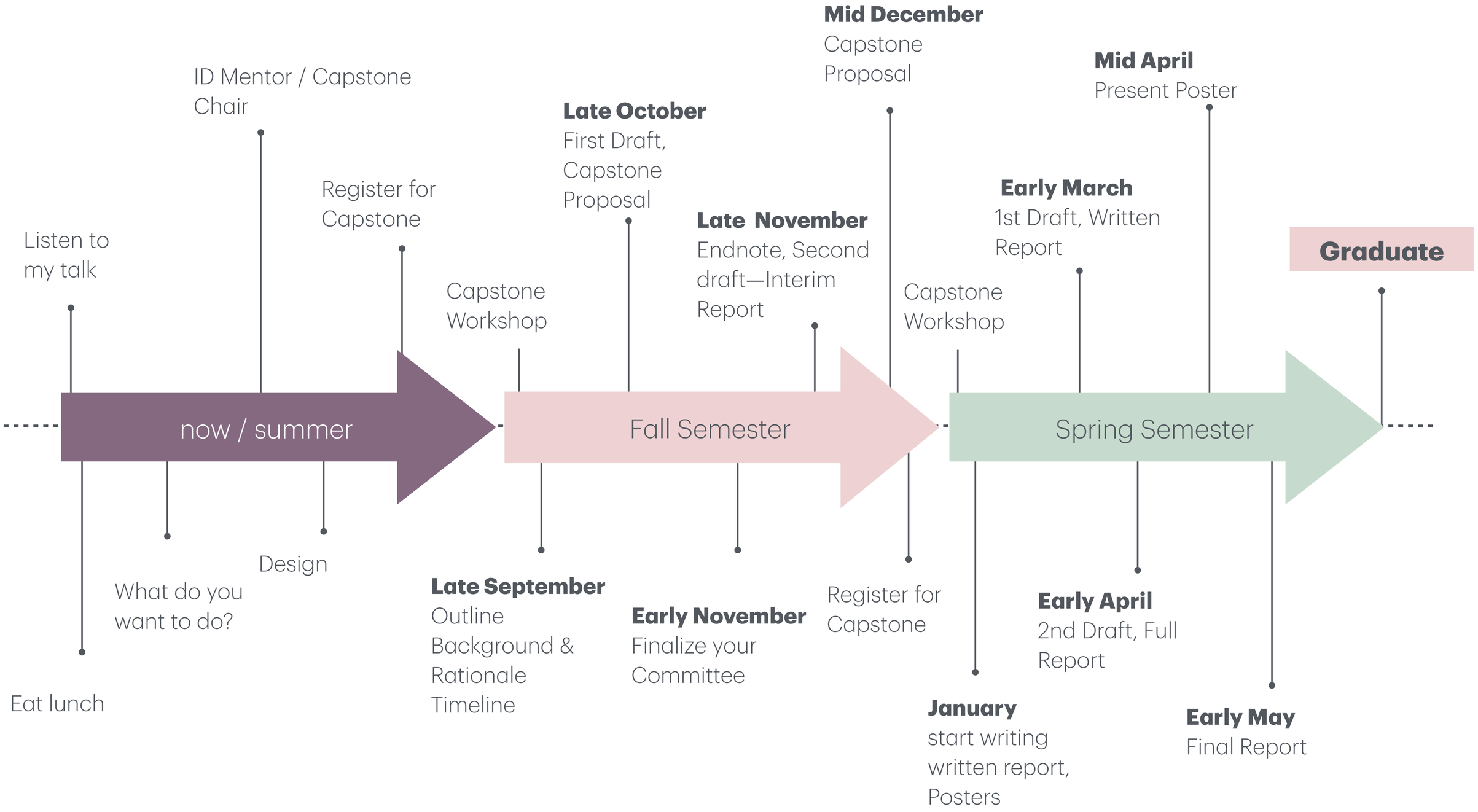
Capstone Workshop

Project Approach and Figures

Ernesto Salcedo, PhD


Listen to my talk
ID Mentor / Capstone Chair
Register for Capstone
Capstone Workshop
Late October
First Draft, Capstone Proposal
Late November
Endnote, Second draft—Interim Report
Mid December
Capstone Proposal
Capstone Workshop
Early March
1st Draft, Written Report
Mid April
Present Poster
Graduate
now / summer
Fall Semester
Spring Semester
Eat lunch
What do you want to do?
Design
Late September
Outline
Background & Rationale
Timeline
Early November
Finalize your Committee
Register for Capstone
January
start writing written report, Posters
Early April
2nd Draft, Full Report
Early May
Final Report

Capstone Proposal

Modeled after an NIH Proposal

- Title
- Significance
- Innovation
- Approach
- Budget
- Timeline
- Citations

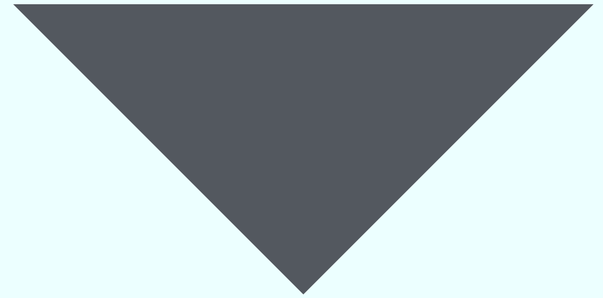
Significance

Sets the stage — why you proposing what you are proposing

- Can be Broken down in Sections
  - **Background information**. What is known.
  - **Rationale**. What is not known (and something should be done about this)
  - **Hypothesis**. A testable statement
  - **Specific aims**. Stated objectives or goals
  - **Outlook**. Why is this important?

Significance

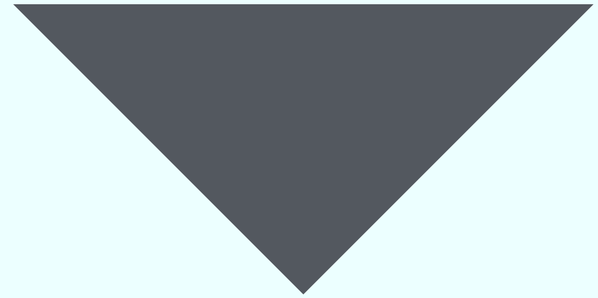
From Broad to Specific



- **Background**
  - A summary of the current state of affairs
  - Think AND Statements: “We know this AND that AND this.”
  - Only include the background necessary to understand the project
  - No DATA DUMPS. We do not want Wikipedia entries here. Just the info we need to understand the rationale and hypothesis
  - Don’t forget to mention **ANATOMY**. We are an anatomy program here.
- **Rationale**:
  - Hint at problems with the current state of affairs
  - State what’s missing and how your project is going to swoop in and save the day.
  - Think BUT statements. “We know this and that, BUT…”
  - Your rationale sets up your specific aims and hypothesis
  - OUTLOOK:
  - Why should we care?

Significance

From Broad to Specific



- **Central Hypothesis**:
  - Hypotheses are testable statements.
  - “Our new 3D model will improve learning outcomes”
  - Be specific:
    - NOT: social networking sites are harmful (Too general)
    - HOT: Twitter users experience more privacy issues than users not on such social network
  - Your hypothesis should inform the type of experiment that you will be performing

- **Specific Aims**:
  - Your Specific Aims are your objective statements
  - Now that you have set up the problem (in the rationale), you state how you plan to solve this problem
  - Specific Aims are single sentences that summarize what you plan to do:
  - “Chacterize the level privacy issues for US adults”

Innovation

Detail the new

- How does your project add new information?
- What is new and exciting about your project.
- How is this different from a Wikipedia entry
- Reframe your rationale so you discuss what’s new

Capstone Proposal

Project Approach

- The approach is where you describe the experiments that you will conduct for each aim.
  - Where you spell out what you are going to do
  - Restate your specific aim and then expound
- Be sure to include rationale for everything that you propose to do
  - Because of this, we are going to do this
- Organize with Headers and Subheaders
- use bold fonts or an outline or numbering system —or both—be consistently throughout.

RESEARCH PLAN We propose to test the hypothesis that the immune system of the human newborn is comprised of two distinct hematopoietic lineages

Specific Aim 1. To determine the normal range of fetal to adult T cells in the umbilical cord blood of neonates at birth

Hypothesis. Physiologic layering of the human immune system during ontogeny leads to a normal range in the ratio of fetal to adult-type T cells at the time of birth, with some neonates born with a more tolerogenic immune system than others.

Rationale. As described in the above Preliminary Data, the human fetal immune system is **poised to generate a tolerogenic Treg** response upon stimulation, an attribute that is conferred by an HSPC that resides within the fetal liver and bone marrow. After birth, bone marrow-derived HSPC give rise instead to immunoreactive T cells with a reduced propensity to generate Tregs. Teleologically, such "layering" of the immune system would appear to be consistent with, and possibly necessary for, maintenance of the semi-allogeneic state of pregnancy and, reciprocally, for the generation of an active immune response against foreign (e.g., infectious agents) after birth. Similar stage-specific waves of distinct hematopoietic progenitors have also been described in avian and murine models. **A key question that remains unanswered is the following: is there inter- individual variation in the rate at which the fetal-type hematopoietic system is replaced by the adult-type system over time?** In this Aim, we propose to determine whether and to what extent such variability may exist at the time of birth. Given known transcripts that uniquely identify tolerogenic fetal T cells (TF) and immunoreactive adult T cells (TA), the normal range of these two T cell subpopulations in the umbilical cord blood will be determined.

Experimental Approach. Comprehensive phenotypic, transcriptional, and functional analyses will be carried out on umbilical cord blood (UCB) mononuclear cells from a total of 200 normal full-term deliveries. Over an 18-month time frame, 75 of these samples will be obtained on a recharge basis from the Human Cord Blood Bank of the UCSF Clinical and Translational Sciences Institute (see attached letter from Dr. William Balke), 75 will be obtained on a collaborative basis from Dr. Elizabeth Shpall of the University of Texas M.D. Anderson Cancer Center (see attached letter), and 50 will be obtained as part of a prospective study to be carried out with Dr. Shannon Thyne of the Child Health Center at SFGH (see attached letter). Initial studies will focus on naive T cells obtained by a combination of ficoll hypaque gradient enrichment and FACS sorting; excess cells will be viably cryopreserved in liquid nitrogen for future experiments that may interrogate other subpopulations of cells. The following assays will be carried out:

https://www.niaid.nih.gov/sites/default/files//mccunefull.pdf PAGE 29

Capstone Proposal

Rigor and Reproducibility

- Make sure that you clearly state how you are going to be rigorous in your science
    - Clearly State your n and what power that is going to give you

Aim 3: Male and female mice will be **randomly** allocated to experimental groups **at age 3** months. At this age the accumulation of CUG repeat RNA, sequestration of MBNL1, splicing defects, and myotonia are fully developed. The compound will be administered at **3 doses** (25%, 50%, and 100% of the MTD) for 4 weeks, compared to vehicle-treated controls. IP administration will be used unless biodistribution studies indicate a clear preference for the IV route. A group size of **n = 10** (5 males, 5 females) will provide **90% power** to detect a **22% reduction** of the CUG repeat RNA in quadriceps muscle by qRT-PCR (**ANOVA**, α set at **0.05**). The treatment assignment **will be blinded** to investigators who participate in drug administration and endpoint analyses. This laboratory has previous experience with randomized allocation and blinded analysis using this mouse model [refs]. Their **results showed good reproducibility** when replicated by investigators in the pharmaceutical industry [ref].

Capstone Proposal

Keep it simple

- Comprehensive but concise
- Don’t go too crazy with the details
- We don’t need a step-by-step protocol for everything you plan to
  - Just an overview
  - e.g. For 3D modeling, You can just the mention the software that you are using and for what purpose (segmentation, rendering, etc.)

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Budget

Critical Funds needed?

- Expectation: your mentor should have most of the funds
- Exception: if you are doing something that is slightly out of the scope of what you mentor typically does
- *And,* it's in the purview of the MHA program (generating education materials, 3D tools, image processing, etc.), then you can request funds
- *And*: If you can't successfully and fully interrogate your hypotheses without these funds
- Then, you can request funds (Maximum request is $1000)
  - typically, requests are much smaller than this.
- To request funds, you need a Rationale and a Line-Item budget

Timeline

The power of working backwards

- Create a timeline, with set deadlines
  - Include the Capstone Workshop assignment deadlines
    - Draft of the Capstone Proposal etc.
  - Data collection
  - Data Analysis
- You can change your timeline if needed

Citations

Citation Managers

- A citation manager helps organize your citations.
- CU Anschutz offers a site license for EndNote.
- **Assignment:** Learn Endnote (library offers course)
  - upload an example citation section that lists a selection of publications formatted
  - Use whatever format for citations that you want.
- Note If you have used a citation manager before, and you still know how to use it, you can use that

Tense and Formatting

Free and Clear

- Write the Proposal in present future tense: “Anatomy is great. We will do this and we will do that.”
- No specific formatting requirements
  - Many journals are now accepting Free Format submissions
    - meaning they will format the manuscript for you if you are article is accepted
  - Just don’t use any weird fonts or font sizes
    - Font Size: 11 or larger
    - Fonts: Arial, Georgia, Helvetica, Palatino Linotype recommended
  - Use Single-Spacing

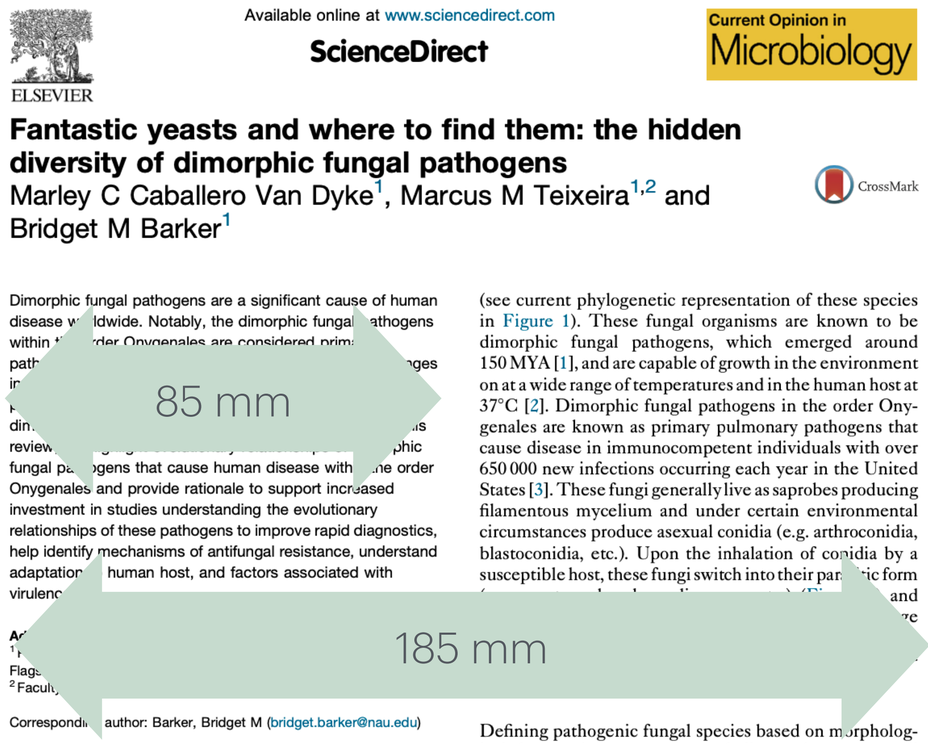
Figures

include them

Figures

Formatting

- Be consistent in your figure formatting
- Figures should be fit either
  - one column (85 mm, 3 3/8”, 20 picas)
  - or two columns (185 mm, 6 13/16”, 41 picas).
- The length of an illustration cannot exceed 227 mm (9”, 54 picas).
- Journal quality reproduction requires grey scale and color files at resolutions of 300 dpi.



Available online at www.sciencedirect.com
ScienceDirect
Current Opinion in Microbiology

Fantastic yeasts and where to find them: the hidden diversity of dimorphic fungal pathogens

Marley C Caballero Van Dyke[1], Marcus M Teixeira[1,2] and Bridget M Barker[1]

Dimorphic fungal pathogens are a significant cause of human disease w[illegible]ldwide. Notably, the dimorphic fungal [illegible]athogens within t[illegible]rder Onygenales are considered prim[illegible] path[illegible]ges in[illegible] din[illegible]is review[illegible]phic fungal pa[illegible]ogens that cause human disease with[illegible]e order Onygenales and provide rationale to support increased investment in studies understanding the evolutionary relationships of these pathogens to improve rapid diagnostics, help identify mechanisms of antifungal resistance, understand adaptation[illegible] human host, and factors associated with virulenc[illegible]

Ar[illegible]
[1] [illegible]
Flags[illegible]
[2] Faculty[illegible]

Correspondi[illegible] author: Barker, Bridget M (bridget.barker@nau.edu)

Current Opinion in Microbiology 2019, **52**:55–63

This review comes from a themed issue on **Host–microbe interactions: fungi**

Edited by **Chad A Rappleye** and **Duncan Wilson**

For a complete overview see the Issue and the Editorial

Available online 7th June 2019

https://doi.org/10.1016/j.mib.2019.05.002

Introduction

The fungal kingdom contains millions of ubiquitous fungal species, and most pose no or trivial direct threat to human health. However, a handful of species can cause devastating disease in both immunocompetent and immunocompromised individuals. Although plants can also be affected by fungal pathogens, this review highlights a distinct group of dimorphic fungal pathogens that cause disease in humans. This specific group of fungi that cause systemic infections is nested within the order Onygenales (Eurotiomycetes, Ascomycota) which include *Coccidioides*, *Histoplasma*, *Blastomyces*, *Paracoccidioides*, *Emmonsia*, and *Emergomyces* (see current phylogenetic representation of these species in Figure 1). These fungal organisms are known to be dimorphic fungal pathogens, which emerged around 150 MYA [1], and are capable of growth in the environment on at a wide range of temperatures and in the human host at 37°C [2]. Dimorphic fungal pathogens in the order Onygenales are known as primary pulmonary pathogens that cause disease in immunocompetent individuals with over 650 000 new infections occurring each year in the United States [3]. These fungi generally live as saprobes producing filamentous mycelium and under certain environmental circumstances produce asexual conidia (e.g. arthroconidia, blastoconidia, etc.). Upon the inhalation of conidia by a susceptible host, these fungi switch into their par[illegible]ic form [illegible] and [illegible]re

Defining pathogenic fungal species based on morphological characteristics poses many challenges because not all fungi are cultivable in media, not all fungal pathogens easily produce sexual fruiting bodies, and some fungi are homothallic (self-fertile) and therefore will not exhibit a detectable inheritance pattern. Before the genomic era, Genealogical Concordance for Phylogenetic Species Recognition (GCPSR) was the method of choice for defining species boundaries within Onygenales and other fungi [5]. This approach is based on Multi Locus Sequencing Type (MLST) to assess sequence variation of conserved housekeeping genes or other neutral loci. The genetic background of centennial species (i.e. *Coccidioides immitis*, *Paracoccidioides brasiliensis*, *Histoplasma capsulatum*, and *Blastomyces dermatitidis*) were resolved leading to new phylogenetically isolated species and new dimorphic fungal pathogens were described (e.g. *Emergomyces*) [5].

Advances in molecular phylogenetics and population genetics based on genomic science have significantly improved our ability to accurately define fungal species limits and hybridization events that shaped the Onygenalean clade [6]. Sequencing the genomes of Onygenalean fungal pathogens also provides information to better understand shared and unique adaptive traits between species complexes, such as metabolism, mating patterns, gene gain or loss, and chromosomal variations that may be associated with infection and disease progression [1].

Figures

Figure Panels

- Use them
  - Don’t just create a series of single image figures.
  - Collect related figures into panels
- Every Figure needs a Figure Legend
  - figure legends explain the figure (without referring to the text)

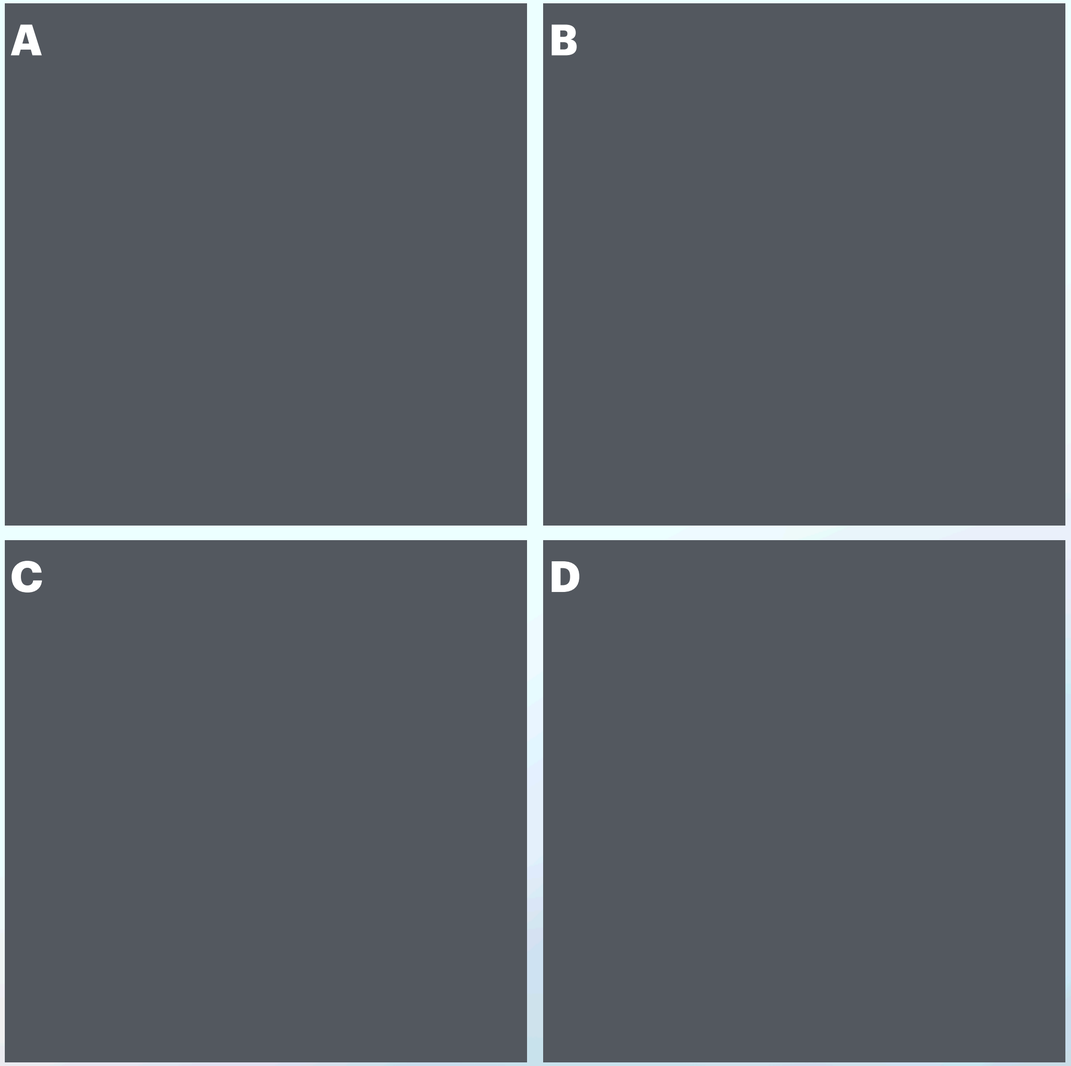


Figure 1: Yeast can be found all over. **A**. And image of a Yeast. **B**. Evolution of yeast **C**. Distribution of Yeast in America. **D**. Common mutation in yeast allele

Figures

Layout

- For half-width figures, text should flow around the figure like this
- Wrap Text: Tight
- Set:Layout: Wrap Text: Tight

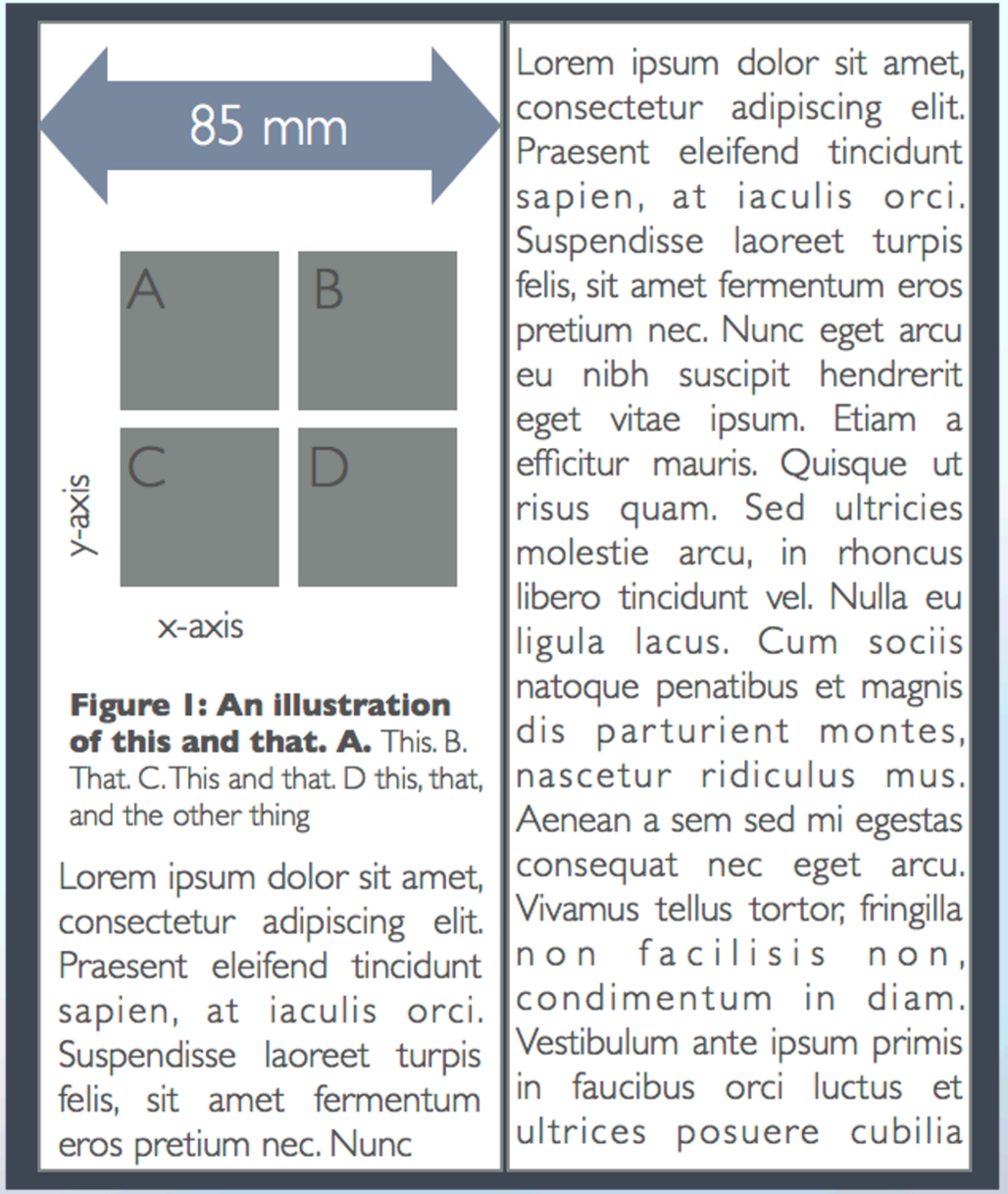


Figure 1: An illustration of this and that. A. This. B. That. C. This and that. D this, that, and the other thing

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