



Photo: Ignatius Angarawai, ICRISAT

Farmers in the field with Improved Deko (12KNICSV-188).

## New sorghum variety with 3 times higher iron content released in Nigeria

The release of two new nutritionally high sorghum varieties, one with three times higher iron content, will be a boost for farmers as well as the malnourished populations, especially children in Nigeria. Both varieties have yields that are double that of the local varieties and are also short duration, allowing farmers to adapt better to climate change.

One of the new varieties has iron content three times higher at 128.99 ppm compared to 40 ppm. The improved varieties yield 2.4-2.8 tons per ha, compared to yields of less than one ton per ha from local varieties. Initial screenings were encouraging as they showed that the new varieties were resistant to *Striga* compared to other varieties in the trial.

“Sorghum has been recommended for infants, the elderly, pregnant and lactating mothers because of its high caloric and nutritional value. There are cases of ‘hidden hunger’ (deficit of iron and zinc) among low income farmers who sell most of their produce. Sorghum is naturally high in iron and zinc,” said Dr Ignatius Angarawai, Scientist-Sorghum Breeding, ICRISAT-Nigeria.

He also stated that, “The newly released varieties can help overcome periods of drought especially terminal drought problems prevalent in the Sahel and Sudan savannah agroecologies of Nigeria because they are early maturing, with 50% flowering in 67 days against the average 90 days for other varieties.”

The improved open pollinated varieties were developed by a team of scientists in the Nigerian national agricultural research system and ICRISAT. The new varieties involved crossing local Nigerian germplasm with improved lines from ICRISAT’s collection in Mali. The new varieties retain desirable traits such as bold and white grains preferred by farmers and traders.

The two varieties, 12KNICSV-188 and 12KNICSV-22 were approved for registration and release as SAMSORG 45 and SAMSORG 46, respectively, by the National Committee on Naming, Registration and Release of Crop Varieties, Livestock Breeds and Fisheries, during their 23rd seating at the National Centre for Genetic Resources and Biotechnology (NCGRAB), Nigeria, on 4 February.

## New sorghum varieties... from page 1

ICRISAT-Nigeria team acknowledges the efforts and contributions of former ICRISAT scientists Eva Weltzien Rattunde and Henry Frederick Weltzien Rattunde towards the development of these two improved sorghum varieties. ■

For more on Sorghum see: <http://exploreit.icrisat.org/page/sorghum/882>  
For more on Nigeria see: <http://exploreit.icrisat.org/page/nigeria/703>

**Projects:** Agricultural Transformation Agenda Support Program (ATASP-1) and Identification of Micronutrient-Dense Sorghums for Better Health in West and Central Africa (WCA) and India

**Partners:** Institute for Agricultural Research (IAR), Nigeria, State Agricultural Development Programs (ADPs), Federal Ministry of Agriculture and Rural Development (FMARD) and ICRISAT

**Investor:** African Development Bank and HarvestPlus

**CGIAR Research Programs:** Dryland Cereals and Dryland Systems

“

Among the five varieties demonstrated, Improved Deko (12KNICSV-188) and Improved Zabuwa (12KNICSV-22) are the best. We are very happy with Improved Deko because of the uniformity, extra earliness and panicle size. The variety will ensure that we have food even in years with low rainfall like this year (2015) and we will harvest before the Fulani cattle rearers can do damage to the late crops. ICRISAT, the Institute for Agricultural Research (IAR) and the Government as a matter of urgency should ensure seed availability for farmers. We are ready to buy.

”

– Mr Mohammed Madaki

Ward Head of Baure, Yamaltu Deba  
Local Government Area, Gombe State.

## Youth invited to become agricultural entrepreneurs – the Youth Agripreneurs Project (YAP)

Inviting young agricultural entrepreneurs from across the globe to apply for the Youth Agripreneurs Project (YAP), a pilot project that will provide seed funding to facilitate young ‘agripreneurs’ to start up their project.

Ten selected agripreneurs, in addition to getting a US\$5000 grant, will attend the GCARD3 global event in Johannesburg (South Africa), integrate into panel discussions; and attend various mentoring and training that will help make their project a success. They will be integrated into the YPARD mentoring program as well.

The applicants should be below 40 years of age and submit a proposal that is agri-related, is practical, realistic, is hands-on, sustainable and has a direct impact

on the rural community. Projects run by a group, an organization, institute or a small company (with an annual turnover of less than US\$50,000) are also accepted. The proposal has to be submitted by the person who would be the project coordinator, and will be the mentee in the YAP project.

This is being organized by GFAR (Global Forum on Agricultural Research), the YPARD (Young Professionals for Agricultural Development) and CGIAR.

Online submission is open until 15 March 2016 (midnight CET). Each person can submit two proposals. For more details visit <http://blog.gfar.net/2016/02/17/calling-on-all-young-agripreneurs-submit-your-project/> ■

## New video on IYP vlog



### A stable price for a staple crop

Watch Dr David Bergvinson talk about the need to stabilize production and prices so that pulse production remains sufficient to meet the growing demands of society.

ICRISAT participated at the 2016 Pulses Conclave in the Indian city of Jaipur, Rajasthan, delegates from around the world gathered to discuss the best way to stabilize and increase the value of pulses to benefit the farmer as well as the consumer. Experts spoke on global markets, health and nutrition and the price of pulses.

<http://www.icrisat.org/a-stable-price-for-a-staple-crop/>



# Genome code of cultivated groundnut cracked

In a scientific breakthrough that promises accelerated gene discovery and development of improved cultivars, researchers have completed high quality sequencing of the ancestral genomes of groundnut. This will lead to better groundnut varieties with enhanced pod and oil yield, greater resistance to diseases, tolerance to drought and heat, and better oil quality.

The groundnut grown today is the result of hybridization between two wild species, *Arachis duranensis* (V14167, A-genome ancestor) and *A. ipaensis* (K30076, B-genome ancestor). The hybrid was cultivated by ancient inhabitants of South America. Since the ancestors were two different species, today's groundnut is a tetraploid, ie, it carries two separate genomes which are designated A and B sub-genomes.

Comparison of the DNA sequences of one of the wild species with the cultivated groundnut showed that they are 99.96% identical.

"It's almost as if we had travelled back in time and sampled the same plant that gave rise to cultivated peanuts from the gardens of these ancient people," said David Bertoli, International Peanut Genome Initiative (IPGI) plant geneticist of the Universidade de Brasília, who is the lead author of the paper and Visiting Professor, University of Georgia, USA.

The breakthrough was made by researchers of IPGI, led by the University of Georgia and published online in [Nature Genetics](#) on 22 February.

ICRISAT is a member of the IPGI and was involved in project planning, defining the strategy and also contributed to data analysis for the discovery. The IPGI, is a multi-national group of crop geneticists with 39 scientists from 26 organizations in six countries engaged in the groundnut genome sequencing project.

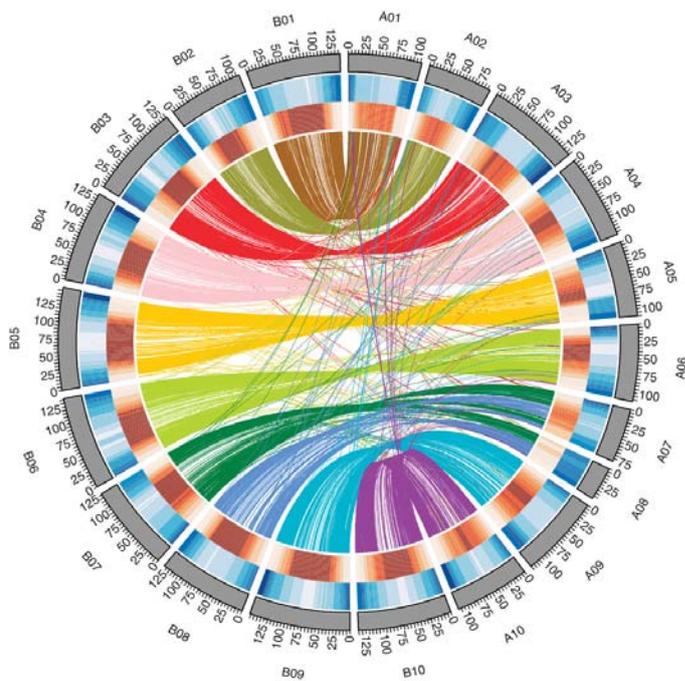
To map the groundnut's genome structure, researchers sequenced the two ancestral parents, because together they represent the cultivated groundnut. The sequences provide researchers access to 96% of all groundnut genes in their genomic context. The genome sequence

assemblies and additional information are available at [http://peanutbase.org/browse\\_search](http://peanutbase.org/browse_search).

The new groundnut genome sequence will be available to researchers and plant breeders across the globe to aid in the breeding of groundnut varieties with desired traits. It is also useful for crop improvement to enable sustainable and resilient groundnut



*The wild groundnut species, Arachis ipaensis (left) and Arachis duranensis (right) that provide the genetic blueprint for today's modern varieties.*



*Groundnut genome sequence*

Source: Paper published in *Nature Genetics*

production that will improve the livelihoods of smallholder farmers. The genome map can also be used to harness genetic diversity by broadening the genetic base of cultivated groundnut gene pool.

"Rich in protein and edible oil, groundnut is central to the financial and nutritional well-being of millions of farmers and consumers across the semi-arid tropics of Asia and sub-Saharan Africa," said Dr David Bergvinson, Director General, ICRISAT.

Groundnut (*Arachis hypogaea*) is an important crop both commercially as well as nutritionally. Globally, farmers cultivate about 25.7 million ha of groundnut each year, producing about 42 million tons. While the oil and protein rich legume is seen as a cash crop in the developed world, it remains an important subsistence crop in developing nations.

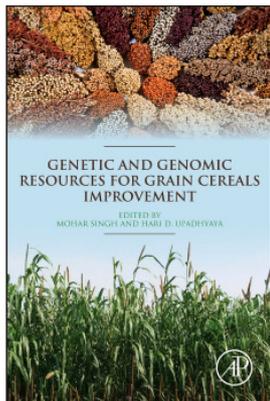
"Improving groundnut varieties to be more drought, insect and disease resistant using the genome sequence, can help farmers in developing nations produce more groundnuts with fewer pesticides and other chemicals and help these farmers feed their families and build more secure livelihoods," said Dr Rajeev Varshney, Research Program Director – Grain Legumes and Director, Center of Excellence in Genomics, ICRISAT.

ICRISAT led a global research partnership for decoding the genome sequence of pigeonpea in 2011, chickpea in 2013 and is currently leading the genome sequencing of pearl millet. ■

For more on groundnut see [ExploireIT – groundnut: http://exploreit.icrisat.org/page/groundnut/686](http://exploreit.icrisat.org/page/groundnut/686)

## New publications

### Genetic and Genomic Resources for Grain Cereals Improvement



**Edited by:** Mohar Singh and Hari D Upadhyaya

**Published:** 2015. Academic Press, Elsevier. Pages 384; ISBN: 978-0-12-802000-5

This is the first book to bring together the latest available genetic resources and genomics to facilitate the identification of specific germplasm, trait mapping, and allele mining that are needed to more effectively

develop biotic and abiotic-stress-resistant grains. As grain cereals, including rice, wheat, maize, barley, sorghum, and millets constitute the bulk of global diets, both vegetarian and non-vegetarian, there is a greater need for further genetic improvement, breeding, and plant genetic resources to secure the future food supply.

ICRISAT scientists contributed the following chapters:

#### Sorghum

**Authors:** Yi-Hong Wang, Hari D Upadhyaya, Ismail Dweikat

#### Pearl millet

**Authors:** Santosh K Pattanashetti, Hari D Upadhyaya, Sangam Lal Dwivedi, Mani Vetriventhan and Kothapally Narsimha Reddy

#### Finger and foxtail millets

**Authors:** Mani Vetriventhan, Hari D Upadhyaya, Sangam Lal Dwivedi, Santosh K Pattanashetti and Shailesh Kumar Singh

#### Proso, barnyard, little, and kodo millets

**Authors:** Hari D Upadhyaya, Mani Vetriventhan, Sangam Lal Dwivedi, Santosh K Pattanashetti and Shailesh Kumar Singh

<http://store.elsevier.com/Genetic-and-Genomic-Resources-for-Grain-Cereals-Improvement/Mohar-Singh/isbn-9780128020005/>

### The 5<sup>th</sup> International Symposium for Farming Systems Design, 7-10 September, 2015, Le Corum conference center, Montpellier, France

The proceedings of the conference aim to serve as a compendium of the ongoing research in the Farming Systems Design (FSD) domain when considered worldwide and across the various sectors of agriculture (including fish-based systems). They include all the 250 presentations (orals and posters) selected by the Scientific Committee.

The following ICRISAT papers were presented at the conference:

#### Institutionalizing Systems Approaches for Improving Agricultural Livelihoods in an Arid Ecoregion of South Asia

**Authors:** Kumar S, Whitbread A and Ramilan T

<http://oar.icrisat.org/9338/>

### Re-designing smallholder farming futures for reduced vulnerability to climate change in semi-arid southern Africa

**Authors:** Homann-Kee Tui S, Katrien D, Patricia M, Arthur CG, Olivier C, Lieven C and Valdivia R

<http://oar.icrisat.org/9206/>

### Dry root rot (*Rhizoctonia bataticola* (Taub.) Butler): an emerging disease of chickpea – where do we stand?

**Authors:** Mamta Sharma, Raju Ghosh and Suresh Pande

**Published:** 2016. Archives of Phytopathology and Plant Protection, ISSN 0323-5408 (Print), 1477-2906 (Online), Taylor & Francis Online, UK

**Abstract:** Dry root rot caused by *Rhizoctonia bataticola* (*Macrophomina phaseolina*) of chickpea (*Cicer arietinum* L.) is gaining importance in the changed scenario of climate when growing crop is predisposed to high temperature and moisture stress. Being mainly a soil-inhabiting pathogen, many environmental and soil factors are responsible for the development of disease. No systematic research related to the biology, ecology and epidemiology of dry root rot in chickpea has been conducted so far. Research is needed to improve the identification and characterization of variability within its epidemiological and pathological niches. Limited literature available on host plant resistance for dry root rot indicated lack of resistant sources for this disease. The present article discusses current status of the disease in the context of climate change and possible management options to alleviate the problem.

<http://dx.doi.org/10.1080/03235408.2016.1140564>

### Evaluation of intensity and duration of seed dormancy in a recombinant inbred population derived from Spanish bunch genotypes

**Authors:** Naganagoudar YB, Kenchangoudar PV, Motagi BN, Gowda MVC, Nadaf HL and Pujer S

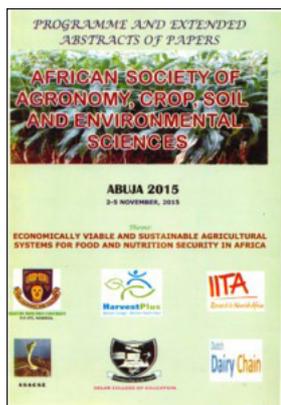
**Published:** 2015. In: Proceedings of the 8th International Conference of the Peanut Research Community-Advances in Arachis through Genomics and Biotechnology (AAGB-2015), Brisbane, Australia, November 4 - 7, 2015.

**Abstract:** Pre-harvest sprouting in groundnut (*Arachis hypogaea* L.) seeds belonging to subspecies *jastigiara* (Spanish bunch) is undesirable. Since it leads to in vitro germination resulting in substantial loss of seeds, both in quantity and quality. A short period of dormancy is therefore desirable in the sub-species to reduce such losses. Evaluation of fresh seed dormancy was conducted for two seasons to determine the intensity and duration of dormancy in recombinant inbred population with 268 RILs developed from crosses involving moderately dormant (GPBD-4) and non-dormant (TAG-24) parents. The intensity of dormancy ranged from 0 to 100% in summer season while 0 to 90% in *kharif* season. There was large variation in the intensity of dormancy which could be related to genetic differences between the entries tested. RIL nos.

165, 259, 160, 172, 209, 254, 213, 247, and 248 recorded very high values (> 70 %) of intensity of dormancy in both the seasons. The variation for dormancy in terms of duration as revealed by germination of 70% (G 70 estimates) was subsequently large as compared to the intensity of dormancy among the RILs. The RIL nos. 5, 40, 84, 165, 183, 209, 213, 248, 254, 259 and 265 were found to have more than two weeks of dormancy (based on G70 count) in both the seasons. These dormant lines can be utilized in breeding for fresh seed dormancy under Spanish background.

<http://oar.icrisat.org/9226/>

### Efficiency of molecular markers to select for *Striga gesnerioides* resistance in cowpea [*Vigna unguiculata* (L.) Walp]



**Authors:** Omoigui LO, Kamara AY, Timko MP, Ajeigbe H, Ayeni DF and Motagi BN

**Published:** 2015. In: 1st Annual Conference Proceedings of the African Society of Agronomy, Crop, Soil and Environmental Sciences (ASACSES), November 02-05, 2015, Abuja, Nigeria.

**Abstract:** *Striga gesnerioides* (Willd) Vatke is a major biological constraint to cowpea

productivity in the d) savannas of sub-Saharan Africa. Over the last two decades, the use of molecular markers in crop improvement has gained prominence owing to its ability to shorten the breeding cycle. The available molecular marker techniques are being improved upon and continuously tested for higher precision, shorter duration of application and better cost effectiveness. In the present study, a total of four molecular markers developed for selecting *Striga* resistant cowpea were used to genotype F2 population derived from a cross between Borno Brown and [T97K-499-35 to identify markers more closely linked to *S. gesnerioides* resistance. SSR1 and 2 were found to be tightly linked to *Striga gesnerioides* with a genetic distance of 1 and 2 cm. The selection efficiency of SSR-1 and SSR-2 were 99 and 98% and was better than that of C 42-B 85.5%.

<http://oar.icrisat.org/9225/>

### Assessing the prospects of *Streptomyces* sp. RP1A-12 in managing groundnut stem rot disease caused by *Sclerotium rolfsii* Sacc

**Authors:** Jacob S, Sajjalaguddam RR, Kumar KVK, Varshney R and Sudini HK

**Published:** 2016. Journal of General Plant Pathology. pp. 1-9. ISSN 1610-739X (Unpublished)

**Abstract:** Biological control of stem rot of groundnut caused by the soilborne pathogen *Sclerotium rolfsii*, using actinomycetes is a viable alternative to existing fungicidal management. Though actinomycetes are prolific antibiotic producers, reports pertaining to their use in groundnut disease management are limited. Here, actinomycetes were isolated from groundnut rhizospheric soils and

screened for antagonism against *S. rolfsii* through a dual culture assay. Culture filtrates and crude extracts of the potential candidates were screened further for extracellular antifungal activity and characterized for biocontrol and plant-growth-promoting traits. A promising candidate was tested under greenhouse conditions as whole organism as well as crude extracts. Isolate RP1A-12 exhibited high antagonism against *S. rolfsii* in dual culture assay (69% inhibition), culture filtrate assay (78–100% inhibition at various concentrations) and crude extract assay (100% inhibition with 1% crude extracts). Moreover, germination of sclerotia of the test pathogen was inhibited with 1% crude extracts. Strain RP1A-12 produced hydrogen cyanide, lipase, siderophores and indole acetic acid. Oxalic acid production by *S. rolfsii* was also inhibited by crude extracts of RP1A-12. In greenhouse studies, RP1A-12 reduced stem rot severity. Overall, our results suggest that isolate RP1A-12 has potential biocontrol capabilities against stem rot pathogen. Molecular characterization based on 16S rRNA gene sequencing of RP1A-12 identified it as a species of *Streptomyces*, closely related to *S. flocculus*.

<http://oar.icrisat.org/9274/>

### Transcriptome analyses reveal genotype- and developmental stage-specific molecular responses to drought and salinity stresses in chickpea

**Authors:** Garg R, Shankar R, Thakkar B, Kudapa H, Krishnamurthy L, Mantri N, Varshney RK, Bhatia S and Jain M

**Published:** 2016. Scientific Reports, 6 (19228). 01-15. ISSN 2045-2322

**Abstract:** Drought and salinity are the major factors that limit chickpea production worldwide. We performed whole transcriptome analyses of chickpea genotypes to investigate the molecular basis of drought and salinity stress response/adaptation. Phenotypic analyses confirmed the contrasting responses of the chickpea genotypes to drought or salinity stress. RNA-seq of the roots of drought and salinity related genotypes was carried out under control and stress conditions at vegetative and/or reproductive stages. Comparative analysis of the transcriptomes revealed divergent gene expression in the chickpea genotypes at different developmental stages. We identified a total of 4954 and 5545 genes exclusively regulated in drought-tolerant and salinity-tolerant genotypes, respectively. A significant fraction (~47%) of the transcription factor encoding genes showed differential expression under stress. The key enzymes involved in metabolic pathways, such as carbohydrate metabolism, photosynthesis, lipid metabolism, generation of precursor metabolites/energy, protein modification, redox homeostasis and cell wall component biogenesis, were affected by drought and/or salinity stresses. Interestingly, transcript isoforms showed expression specificity across the chickpea genotypes and/or developmental stages as illustrated by the AP2-EREBP family members. Our findings provide insights into the transcriptome dynamics and components of regulatory network associated with drought and salinity stress responses in chickpea.

<http://oar.icrisat.org/9276/>

## Farewell



**Mr R Vijaya Kumar**, Senior Manager, Field Research Operations (Pigeonpea Breeding), Grain Legumes, Patancheru, India, concludes his assignment on 29 February after over 39 years of valuable and dedicated service to ICRISAT.



**Mr AG Bhasker Raj**, Manager, Field Research Operations (Pearl Millet Breeding), Dryland Cereals, Patancheru, India, concludes his assignment on 29 February after over 38 years of valuable and dedicated service to ICRISAT.

We wish them all success in their future endeavors.

## Readers' comments

Many thanks for drawing my attention to the story of initial successes in growing new varieties of groundnut, developed under the ICRISAT groundnut breeding program in Malawi established almost three decades ago. Kenya's Rift valley agriculture offers an excellent opportunity to fit groundnut in the existing cropping systems, and expand acreage under this crop (*Happenings No. 1712*). Groundnut stands out for its multiple uses as nutritious food for humans and animals, and raw material for several enterprises. I would be most interested in following up the successes in the near future.

**Dr YL Nene**

*Chairman Emeritus, Asian Agri-History Foundation, Hyderabad, India*

I thank you for the ICRISAT Happenings highlighting three successful events.

1. Seed revolving fund experience in Malawi: This successful innovation in producing and making available locally the certified seeds under public-private-farmers' partnership is commendable for replication of the model for saturation of the area(s) with high yielding varieties seeds in short span of time.

In this regard, the model of Seed village cum Grain village model innovated and implemented by MSSRF (MS Swaminathan Research Foundation) in select villages in Tamil Nadu and Odisha is another successful model to attain seed self-sufficiency in the village itself, by involving a few progressive farmers as seed farmers of the village and multiplying the seeds required for that village and storing them in farmers -owned village seed bank. Seeds of different varieties of the crop stored in this way, helps in switching over to contingency crop-variety planning under rainfed agriculture as per the current behavior of the monsoon. (Reference-Annual reports of the MSSRF).

2. Soil testing and promotion of integrated nutrient management by farmers in the districts of Andhra Pradesh and Telangana dovetails into the national soil testing mission for testing and issue of soil health cards to farmers. In my view, soil testing is the first entry point for the extension personnel to engage with farmers to upgrade soil fertility of their farm and in the process, impart all improved methods of cultivation and management, suited to the size of his family farm and assets, until the last mile to the farm is covered and achieved by the local extension agency.
3. Enhancing the competence and competitiveness of farmers' producer companies/organizations and cooperatives along with skill training of the members in value addition and marketing in the supply chain is the need of the hour. Aply the Government has a separate Ministry for Skill Development and Entrepreneurship, and the canvas now is from R&D to R,T(Training)&D.

**M Velayutham**

*Executive Director, MS Swaminathan Research Foundation, Chennai, India*



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ICRISAT's scientific information: [EXPLOREit.icrisat.org](http://EXPLOREit.icrisat.org)  
DG's Journal: [dgblog.icrisat.org](http://dgblog.icrisat.org)

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