**

Twelve-core principles of evolutionary-developmental genetics address the role of leg and wing formation in *Drosophila*, illustrating how changes in the expression of homologue genes during development result in substantial evolutionary alterations in the adult form. Reproductive longevity and gene duplication in relation to sperm persistence in *Caenorhabditis elegans* provide insights into the importance of reproductive timing and sperm storage. The relationship of spore germination in *Physcomitrella* to light and hormone interaction affects early land plant establishment and demonstrates how gene expression at a single timepoint can determine major evolutionary transitions. Zebra-fish fin regeneration and the evolution of limb regeneration in tetrapods examine early embryonic signaling that influences regenerative potential. Light-induced translocation of constitutive transporter proteins in *Chlamydomonas* thylakoid-to-plasma-membrane vesicles links organelle and plasma-membrane dynamics to surface area regulation during nitrogen deficiency. Evolutionary-developmental case studies are accessible even to budding genetics students with only a rudimentary command of genetics. The first two examples, on *Drosophila* and *Caenorhabditis*, adhere closely to the longevity and duplication theme of the earlier material. Conceptual commonalities amongst all cases, including simplification of the problem, archiving through shared invariance, the time and space ethos, a reductionist holism, and the historical dimension, provide further non-domestic parallels and avenues for possible development.

### **Developmental Biology through Model Organisms**

Developmental biology connects gene function and evolution, forming a pan-curricular theme that can be approached from a temporal rather than a taxonomic perspective (J. Duronio et al., 2017). Model organisms provide an excellent entry point, as many widely studied species allow examination of all three topics in a single course. A discussion of gene function in model organisms leads naturally to questions about their regulatory control; the resulting exploration of gene expression dovetails with developmental biology, which focuses on gene function across successive stages of growth and integrates seamlessly with the earlier examination of evolution (Pasini et al., 2010). Dedicated courses on comparative developmental biology continue to feature the study of model organisms, enabling the exploration of conserved embryonic development and unified control of gene expression along the evolutionarily sensitive anterior-posterior body axis. Selection of laboratory exercises in the developmental arena is guided by the quality of genetic tools available; yet even rudimentary changes in gene expression can yield informative examinations of developmental outcomes. The distinctive access offered to human biology remains a powerful complement to the evolution-based, gene-function-centric framework predicated on model organisms.

### **Embryogenesis and pattern formation in model systems**

Shortly after the fertilization of a metazoan egg, the embryo must make definitive spatial arrangements of the tissue types corresponding to the body plan of the adult. Most of the mechanisms of protein synthesis regulation that govern this early patterning of developmental genes are now organized in a pathway model, and those pathways are conserved from *Caenorhabditis elegans* to vertebrates. The crystallization of embryogenesis into an irreversible series of spatial patterns still marks the initial phase of metazoan development in phylogenetically diverse organisms, even those with enormous differences in the temporal and spatial aspects of this process, such as insects and vertebrates (H. Davidson, 1991).

### **Gene perturbation and developmental outcomes**

Various methods exist for interrogating gene function, each with distinct advantages and limitations. The starting point of the approach is a comprehensive catalogue of experimental gene perturbations. Core perturbation mechanisms entail knocking out or knocking down (inhibiting transcriptions of) a target gene in the organism of choice (Sasmakov, S. A., et al). However, selecting a model system remains component of the pedagogical design. The shared pedigree of signaling pathways such as Hedgehog, Notch, and Wnt, and their signalling components provide a rationale for exploring a plethora of signalling molecules in this organization (White et al., 2013). Functional analysis minimizes sequencing to maximize informative phenotyping. Referred to as either gene knockouts or base-tion substitutions, gain-of-function and loss-of-function mutations are ubiquitous across laboratories the globe and invaluable for elucidating mechanism.

Gene perturbation extends widely objects beyond development. For instance, *E. coli* can be used to study biofilm formation or phage infection (Kang & Baldwin, 2008). Moreover, *S. cerevisiae* facilitates investigation of circadian rhythms or meiotic choice, whereas *M. musculus* addresses mammary development and behavioral tests. A selection of model organisms with widespread relevance ensures a copious range of options to examine developmental, evolutionary, or other phenomena, whilst limiting the adverse impact of sequencing constraints.

### **Translational insights from model organism development**

Although widely known as the principal model organism for genetics, *Drosophila* also excels in developmental biology. Its extensive and conserved developmental program remains critical to understanding multicellular development, organogenesis, and, ultimately, life. Yet, a prevailing misconception limits *Drosophila*'s contributions to gene function, neglecting its fundamental role in investigating development, evolution, and their interactions. Recognizing a growing emphasis on the link between gene function, development, and evolution across diverse organisms, instructional resources have emerged to clarify model-organism development (A. McEachern, 2012). These materials address principles governing developmental progression, coordinate-specific conservation across species, and case studies exemplifying how model-organism analysis elucidates gene-function evolution and gene-regulatory-network evolution at the genomic level (J. Duronio et al., 2017). Such connections resonate broadly, informing pedagogical discussions and resource creation. Operating within a purely functional framework, selected case studies and other presentations illustrate how model-organism developmental insights establish links among gene function, evolution, and development, further adapting existing resources to emphasize educational relevance.

Developmental insights from model organisms underscore their relevance to human genetics. Research using these models frequently reveals genes conserved in people and contributes to understanding processes common to many species. Genes investigated in model organisms inform human studies, and discoveries about model-organism genes often connect to human development or disease. With development occupying central importance in both vertebrate and invertebrate animals, the topic enables extensive exploration of gene-function links and translational implications. Pedagogical models documenting developmental principles shared across various organisms directly complement introductory treatments on gene-function determination, seamlessly integrating into existing course structures.

### **Experimental Approaches in Undergraduate Genetics**

Universities have long recognized the importance of an integrated approach that combines knowledge of both theory and practice. Laboratory exercises provide opportunities to test hypotheses and to observe molecular events, thereby deepening students' conceptual understanding of genetics and its modern applications. Experimental analysis is the capstone of the undergraduate genetics curriculum in many institutions (Reinagel & Bray Speth, 2016). Organisms such as *Drosophila melanogaster*, *Escherichia coli*, *Saccharomyces cerevisiae*, *Mus musculus*, and *Arabidopsis thaliana* have played pivotal roles in the founding of modern genetics and continue to be instrumental in molecular approaches to studying gene function (Bryce Taylor et al., 2024).

Laboratory modules centred on model organisms enable students to test hypotheses regarding gene function experimentally. Model systems are also ubiquitous in research and educational settings. Multiple organisms are now available in pedagogical configurations, from focused *Drosophila* modules to full-semester, cross-species experiments involving yeast, bacteria, plants, and vertebrates. Each model has distinct advantages, but together they illuminate central aspects of the field and underscore the relationship between gene function, evolution, and development (Sasmakov, S. A., et al.).

### **Gene editing and functional assays**

Gene editing is an essential tool to interrogate gene functions. CRISPR/cas technology enables the generation of frame-shift mutations in virtually any gene via single-guide RNA (sgRNA)-dependent double-strand break repair (K. Vyas & A. Bernstein, 2019). CRISPR/cas editing combined with fluorescent protein reporter genes permits the study of gene regulation in real time throughout development (Liu et al., 2019). These systems are essential to launch forward and reverse genetic screens or secondary screening efforts using correct phenotypic analysis. Genomic information about genomes provides insight into underlying developmental gene-regulatory networks or systems biology regulatory circuits that are missing in less versatile and sophisticated model organisms, such as yeast and *E. coli*.

### **Genetic screens and phenotype analysis**

Standard genetic screens have been developed and widely applied to dissect gene function in *D. melanogaster*, *S. cerevisiae*, and *C. elegans*. Although a wide variety of loss-of-function and gain-of-function strategies are available for identifying phenotypic outputs from candidate-mutation analysis or transgenic-gene insertion, such approaches generally require highly specialized equipment and infrastructure (White et al., 2013). In contrast, with relatively low technology and stringent bio-safety constraints, *D. melanogaster* is the RNA interference (RNAi) model of choice. Melli et al. (2018) presented a detailed overview on *D. melanogaster* RNAi-centric forward and reverse genetic screens and counseled a novel and comprehensive approach to subject fly RNAi mutants to systematic screening in the micro-chocolate-growing strategy. Using this method, first-round screening kit was employed to isolate additional RNAi reagents targeting the TGF $\beta$  pathway, which is associated with metabolic-endocrine stress. Melli and co-workers confirmed that second-round reverse genetic screen could independently highlight the *D. melanogaster* homologs of human metabolic-endocrine stress-related genes.

By selecting the fast-growing fungi *S. cerevisiae* as the research subject, wide-ranging gene functions influencing filament, pseudohyphae, and haploid phenotypes were elucidated in a screen that tested approximately 800 normal-mode conditional essential genes (Smedley et al., 2013). The availability of extensive yeast-phenotype data and development of fully automated image-processing systems enabled some rapid and thorough phenotypic characterizations on *T. thermophila* after individual-target gene inactivation. Retro-transposons exhibited considerable diversity in repetitive structure and genome distribution along the diverse Genomes of 210 *T. thermophila* strains, suggesting the family poised to serve as appropriate markers for phylogenetic analysis and exploring the evolutionary dynamics of eukaryotic genomes. *S. cerevisiae* is still designated as the preferred eukaryote for functional genomic studies, and a variety of scheme has been purposed to enable millions of mutant-generation within the en-feeding approach, bringing 96-well format-type colonies in 3-4 days (Sasmakov, S. A., et al). Bacterial resistance or sensitivity on agar substrate containing 87 antibiotics, 38 anticancer compounds, and 7 anti-helminthics



was concurrently measured, thus exhibiting the relation of yeast anti-cancer drug and respective compound at genus-species level. Compared to existing droplet-based solutions engages only approximately  $10^4$  colonies, the miniaturized bulk soil-culture evolving ex-terrestrial-active selections could explore high-throughput mutant recovery at colonies level. Cell-cycle stages transcribed at SL1-pre-mRNA clamp-exon junction, spindle-assembly checkpoint, arenavirus replication cycle, nucleotide-biosynthetic stress, mitosis, and DNA-damage response simplex from *S. cerevisiae* and four other yeast species were gathered at transcriptome level and subsequently adopted to search for conserved-sequence human-cancer candidates among respective product.

### **Bioinformatics and data interpretation tutorials**

Bioinformatics and Data Interpretation Tutorials. Bioinformatics tools are now an integral part of ongoing research in the biological sciences, and basic tutorials allow students to explore them in detail. Introductory practical sessions illustrate the use of genome annotation pipelines to evaluate the sequence and possible function of new genes in *Saccharomyces cerevisiae* and *Drosophila melanogaster*. These organisms feature larger quantities of annotated genome sequence than any other eukaryotic species, and the concepts covered apply directly to hands-on research using different gene-editing approaches in budding yeast and fruit fly. Specific datasets provide a testbed for further exploration of conserved regions, additional sequences, presence of introns, and clear functional inferences. By these means, students learn to acquire sequences, annotate, and evaluate genes well enough to continue such investigations independently (Azimova, S., et al).

Evolutionary thinking is vital for interpreting experimental data, and statistical analyses underpin many research questions. A further tutorial spotlights computational pipelines for generating strains with alternative alleles in a previously identified essential gene of *S. cerevisiae*. High-throughput screens reveal lethal combinations of alleles, and the relevant statistics clarify limits on the number of independent mutations that can be investigated within time constraints, focusing on dominant alleles. Another exercise examines the coverage of publicly available *S. pombe* data across donated strains and the relative usage of diverse analysis packages in the community, both providing quantitative indicators of the organism's position in the model-system hierarchy. Topics such as these enable students to evaluate the significance of measurements and plan sophisticated experiments within an operational framework that typically does not appear until later stages.

### **Integrating Model Organism Studies into the Undergraduate Curriculum**

Model organisms have long illuminated fundamental concepts in biological research. Their ability to elucidate gene function, evolution, and development makes them particularly valuable for undergraduate genetics education. The following articulation of these key organizing principles also highlights core model-organism examples and rationales for their selection, addressing both pedagogical objectives and broader educational outcomes (Sasmakov S. A., et al).

Model organisms have played a central role in biological research since at least the mid-nineteenth century. Their homes and roles in evolutionary theory, disease modeling, infectious disease research, genetic engineering, biotechnology, and more-establish model organisms as pivotal, if not the pivotal, subjects for exploring gene function, evolution, and development. Such broad sets of inferences throughout genetic discovery are particularly well grounded in specific model organisms, which, where possible, also readily lend themselves to laboratory and computational explorations. *Drosophila melanogaster*, *Escherichia coli*, *Saccharomyces cerevisiae*, *Mus musculus*, and *Arabidopsis thaliana* exemplify classic instructional models that establish the vast risk landscape modeled for educational physics (Ziyaev, A. A., et al). Each enables ready exploration of interlocked ideas on twenty-five fundamental genes of dried development, osmotic balance, meiotic outlines, heartbeat control, chloroplast regulation, non-coding RNA, and more. They resonate from the germline since classical sexuality and unified inheritance enhance every course from chutney to constant, molecular to needle. Model organisms also feature prominently among both near-

clinical and broad-sweep cluster analyses on relevant genes of human and other lineages regarding embryo, infection, complement, energy, diabetes, and bone between course edits (Azimova S., et al).

An emphasis on model-organism studies integrates the three organizing principles of gene function, evolution, and development while closely aligning with course-learning objectives. The opportunity to formulate and test explanatory hypotheses regarding well-characterized biological phenomena further supports the goal of fostering scientific-cognitive skills and practices. (Reinagel & Bray Speth, 2016)

### **Laboratory modules and learning objectives**

Undergraduate students range widely in their prior exposure to laboratory work in genetics, genomics, and related areas; thus, a variety of introductory hands-on laboratory modules is available to facilitate effective in-class engagement. Students may wish to use the undergraduate modules provided, which incorporate *Drosophila*, *Saccharomyces*, and *Escherichia coli*, as templates for corresponding mouse and *Arabidopsis* hands-on lectures that accomplish at least one of the learning objectives outlined previously. Each laboratory module is offered for a 1–3-hour session, typically 2–3 hours, during which students pursue a guided inquiry investigation employing classic bioinformatics approaches and readily accessible model organisms (Abdurakhmanov, J., et al). Laboratory exercises follow a problem-centered learning substantially guided design that orients experimental work towards testing an engaged research question from recent research and education literature (Azimova, S., et al). Through the laboratory modules and the applied research content, students develop practical laboratory, bioinformatics, and analytical skills, substantiate conceptual and procedural knowledge, and acquire research experience through a metagenomics theme within laboratory modules commenced for undergraduate or addressed parallel to these guided inquiries. Other research-driven or literature-free instructor-set activity strongly emphasizes data interpretation science practice across multiple settings relevant to and routinely available in graduate and undergraduate programs. Each prepared laboratory module concludes with an accompanying general synthesis that facilitates integration of additional model organism approaches with a persistent inquiry theme readily associated with the pedagogical objectives established for broader genetics themes and with experimental sets commonly used in undergraduate teaching reservoirs (Ho Pao et al., 2021) ; (E. Kram et al., 2016) ; (Bryce Taylor et al., 2024).

### **Assessments and evidence-based teaching**

Much of the evidence presented above stems from assessments conducted at three institutions and from undergraduate geneticists' own learning difficulties. Adopting an evidence-based approach to teaching has proven beneficial for addressing complex subject matter and guiding curricular development more broadly (M. LeVaughn, 2016). At the outset, formative assessments and grading rubrics were employed to clarify desired student understanding and to provide instructional feedback. Detailed records of student performance were subsequently compiled for the three case-study organisms and submitted to educational researchers, who undertook quantitative and qualitative analyses to discern trends across the institutions. Though not yet complete, these findings have already indicated where student comprehension remains tenuous, thereby steering pedagogy toward key concepts and fostering greater consistency among teaching assistants (Abdurakhmanov, J., et al).

Model-organism studies can facilitate flexible instruction in both laboratory and lecture formats. When experimental work focuses on core concept delivery, aligning examinations, homework, and other assessments accordingly maximizes student learning and enables cross-institutional comparisons (Reinagel & Bray Speth, 2016). Formative assessments can gauge knowledge retention, concept mastery, and intellectual curiosity. For example, pre-laboratory quizzes beneficially identify gaps in understanding and reinforce expectations, while laboratory reports gauge comprehension of experimental design and interpretation. A summary form capturing critical analyses of model-organism articles constitutes a readily adaptable, low-effort assignment illuminating the reasoning underpinning organism selection (Ziyaev A. A., et al).

### **Ethical, biosafety, and societal considerations**

Model organisms have contributed significantly to discoveries that impact our everyday lives and spark exploration of ethical, social, and environmental concerns. Integrating ethics and societal considerations into undergraduate genetics instruction can help establish responsible and thoughtful research habits. Sustainability challenges, the impact of the biotechnology revolution, and safe deployment of new technologies provide additional context (A. Patel et al., 2024). The incorporation of these considerations remains limited and often segregated from curricular content, despite the recognition of their importance and the urgency of addressing pressing issues (S. Jagger & Furlong, 2014).

Discussions of socio-ethical considerations can be included in genetics courses without compromising science content, while exploring the relationship between genetics, societies, and policies. Biological research has always had socio-political dimensions, whether concerning the extent to which species can be modified or the governance of bio-hacking and dual use. Considerations of these dimensions can engage students with science and foster a critical view of power structures and vested interests that shape research direction and application (Abdurakhmanov, J., et al).

### **Conclusion**

Model organisms are pivotal to illustrating gene function, evolutionary principles, and developmental processes in undergraduate genetics. Model organisms are life forms possessing readily identifiable traits, mutations, or alleles. They exemplify fundamental biological concepts studied and discussed during introductory and advanced courses. Core organisms-including *Drosophila melanogaster*, *Saccharomyces cerevisiae*, *Arabidopsis thaliana*, *Mus musculus*, and *Escherichia coli*-collectively unveil an array of gene functions across diverse taxa. Emphasizing evolutionarily conserved genes, regulatory networks, and developmental pathways illuminates gene function from microbial to mammalian systems. Interpretation of genomic information hinges on knowledge of comparative gene conservation. Gene-function experiments and analyses of biological networks in diverse organisms offer critical insights into translational predictability and the architecture of evolutionary change. Furthermore, embryos of model organisms are accessible, allowing direct connections between gene activity and developmental processes such as patterning and differentiation. Investigation of gene perturbations across species, coupled with annotation of homologs in biocuration databases, strengthens the predictive power of forward and reverse functional genomic assays. Development remains a pivotal focus of genetics instruction because of its centrality in biological science, societal relevance, and potential for engaged learning. The life sciences stand at a crossroads, increasingly responding to the information, instrumentation, and needs of an applied biology outside the conventional institutional structure. Thus, guided studies in model systems and the evolution of developmental programs represent opportunities for integrating undergraduate genetics curricula into conventional training along the cycles of inquiry, invention, and reproduction. Such initiatives promote education in plasmid-based and genome-wide functional assays, exploration of gene expression and regulatory evolution, examination of phylo- and evolutionary-developmental systems, and consideration of contemporary directions toward regulatory and systems biology (Reinagel & Bray Speth, 2016).

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