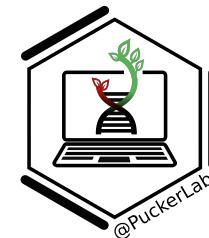
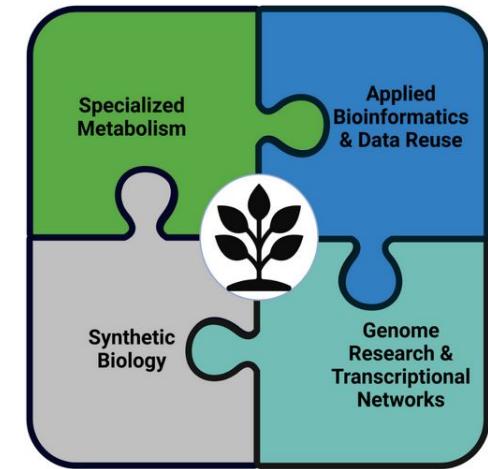


Prof. Dr. Boas Pucker

PBPM-BP-01: Plant

Systematics & Model Plants

- Biochemistry at HHU Düsseldorf
- (Systems) Biology at Bielefeld University
- Doctoral student (CeBiTec, Bielefeld University)
 - Genomics & Bioinformatics; synthetic biology (iGEM)
- Post doc (Ruhr-University Bochum)
- Post doc (Department of Plant Sciences, Cambridge, UK)
- Plant Biotechnology & Bioinformatics, TU Braunschweig (2021-2025)
- Plant Biotechnology & Bioinformatics, Uni Bonn (since 2025)
 - Evolution of specialized plant metabolism (genetics!)
 - Applied bioinformatics
 - Genomics/transcriptomics



No PBPM0 lecture on December 3rd 2025

Instead: Inaugural lecture in main building (lecture hall VIII, 11am (c.t.))

“Big Data-Driven Discoveries in Specialized Plant Metabolism”

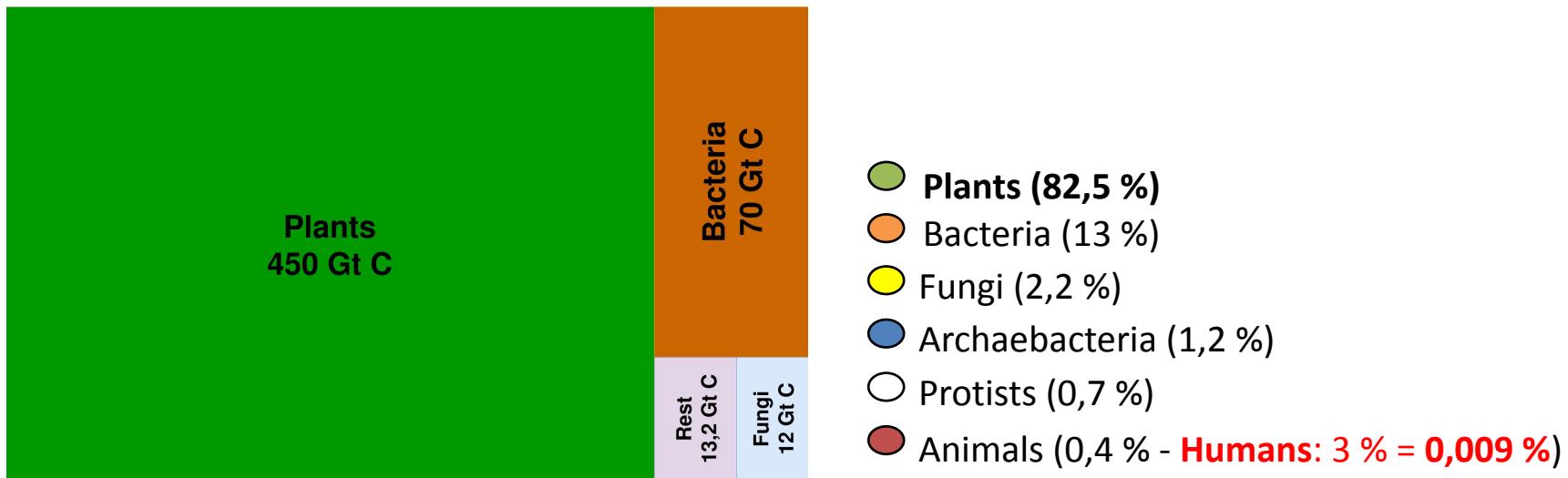
Availability of slides

- All materials are freely available (CC BY) - after the lectures:
 - eCampus: PBPM0 - Plant Biochemistry, Physiology and Molecular Biology (LEC)
 - GitHub: <https://github.com/bpucker/teaching/PBPM>
- Questions: Feel free to ask at any time
- Feedback, comments, or questions: [pucker\[a\]uni-bonn.de](mailto:pucker[a]uni-bonn.de)



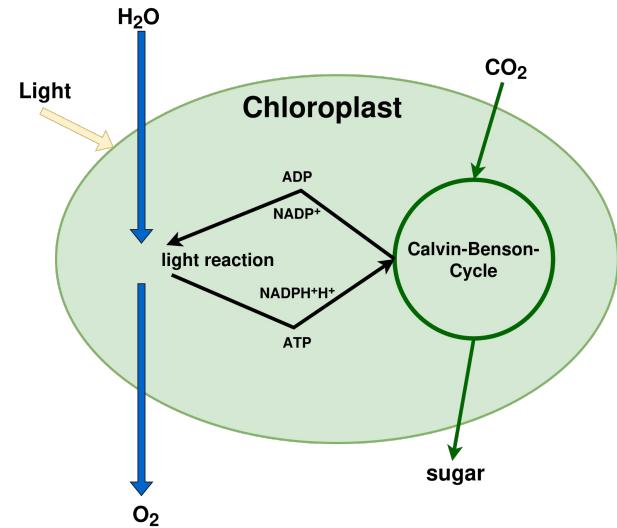
My figures and content can be re-used in accordance with CC BY 4.0, but this might not apply to all images/logos. Some figure were constructed using bioRender.com.

Global biomass composition



Why plants?

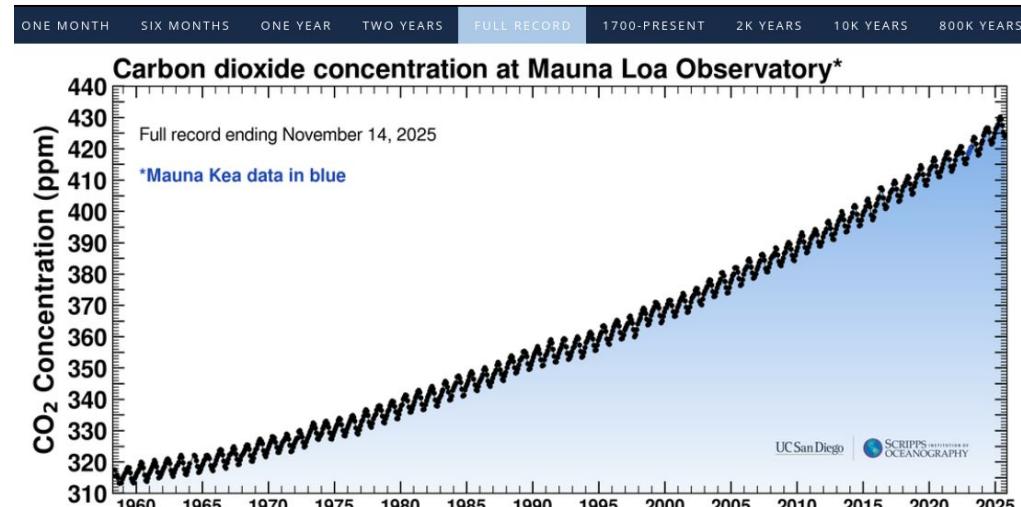
- Autotrophic organisms: synthesize all organic components necessary for building cells themselves
 - from inorganic macroelements (C, H, O, S, N, P, Mg, K, Ca)
 - and microelements (B, Cl, Cu, Fe, Mo, Mn, Si, Zn)
- Starting points of food chains: organic building blocks are essential for animals and must be obtained through food
- Dominant biomass: 200 times greater than that of animals
- Fundamental role in global cycles



Keeling curve

- Atmospheric CO₂ development tracked over time
- Significant increase during last decades
- Importance of forests in the northern hemisphere

*Latest CO₂ reading: 427.55 ppm



*Mauna Loa Observatory data from the most recent month is [preliminary](#)

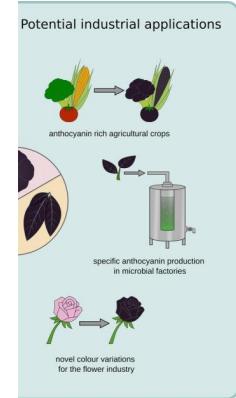
Crops - human nutrition



- Cereals make up >60% of global calorie production
- Maize is one of the largest contributors (about 20% of global human calories)
- Wheat is a key calorie source (~15% of cereals)
- Rice is especially important in Asia (>15% of global caloric intake)
- Cassava (a starchy root/tuber) >15% of caloric intake in Tanzania
- Potato has high calories per hectare

Biosynthesis of specialized metabolites

- Plants are vital sources of medicines (e.g., willow bark → aspirin)
- Plant biodiversity is a pharmaceutical reservoir for future drugs
- Anthocyanins & carotenoids from plants provide natural food colorants
- Plants supply key textile fibers such as cotton, linen, and hemp
- Natural fibers are renewable, biodegradable, and central to global industries
- Natural rubber from rubber trees is essential for tires



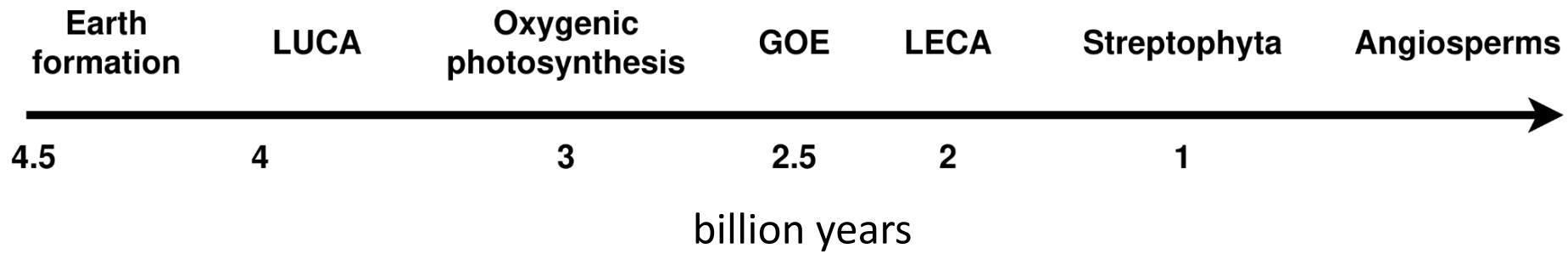
Mental health

- Stress reduction: being around plants can lower cortisol levels
- Plants can decrease depressive moods and symptoms
- Reduction in anger and hostility; increase in feelings of happiness
- Improved air quality from plants can benefit cognitive performance and overall health
- Gardening in communal spaces can help foster a greater sense of community
- Caring for plants can encourage self-expression and provide a sense of fulfillment



Evolutionary times and major events

- Land plants inhabit Earth for ~475 million years; enabled colonization of land by metazoans
- LUCA = Last Universal Common Ancestor
- GOE = Great Oxidation Event (“Great Oxygen Catastrophe”)
- LECA = Last Eukaryotic Common Ancestor



Plant Systematics

Nomenclature

- Taxonomic levels of divisions, classes, orders, and families can be recognized by their suffixes
- Species names are binomial (or “binary”) names according to Linnaeus
 - genus and specific epithet
- **Taxonomic levels:**
 - **Division: -phyta**
 - **Class: -opsida**
 - **Order: -ales**
 - **Family: -aceae**
 - **Example: Foxglove (*Digitalis purpurea*)**
 - Division: Tracheophyta
 - Class: Magnoliopsida
 - Order: Lamiales
 - Family: Plantaginaceae



What to italicize?

- Classical: only the species name is used, e.g., *Digitalis purpurea* or *Arabidopsis thaliana*
- Thines *et al.*, 2020: all taxonomic names should be written in italics

Setting scientific names at all taxonomic ranks in italics facilitates their quick recognition in scientific papers

Marco Thines  Takayuki Aoki, Pedro W. Crous, Kevin D. Hyde, Robert Lücking, Elaine Malosso, Tom W. May, Andrew N. Miller, Scott A. Redhead, Andrey M. Yurkov & David L. Hawksworth

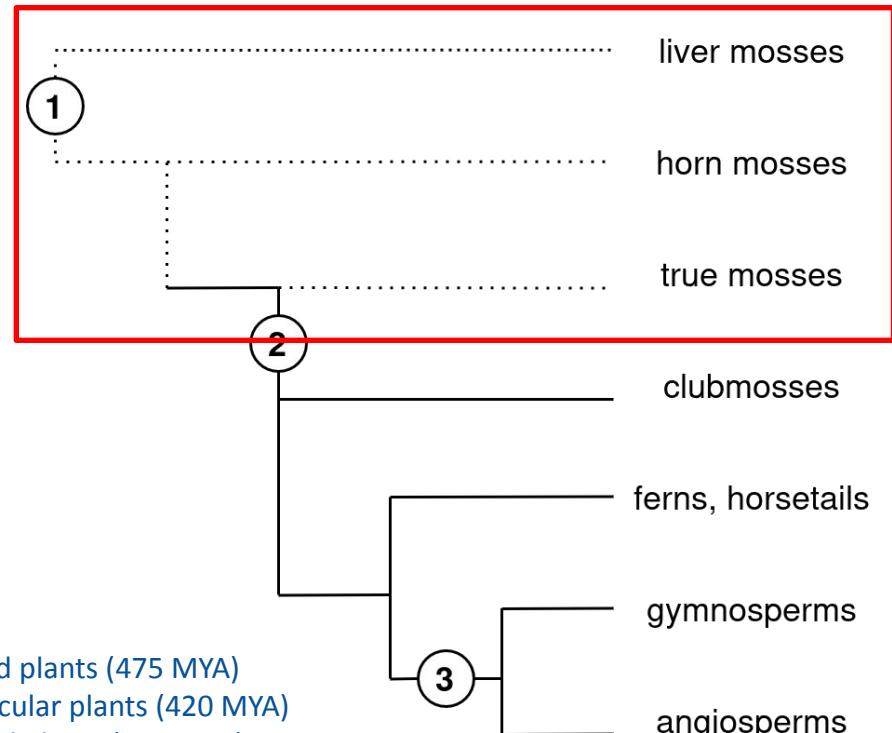
IMA Fungus 11, Article number: 25 (2020) | [Cite this article](#)

39k Accesses | 28 Citations | 40 Altmetric | [Metrics](#)

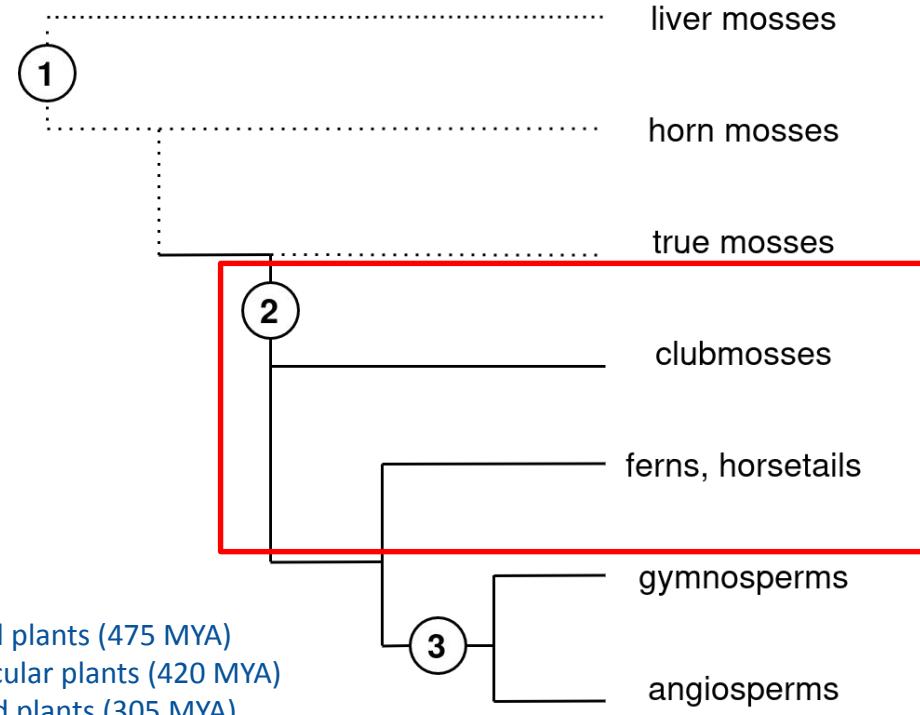
Abstract

It is common practice in scientific journals to print genus and species names in italics. This is not only historical as species names were traditionally derived from Greek or Latin. Importantly, it also facilitates the rapid recognition of genus and species names when skimming through manuscripts. However, names above the genus level are not always italicized, except in some journals which have adopted this practice for all scientific names. Since scientific names treated under the various Codes of nomenclature are without exception treated as Latin, there is no reason why names above genus level should be handled differently, particularly as higher taxon names are becoming increasingly relevant in systematic and evolutionary studies and their italicization would aid the unambiguous recognition of formal scientific names distinguishing them from colloquial names. Several leading mycological and botanical journals have already adopted italics for names of all taxa regardless of rank over recent decades, as is the practice in the *International Code of Nomenclature for algae, fungi, and plants*, and we hereby recommend that this practice be taken up broadly in scientific journals and textbooks.

- ... are closely connected.
- Molecular sequence data enable unravelling of phylogenetic relationships
- Systematics of flowering plants is of particular interest



- Monilophyta: common group of all “true” ferns, including horsetails, but excluding clubmosses
- Evolutionary timeframes: earliest land plants have been inhabiting the planet for more than 475 million years
- Flowering plants have existed at least since the beginning of the Cretaceous period (about 140 million years ago – but probably already 250 million years ago, Smith et al. 2010, PNAS)



1 = Origin of land plants (475 MYA)

2 = Origin of vascular plants (420 MYA)

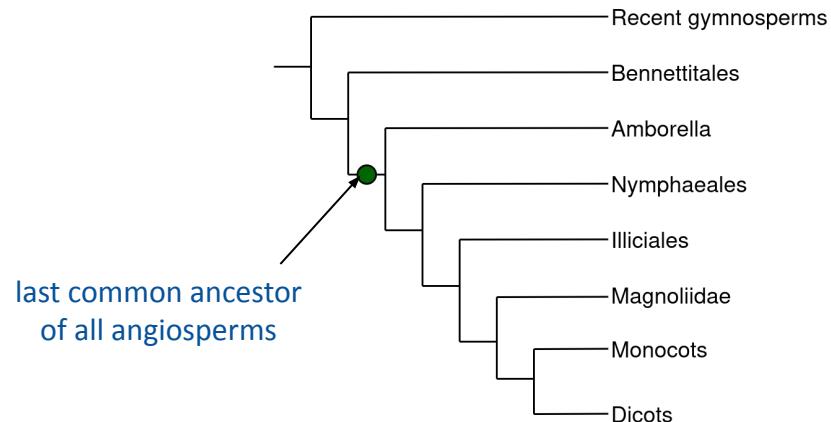
3 = Origin of seed plants (305 MYA)

Basal angiosperms

- Evolutionary lineages should not be described as “low” or “high”
- Evolutionary age of all extant lineages is the same
- Extant = currently (still) living
- Ancestral = characteristic of the ancestors



Water lilies (e.g., *Victoria cruziana*) are representatives of a very ancient group. Only the lineage of *Amborella* is older.



Land plants: embryophyta

Ferns and 'close relatives'

4 classes of gymnosperms
(phylogeny not fully resolved)

Taxonomy browser (NCBI)

- **Bryophyta (Mosses)**

- Anthocerotopsida (Hornworts)
- Marchantiopsida (Liverworts)
- Bryopsida (Leafy mosses), *Funariales*, *Funariaceae*, *Physcomitrium patens*



<http://www.moss.leeds.ac.uk/images/slide6.gif>

- **Lyco(podio)phyta (Clubmosses)**



- **Monilophyta**

- Equisetopsida (Horsetails), ..., *Equisetum arvense*
- Psilotopsida
- Pteridopsida (Ferns)



Andrew Butko, CC BY-SA 3.0

- **Spermatophyta (Seed plants)**

- Coniferopsida
- Ginkgopsida, ..., *Ginkgo biloba*
- Cycadopsida
- Gnetopsida,, *Welwitschia mirabilis*
- Magnoliopsida (Flowering plants, Angiosperms)
 - Basal dicots
 - Monocots, *Poales*, *Poaceae*, *Oryza sativa*
 - Eudicots, *Brassicales*, *Brassicaceae*, *Arabidopsis thaliana*



<https://www1.wdr.de/lokalzeit/unterwegs/botanische-gaerten-bonn-kolonialismus-100.html>



Angiosperms: monocots vs. dicots



Miya.m, CC BY-SA 3.0



Maksym Kozlenko, CC BY-SA 4.0



Frank C. Müller, CC BY-SA 4.0



Richard Bartz, CC BY-SA 2.5

Poales (monocots)

- ~20 families and >20,000 species, dominated by the Poaceae
- Evolved around 66–70 MYA, adapting to open, disturbed habitats (grasslands)
- Poaceae (grasses) crucial for agriculture: cereal crops
- Fiber and construction materials (e.g., bamboo, reeds)
- Intercalary meristems for regrowth and reduced floral structures (wind pollination)
- Frequent C₄ or CAM photosynthesis (efficient in heat, drought, high-light)



Brassicales (dicots)

- about 17 families and >4,000 species, Brassicaceae (mustard family) is largest family
- includes model organism *Arabidopsis thaliana*
- hallmark feature of Brassicaceae are glucosinolates (mustard oil compounds)
- damaged tissues breaks glucosinolates down to form isothiocyanates, which deter herbivores and pathogens
- many major crops:
 - *Brassica oleracea* (cabbage, broccoli, kale, cauliflower)
 - *Brassica napus* (canola/rapeseed)
 - *Raphanus sativus* (radish)
 - *Sinapis alba* (white mustard)



Caryophyllales (dicots)

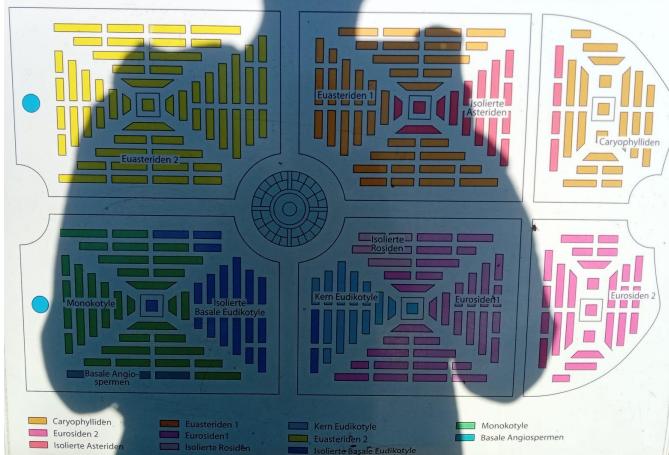


- Comprising about 37 families and >12,000 species
- Specialized and ecologically diverse lineages: cacti, carnations, amaranths, and ice plants
- Major evolutionary radiation into arid, saline, and nutrient-poor environments
- Betalains are nitrogen-containing pigments found only in Caryophyllales
- Many exhibit CAM or C₄ photosynthesis (adaptation to extreme environments)
- Economically valuable species: Beet (*Beta vulgaris*) (sugar and fodder); amaranths and quinoa (pseudocereals)



- Comprising ~8 families and >2,600 species; Cucurbitaceae is largest and most economically important
- Typically have vining or climbing habits with tendrils for support
- Fruits are often pepos (specialized type of berry with a thick rind)
- Special strategies for seed dispersal
- Many species have cucurbitacins (deters herbivores)
- Key food crops: cucumber (*Cucumis sativus*), melons (*Cucumis melo*), pumpkins and squashes (*Cucurbita* spp.), watermelon (*Citrullus lanatus*)

Angiosperm systematics in the Palace Garden



Artificial Intelligence in Botany

Mehr als 30.000 Pflanzenarten

Bestimme mit der Flora Incognita App mehr als 30.000 Pflanzenarten und erweitere deine Pflanzenkenntnisse.

Umfangreiche Pflanzensteckbriefe

Erfahre viele interessante Fakten über Pflanzen, z.B. Merkmale, Schutzstatus und Verbreitung.

Speichere deine Pflanzenfunde

Speichere deine Observatioen und leiste einen wichtigen Beitrag für die Wissenschaft.



Kosten- und werbefrei

Die Flora Incognita App ist kosten- und werbefrei und ist dank des Offline-Modus auch für Schulen- und Umweltbildungseinrichtungen geeignet.

- rRNA genes (e.g., 16S/18S rRNA): Highly conserved regions & more variable regions)
- Chloroplast/mitochondrial genes (e.g., *rbcL*, *matK*, *cox1*)
 - Widely used in plants (*rbcL*, *matK*) and animals (*cox1*)
 - Useful for barcoding and phylogenetic studies
- Protein-coding nuclear genes: EF-1 α , actin, tubulin (where rRNA is too conserved)
- Non-coding regions (e.g., ITS, intergenic spacers)
 - Higher mutation rate, useful for resolving relationships among closely related species

- Whole-genome re-sequencing data / Single Nucleotide Variants (SNVs)
 - High-resolution phylogenies & robust inference at all taxonomic levels
- Conserved orthologous markers
 - Single-copy genes to avoid paralogy issues
 - Facilitate comparison across broad taxonomic groups

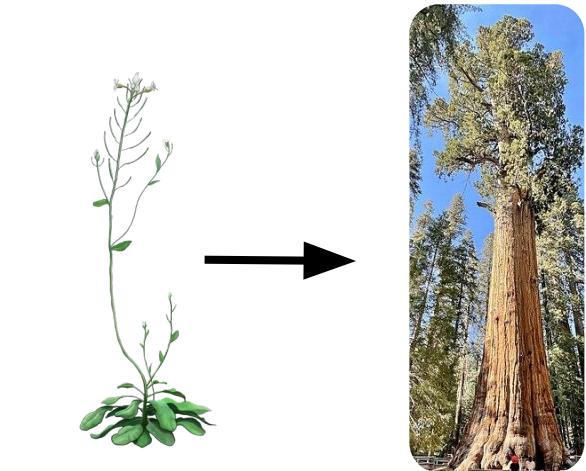
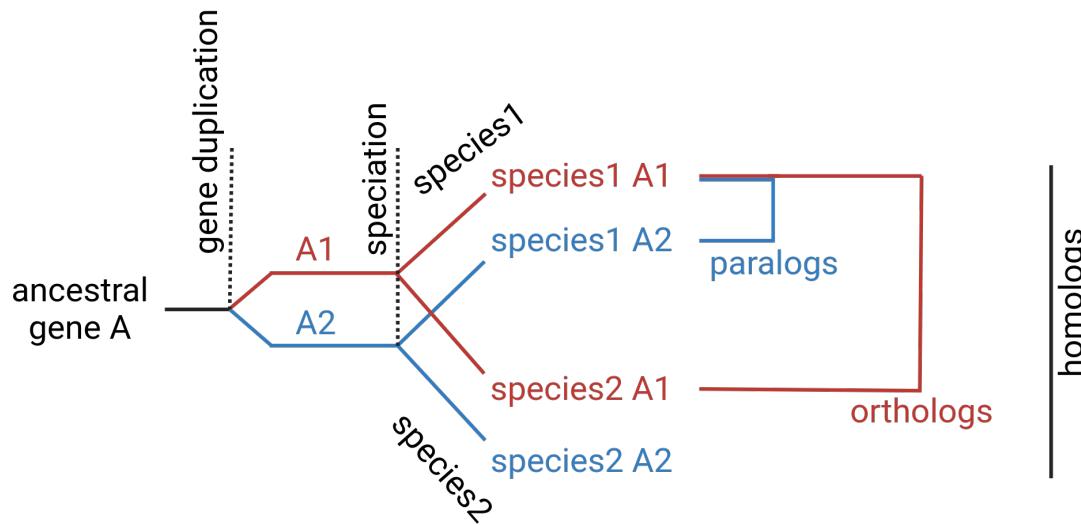
Model organisms

General properties of a model organisms

- Definition: characterized by outstanding features for research
- Short generation time
- Small size, low demands on culture conditions, low laboratory maintenance costs
- Many offspring, seed production
- Well-defined classical genetics (populations, traits, crossability, etc.)
- Transformability for creation of transgenic lines: knock-outs (KO), overexpression
- Transferability of findings to non-model organisms
- Available genome sequence

Knowledge transfer between plant species

- Homology-based transfer of knowledge between plant species
- Ortholog = same gene in different species



DataBase Center for Life Science (DBCLS), 2021

Marty Aligata, 2022

Arabidopsis thaliana

- True dicot flowering plant, order (Brassicales), family (Brassicaceae), related to crop plants such as rapeseed and cabbage.
- Very small genome (approx. 145 Mbp); fully sequenced since 2000
- About 28,500 protein-coding genes on 5 chromosomes
- Short generation time: ~6–8 weeks
- Well-described classical genetics
- Normally self-fertilizing (“selfing”), but also easily crossable
- Cosmopolitan with a large collection of different ecotypes
- Up to 10,000 seeds per plant
- Small plant (lab-suitable), e.g., for large-scale mutant screenings for phenotypes/traits
- Mutant collections (e.g., GABI-Kat: <https://www.gabi-kat.de/>)
- Easily transformable via *Agrobacterium tumefaciens*
- Con: no symbioses with nitrogen-fixing bacteria or mycorrhizal fungi



(A2 YB-SO) (gj, enaferd, ziegobdenAaif) (www.groeiobservatorium.nl)\agfh

Oryza sativa

- Rice: extremely important crop for daily food supply of at least 2.5 billion people
- Since 2003: first genome sequence (500 Mbp) available; now complete genome sequence published
- Monocot with considerable evolutionary distance (>100 million years) from *Arabidopsis*
- Proportion of research in China is increasing; strong focus on rice is making it one of the most important model organisms

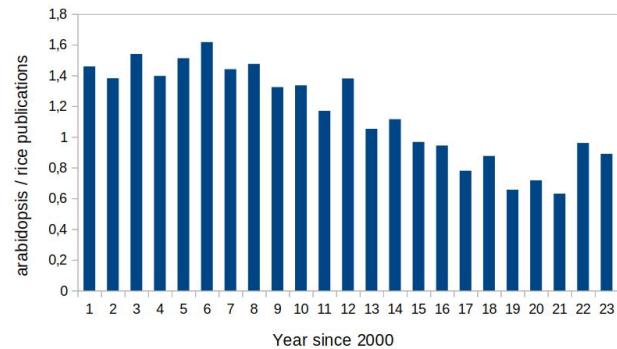


Oryza sativa

What is the most important model organism?

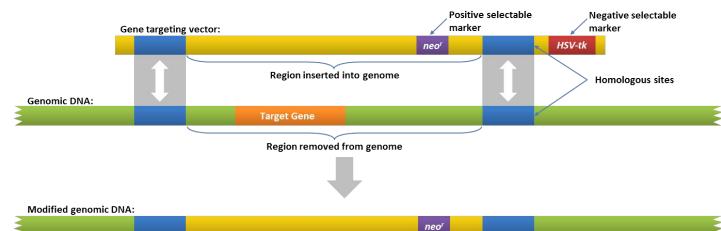
- *Arabidopsis thaliana*:
 - Publications: >120,000 (2024)
 - Mutant lines: >1,000,000 available (NASC, ABSRC)
 - Generation time: ~6 weeks from seed to seed
 - Transformation efficiency: >95% via floral dip

- *Oryza sativa*:
 - Publications: ~70,000 (2024)
 - Mutant lines: >500,000 available (T-DNA, TE, CRISPR libraries)
 - Generation time: ~3–4 months
 - Transformation efficiency: 60–90% (varies by subspecies)



Physcomitrium patens

- Leafy moss: the green plant is a haploid gametophyte ($1n$)
- Mosses exhibit efficient homologous recombination (enables knock-outs); allows the targeted integration of a transgene at a specific genomic location
- Genetic manipulation of the gametophyte has an immediate effect, because no second allele is present
- Genome sequence (480 Mbp) has been published
- Biotechnologically interesting because it can be cultivated in bioreactors



BioStu, CC BY-SA 3.0



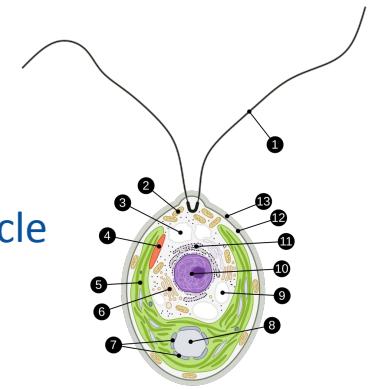
<https://de.wikipedia.org/wiki/Moosbioreaktor>



- Extensive classical genetics and mutant collections (e.g., kernel color, growth traits)
- Large genome (~2.3 Gbp); studies on genome structure, transposons, and gene regulation
- Important for comparative studies with other cereals (rice, wheat, sorghum)
- Easily crossable; distinct male and female flowers enable controlled breeding
- Major crop, linking fundamental research to agriculture
- Transposon tagging, transformation systems, and genomic resources
- Ideal for quantitative genetics, epigenetics, and systems biology

Chlamydomonas reinhardtii

- Unicellular green alga; simple, haploid eukaryote with well-defined life cycle
- Rapid growth (~1 day generation time under optimal conditions)
- Easily mutagenized; classical and reverse genetics possible
- Nuclear, chloroplast, and mitochondrial genomes can be manipulated
- Model for cilia and flagellar motility, assembly, and signaling
- Insights into chloroplast biology, light responses, and carbon fixation
- Cultivable in bioreactors; used for biofuel and recombinant protein production
- Genome sequenced: Well-annotated nuclear, chloroplast, and mitochondrial genomes



Populus trichocarpa (poplar)

- Woody perennial plant (tree biology and forest ecology)
- First tree with a sequenced genome (approx. 485 Mbp; published 2006)
- Fast-growing compared to other trees
- Large, well-characterized populations
- Ideal for investigating secondary growth, lignin, and cellulose biosynthesis
- Transformation and molecular tools available
- Ecological and physiological research on drought, temperature, and stress responses
- Model for biomass production and sustainable forestry



Antirrhinum majus (snapdragon)

- Classic genetics model (flower color & shape)
- Insights into floral organ identity and symmetry
- Enables controlled hybridization experiments (easily crossable)
- Mutant collections facilitate studies of gene function and regulation
- Molecular tools: Transposon tagging, transformation, and in situ hybridization
- Sequenced genome allows functional genomics research



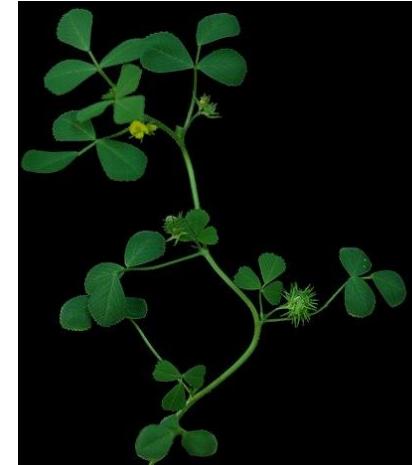
Petroselinum crispum (parsley)

- Family: Apiaceae (carrot family); biennial herb
- Genome size: ~2.2 Gb (only draft in 2025)
- Used to study gene regulation in response to environmental stimuli
- Investigation of phenylpropanoid pathway (flavonoids, lignin)
- Research on plant defense responses to pathogens (fungal elicitors)
- Cell suspension cultures model; protoplast transformation (transient expression assays)
- Helped define early signal transduction cascades involving ROS and calcium



Medicago truncatula (barrel medic)

- Family: Fabaceae (legume family); annual, self-fertilizing diploid
- Genome: ~500 Mb; fully sequenced and well-annotated
- Model for legume biology (closely related to crops)
- Short generation time and ease of transformation
- Forms root nodules with *Sinorhizobium meliloti* (nitrogen fixation)
- Forms arbuscular mycorrhizal associations (model for plant–microbe interactions)



Digitalis purpurea (common foxglove)



- Produces cardiac glycosides and secondary metabolites
- Moderate genome size facilitates genomic and functional studies
- Specialized metabolite pathways can be investigated and engineered
- Insights into floral development & pollination
- Diverse ecotypes enable studies of adaptation & evolution
- Potential for transformation, gene editing, and metabolic engineering

More model species

- Other model plants:
 - tobacco (*Nicotiana tabacum*)
 - potato (*Solanum tuberosum*)
 - tomato (*Lycopersicon esculentum*)
 - „C-fern“ (*Ceratopteris richardii*)
- „Plant Science’s next top models“ (Cesarino *et al.*, 2020):
 - *Marchantia polymorpha* (liverwort)
 - *Eutrema salsugineum*
 - *Phragmites australis*
 - *Pisum sativum*
 - *Setaria viridis*
 - *Striga hermonthica*



- Global importance of plants (biomass)
- Role of plants during evolution (oxygen)
- Plant systematics / nomenclature
- Properties of model organisms
- Examples of model organisms

Time for questions!

Questions

1. Why are plants important?
2. Which major events took place in the last 4.5 billion years?
3. Which taxonomic levels are frequently used to classify plants?
4. Please name three species-rich orders of plants!
5. What are important properties of a model organism?
6. Whis species are important plant model organisms?
7. Which model species would be a good choice to understand vegetables?