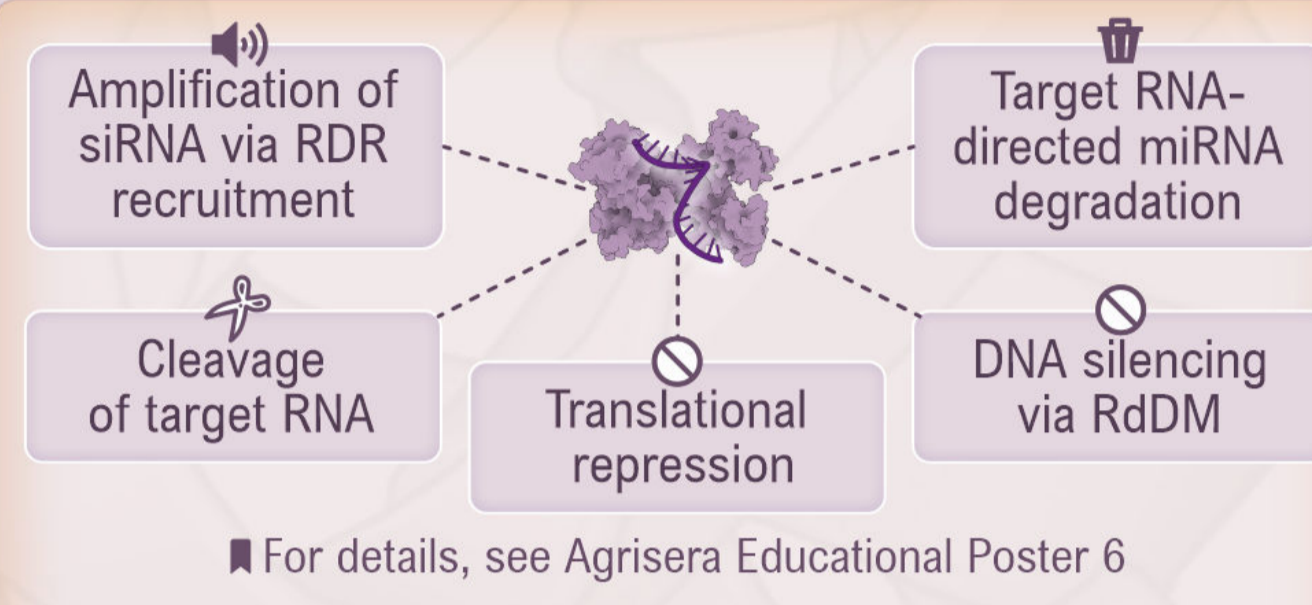
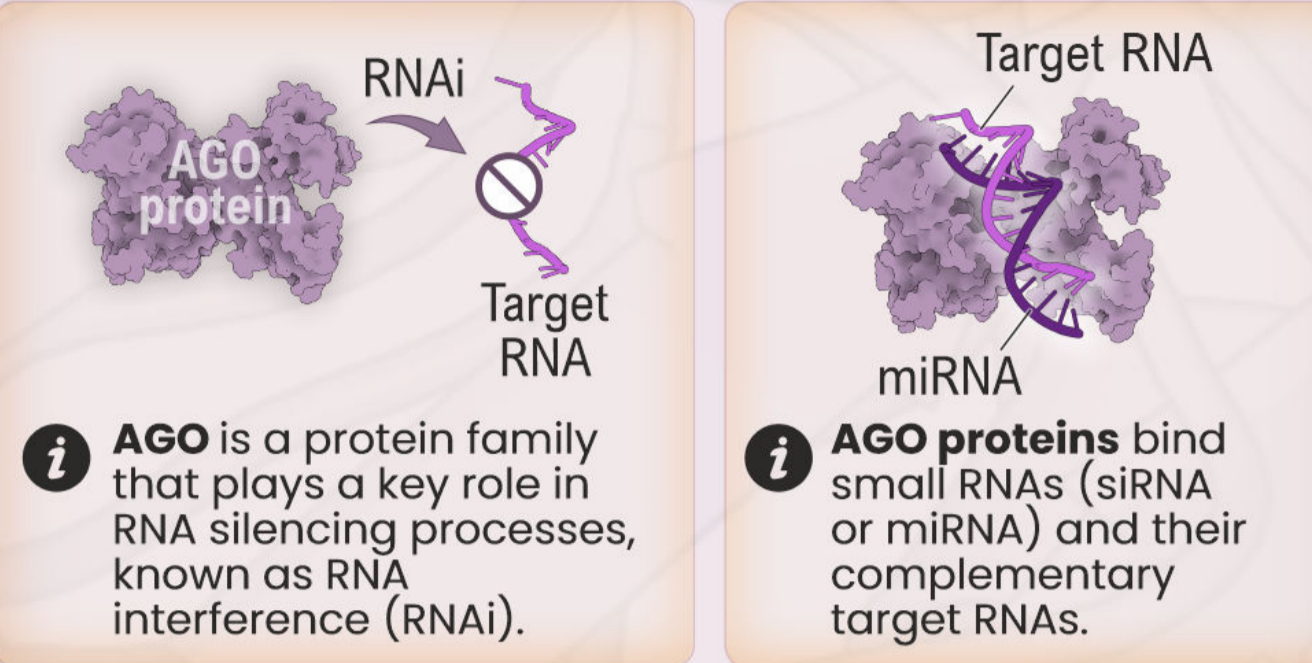
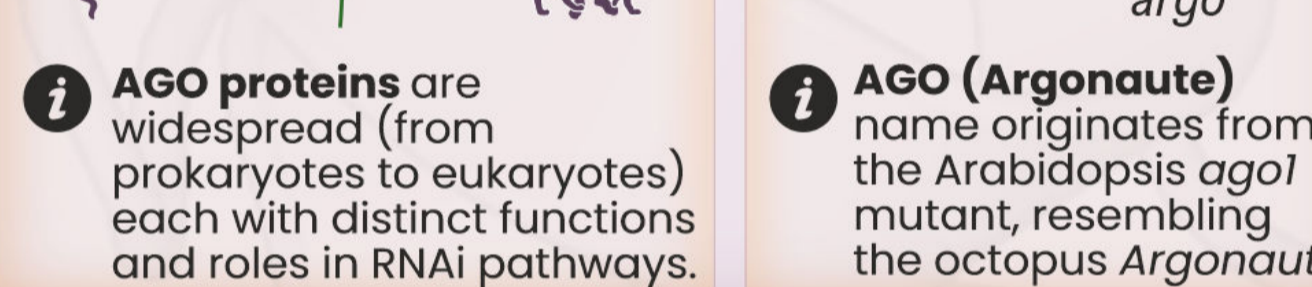
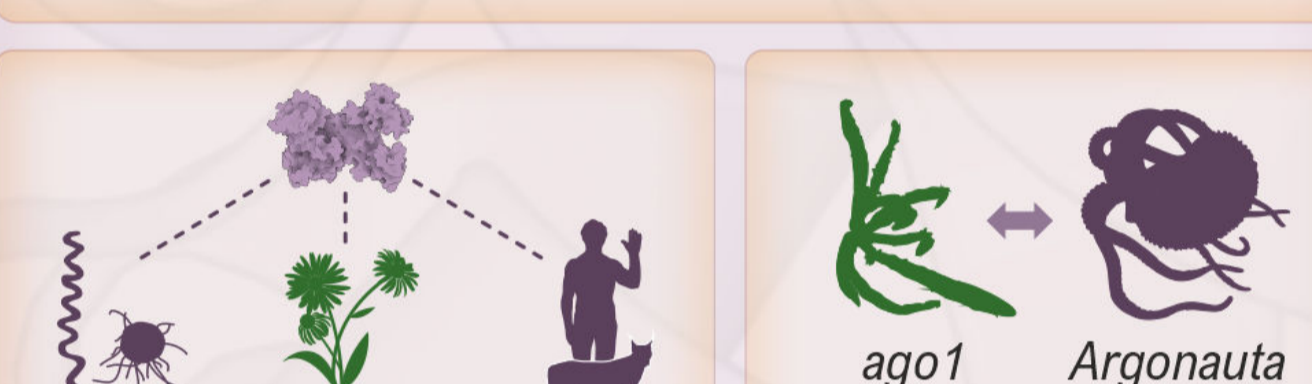


# Plant Argonautes: Protein Effectors of Small RNAs

## AGO proteins: Basic Information



For details, see Agrisera Educational Poster 6



**Plant Argonautes Poster:** Protein effectors of small RNAs. For further information, see [1-11] and references therein. Send questions and comments to Prof. Blake Meyers (BMeyers@danforthcenter.org) and/or to Dr. Dmitry Shevela (info@scigrafik.se).

**Abbreviations:** AGO, Argonaute; hc-siRNA, heterochromatic siRNA; HD-ZIP III, class III homeodomain-leucine zipper transcription factor; L1, linker domain 1; L2, linker domain 2; MID, middle domain; miRNA, microRNA; N, N domain; PAZ, PIWI-Argonaute-Zwille; phasiRNA, phased, secondary siRNA; PIWI, P-element induced wimpy testis; Pol, RNA polymerase; RdDM, RNA-directed DNA methylation; RDR, RNA-dependent RNA polymerase; RNAi, RNA interference; siRNA, small interfering RNA; SAM, shoot apical meristem; tasiRNA, trans-acting RNA; vsiRNA, virus-derived siRNA.

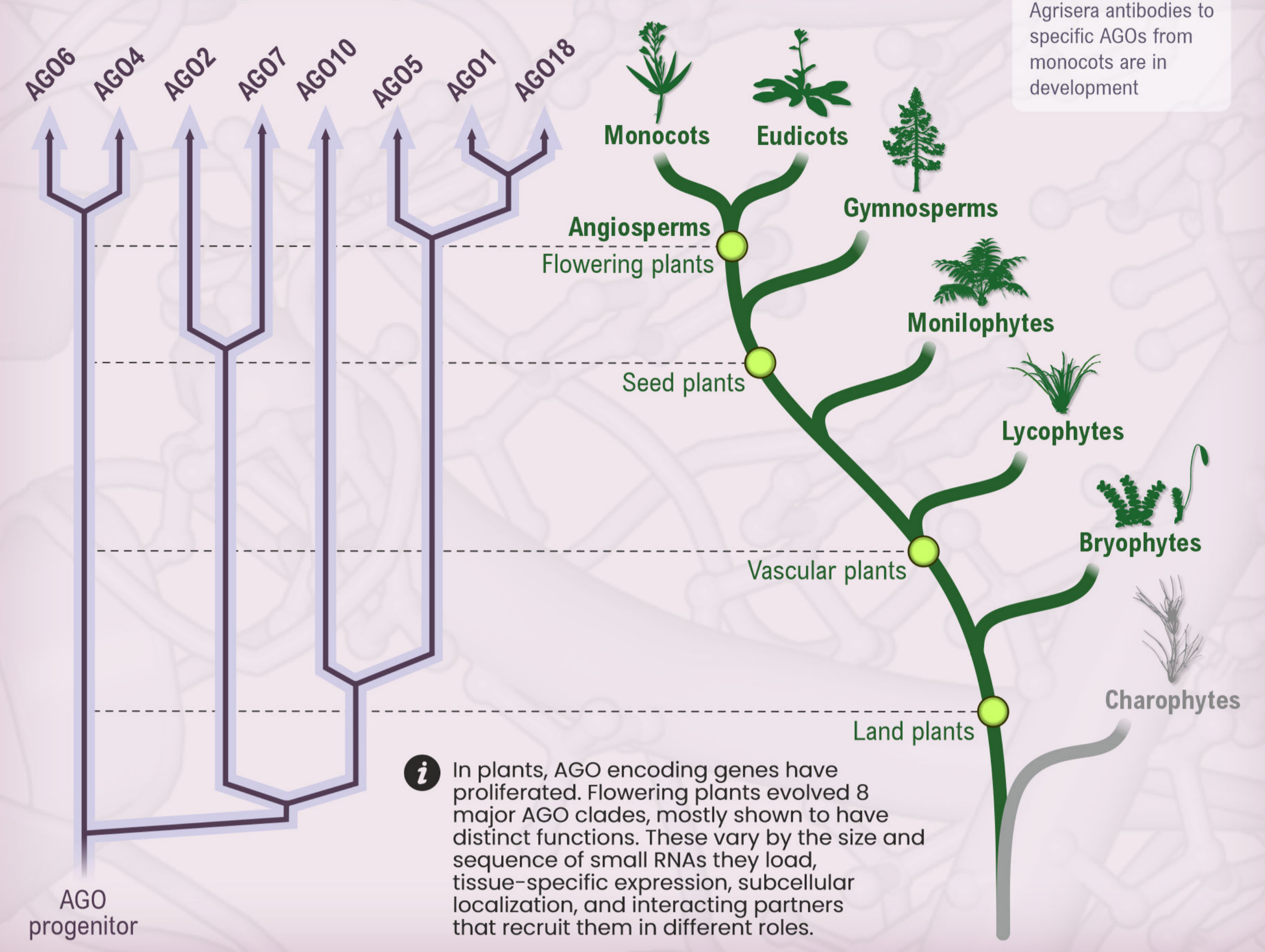
**Notes:** Complexes and cofactors were generated using Protein Imager software using coordinates of the following PDB codes: 4w5r and 7swf.

**Acknowledgements:** We thank Prof. Peter Brodersen, Dr. Joanna Porankiewicz-Asplund, and Edith Kalén for their valuable comments and corrections, and Camilla Engler for assistance in identifying Arabidopsis AGO domains. We are highly grateful to Agrisera for sponsoring the poster design, printing, and free distribution at conferences around the world.

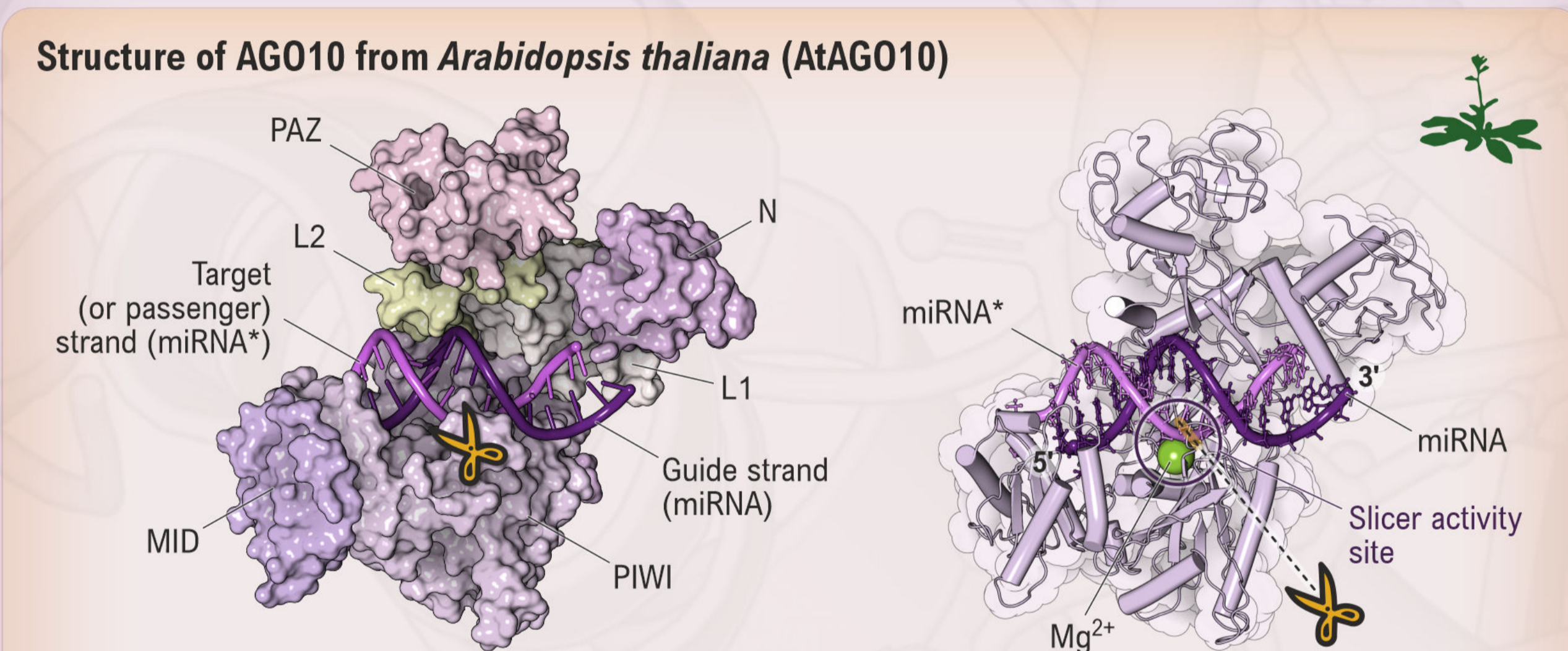
**Citation:** Meyers B, Zhan J, Shevela D, Bologna N, Mosher R (2023) Plant Argonautes: Protein Effectors of Small RNAs, *Agrisera Educational Poster 7*. doi:10.6084/m9.figshare.24006819

**References:** [1] Belanger S, Zhan J, Meyers BC (2023) Phylogenetic analyses of seven protein families refine the evolution of small RNA pathways in green plants. *Plant Physiol.* 192: 1183-1203; [2] Cai H, Liu L, Zhang M, Chai M, Huang Y et al. (2021) Spatiotemporal control of miR398 biogenesis, via chromatin remodeling and kinase signaling, ensures proper ovule development. *Plant Cell* 33: 1530-1553; [3] Cuenda-Gil D, Slotkin RK (2016) Non-canonical RNA-directed DNA methylation. *Nat. Plants* 2: 16163; [4] Duan CG, Zhang H, Tang K, Zhu X, Qian W et al. (2015) Specific but interdependent functions for Arabidopsis AGO4 and AGO6 in RNA-directed DNA methylation. *EMBO J.* 34: 581-592; [5] Fang X, Qi Y (2016) RNAi in plants: An Argonaute-centered view. *Plant Cell* 28: 272-285; [6] Li Z, Li W, Guo M, Liu S, Liu L et al. (2022) Origin, evolution and diversification of plant ARGONAUTE proteins. *The Plant J.* 109: 1066-1097; [7] Liu Y, Teng C, Xia R, Meyers BC (2020) PhasiRNAs in plants: their biogenesis, genetic sources, and roles in stress responses, development, and reproduction. *Plant Cell* 32: 3059-3080; [8] Martin-Merchan A, Moro B, Bouet A, Bologna N (2023) Domain organization, expression, subcellular localization, and biological roles of ARGONAUTES proteins in Arabidopsis thaliana. *J. Exp. Bot.* 74: 2374-2388; [9] Roussin-Léveillé C, Silva-Martins G, Moffett P (2020) ARGONAUTES represses age-dependent induction of flowering through physical and functional interaction with miR156 in Arabidopsis. *Plant Cell Physiol.* 61: 957-966; [10] Tamotsu H, Koizumi K, Briones AV, Komiyama Y (2023) Spatial distribution of three ARGONAUTES regulates the anther phasiRNA pathway. *Nat. Commun.* 14: 3333; [11] Zhou Y, Honda M, Zhu H, Zhang Z, Guo X et al. (2015) Spatiotemporal sequestration of miR165/166 by Arabidopsis Argonaute10 promotes shoot apical meristem maintenance. *Cell Rep.* 10: 1819-1827.

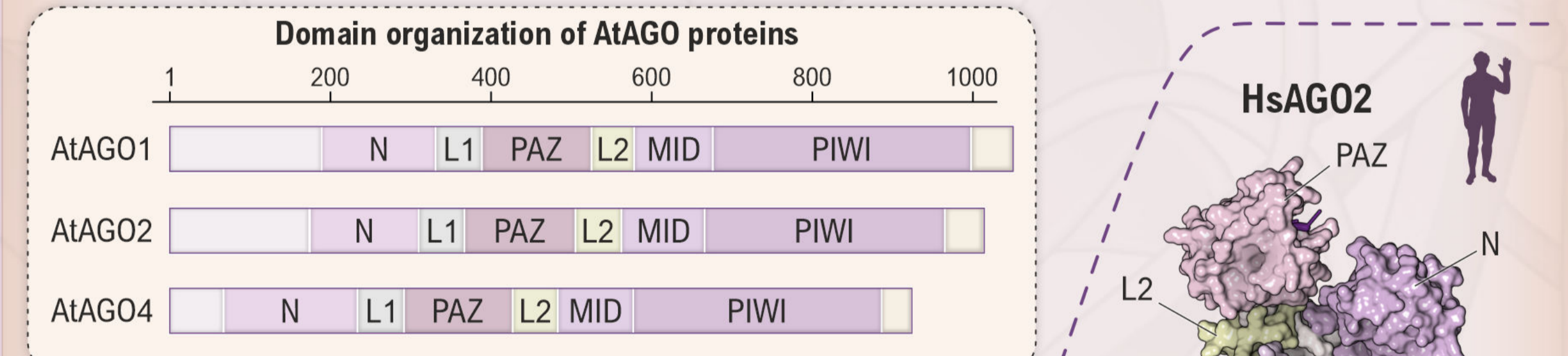
## Evolutionary History of AGO Proteins in Plants



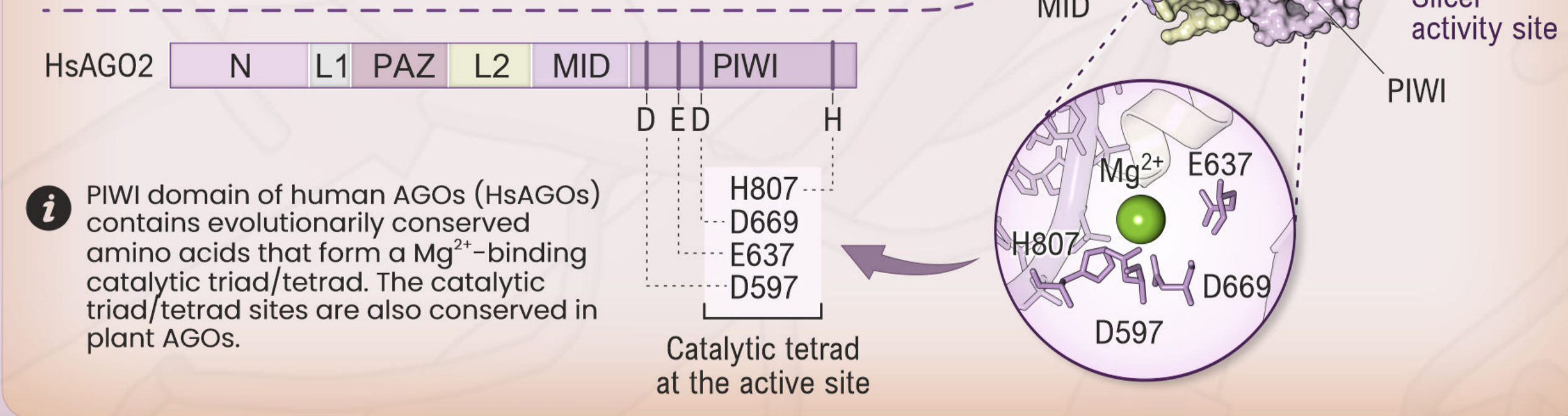
## Structure of AGO Proteins: Domains and Their Functions



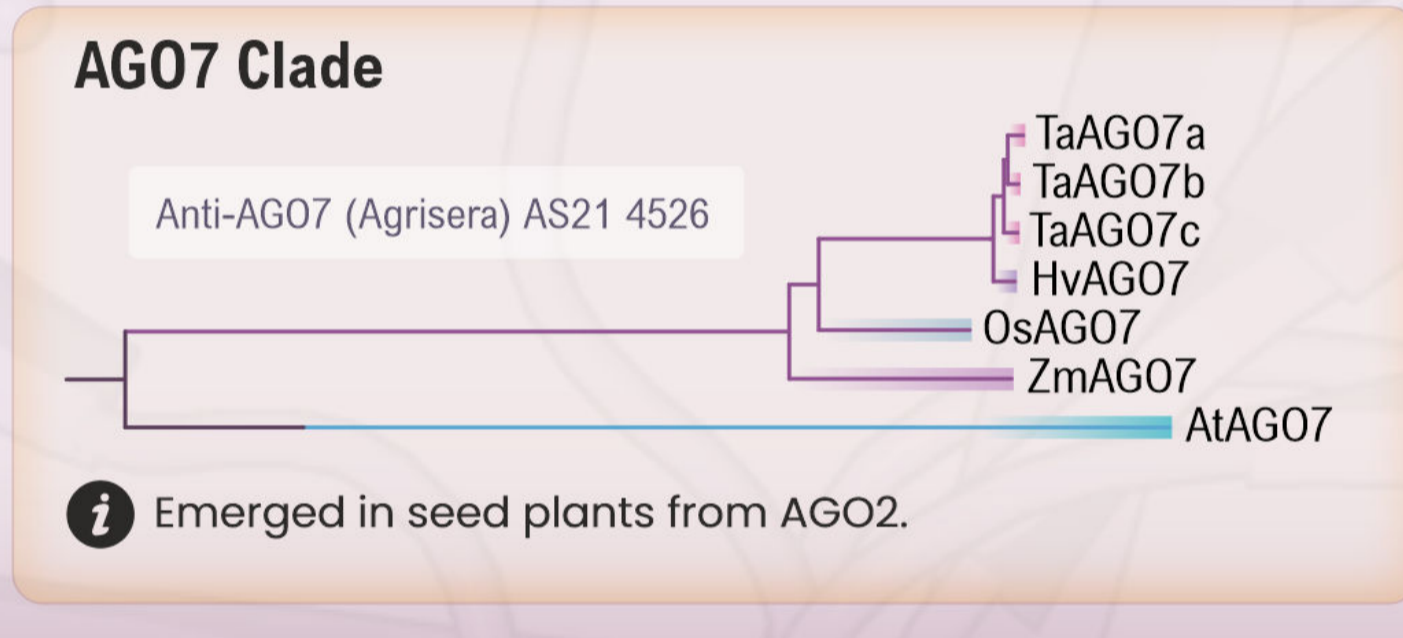
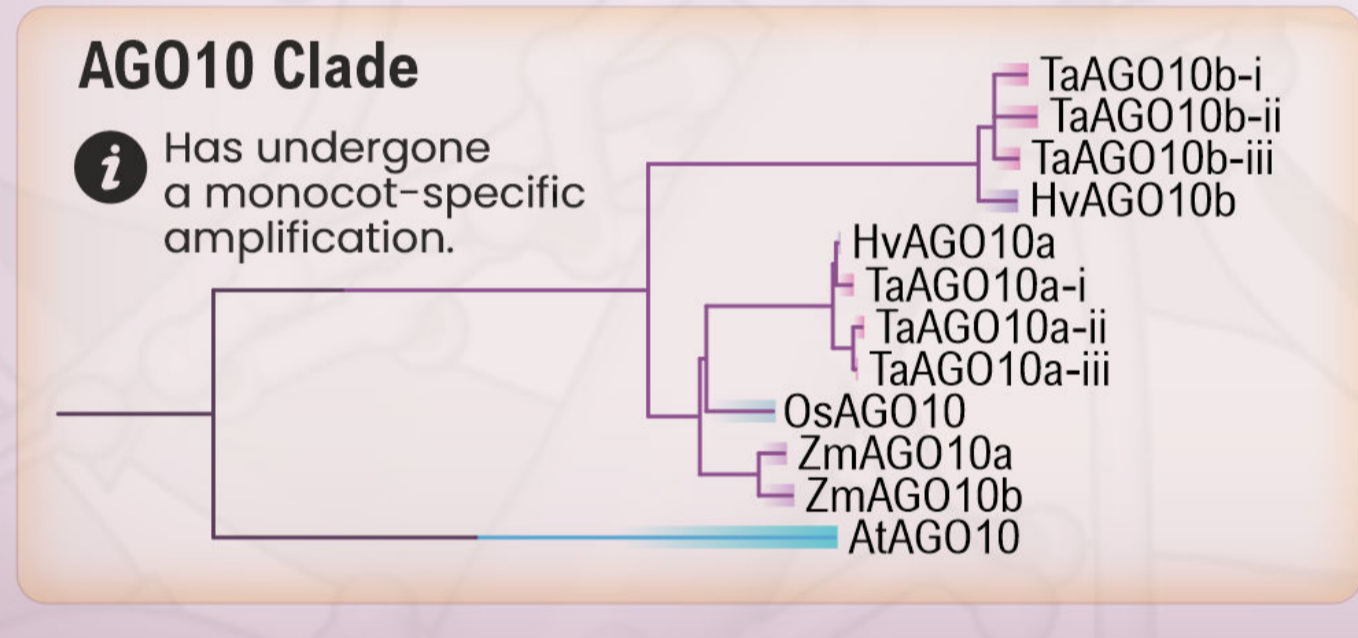
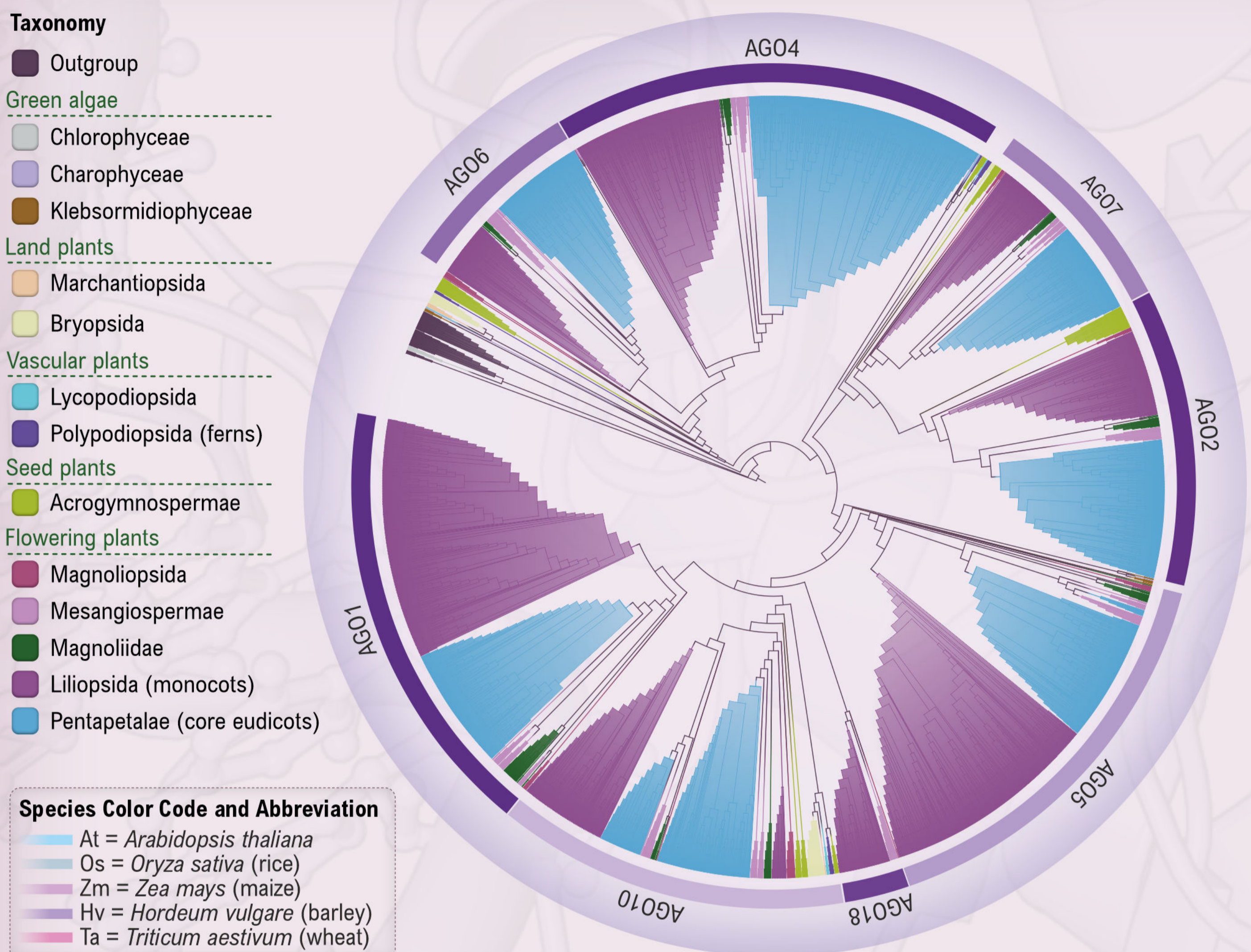
Four key functional domains common to all AGO proteins. **N-domain** (N) is needed for unwinding duplex small RNAs and for loading guide strand (miRNA). **PAZ domain** anchors the 3' end of miRNA. **MID domain** binds the 5' end of miRNA. **PIWI domain** cleaves the target (or passenger) strand by its catalytic triad/tetrad. N and PAZ domains are connected by L1, while the PAZ and MID domains are connected by L2.



In addition to the four domains (N, PAZ, MID, and PIWI), all AGO proteins display an unstructured and less conserved amino-terminal extension located before the N-domain.



## Maximum-Likelihood Phylogeny of Plant AGO Family Proteins



## AGO proteins: Biological Roles in Plants

Proteins	RNAs bound	Function
AGO1	miRNA, tasiRNA, vsiRNA, phasiRNA	Plant development, Antiviral defense, phasiRNA trigger complexes, Effector of phasiRNAs
AGO5	siRNA, miR156, vsiRNA, phasiRNA	Megagametogenesis, Antiviral defense, Regulation of flowering, Anther development, Effector of 21-nt phasiRNAs
AGO10	miR165, miR166, vsiRNA, miR398	SAM development, miR165/166 degradation, Antiviral defense, Ovule and female gametophyte development
AGO18	miR168, phasiRNA	Antiviral defense, Reproductive phasiRNA loading

