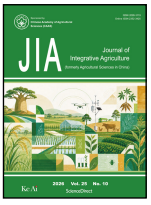
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EDITORIAL

Advancing China–Africa agricultural science and technology cooperation: Innovation and pathways

The United Nations Sustainable Development Goal (SDG) 2 aims to achieve Zero Hunger by 2030. Yet global hunger and food insecurity remain stubbornly high, and the challenge is nowhere more pressing than across Africa, where smallholder farmers still account for the great majority of agricultural production and where yield gaps, emerging pests and diseases, and climate stress continue to constrain productivity. China, as the world's largest agricultural producer and a long-standing partner of African nations in agricultural development, is well placed to share technologies, germplasm, and experience to help close these gaps, while African science, in turn, offers genetic resources, field evidence, and context-specific knowledge that enrich global agricultural research.

Against this background, the Chinese Academy of Agricultural Sciences (CAAS) and the African Academy of Sciences (AAS) jointly established the China–Africa Agricultural Science and Technology Innovation Alliance (CAASTIA). At the Alliance's First General Assembly, held on October 26–28, 2025, CAAS and AAS jointly launched this Special Focus of the Journal of Integrative Agriculture (JIA), "Advancing China–Africa Agricultural Science and Technology Cooperation: Innovation and Pathways," to showcase collaborative and complementary research across five priority areas identified by the Alliance: rice technology and adaptation, tea sector transformation, livestock production and breeding, plant protection and green control, and agricultural extension and poverty reduction.

This first collection under the Special Focus comprises six papers contributed by research teams from China, Ghana, Kenya, Côte d'Ivoire, Sudan, Australia, and Kenya's national agricultural research system, spanning four of the Alliance's five priority directions: rice technology and adaptation, tea sector transformation, livestock production and breeding, and plant protection and green control. Together, the papers move from gene to genome, from laboratory to field, and from single-farm trial to continental meta-analysis, illustrating the range of tools that China–Africa cooperation can bring to bear on shared agricultural challenges.

Rice underpins food security across both Asia and Africa, and two papers in this Special Focus show how the genetic diversity of African cultivated rice, *Oryza glaberrima*, and the disease pressures of African rice-growing systems can inform breeding for both continents. He *et al.* (2026) isolated a chromosome segment introgression line carrying a fragment of *O. glaberrima* and used map-based cloning to identify *OgGS3.2*, an ortholog of *OsSLR1*, as the gene underlying a substantial increase in grain size. A single nucleotide substitution in *OgGS3.2* was identified as the causal mutation, and haplotype analysis of African rice germplasm confirmed that most accessions carry the favorable allele, providing breeders with a validated genetic resource for yield improvement in Asian cultivated rice.

Complementing this genetic advance, Tawiah *et al.* (2026) reviewed the evolutionary dynamics of rice yellow mottle virus (RYMV), one of the most destructive viral diseases of rice in Sub-Saharan Africa. The authors synthesized evidence on the phylogeographic diversification of the virus and the distinct molecular mechanisms and durability of the three major resistance genes, *RYMV1*, *RYMV2*, and *RYMV3*, most of which trace back to *O. glaberrima*. Their evolution-informed framework highlights marker-assisted gene pyramiding, genomic selection, and region-specific, diversified variety deployment as the most promising routes to durable resistance, and points to genome editing and AI-assisted breeding as emerging tools that will need careful integration into future strategies. Read together, these two studies underscore the continuing value of African rice germplasm, both as a source of favorable yield alleles and as a proving ground for understanding host–pathogen coevolution, for breeding programs on both continents.

Tea is a vital cash crop and a growing point of shared interest for China–Africa cooperation, but intercropping outcomes in tea gardens have long been reported inconsistently across studies. Zhang J *et al.* (2026) addressed this by conducting a meta-analysis of 157 paired observations drawn from 41 published studies. Intercropping significantly increased tea yield by 11.9% and improved quality indicators, raising free amino acid content by 19.08% while lowering the tea polyphenol-to-amino-acid ratio; it also improved soil nutrient status and pH. Importantly, the study identifies which factors govern these outcomes: initial soil organic matter and pH mainly determine yield and quality responses, whereas companion-crop type and climatic

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variables such as mean annual temperature and precipitation mainly drive soil improvement, with leguminous intercrops delivering the strongest overall benefits. These findings give tea growers and extension services an evidence base for selecting intercropping strategies suited to local soil and climate conditions.

Two papers in this section address viral diseases that threaten swine and poultry production, respectively, both of which are major economic concerns for smallholder and commercial livestock systems in China and Africa alike. Ibrahim *et al.* (2026) conducted a systematic review and meta-analysis of porcine epidemic diarrhoea virus (PEDV) across 133 studies from 22 countries. By integrating animal- and herd-level data and explicitly accounting for diagnostic-method bias, the authors show that PEDV should be understood as an endemic, persistently circulating pathogen sustained by subclinical infection in sows and by silent transmission within herds, rather than as a disease characterized solely by sporadic outbreaks. Their harmonized prevalence estimates and evidence-based framework offer a foundation for more standardized global surveillance and more effectively targeted vaccination and biosecurity measures.

Li *et al.* (2026) turned to avian leukosis virus subgroup J (ALV-J), a major oncogenic threat to the poultry industry, and examined the poorly understood role of TCRγδ$^+$CD8α$^+$ T cells in the antiviral response. Comparing MHC-homozygous B21 chickens with outbred White Leghorn chickens, the authors demonstrated stronger and earlier expansion and cytolytic activation of these T cells in the more resistant B21 line, and identified the viral Gag and Pol proteins, and specific peptides within them, as the dominant targets recognized by chicken TCRγδ$^+$CD8α$^+$ T cells. This is the first demonstration that these cells can recognize defined viral peptides in chickens, opening the way for peptide-based vaccine design against ALV-J and a deeper understanding of MHC-linked disease resistance in poultry.

Fall armyworm (*Spodoptera frugiperda*) remains one of the most damaging pests to smallholder maize production since its arrival in Africa in 2016 and in China in 2019. Zhang *et al.* (2026), working under the FAO-China South-South Cooperation Fall Armyworm Project, conducted on-farm trials at two sites each in Kenya and Ghana to compare botanical, biological, and chemical control options, delivered either by knapsack spray or as low-cost sand-mediated whorl application, alongside a screen of local maize varieties for natural resistance. Emamectin benzoate and chlorantraniliprole consistently provided the strongest control; sand-mediated delivery proved a practical, low-cost alternative to spraying, and several locally available varieties, such as Omankwa in Ghana and Pioneer, SC 73 Tumbo, and WH508 in Kenya, showed significantly lower leaf damage than susceptible checks. By directly comparing treatments side by side under farmers' own field conditions, this study gives smallholders and extension agents concrete, locally adapted guidance for integrated fall armyworm management.

Although these six studies range from molecular genetics and cellular immunology to global meta-analyses and multi-country field trials, they share a common purpose: translating rigorous science into practical tools that smallholder farmers in China and Africa can use. Whether by identifying a favorable grain-size allele in African rice, mapping the evolutionary logic of durable virus resistance, clarifying how intercropping benefits tea gardens, reframing the true epidemiology of a costly swine pathogen, revealing how chicken T cells recognize a poultry oncovirus, or validating a low-cost pest-control package for maize farmers, each paper advances the shared goal of more productive, resilient, and sustainable agri-food systems.

This Special Focus is intended as the first of an ongoing series arising from the CAASTIA partnership between CAAS and AAS. We hope it will encourage further joint research, germplasm exchange, and knowledge sharing across the remaining priority areas of the Alliance, particularly agricultural extension and poverty reduction, and we look forward to future contributions that continue to strengthen China–Africa agricultural science and technology cooperation in service of the Zero Hunger goal.

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Declaration of competing interest

The authors declare that they have no conflict of interest.

Declaration of generative AI and AI-assisted technologies in the writing process

The authors declare that they did not use AI in the preparation and writing of this manuscript.

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