



ABSTRACT

Rice is a staple food for more than half of the world's population. In addition to the two domesticated rice species, *Oryza sativa* (Asian rice), and *Oryza glaberrima* (African rice), the genus *Oryza* contains 25 wild species. The rice wild relatives store a virtually untapped reservoir of genetic variation that can be harnessed to help solve world food security issues by 2050. The International *Oryza* Map Alignment Project (IOMAP) was established in 2003 to characterize the genetic diversity of wild rice species by comparing their genome sequences and studying their genomic variations.

The data generated is used to investigate population structures of the *Oryza* species to aid in the classification of subpopulations and pinpoint genomic regions associated with adaptation to particular ecosystems that facilitate genome engineering for crop improvement. Another approach to provide food security and sustainable rice production is to rapidly domesticate (i.e., neo-domesticate) wild plant species as a food source, especially for the staple crops eaten and depended upon worldwide.

OBJECTIVES

1. Create a comparative genomics platform for the genus *Oryza*
2. Increase the number and biodiversity of available crops
3. Develop crops that can grow on marginal lands
4. Reduce the traditional time-frame for generating new crops from decades to a few years

APPROACH

Platinum Standard Reference Genome Sequence (PSRefSeq) refers to a new standard of near-gap free reference genomes. PSRefSeqs are being generated for all 25 wild *Oryza* species using cutting edge ultra-long read sequencing technology and high-resolution optical maps

Neo-domestication: a path for future food security

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Leveraging Wild Rice to Find an Answer to the 10 Billion People Question



HALOPHYTE RICE

Oryza coarctata is the only halophyte in the *Oryza* genus and can thrive in salinity levels equal to brackish water⁴. For decades, rice breeders have tried to introgress the halophyte characteristics of *O. coarctata* into cultivated rice with no success as offspring are sterile⁵.

As the platinum reference genome is available, *O. coarctata* is an ideal candidate for neo-domestication and, if successful, would allow farmers to grow rice on land that otherwise is unable to support conventional rice farming practices.

This work is currently being carried out at Center for Desert Agriculture in collaboration with the University of Dhaka, Bangladesh.



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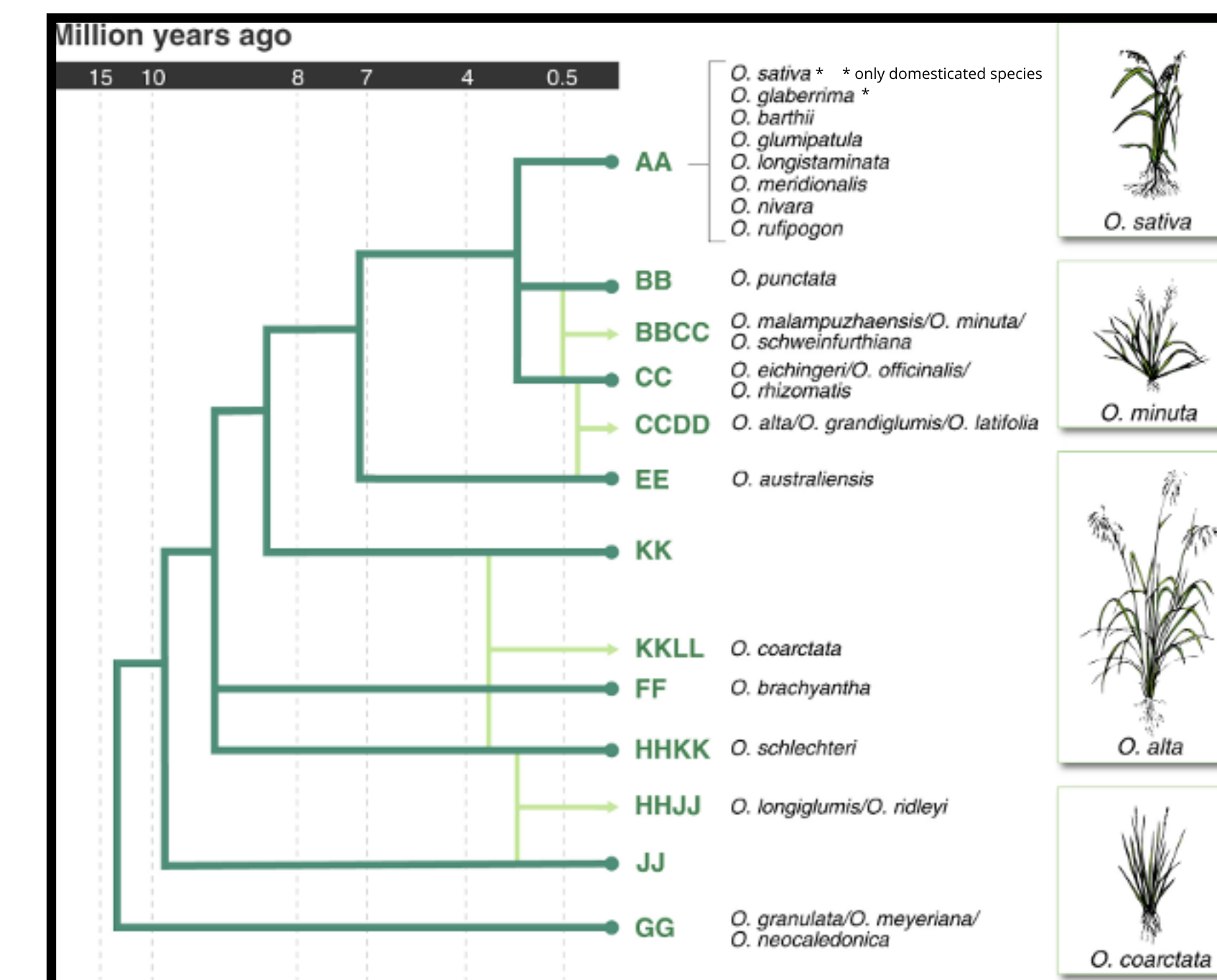


Figure 1. Phylogenetic tree of the *Oryza* genus¹. The tree portrays how the known rice species evolved from common ancestors and highlights genetic relationships between both cultivated and wild rice.

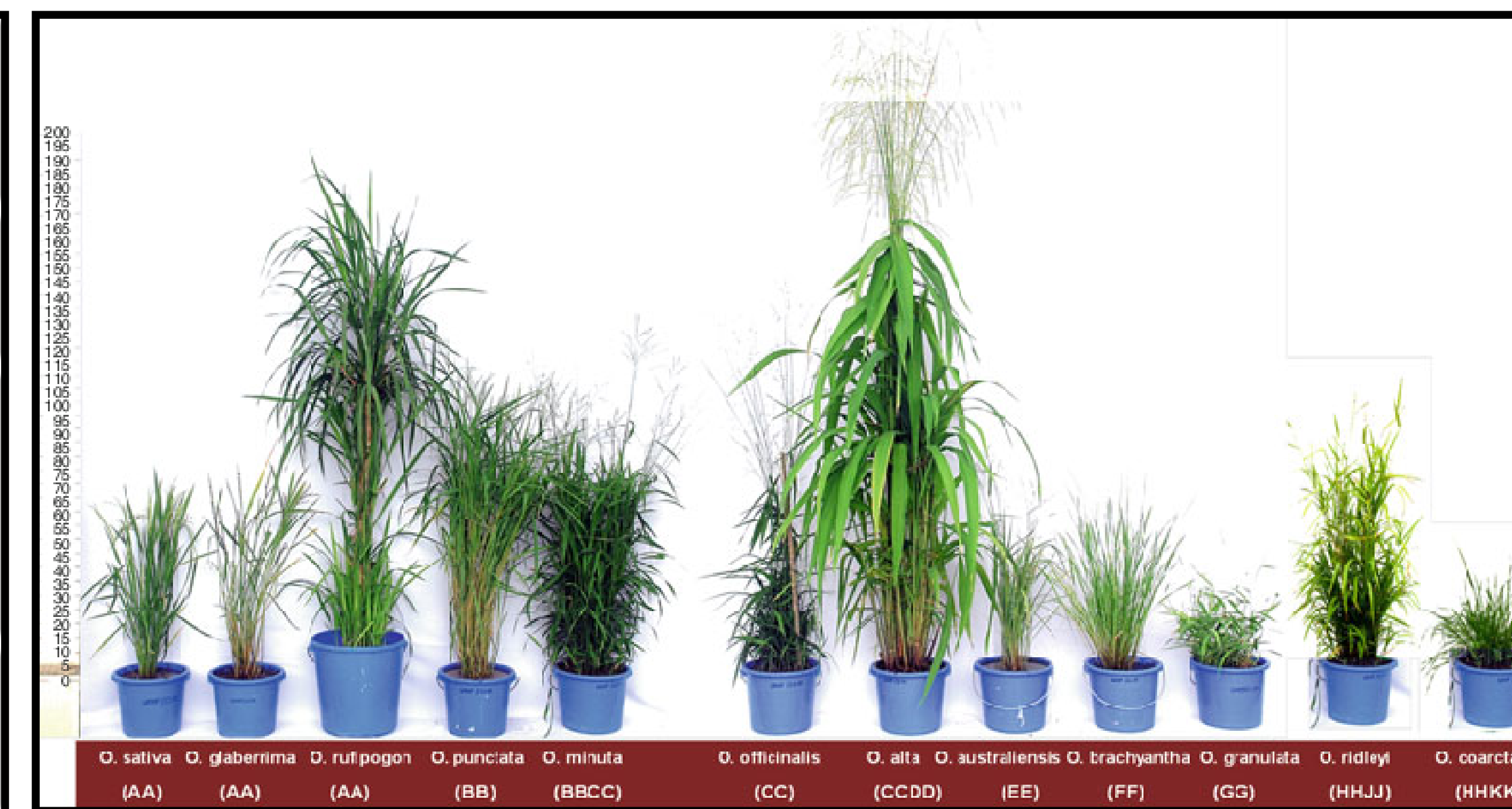


Figure 2. Phenotypic diversity of select *Oryza* species². The vast genetic diversity of the wild relatives (WRs) of rice includes beneficial traits such as resistances to diseases or the ability to grow in salty water and poor nutrient soils.

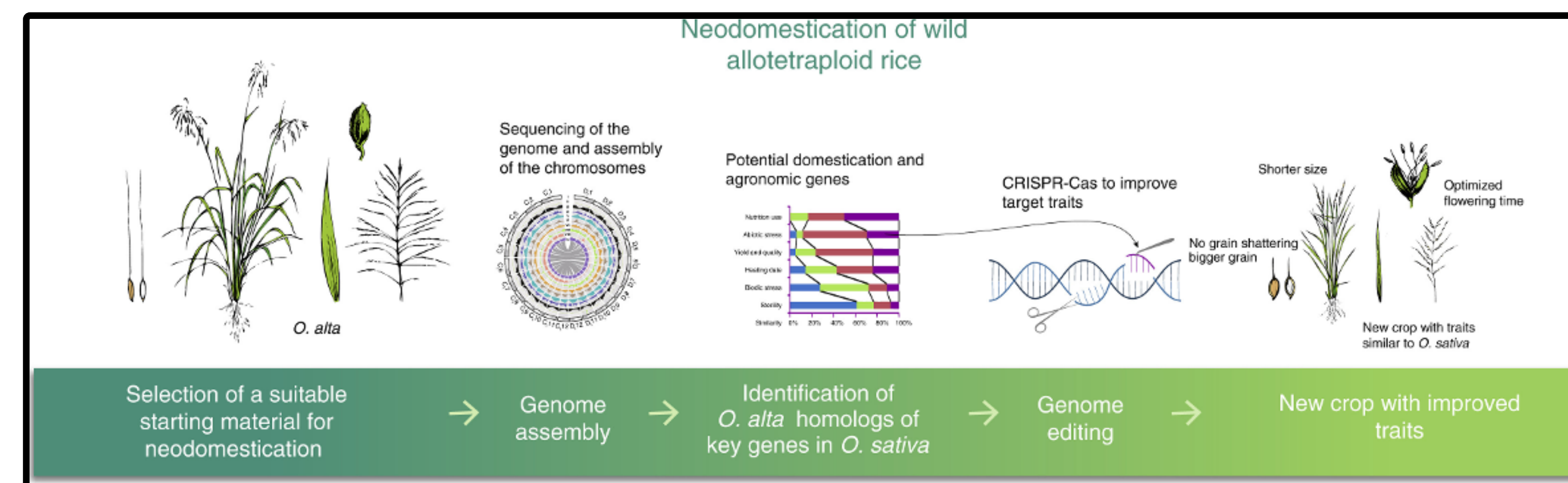


Figure 3. Roadmap of key steps for *O. alta* neo-domestication¹. Neo-domestication, or rapid domestication, of wild plants utilizes genome editing to introduce domestication traits whilst still preserving naturally acquired adaptation traits. As a proof of concept, the overall process has successfully been done in 1 out of 25 wild relatives of rice: *Oryza alta*. This successful rapid process utilizes 3rd generation sequencing to build the genome, identify domestication genes, down-regulate target genes using genome editing and validate the down-regulation of genes linked to domestication, outlined above, to create a cultivable and edible new rice species

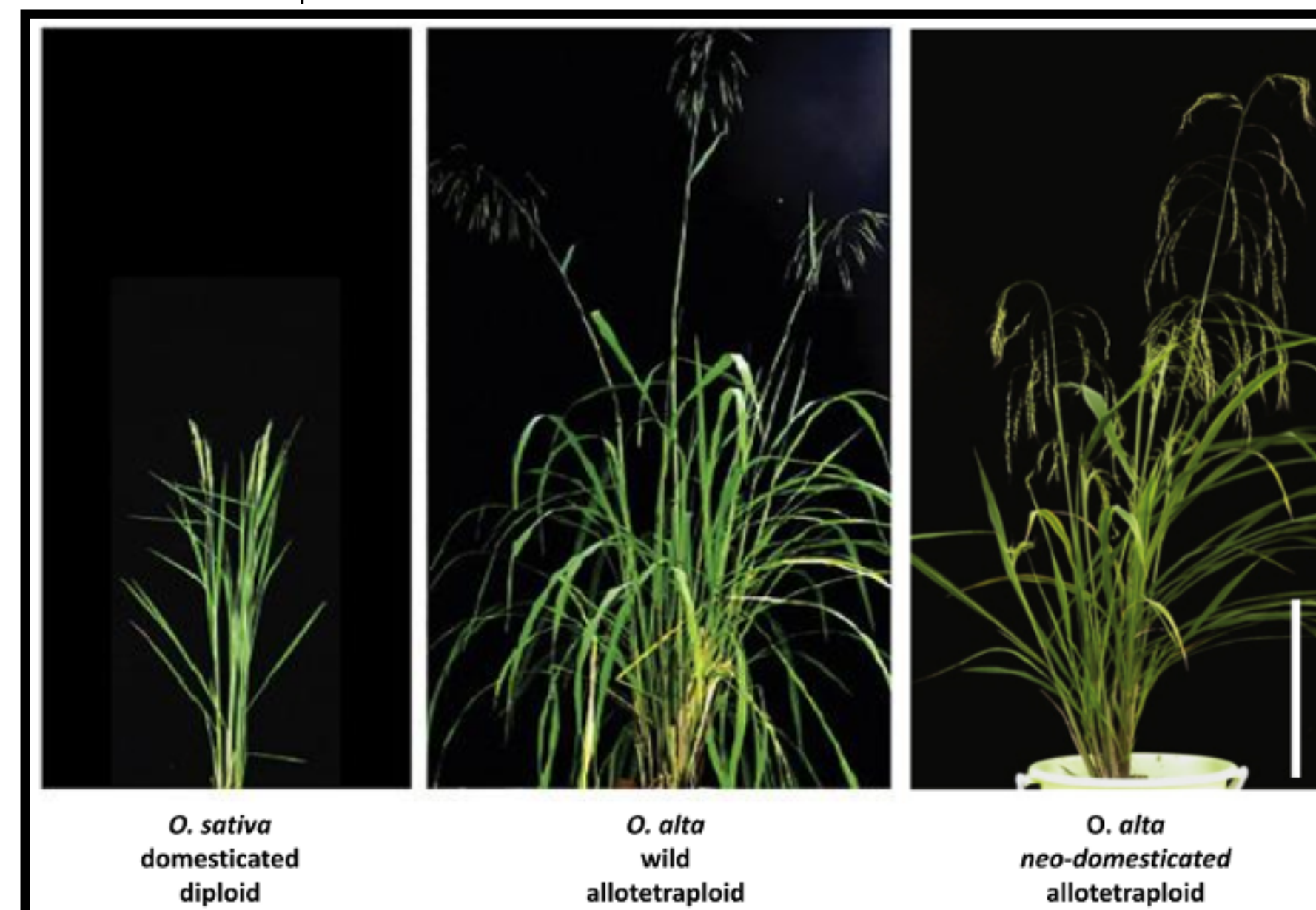


Figure 5. Phenotypes of wild and neo-domesticated *O. alta*. Targeting the 10 domestication genes produced a shorter plant with no seed shattering and bigger grain size which is similar to domesticated rice.

Genes in <i>O. sativa</i>	Domesticated Trait	Genes in <i>O. alta</i>	Origin	Identity	Coverage (<i>O. sativa</i>)	Coverage (<i>O. alta</i>)
Ar-2LBA1	Awn length	OaC04g119810	CC	99.9%	99.9%	99.9%
CSH1	Shattering	OaC01g121490	CC	99.9%	99.9%	99.9%
SH4	Shattering	OaC01g114650	DD	99.9%	99.9%	97.1%
OaL61	Particle shape	OaC04g104700	CC	99.9%	99.9%	99.9%
rice	Pericarp color	OaC07g110300	DD	99.9%	99.9%	99.9%
BH4	Hull color	OaC04g119650	DD	99.9%	97.0%	96.3%
CHWSGSE2q SW	Grain width	OaC05g109410	CC	99.9%	99.9%	99.9%
Ar-1	Awn length	OaC04g130280	DD	99.9%	97.5%	97.1%
GA4HRAE2	Awn length	OaC08g105550	CC	99.9%	97.2%	96.2%
PROG1	Tiller angle	OaC07g155220	CC	99.9%	99.9%	99.9%
CSH1	Shattering	OaC01g121490	DD	99.9%	99.9%	99.9%

Figure 4. *O. alta* homologs of 10 domestication related genes of *O. sativa*³. These genes were targeted in *O. alta* neo-domestication via gene editing

Lead Sequencing Group		Lead Sequencing Group	
<i>Oryza barthii</i>	AGI, Arizona, USA ¹	<i>Oryza rhizomatis</i>	NIG, Mishima, Japan ⁶
<i>Oryza glumipatula</i>	UFP, Pelotas, Brazil ²	<i>Oryza alta</i>	CAS, Beijing, China ³
<i>Oryza longistaminata</i>	CAS, Beijing, China ³	<i>Oryza grandiglumis</i>	CDA, KAUST, KSA ⁸
<i>Oryza meridionalis</i>	SCU, Lismore, Australia ⁴	<i>Oryza latifolia</i>	CDA, KAUST, KSA ⁸
<i>Oryza nivara</i>	AS, Taipei, Taiwan ⁵	<i>Oryza australiensis</i>	UP, Perpignan, France ⁹
<i>Oryza rufipogon</i>	NIG, Mishima, Japan ⁶ /NCGR, New Mexico, USA ⁷	<i>Oryza coarctata</i>	HZAU, Wuhan, China ¹⁰
<i>Oryza punctata</i>	CDA, KAUST, KSA ⁸	<i>Oryza brachyantha</i>	CAS, Beijing, China ³
<i>Oryza malampuzhaensis</i>	CDA, KAUST, KSA ⁸	<i>Oryza schlechteri</i>	CDA, KAUST, KSA ⁸
<i>Oryza minuta</i>	CDA, KAUST, KSA ⁸	<i>Oryza longiglumis</i>	CDA, KAUST, KSA ⁸
<i>Oryza schweinfurthiana</i>	CDA, KAUST, KSA ⁸	<i>Oryza ridleyi</i>	CDA, KAUST, KSA ⁸
<i>Oryza eichingeri</i>	NIG, Mishima, Japan ⁶	<i>Oryza granulata</i>	CAS, Beijing, China ³
<i>Oryza officinalis</i>	NIG, Mishima, Japan ⁶	<i>Oryza meyeriana</i>	CDA, KAUST, KSA ⁸

Figure 6. Target species for neo-domestication. 1. AGI, Arizona Genomics Institute 2. UFP, Universidade Federal de Pelotas 3. CAS, Chinese Academy of Sciences 4. SCU, Southern Cross University 5. AS, Academia Sinica 6. NIG, National Institute of Genetics 7. NCGR, National Center for Gene Research 8. CDA, Center of Desert and Agricultural 9. UP, Université de Perpignan 10. ICAR, Indian Council of Agricultural Research.