FERNAND LAMBEIN
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NEWS LETTER

What's new around *Lathyrus*?

People

Prof. Dr. TR Sharma is serving as National Professor–BP Pal Chair at the National Institute for Plant Biotechnology, Indian Council of Agricultural Research (ICAR), with decades of leadership in crop genomics and biotechnology.
He has made foundational contributions to genome sequencing, molecular breeding, and resistance gene discovery in crops such as rice, pigeonpea, wheat, and grasspea.

Science

Madke *et al.* tested gamma-ray–induced mutants of cultivar NLK-73 and identifies several M_4 lines with higher yield and lower β-ODAP content, demonstrating that mutation breeding can rapidly generate safer, high-yielding grasspea varieties

Sanches *et al.* performed a GWAS study on 194 grasspea accessions to uncover genetic markers linked to drought and flood tolerance. They show drought and waterlogging rely on mostly separate genetic pathways.

INTERNATIONAL LATHYRUS DAY

08.06.2026

Dubrovnik, Croatia

Join us to shape the future of grasspea science. Explore the full program to learn more about what's in store.

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TILAK RAJ SHARMA

Meet the keynote speaker of the Lathyrus Day: Prof. Dr. TR Sharma! As plant molecular biologist, Prof. Sharma has shaped national research agendas for more than a decade.

Prof. Tilak Raj Sharma is widely recognized as one of India's leading plant molecular biologists, known for combining scientific depth with visionary leadership. Currently serving as National Professor–BP Pal Chair at the National Institute for Plant Biotechnology, Indian Council of Agricultural Research (ICAR), he has played a pivotal role in shaping Indian agricultural biotechnology for more than a decade. Over his career, he has held key positions including Deputy Director General of the Indian Council of Agricultural Research (ICAR), and Director & Vice Chancellor at IARI, in addition to several other leadership roles across major national research institutes.

His scientific journey has been enriched by global exposure. TR Sharma completed three postdoctoral trainings in plant molecular biology and genome analysis at the University of Alberta, Canada, and at Cold Spring Harbor Laboratory, USA, and represented India in academic and scientific forums across 15 countries.

Prof. Sharma is among the few scientists elected as a Fellow of all four national science academies of India, underscoring the importance of his contributions to agricultural science. He is also a two-time recipient of the J.C. Bose National Fellowship, along with numerous other national and international honors.

For over 35 years, his research has advanced plant genomics and plant disease resistance, producing groundbreaking work that continues to shape crop improvement efforts in India and globally.

Building on this distinguished legacy, Prof. Sharma will deliver the keynote speech at the 2026 International Lathyrus Day, held on 8 June 2026 in Dubrovnik.

What initially sparked your interest in studying biotechnology and pursuing a career in plant science?

From an early age, I was fascinated by plant development, this curiosity guided me toward studying biology and agriculture. My PhD research focused on inducing and transferring resistance to Alternaria blight in mustard (*Brassica juncea*) using advanced crop-improvements methods such as mutation breeding, interspecific hybridization via ovary and ovule culture, and somaclonal variation.

During my first postdoctoral training at the University of Alberta, Edmonton, I continued this work by studying how plant cells grow in isolation and by using DNA-based methods to identify plant diseases. I later expanded into plant tissue culture and the molecular

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biology of plant disease resistance before joining the International Rice Genome Sequencing Project in 2000 at IARI, New Delhi. Two additional postdoctoral trainings at Cold Spring Harbor Laboratory allowed me to work extensively on large-scale efforts to decode the rice genome, where I contributed to preparing, assembling, and interpreting the DNA sequences.

Since then, I have contributed to decoding the genomes of rice, tomato, pigeonpea, jute, wheat, mango, guar, tea, grasspea, and several plant pathogens.

However, for more than three decades I worked on improving rice. One of my greater achievements was the discovery of a key gene, Pi54, that helps rice defend itself against blast disease, a major threat to rice production worldwide. I also identified related versions of this gene in other rice types, as well as natural variants found in traditional varieties, and DNA switches that activate the plant's defence system when it is attacked. Pi54 has since been incorporated into more than 40 rice varieties in India and several other countries, playing an important role in strengthening rice crops and supporting quieter but impactful progress in rice breeding.

Working with Dr. Pramod Kandoth and Dr. Anjali Verma, Prof. TR Sharma developed the first grasspea transformation protocols and decoding its large genome.

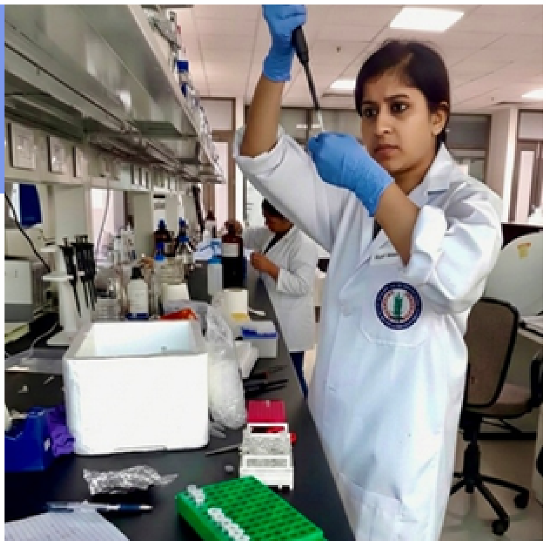
How did you approach the study of grasspea? What attracted you to dive into this crop?

When I joined the National Agri-Food Biotechnology Institute (NABI) as Executive Director, I focused on nutritionally rich but under-researched crops. Grasspea stood out due to its climate resilience, nitrogen-fixing ability, high nutritional value, and its importance as a pulse and fodder crop in marginal lands.

However, its cultivation is limited by anti-nutritional factors, particularly the neurotoxin β-ODAP. This combination of resilience and scientific gaps makes grasspea an ideal research target.

Together with Dr. Pramod Kaitheri Kandoth and our PhD student Dr. Anjali Verma, our initial goal was to use genome editing to knock down genes involved in β-ODAP biosynthesis. However, we quickly realized that the crop lacked essential resources: a reference genome, reliable transformation protocols, and detailed gene annotations.

Dr. Verma (later supported by the Lambein Fund for a postdoctoral fellowship at the Frank Van Breusegem Lab featured in issues IV and V of our newsletter, *ed. note*) subsequently developed transformation protocols and carried out extensive gene expression studies, while Dr. Kandoth undertook the challenging task of decoding the grasspea genome, which is significantly larger than those of many major crops.



Dr. Anjali Verma in the lab.

TILAK RAJ SHARMA

What major scientific advances has your team contributed to grasspea research?

Dr. Anjali Verma developed the first *Agrobacterium rhizogenes*–mediated hairy root transformation system and a CRISPR/Cas genome-editing platform for grasspea, enabling functional characterization of genes.

Her transcriptome analysis revealed that contrasting ODAP levels correlate with stress-related gene expression.

Our group at NABI also produced the first draft genome sequence of grasspea. We worked on a variety called Pusa-24 and decoded its (3.0 Gb) genome, which is very large: about 3.8 billion DNA letters. In this genome, we identified over 50,000 genes that make proteins and confirmed that almost all the genes (98.3%) normally found in green plants (*Viridiplantae*) are present and well conserved in grasspea. Importantly, we also found several genes that are involved in making β-ODAP, the compound responsible for grasspea's neurotoxin, and genes that help the plant respond to stress.

Why is improving grasspea socially important today?

Grasspea improvement holds strong societal relevance because historical outbreaks of lathyrism led to cultivation bans in parts of India, creating both stigma and lost opportunities for farmers who rely on hardy pulse crops. Understanding the molecular basis of β-ODAP toxin production and developing low-ODAP varieties without compromising yield or nutritional quality is therefore essential. Our broader goal is to reposition grasspea as a climate-resilient, protein-rich food and fodder crop, particularly valuable for marginal environments. By integrating genomics, wild relatives, and genome-editing tools, we aim to unlock the full potential of this underutilized species for food, feed, and livelihood security.

Dr. Pramod Kaitheri Kandoth.

What breeding and genetic improvement strategies are you using to modernize and improve grasspea?

Our breeding strategy is now guided by the foundational genomic resources our team has generated. The draft genome enables the identification of SSR and SNP markers linked to agronomically important traits, which in turn supports the development of biparental mapping populations and the establishment of core and mini-core sets. ICARDA's extensive collection of more than 4,000 accessions offers rich opportunities for multi-location phenotyping and trait discovery across diverse environments. With transformation protocols in place, genome editing can now be directed toward targeted improvements: reducing ODAP levels, refining plant architecture for mechanized harvesting, and enabling the overall modernization of grasspea.

How is technology accelerating progress in this crop?

Technology plays a central role in transforming grasspea from an orphan crop into a genome-enabled species.

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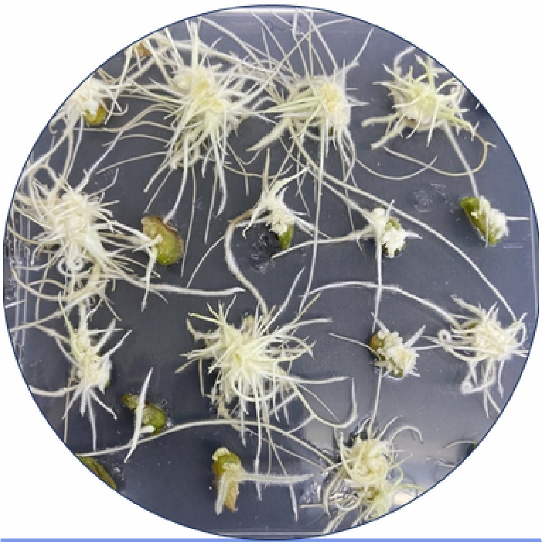
Modern genomics-assisted breeding and CRISPR-based genome-editing platforms allow the development of improved varieties in significantly shorter timeframes. At ICAR, we integrate these tools with traditional breeding approaches and the use of wild relatives to create low-ODAP cultivars that enhance both food and feed safety. Together, these technologies make it possible to pursue "designer *Lathyrus*" varieties tailored for resilience, nutritional quality, and farmer-friendly traits.

Are there emerging threats or opportunities you are monitoring in grasspea research?

After more than eight years working on this crop, we have learned that grasspea continues to pose technical challenges for molecular biology research, particularly due to limited public datasets and constraints in available methodologies. Consumer acceptance also remains a concern, largely shaped by the historical association with lathyrism and past cultivation bans.

Despite these challenges, the opportunities are substantial. There is strong potential to develop dwarf, early-maturing, low-ODAP, and mechanization-friendly varieties that can enhance both productivity and safety.



Agrobacterium rhizogenes mediated hairy root transformation in grasspea. Developed by Dr. Anjali Verma.

Grasspea's naturally high protein content also positions it as a promising biofortified fodder crop for livestock systems. In addition, the crop's remarkable stress-tolerance genes represent valuable resources that could be harnessed to improve resilience in other species. Together, these avenues make grasspea an important and forward-looking target for innovation.

LATEST PUBLICATIONS

Genetic Improvement of grasspea (*Lathyrus sativus* L.) through gamma-ray-induced mutagenesis: evaluation of M4 progenies for yield, agronomic traits, and low ODAP content.

Madke V.S., Manwar R.M., Nandeshwar B.C., Ali U.M.

Sci Rep (2026).
doi: 10.1038/s41598-026-41769-9

This study evaluates how gamma-ray mutagenesis can be used to create improved grasspea lines with higher yield and lower β-ODAP content. Seeds of cultivar NLK-73 were exposed to different doses of gamma rays, and 29 mutant lines were advanced to the M_4 generation and tested in field trials. The authors found significant genetic variability for all agronomic and biochemical traits, including flowering time, plant height, pods per plant, seed yield, and ODAP levels.

Several mutants—particularly NLM-12, NLM-20, and NLM-23—outperformed the original variety with higher seed yield (23–24.5 g/plant) and substantially reduced ODAP content, making them strong candidates for breeding programs. Overall, the study demonstrates that mutation breeding effectively broadens genetic diversity in grasspea and can accelerate the development of safer, high-yielding cultivars.

Integrating natural variation through GWAS - genetics of drought and flood tolerance in grass pea reveal independent yet interconnected mechanisms.

Sanches M., Vuylsteke M., Santos C., Mhamdi A., Araújo S., Van Breusegem F., Patto M.C.V.

BMC Plant Biol. 2026 Feb 5;26(1):442.
doi: 10.1186/s12870-026-08229-y

This study investigates how *Lathyrus sativus* (grasspea) tolerates both drought and flooding by combining extensive phenotyping with a genome-wide association study (GWAS). The authors analyzed 194 diverse accessions under well-watered, mild drought, and partial-submergence conditions and linked their physiological and stress-response traits to 5,651 SNP markers.

The study identifies 130 SNPs associated with different stress-response traits and shows that drought and flooding tolerances rely on largely distinct genetic pathways, although some overlapping mechanisms, such as redox regulation and carbohydrate metabolism, also appear. These findings provide valuable markers and candidate genes for breeding grasspea varieties with improved and combined water-stress resilience.

LATEST PUBLICATIONS

The LsBAHD3-LsAAE3 Module Catalyses Biosynthesis of β-N-Oxalyl-L-α,β-Diaminopropionic Acid in *Lathyrus sativus* and *Pisum sativum.*

Zhang Y., Song Y., Shang T., Tang Y., Chen H., Ma H., Zhang X., Miao Z., Lan B., Wang L., Cao N., Liu X., An Z., Lian R., Yang T., Chen P., Jiao C., Xu Q.
Plant Cell Environ. 2025 Sep 3.
doi: 10.1111/pce.70167

Agrobacterium *rhizogenes*-Mediated Hairy Root Transformation for Genome Editing in Recalcitrant Legume *Lathyrus sativus.*

Verma A., Kaur L., Kandoth P.K.
Curr Protoc. 2025 Nov; 5(11):e70256.
doi: 10.1002/cpz1.70256

Drivers of Grasspea (*Lathyrus sativus* L.) Market Supply and Its Sustainability Payoffs: Evidence From Jama District, Ethiopia.

Yigezu Y., Sidell Z., and Astatkie T.
Legume Science7. 2025 Nov; no. 4: e70065
doi: 10.1002/leg3.70065

The Business Case For Grasspea In Ethiopia: An Action Plan To Provide Ethiopian Farmers With A Safe, Nutritious And Climate-Smart Protein Source.

Heaton M., Chole H.
Norwich Institute for Sustainable Development. 2025 Sept.
doi: 10.6084/m9.figshare.30094414

Microwave-Induced Structural Remodeling of Legume Proteins: Structure-Function-Nutrition Relationships and Their Improved Performance in Wheat Flour Fortification.

Patil N. D., Kumar P., Bains A., Sharma A., Sridhar K., Chawla P., Inbaraj B. S.
Foods 2026, 15(3), 580.
doi: 10.3390/foods15030580

LATEST PUBLICATIONS

Ultrasound Modification of Grasspea Starch: Amplitude-time Effects on Gel Strength and Structural Properties

Heydarian M., Koocheki A., Shahidi F., Mozafarpour R.
Int J Biol Macromol 2025 Dec;333(Pt 1):148857.
doi: 10.1016/j.ijbiomac.2025.148857

People

Science

Good to know

INTERNATIONAL LATHYRUS DAY

Organized as a satellite event to the 5th International Legume Society Conference, this edition expands the focus beyond molecular and physiological research to the practical applications of grasspea.
Once again, scientists from around the world will contribute with their perspectives, ensuring a dynamic and diverse exchange of ideas.

08.06.2026

Dubrovnik, Croatia

Program

Time	
09:00	Welcome and kick off
09:30	Opening Keynote **Prof. Dr. Tilak Raj Sharma**

Session 1 – In the Lab: molecular, genetic and physiological Research on grass pea
Chair: **Carlota Vaz Patto**

10:30 – 12:30

CRISPR/Cas-based manipulation of transcriptional reprogramming and stomatal immunity against pathogen invasion of African yam bean (*Sphenostylis stenocarpa*) and grasspea (*Lathyrus sativus*).
Okung Unung, *NABDA*

Aphanomyces euteiches causes disease in *Lathyrus sativus* with a globally diverse, polygenic resistance landscape.
Sara Rodríguez Mena, *CSIC*

High-throughput phenotyping reveals genotypic variation in drought response and water-use strategies in *Lathyrus* spp. under progressive soil drying.
Kamal Hejjaoui, *CAES*

From "Poor Man's Meat" to safe climate-smart protein: pioneering genome editing of grasspea (*Lathyrus Sativus*) for improved yield in a changing climate.
Keya Akter, *VIB*

Time	
12:30	Lunch break
13:30	QUIZ

Session 2 – Bridging the gap: grasspea from the lab to the field
Chair: **Diego Rubiales**

14:00 – 15:20

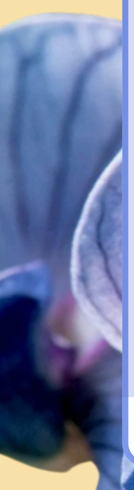
Farmers video
Shivali Sharma, Petra Pajdakovic, *Crop Trust*

Bridging the gaps in Ethiopia: grasspea in the field.
Dagnachew Bekele, *EIAR*

Patterns and determinants of grasspea (*Lathyrus sativus*) consumption among rural households in major cultivating districts of Ethiopia: a cross-sectional study.
Azeb Atnafu

Plenary session
Maria Carlota Vaz Patto, **Shivali Sharma**

Time	
15:20	Wrap up and Welcome Reception



WHAT'S GOING ON AROUND *LATHYRUS*?

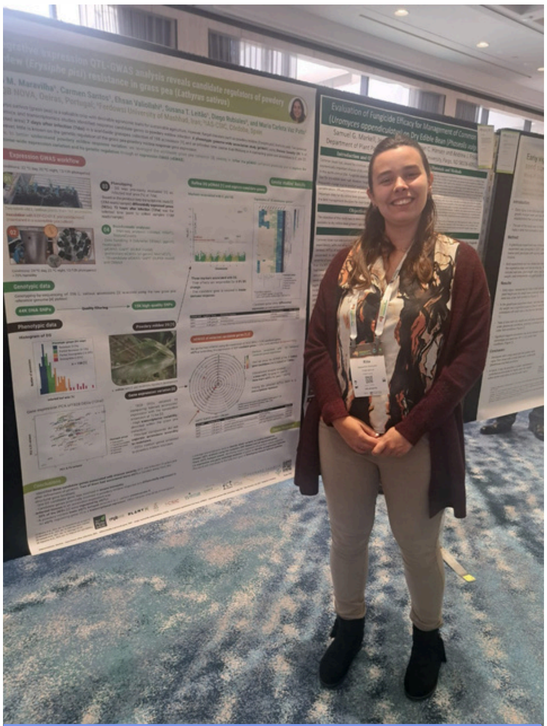
FROM OUR AWARDEES:

Hello dear reader,

My name is Rita Maravilha Marques, and I am a final-year PhD student from Portugal working on grasspea resistance to powdery mildew. Thanks to the generous support of the Fernand Lambein Fund, I had the opportunity to attend the 8th International Food Legume Research Conference and the 5th Australian Pulse Conference in Perth, Western Australia. This unforgettable experience broadened my scientific perspective and strengthened my passion for grasspea research.

Although the program covered many grain legumes, I was happy to see grasspea featured in several sessions. Priyanka Gupta, also supported by the Fund, highlighted the crop's resilience and shared UPGRADE project results identifying ten stress-tolerant, low-ODAP lines. In breeding and phenotyping talks, Moez Amri showcased high-throughput tools using grasspea as a successful test case in his PHENO-MA platform. Sanjeev Gupta emphasized its climate-smart potential and valuable health-related compounds, while noting that β-ODAP levels below 0.2% are considered safe. Grasspea-related biotic stress was also covered in Youness En-Nahli's presentation on Orobanche crenata, offering useful insights for managing parasitic weeds in legume systems.

Even though grasspea appeared throughout the conference, its coverage was still modest compared to major pulses. That is why the closing keynote by Mark Sweetingham was especially meaningful to me. He honoured lupin breeder John Gladstone and drew clear parallels between lupin and grasspea, both "orphan crops" with huge but underused potential. Lupin's remarkable domestication journey was presented as an inspiring model for what grasspea could also achieve with sustained effort and international collaboration. Seeing grasspea recognized in this way was both exciting and motivating.



Rita next to her poster at the conference.

On a personal note, I was honoured to receive the Best Poster Award, something that would not have been possible without the Fernand Lambein Fund. The conference enriched my knowledge, connected me with researchers, breeders, and farmers from around the world, and opened doors for future collaborations. I left the event with new friendships, inspiring conversations, and a renewed motivation to continue working for the advancement of grasspea research. For all of this, I am truly grateful.

Rita Maravilha Marques,

ITQB NOVA, Oeiras, Portugal

Do you have ideas to improve our newsletter or you want to suggest some contents to be covered in the future?

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Pictures: Jean-Pierre Dubois, Suraijt Koley

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