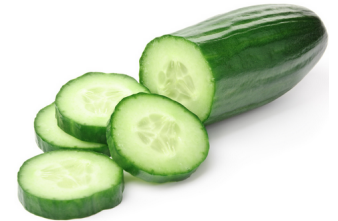


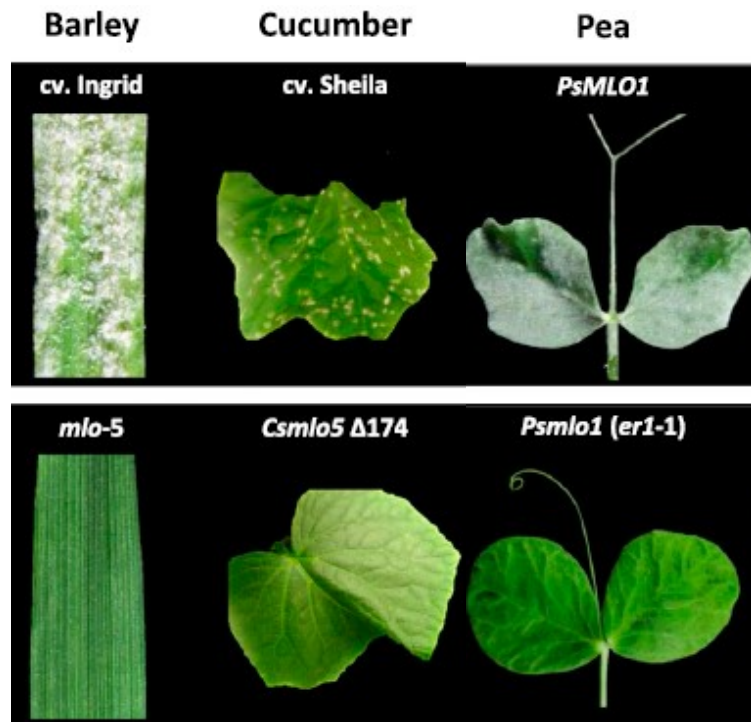
Powdery Mildew

What drives the genetic evolution of powdery mildew, a pathogen of staple and cash crop?

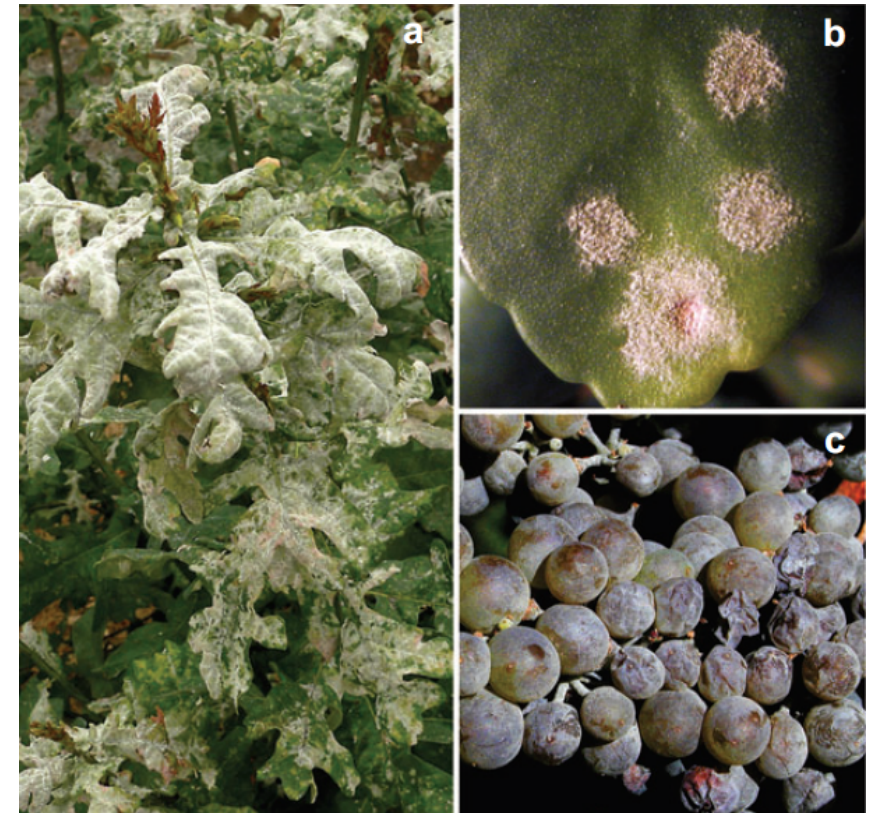
What is your daily food?



Powdery Mildew: Hosts



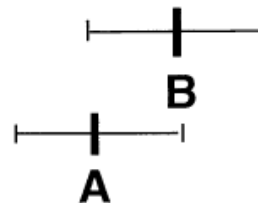
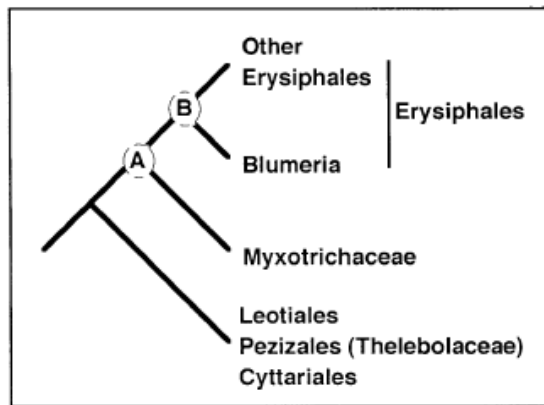
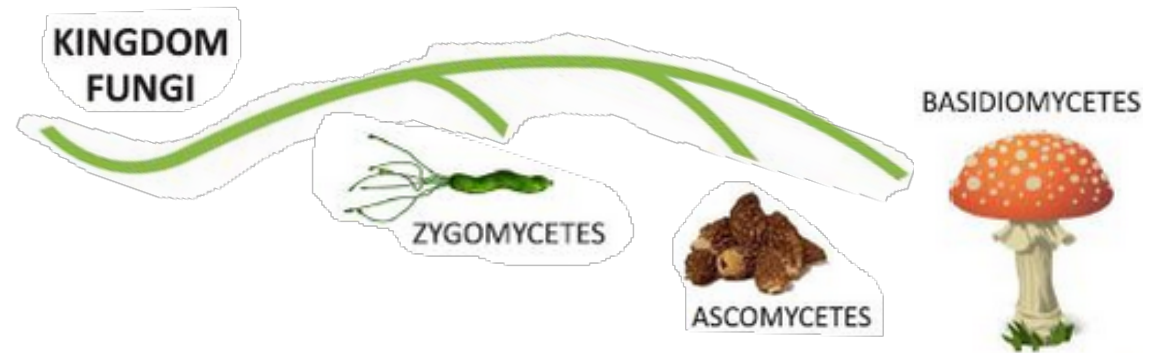
Kusch and Panstruga 2017



a: oak tree
b: christmas kalanchoe
c: grape vine

Glaw 2008

Phylogeny & Origin



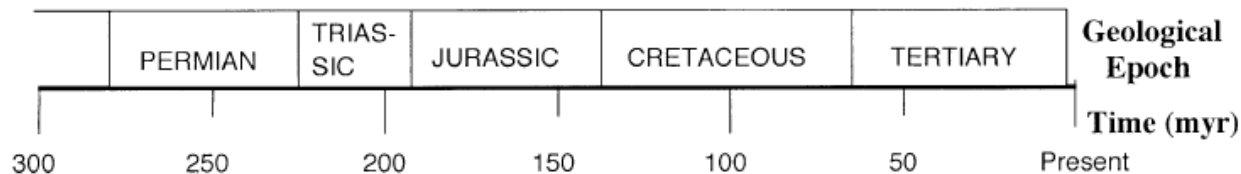
Molecular clock
1.26%/100myr
(Berbee and Taylor 2001)

Split of angiosperms
from other seed plants

Split of monocots
from dicots

Diversification of
angiosperms

Evolutionary events
of plants



5 major clades:

Cystothecaceae
Phyllactinieae
Erysipheae
Golovinomyceteae
Blumerieae

Takamatsu *et al.* 2004

Powdery Mildews & Lifestyles of pathogens

- *Erysiphe pisi*



- *Erysiphe necator*

- *Golovinomyces orontii*

- *Golovinomyces cichoracearum*

- *Blumeria graminis*

- *Blumeria graminis* f. sp. *hordei*

- *Blumeria graminis* f. sp. *tritici*

- *Oidium heveae*



- Biotroph

- **Obligate biotroph**

- Hemibiotroph

- Necrotroph

- Saprotroph

What drives the genetic evolution of powdery mildews?

Genome Expansion and Gene Loss in Powdery Mildew Fungi Reveal Tradeoffs in Extreme Parasitism

Spanu *et al.* 2010

Powdery Mildews Are Characterized by Contracted Carbohydrate Metabolism and Diverse Effectors to Adapt to Obligate Biotrophic Lifestyle

Liang *et al.* 2018

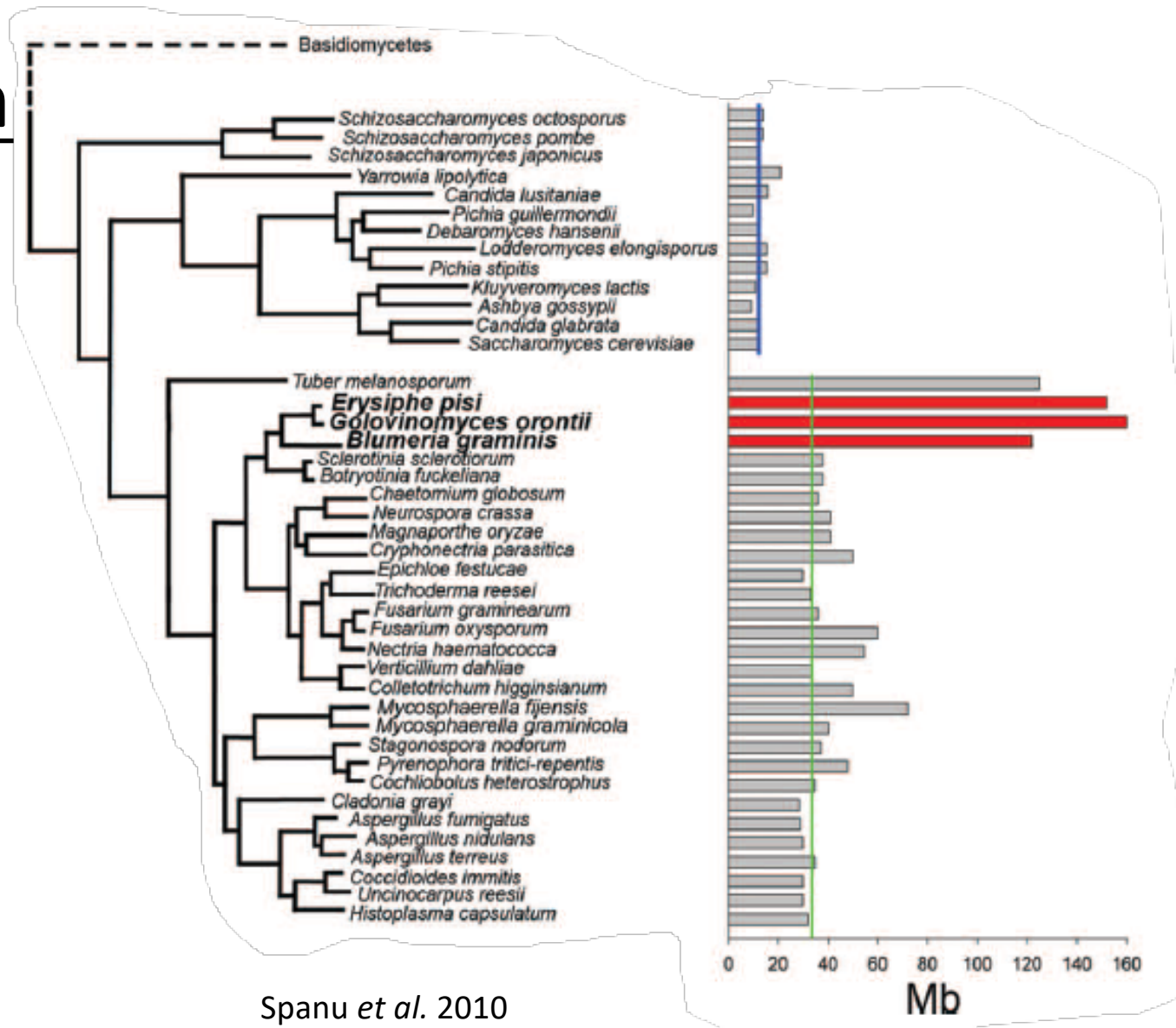
What is the molecular basis of obligate biotrophs?

Genome Expansion

- 64% TEs

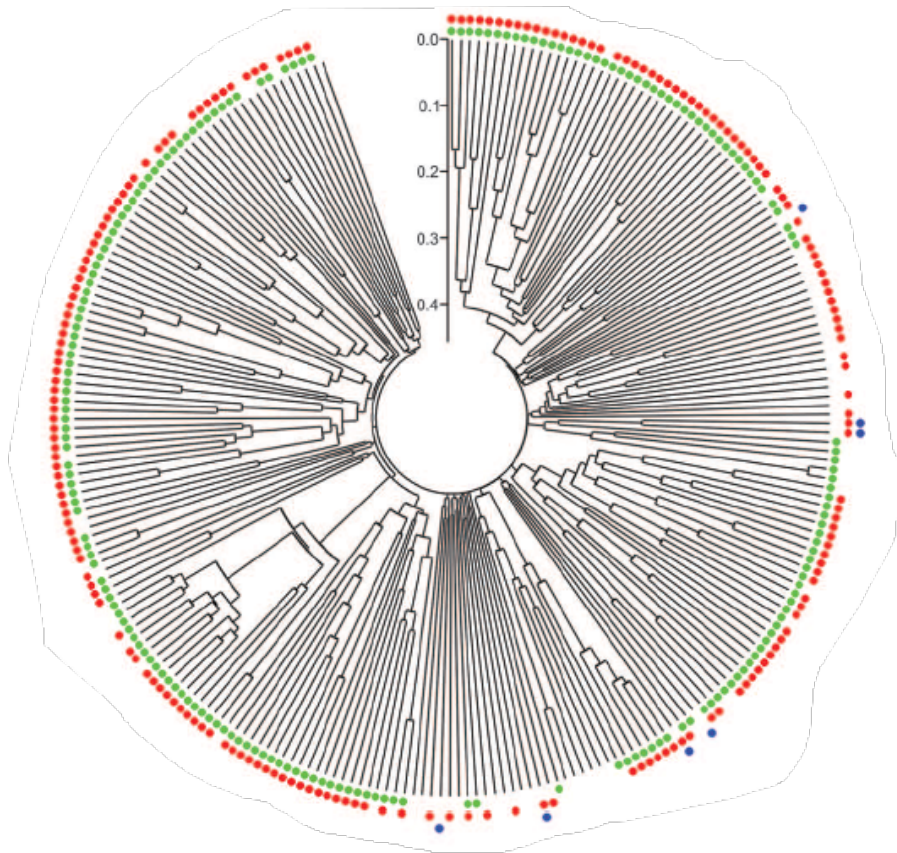
- CSEPs

Candidates for secreted effector proteins



CSEPs

—————→ Highly specialised to hosts



Spanu *et al.* 2010

Further studies in Liang *et al.* 2018:

Blumeria graminis f. sp. *hordei* (Bgh)
Blumeria graminis f. sp. *tritici* (Bgt)

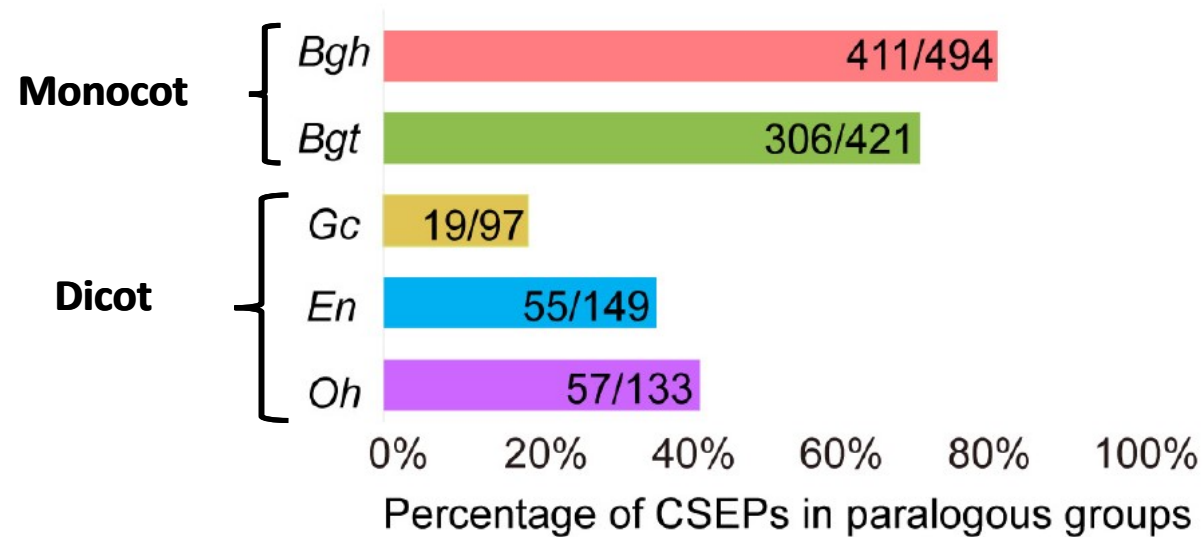
Golovinomyces cichoracearum (Gc)
Erysiphe necator (En)
Oidium heveae (Oh)

Hosts:

**Monocoty-
ledons**

**Dicoty-
ledons**

CSEPs: Mono- vs. Dicotyledonous Pathogens



Liang *et al.* 2018



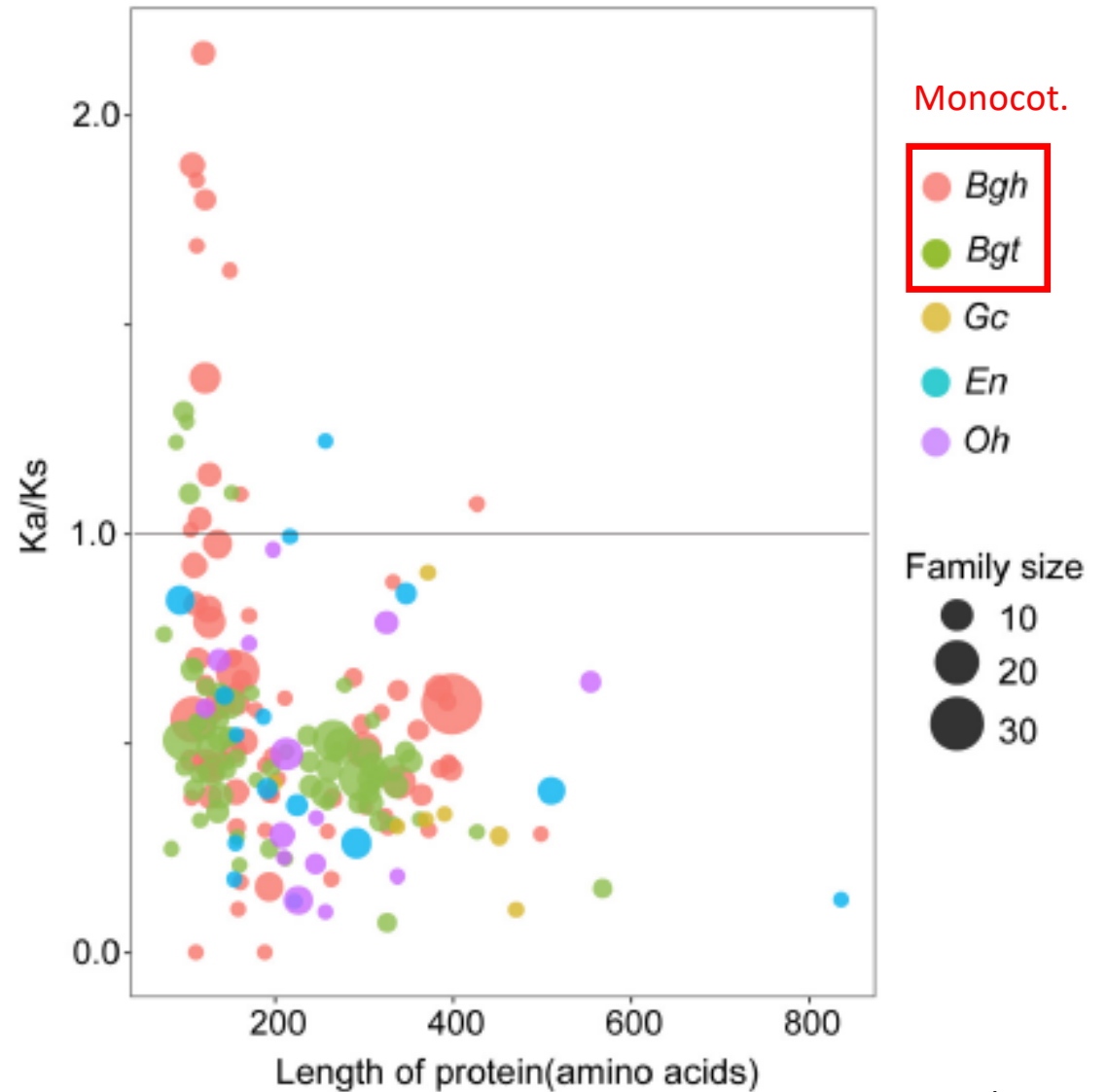
Strong CSEP duplication in
monocotyledonous pathogens

CSEPs: Selection Forces in Mono- and Dicotyledonous Pathogens

substitution rate K_a/K_s :

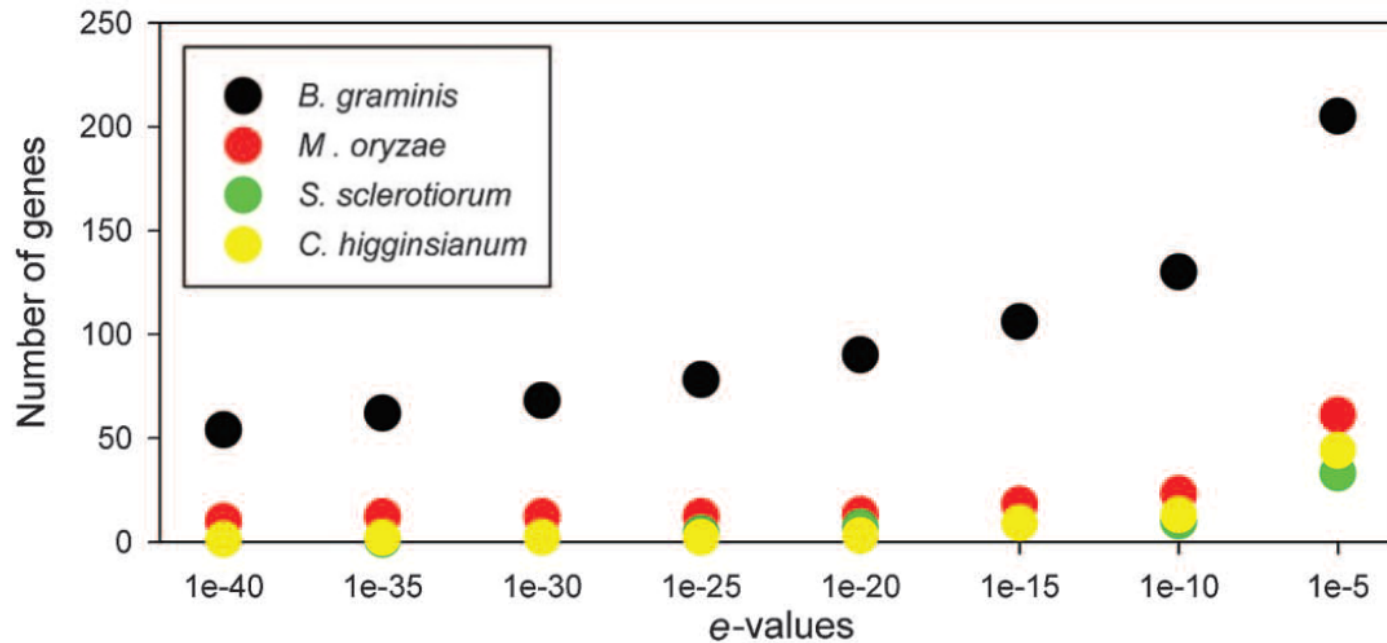
- K_a = non-synonymous
- K_s = synonymous
- High ratio = $K_a > K_s$
-> positive selection
- Low ratio = $K_a < K_s$
-> purifying selection

➡ Different selection forces



Liang *et al.* 2018

Missing Genes?



Spanu *et al.* 2010

MACGs = missing ascomycete core genes

- metabolism
- regulatory proteins

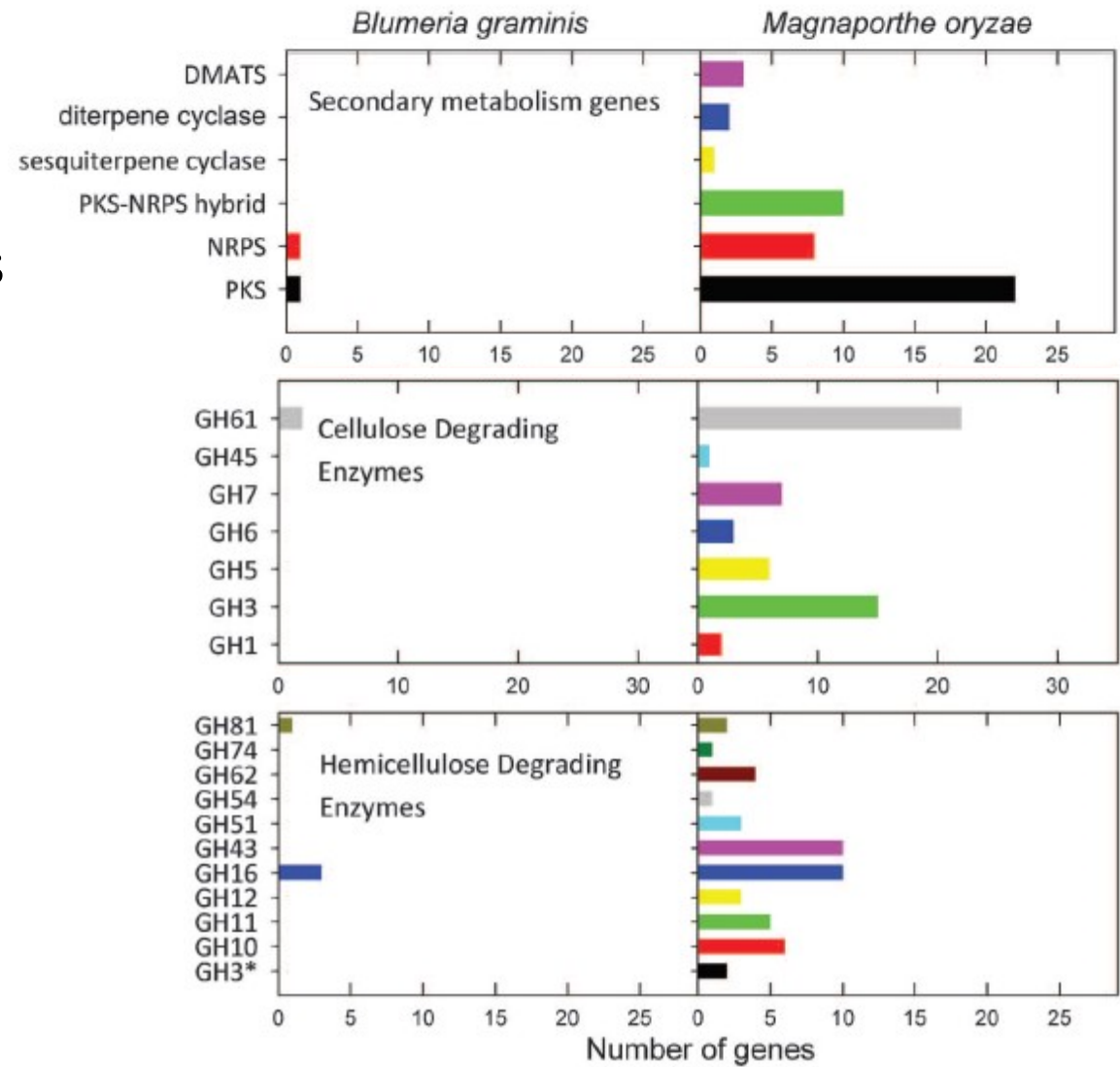
MACGs

special metabolites for pathogens

biosynthesis catalyzing enzymes

- NRPS = nonribosomal peptide synthetases
- PKS = polyketide synthases

➔ less pathogenicity?



Spanu *et al.* 2010

MACGs

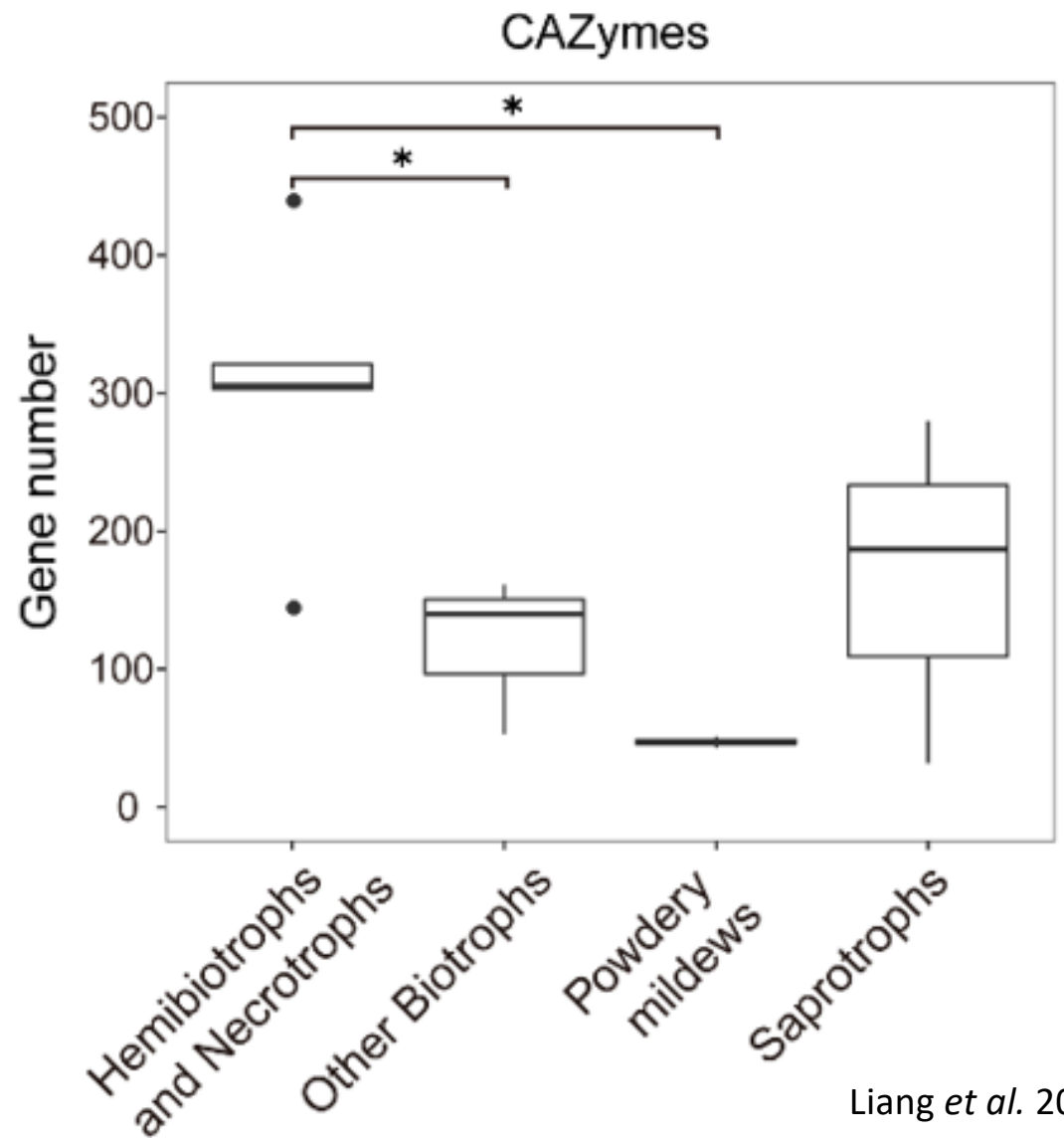
CAZymes

carbohydrate active enzymes

-> host cell wall degradation

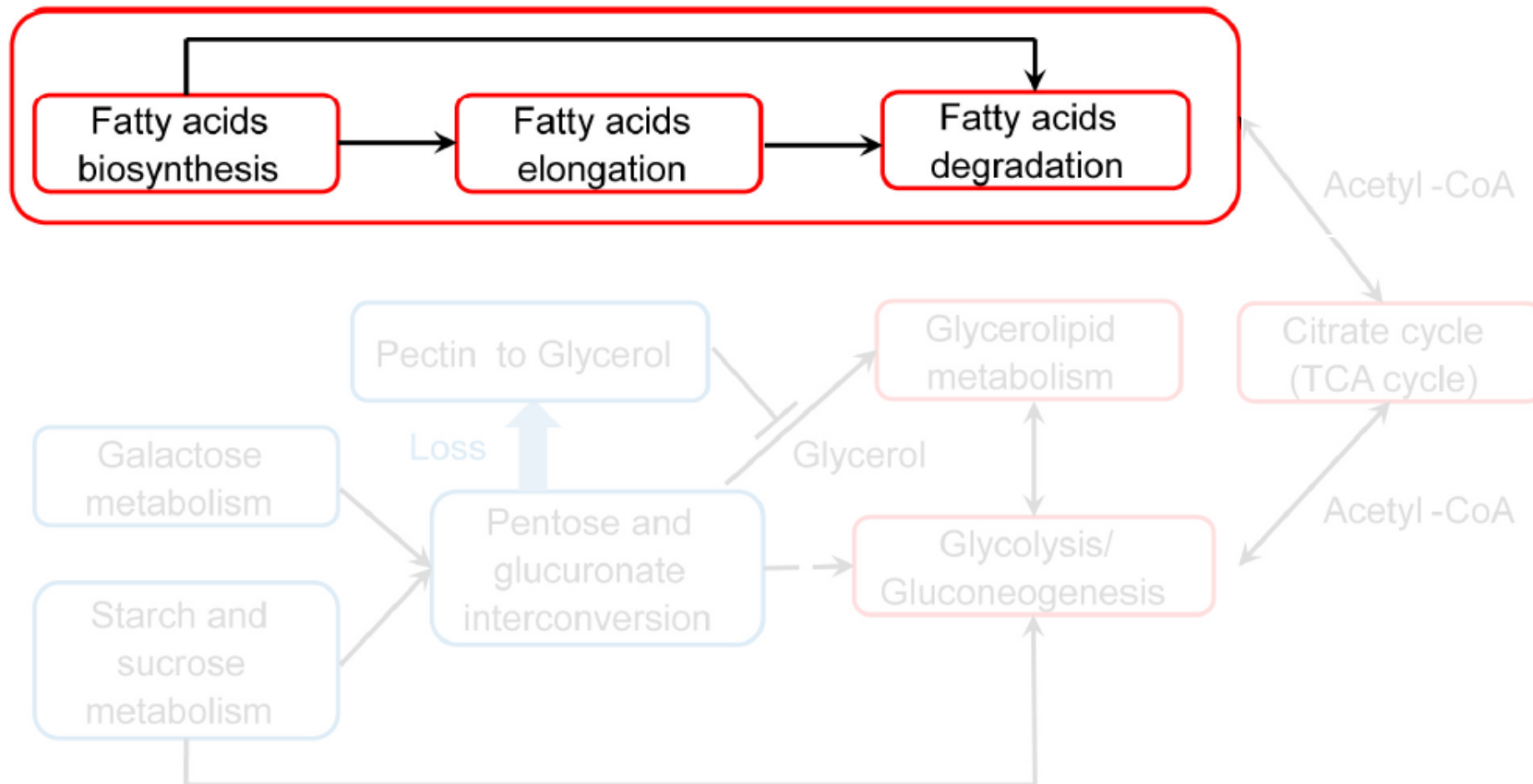


No energy source?



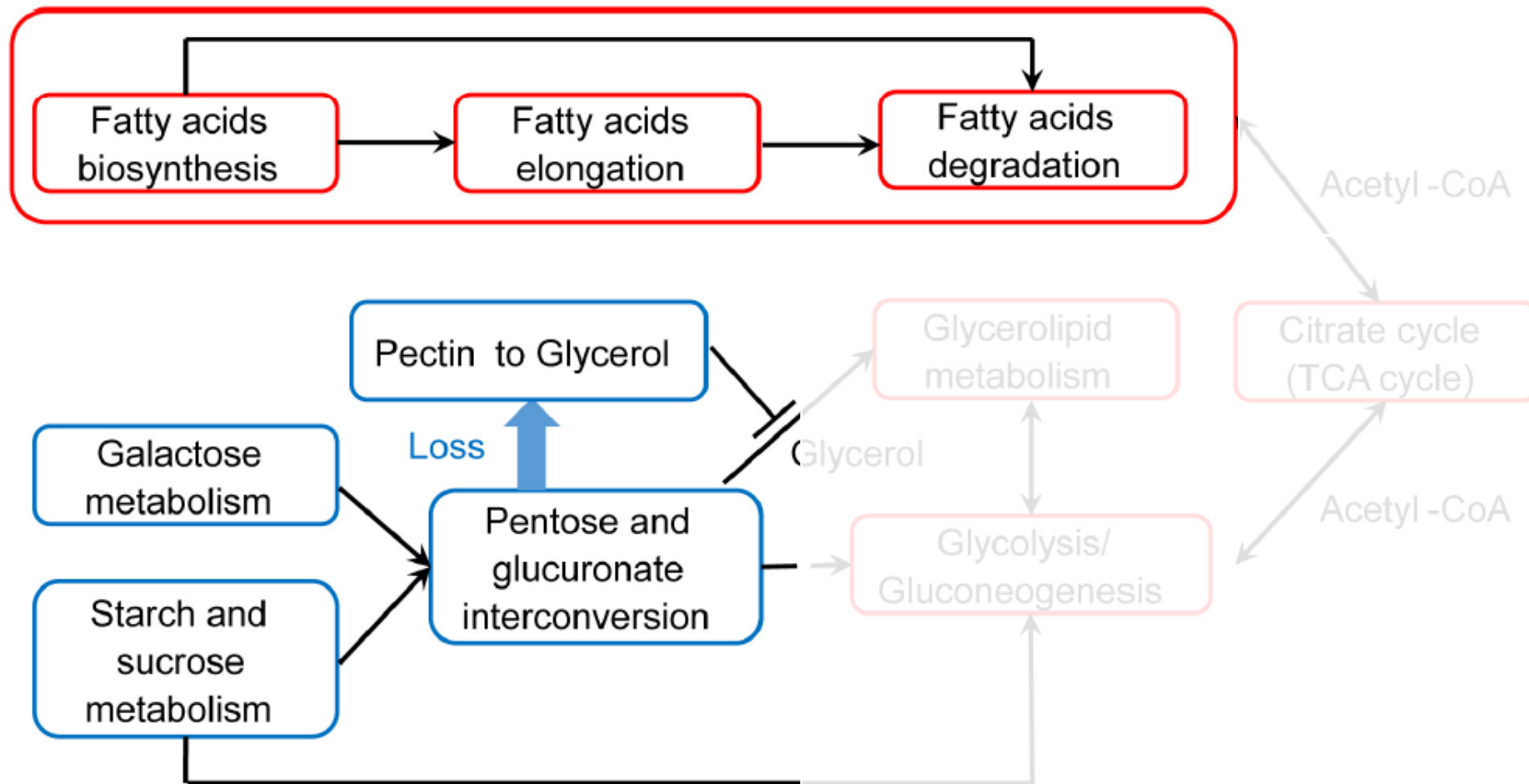
Liang *et al.* 2018

More Lipid Metabolism Genes



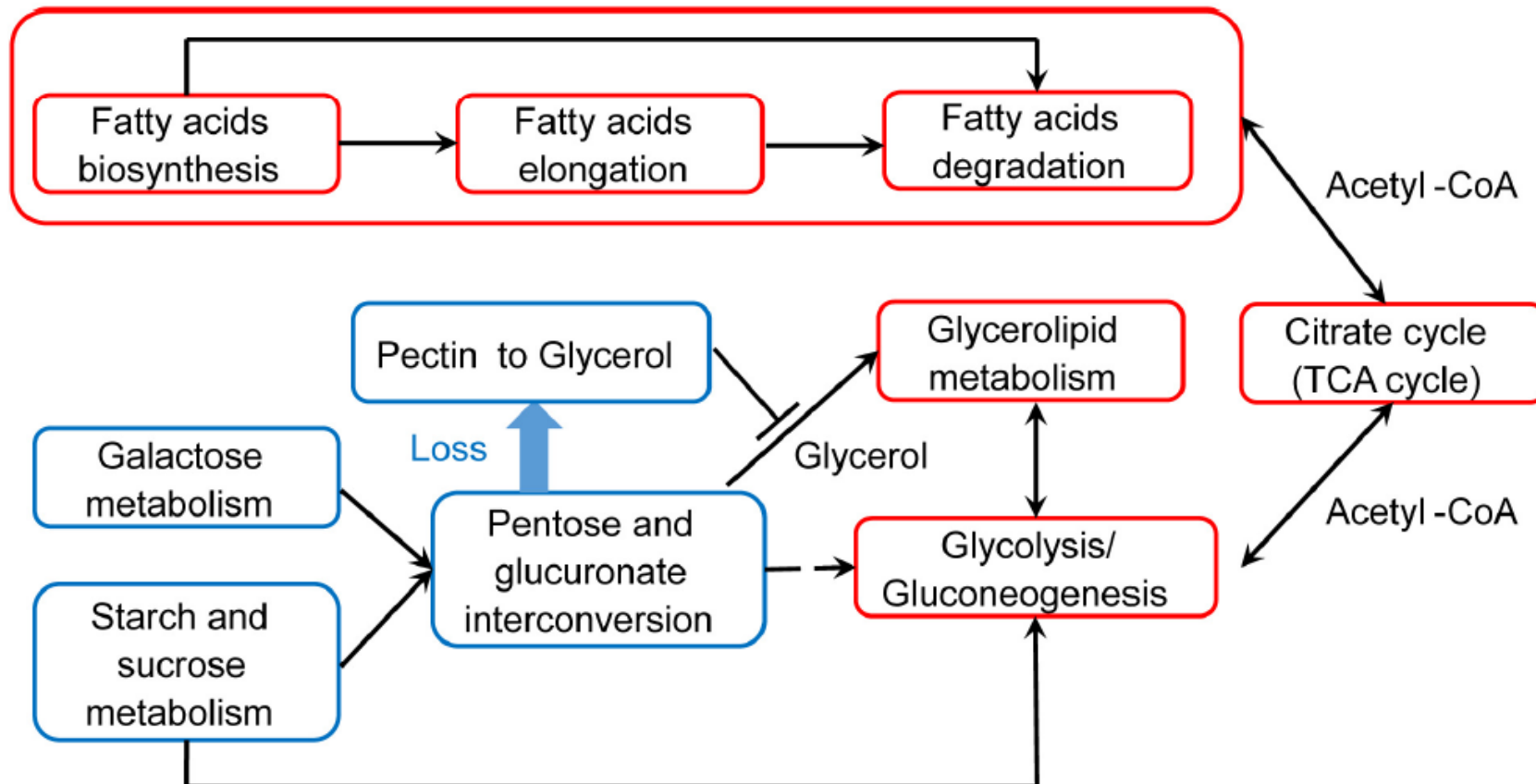
Liang *et al.* 2018

More Lipid Metabolism Genes



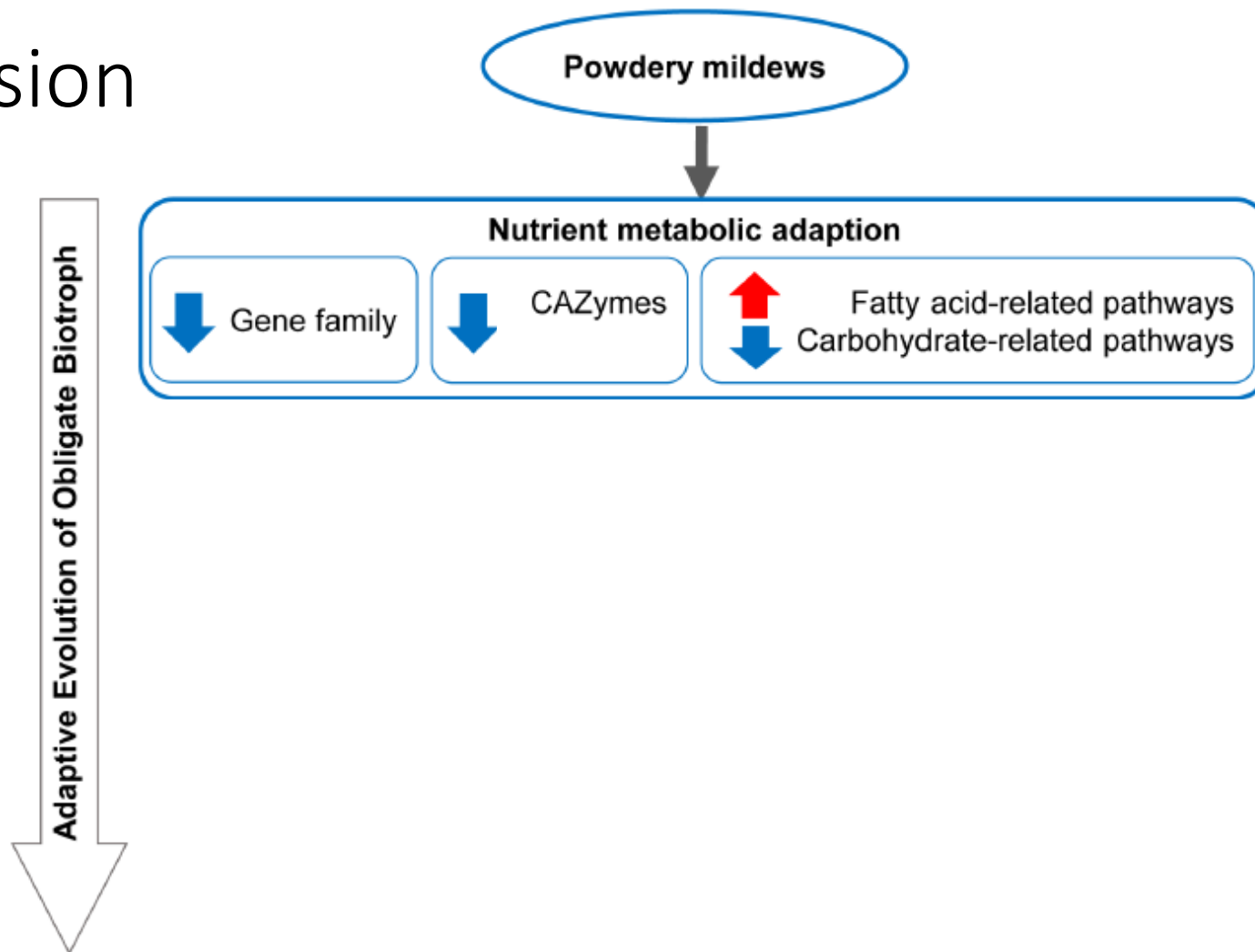
Liang *et al.* 2018

More Lipid Metabolism Genes



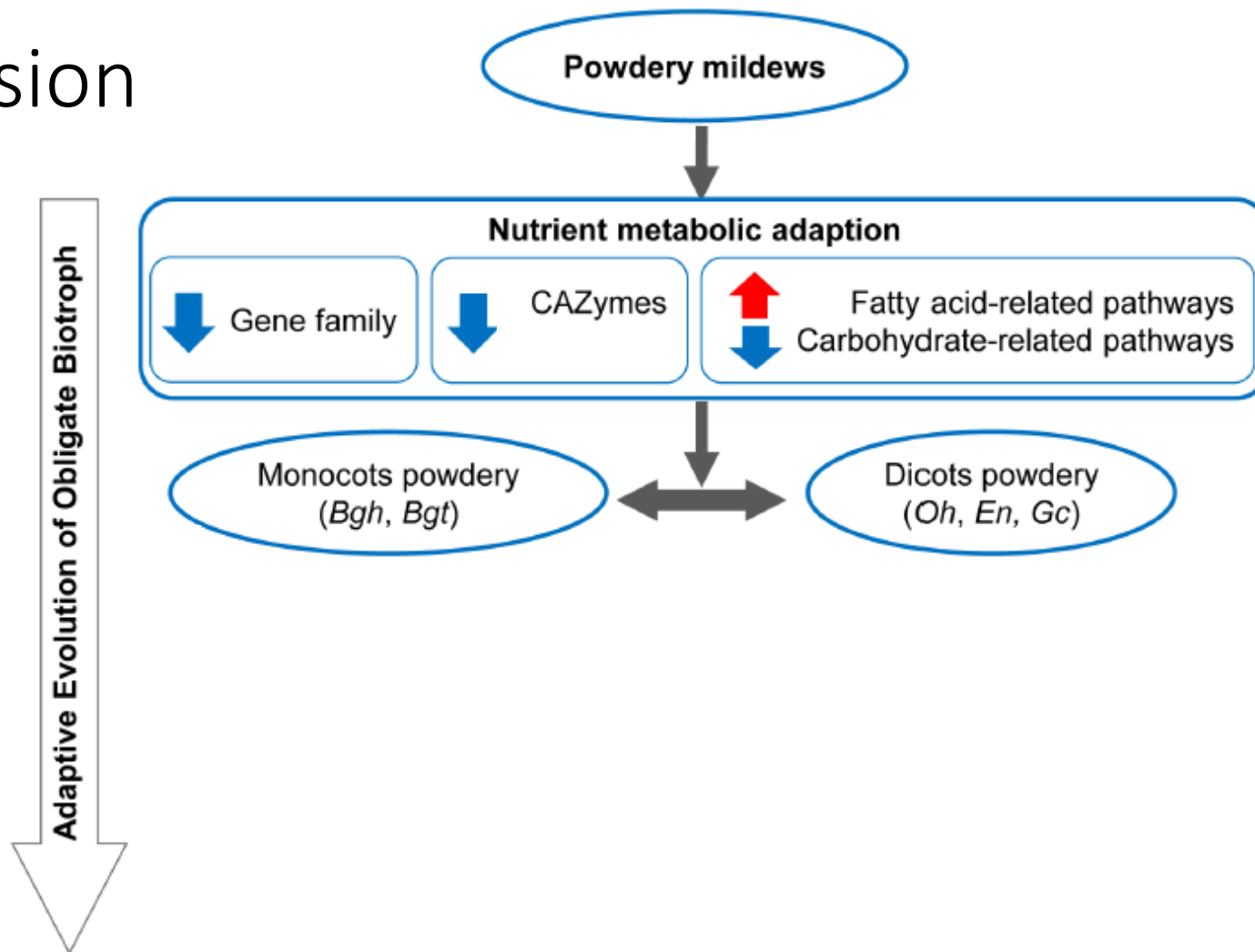
Liang *et al.* 2018

Conclusion



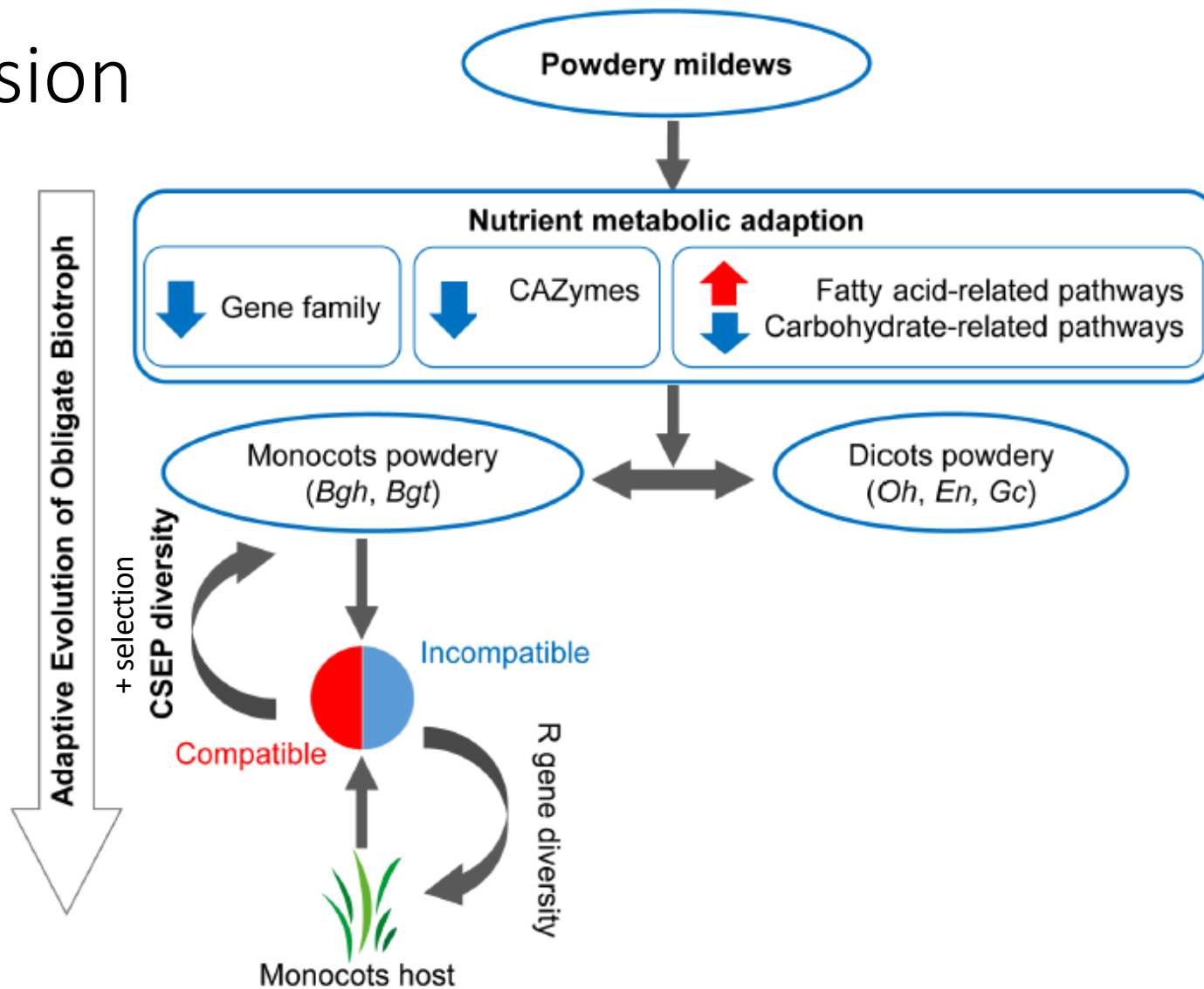
Adapted from Liang *et al.* 2018

Conclusion



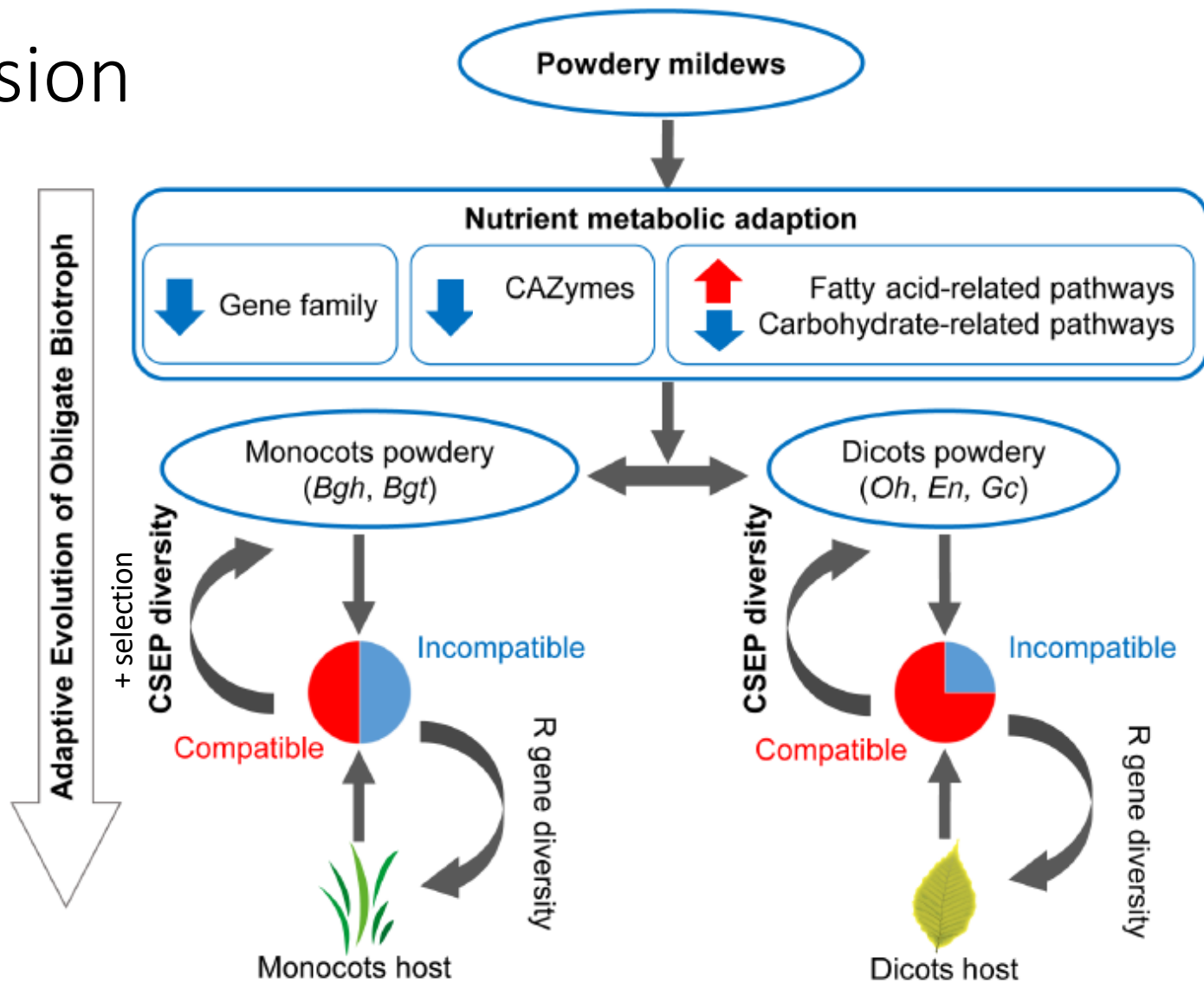
Adapted from Liang *et al.* 2018

Conclusion



Adapted from Liang *et al.* 2018

Conclusion



Adapted from Liang *et al.* 2018

Thank you for your attention

Questions?

Discussion: What drives the genetic evolution of powdery mildew?

- Adaptation
-> direct and indirect?
- Environment:
 - Climate change
 - Geographical aspects
- Which environmental aspects allowed them to develop to highly specialised pathogens?

References

- Glawe, D. A. (2008). The powdery mildews: a review of the world's most familiar (yet poorly known) plant pathogens. *Annu. Rev. Phytopathol.*, 46, 27-51.
- Kusch, S., & Panstruga, R. (2017). mlo-Based Resistance: An Apparently Universal "Weapon" to Defeat Powdery Mildew Disease. *Mol Plant Microbe Interact*, 30(3), 179-189. doi:10.1094/mpmi-12-16-0255-cr
- Liang, P., Liu, S., Xu, F., Jiang, S., Yan, J., He, Q., . . . Miao, W. (2018). Powdery Mildews Are Characterized by Contracted Carbohydrate Metabolism and Diverse Effectors to Adapt to Obligate Biotrophic Lifestyle. *Frontiers in Microbiology*, 9(3160). doi:10.3389/fmicb.2018.03160
- Menardo, F., Praz, C. R., Wyder, S., Ben-David, R., Bourras, S., Matsumae, H., . . . Roffler, S. (2016). Hybridization of powdery mildew strains gives rise to pathogens on novel agricultural crop species. *Nature Genetics*, 48(2), 201.
- Spanu, P. D., Abbott, J. C., Amselem, J., Burgis, T. A., Soanes, D. M., Stüber, K., . . . Gurr, S. J. (2010). Genome expansion and gene loss in powdery mildew fungi reveal tradeoffs in extreme parasitism. *Science*, 330(6010), 1543-1546.
- Takamatsu, S. (2004). Phylogeny and evolution of the powdery mildew fungi (Erysiphales, Ascomycota) inferred from nuclear ribosomal DNA sequences. *Mycoscience*, 45(2), 147-157.
- Takamatsu, S. (2013). Origin and evolution of the powdery mildews (Ascomycota, Erysiphales). *Mycoscience*, 54(1), 75-86.