



Sarawak rice landraces as genetic resources for crop improvement: diversity, key traits, conservation and utilization—A review

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Abstract Asian rice (*Oryza sativa* L.) is fundamental to global food security, yet Malaysia's rice self-sufficiency level (SSL) has declined to 69%, underscoring the need for breeding strategies that exploit locally adapted genetic resources. Sarawak is characterised by an exceptionally high number of indigenous rice landraces, including Geographical Indication (GI) cultivars such as Bario, Biris, and Bajong, collectively forming a broad and structured genetic base well suited for effective rice breeding. This review evaluates the breeding potential of Sarawak rice landraces by synthesizing literature published between 1980 and 2025, drawing on international databases and local grey sources. The reviewed research revealed extensive genetic diversity, with landraces forming multiple genetic clusters and expressing a wide range of agronomically valuable traits, including tolerance to drought, salinity, heat, and flooding, as well as resistance to major diseases such as rice blast. From a breeding perspective, these landraces represent promising donor resources for developing climate-resilient and yield-stable rice cultivars. Desirable quality traits, including aroma, pigmentation, and elevated antioxidant content, further highlight their potential for nutritional improvement

and value-added breeding. However, the effective utilization of these genetic resources is limited by incomplete characterization, genetic erosion, and fragmented conservation and breeding efforts. Overall, the literature confirms that Sarawak rice landraces constitute a strategically important yet underexploited breeding resource. Integrating advanced molecular breeding approaches with participatory breeding, strengthened germplasm management, and supportive policy frameworks will be essential to translate this diversity into improved cultivars that strengthen long-term food security.

Keywords *Oryza sativa* · Rice breeding · Rice landraces · Sarawak · Hybrid rice · Genetic

Introduction

Oryza sativa L., also known as Asian rice, has been the staple food source for more than half of the world's population, exclusively in Asia and Africa (Maraseni et al. 2018). In Malaysia, the Self-Sufficiency Level (SSL) of rice was around 70% from 2009 to 2018, and the country still relies on imports to compensate for the shortfall (Nodin et al. 2023). After the pandemic, the SSL of Malaysia decreased to 69% due to labor shortages, supply chain disruptions, and an increase in staple food consumption (Adnan & Nordin 2021). Among Southeast Asian countries, Malaysia has the smallest total rice planting area at

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689,268 ha, ranking it among the smallest among neighbouring countries (Firdaus et al. 2020). Malaysia has a relatively low SSL (69%), compared to our neighbouring countries, the Philippines (93%), Indonesia (97%), Vietnam (124%) and Thailand (196%) (Omar et al. 2019). The newly implemented goal of Sarawak is to achieve a fully rice self-sufficient level in 2027 (Department of Agriculture Sarawak 2024).

Sarawak, the largest state in Malaysia, holds significant potential to boost rice production through its rich biodiversity of traditional rice landraces (Omar et al. 2022). In this review, the term landrace refers to traditional, locally adapted rice populations that have been maintained by farmers over generations (Ray et al. 2013), unless otherwise specified as a formally recognized cultivar. Permanent rice cultivation has been practiced by local farmers on a small scale. Generally, single cropping during the main season, from October to April, is predominant in Sarawak (Omar et al. 2022). Double cropping is only possible for farmers who have proper infrastructure, irrigation and drainage systems, and access to high-yielding seeds (Sang et al. 2018; Omar et al. 2022). Famous traditional cultivars such as Bario, Biris, and Bajong, all of which have received Geographical Indication (GI) certification from Intellectual Property Corporation of Malaysia (MyIPO) in Sarawak, reflect the unique genetic resources available in this region (<https://landportal.org/library/resources/agrismy2015000785/geographical-indication-gi-certification-sarawaks-traditional>) (Tan 2015; Ganendra 2024; Teo 2025).

Rice can be broadly categorized into two types in Sarawak, which are upland rice and lowland rice. The lowland rice is usually planted in the flooded field with a well-irrigation system, whereas the upland rice is normally planted in the soil with naturally well-drained and no surface water accumulation (Sylvester Embuas et al. 2025). Upland rice commonly possesses higher drought resistance but lower productivity, whereas lowland rice has lower drought resistance but higher productivity than upland rice due to its adaptation to the growing environment (Xia et al. 2019) (see Table 1). The anatomical and physiological traits associated with these adaptive differences have been reported in multiple regional investigations, which are synthesised in the thematic summary of Sarawak rice research (Table 2). Despite Sarawak being the largest state in Malaysia with 12,417,000 hectares (Jamil et al. 2024), but the rice

cultivation has not yet achieved a significant level of production. The total production of paddy (Fig. 1) in Sarawak from 2017 to 2022 was 1,190,917.9 metric tonnes (t), ranked fifth after Kedah (5,409,781 t), Kelantan (1,810,363 t), Perak (1,590,007 t) and Perlis (1,374,861 t) (Department of Statistics Malaysia, n.d. 2025).

This review synthesizes current knowledge on Sarawak's rice landraces, highlighting key traits for breeding, recent research progress, and existing challenges. It further explores emerging opportunities and proposes strategic recommendations to harness diverse and unique genetic resources for future hybrid and inbred rice breeding programs aimed at enhancing food security and sustainable agriculture in Sarawak and beyond.

Literature search and selection

This review is based on a structured but non-systematic search of both international databases and local sources to capture published and grey literature on Sarawak rice landraces and their use in breeding. Between March and November 2025, we searched Web of Science, Scopus, CAB Abstracts and Google Scholar using combinations of the following English keywords: rice, *Oryza sativa*, Sarawak, Borneo, landrace/landraces, traditional cultivars, indigenous rice, upland rice, highland rice, germplasm, genetic diversity, abiotic stress, biotic stress, grain quality, hybrid rice, participatory breeding and Sarawak Department of Agriculture (DOA). Boolean operators and truncations (e.g. "Sarawak AND landrace", "Bario OR Biris OR Bajong") were used to refine the search. The main temporal window was 1980–2025, but older references were included where they provided seminal background on Sarawak rice production or indigenous cultivation practices.

To complement international databases, we systematically screened local and grey sources, including technical reports and statistics from the Department of Agriculture Sarawak, postgraduate theses, internal reports and project documents from Universiti Malaysia Sarawak (UNIMAS), and relevant proceedings or policy documents issued by Malaysian agencies. Reference lists of key papers were checked (backward citation tracking), and additional investigations were identified by consulting researchers and breeders actively working on Sarawak rice.

Table 1 Comparative summary of Sarawak rice landraces based on agro-ecosystem distribution, stress tolerance traits, grain quality attributes, cultural value, and integrated quantitative evidence

Landrace/Group	Agro-ecosystem & Region	Key abiotic stress traits (with numbers)	Key biotic stress traits (with numbers)	Grain quality & market traits (with numbers)	Special status/cultural value	Integrated evidence basis (Quantitative)	References
Bario (GI group)	Upland/Highland (Kelabit highlands, Bario)	Adapted to cool temperatures 19–22 °C; germination: $T_b \approx 10$ °C, $T_{opt} = 32$ –33 °C, $T_{max} \approx 43$ °C; maximum germination around 22.5 °C; upland drought tolerance	Leaf epidermis with dumbbell-shaped silica cells; Score 2 (Moderate resistant) to <i>P. oryzae</i> isolates, inoculated at 4th leaf stage; homogeneous prokaryotic community diversity	Fine elongated grains; soft texture; aromatic; high amylose; moderate GI; pigmented variants (yellow/red/black) with anthocyanins	GI-registered flagship rice; premium niche markets	Germination modeling; SSR differentiation; silica histology; grain quality assays; farmer surveys; Blast scoring adapted and modified from Takahashi et al. (2009, 2014) and Challagulla et al. (2015)	(Wong et al. 2009; Yeo et al. 2018a, b, 2022; Luong & Nori 2023)
Biris (GI)	Rainfed lowland (Simunjan, Kota Samarahan)	Excellent heat tolerance: 95% germination within 2 days at 40 °C; cardinal temperatures $T_b = 9.5$ °C, $T_{opt} = 32.1$ °C, $T_{max} = 43.5$ °C; thermal time 53 °Cd ($T_b = 10$ °C)	Antioxidant activity detected in seedling extracts (seedling stage)	Long slender grain; mean grain length 6.88 mm; low chalkiness; strong aroma; high protein; soft texture	GI-registered; high historical commercial rating	Germination assays; tissue culture regeneration; grain quality analysis; antioxidant assays	(Libin et al. 2012; Yeo et al. 2018a, b; Luong & Nori 2023)
Bajong (GI)	Rainfed lowland (Lubok Nibong, Betong)	Strong drought and salinity tolerance; elevated OsRC12 expression; Na^+ exclusion; Ca^{2+} signaling; stomatal regulation	High leaf silica (dumbbell cells); homogeneous microbial diversity	Aromatic; dark brown husk; black kernel; medium yield	GI-registered; premium niche markets	Physiological stress research; YSB oviposition assays; silica histology	(Yeo et al. 2018a, b, 2022; Cheok et al. 2019) "

Table 1 (continued)

Landrace/Group	Agro-ecosystem & Region	Key abiotic stress traits (with numbers)	Key biotic stress traits (with numbers)	Grain quality & market traits (with numbers)	Special status/cultural value	Integrated evidence basis (Quantitative)	References
Bario sederhana	Commercial landrace (Serian District)	Cardinal temperatures: $T_b = 11.6$ °C, $T_{opt} = 33.1$ °C, $T_{max} = 43.5$ °C; thermal time for germination 63 °Cd ($T_b = 10$ °C); < 35% germination at 40 °C	No formal resistance data	Medium grain; high protein; low fat; low gelatinization temperature; high gel consistency (soft, cooked texture)	Specialty premium rice, preferred by health-conscious consumers	Broken-stick linear germination model; proximate grain analysis	(Luing & Nori 2023)
Bubok (padi bubuk)	Lowland (Sri Aman)	Lowland adaptation	Score 0–2 (Resistant) to <i>P. oryzae</i> isolate B2PG; 3rd leaf stage inoculation	White kernel; yellow husk; aromatic	Target for genetic improvement under EPP11	Seedling blast tests scoring modified from Yu (1987); Pairwise Nei genetic distance to Mamut was 0.4755	(Razak et al. 2018; Cheok et al. 2019; Lai et al. 2019; Yeo et al. 2022),
Bali 1, 2, 3	Lowland (Sri Aman)	Tall culm height 156.52–172.60 cm; drought tolerance target	No formal resistance data	Strong aroma; coloured grain; TGW Bali 3 = 22.4–24.8 g	Target for genetic improvement under EPP11	Genetic similarity: Bali 2 versus Bali 3 Nei's distance was 0.1271	(Razak et al. 2018)
Mamut	Traditional lowland	Culm height ~ 150.77 cm	Field tolerance reported, no data provided	Nil to slight aroma; colored grain; TGW = 23–25 g	Traditional landrace; Target for genetic improvement under EPP11	Agronomic characterization under EPP11	(Razak et al. 2018a, b) Yeo et al. 2018a, b)
Kanowit	Lowland (Kg Melugu Skim, Sri Aman)	Tall plant 170.1 cm; long maturity ~ 120 days to heading to 151 days to flowering	Highly preferred by <i>S. incertulas</i> for oviposition during one month seedling phase (choice test); Score 2 (Moderate resistant) to <i>P. oryzae</i> isolates, inoculated at 4th leaf stage; carries <i>AvrPiz-t/AvrPi-54</i> haplotypes (4th leaf stage)	Linear seed; yellow to golden-brown husk; milky white grain	Traditional landrace	YSB choice tests; Blast rating scoring adapted and modified from Takahashi et al. (2009, 2014) and Challagulla et al. (2015)	(Ling et al. 2020; Clifton et al. 2024; Yeo et al. 2024; Rafael et al. 2025)

Table 1 (continued)

Landrace/Group	Agro-ecosystem & Region	Key abiotic stress traits (with numbers)	Key biotic stress traits (with numbers)	Grain quality & market traits (with numbers)	Special status/cultural value	Integrated evidence basis (Quantitative)	References
Merah (Padi Merah)	Lowland (Kg pesak, kuching)	Shorter grain length; wider grain width versus upland accessions	Resistant to <i>P. oryzae</i> isolate POS17 (H14 haplotype); inoculated at 4th leaf stage	Pale yellow husk; dark brown grain; red bran with anthocyanins	Traditional landrace	Blast phenotype– <i>Avr</i> interaction research. Scoring same as in Kanowit	(Clifton et al. 2024; Yeo et al. 2024; Rafael et al. 2025)
Padi Rendah	Lowland (Serian, kuching)	Lowland adaptation	Score 1–0 (Resistant) to <i>P. oryzae</i> isolate B2PG; 3rd leaf stage inoculation	Linear seed; yellow husk; milky white grain	Traditional landrace	Seedling blast tests scoring modified from Yu (1987)	(F. K. S. Yeo et al. 2018a, b; Lai et al. 2019)
Padi Hiram/Che-lum landraces	Upland and lowland. Bario highlands, Serian (Kg Lebor), Kuching (Kg Pueh, Kg Pesak), Sri Aman, Kota Samarahan, Bau, and Betong	Adapted to rainfed upland and irrigated lowland systems. Upland accessions exhibit larger root and stele diameters (steles ≈ 298.9 µm), supporting water uptake under stress	Score 3–4 (Moderate resistant) to <i>P. oryzae</i> ; 3rd leaf stage inoculation; Yellow stem borer: Low oviposition preference (relative egg mass = 0.05 ± 0.011). Tested on 1-month-old seedling	Black kernel with dark brown or yellow husk; typically aromatic. Grain shape linear to oblong; seed length 0.73–1.00 cm	Premium rice and functional rice due to high anthocyanin-derived anti-oxidant activity, associated with anti-inflammatory and anti-cancer properties	SSR markers show high diversity, Seedling blast tests scoring modified from Yu (1987); Pest resistance test	(Wong et al. 2009; Lee et al. 2011; Yeo et al. 2018a, b; Jasim Aljumaili et al. 2018; Lai et al. 2019; Ling et al. 2020; Clifton et al. 2024)
Other named Sarawak landraces (Mamut, Pandan, Lemak, etc.)	Mixed upland and lowland ecologies across divisions	Diverse local adaptation to specific soil, water and topographic conditions; some tolerant of waterlogging or marginal soils	Leaf silica reported across surveyed landraces; some lines likely carry uncharacterised resistance to major diseases and pests	Wide range of grain shapes, textures and flavours; includes aromatic, waxy and specialty types; some likely suited to mechanisation	Embedded in local cuisines and traditions; several at risk of genetic erosion without systematic conservation	Germplasm surveys; microsatellite diversity research (≥ 6 genetic clusters); DOA documentation; farmer interviews	(Wong et al. 2009; Lee et al. 2011; Razak et al. 2018; Yeo et al. 2018a, b; Clifton et al. 2024; Sylvester Embuas et al. 2025)

Lesion scores follow the 0–5 from Yu (1987) where 0–2 = resistant, 3 = mildly resistant, and 4–5 = susceptible. Blast scoring adapted and modified from Takahashi et al. (2009, 2014) and Challagulla et al. (2015), where 0–1 = resistant, 2 = moderately resistant, and 3–4 = susceptible. Field tolerance indicates a qualitative description only; no quantitative data were reported

Table 2 Thematic synthesis of published rice landraces and their breeding relevance

Theme	Title	Objective summary	Key finding summary	Materials used	Traits studied	Country
Molecular genetics & Genetic diversity	Analysis of Sarawak Bario rice diversity using microsatellite markers (Wong et al. 2009)	The primary objective was to differentiate 8 Bario rice cultivars in Sarawak and to determine their genetic diversity	The study detected a total of 31 alleles among the 8 Bario rice cultivars, showing significant genetic variation. The cultivars clustered into two distinct groups (Group I and Group II). Bario Halus and Bario lowland (Meradong) were highly similar (coefficient 0.917)	8 Bario rice cultivars (seeds/leaves); 12 SSR primers	Genetic diversity, genetic relationships, polymorphism (PIC value), allele size	Sarawak, Malaysia
	Genetic diversity of aromatic rice germplasm revealed by simple sequence repeat (SSR) markers (Jasim Aljumatili et al. 2018)	The objectives were to quantify the genetic divergence of aromatic rice accessions using SSR markers and to identify the potential accessions for introgression into the existing rice breeding program	Analysis of 53 aromatic rice accessions detected 131 alleles across 32 SSR markers (average 4.09 alleles per locus). Cluster analysis revealed ten distinct clusters, indicating significant genetic divergence. Most of the genetic variation (89%) was found within populations	53 rice accessions (50 aromatic + 3 checks) from MARDI; 32 polymorphic SSR markers	Genetic diversity (Nei's index, Shannon's index), allelic diversity, clustering patterns (UPGMA, PCA)	Malaysia (Sarawak, Peninsular Malaysia, Sabah)
	Genetic characterization and analysis of the population of selected Sarawak rice cultivars using SSR markers (Razak et al. 2018)	The study aimed to genetically characterize five selected Sarawak rice cultivars (Bali 1, Bali 2, Bali 3, Bubok, and Mamut), discerning their genetic diversity and population stratification, and developing an SSR marker panel for fingerprinting	The five cultivars studied formed two main genetic groups. Bali 1, Bali 2, and Bali 3 were found to be closely related (lowest pairwise genetic distance and FST values), while Bubok and Mamut formed a separate, distinct group	5 Sarawak cultivars (Bali 1, Bali 2, Bali 3, Bubok, Mamut); 28 polymorphic SSR markers	Allelic variation (allele number, PIC), genetic distance (Nei's 1983), population structure (FST, Bayesian clustering)	Sarawak, Malaysia (Sri Aman)

Table 2 (continued)

Theme	Title	Objective summary	Key finding summary	Materials used	Traits studied	Country
Plant pathology & Pathogen genetics	Genotyping of Sarawak rice cultivars using microsatellite markers (Lee et al. 2011)	The study focused on the genotyping of 53 Sarawak rice cultivars using SSR markers to infer their genetic relationships	A microsatellite marker panel consisting of 12 polymorphic markers was identified. This panel provided a high overall Polymorphism Information Content (PIC) value of 0.969, confirming its effectiveness for differentiating the 53 Sarawak rice cultivars studied	53 Sarawak rice cultivars; 12 selected polymorphic SSR markers	Genetic relationships (UPGMA dendrogram), allelic diversity (43 alleles detected), polymorphism (PIC values)	Sarawak, Malaysia (Southern Sarawak divisions)
	Isolation and characterization of avirulence genes in <i>Magnaporthe oryzae</i> (Jee et al. 2017)	The focus was on the preliminary finding (isolation and characterization) of Avirulence genes (<i>AvrPiz-t</i> , <i>AvrPik</i> , <i>Avr-Pi54</i> , and <i>Avr-Pita1</i>) from the <i>M. oryzae</i> T ^r isolate of Sarawak	The Avirulence (<i>Avr</i>) genes (<i>AvrPiz-t</i> , <i>AvrPik</i> , <i>Avr-Pi54</i> , and <i>Avr-Pita1</i>) were successfully isolated from the <i>M. oryzae</i> T ^r Sarawak isolate. Structural analysis of the gene sequences revealed the presence of a novel signal peptide motif in <i>AvrPiz-t</i> , a motif also found in <i>AvrPiz9</i> , <i>AvrPia</i> , and <i>AvrPii</i>	<i>Magnaporthe oryzae</i> T ^r isolate; Primers for four Avirulence genes (<i>AvrPiz-t</i> , <i>AvrPik</i> , <i>Avr-Pi54</i> , <i>Avr-Pita1</i>)	Isolation of <i>Avr</i> genes, gene/protein structure (3D modeling, signal peptide motifs)	Sarawak, Malaysia
	Isolation and characterization of <i>Pyricularia oryzae</i> isolated from lowland rice in Sarawak, Malaysian Borneo (Hussin. et al. 2020)	The aim was to isolate and characterize rice blast fungus (<i>P. oryzae</i>) from infected leaves in Sarawak and serve as the first step toward understanding variation in the population of <i>P. oryzae</i> from the region	Twelve isolates of the rice blast fungus were successfully isolated and characterized, and all were identified as <i>Pyricularia oryzae</i> with high molecular identity (99.59% to 100%). Colony morphology varied across different media types	12 isolates of rice blast fungus (<i>P. oryzae</i>); Lowland rice leaves; Filtered oatmeal agar and Potato dextrose agar (PDA) culture media	Isolation/identification (ITS sequencing), morphological characteristics (colony surface, pigmentation), growth rate, sporulation rate	Sarawak, Malaysian Borneo (Miri, Serian, Sri Aman, Kuching divisions)

Table 2 (continued)

Theme	Title	Objective summary	Key finding summary	Materials used	Traits studied	Country
Morphological and physiological development of <i>Pyricularia oryzae</i> isolates from North-western region of Sarawak on different media under laboratory conditions (Rafael et al. 2023)		The study aimed to identify the best media for culturing and maintaining <i>P. oryzae</i> isolates from Sarawak by characterizing their morphological and physiological development	Isolates demonstrated morphological variation, but all tested isolates showed flat elevation on Rice Agar (RA) and Glucose Agar (GA). Barley Agar (BA) yielded the highest mean sporulation rate ($1.83 \times 10^5/5$ mL) for <i>P. oryzae</i> isolates	14 <i>P. oryzae</i> isolates; Seven culture media (Oatmeal Agar, Malt extract agar, Cornmeal agar, PDA, RA, BA, GA)	Morphological traits (elevation, colony color, surface), growth rate, sporulation rate	Sarawak, Malaysia (North-western region)
	New haplotypes of AvrPi-54 gene detected in <i>Pyricularia oryzae</i> from Malaysia, India and China (Rafael et al. 2025)	The research focused on amplifying and analyzing the AvrPi-54 gene sequence in <i>P. oryzae</i> isolates from various regions to detect new haplotypes and perform neutrality tests	Neutrality tests indicated that the AvrPi-54 gene sequence deviated from neutrality in the overall population (negative and significant values for Tajima's D and Fu and Li's statistics). The π_{non}/π_{syn} ratio (> 1) suggested the gene was undergoing positive selection	20 <i>P. oryzae</i> isolates from Sarawak; AvrPi-54 gene sequence analysis	Gene structure (SNPs), haplotype diversity, neutrality tests (Tajima's D, Fu and Li's statistics), selection pressure (π_{non}/π_{syn} ratio)	Malaysia (Sarawak), India, China (comparative data)
New variants of AvrPi2-t identified in <i>Pyricularia oryzae</i> from Malaysia (Yeo et al. 2024)	The objective was to analyze the AvrPi2-t ORF sequences in <i>P. oryzae</i> isolates from Sarawak, Thailand, India, and China to identify new haplotypes and conduct population genetic analysis	Eight new haplotypes (H12 to H19) of the AvrPi2-t gene were identified. Population analysis indicated that the gene was under directional natural selection (purifying selection) based on negative and significant neutrality tests. Pathogenicity assays showed highly variable resistance levels among Sarawak landraces inoculated with isolates carrying haplotype H14, ranging from susceptible (Kanowit) to resistant (Selasih, Merawi, Bario)	150 <i>P. oryzae</i> isolates (from Malaysia, Thailand, India, China); Six Sarawak rice landraces (for pathogenicity)	Avirulence gene sequence variation (new haplotypes H12–H19), population genetics (nucleotide diversity), selection pressure (purifying selection), resistance evaluation (disease score on landraces)	Malaysia (Sarawak), Thailand, India, China	

Table 2 (continued)

Theme	Title	Objective summary	Key finding summary	Materials used	Traits studied	Country
Host resistance & Insect interaction	Oviposition behavior of <i>Scirpophaga incertulas</i> , the Yellow Stem borer (Lepidoptera Crambidae) in a non-choice study (Cheok et al. 2019)	The study was designed to provide a preliminary insight into the antixenosis resistance of three Sarawak paddy landraces (Bajong, Bario, and Bubok) toward the yellow stem borer	Female yellow stem borers (<i>Scirpophaga incertulas</i>) showed no preferential oviposition among the three Sarawak landraces (Bajong, Bario, and Bubok) tested in the non-choice environment	Female Yellow Stem-borer (<i>S. incertulas</i>); Three Sarawak paddy landraces (Bajong, Bario, Bubok)	Oviposition preference (site, number of egg masses, size)	Sarawak, Malaysia
	Qualitative resistance of Sarawak rice landraces against <i>Pyricularia oryzae</i> (Lai et al. 2019)	The main goal was the evaluation of qualitative resistance of Sarawak rice landraces against <i>Pyricularia oryzae</i> (rice blast fungus)	Four Sarawak landraces (Padi Semanggang, Padi Perintah, Padi Bubuk, and Padi Rendah) exhibited resistance against the <i>P. oryzae</i> isolate B2PG. Padi Hitam and Padi Entangor showed mild resistance	Six lowland rice landraces; <i>P. oryzae</i> isolate B2PG	Qualitative resistance/susceptibility (disease severity scoring), fungal macro- and micromorphology	Sarawak, Malaysia (Serian division)
Screening for Sarawak Paddy landraces with resistance to Yellow rice Stem Borer, <i>Scirpophaga incertulas</i> (Walker) (Lepidoptera Crambidae) (Ling et al. 2020)	The purpose was to screen Sarawak paddy landraces for resistance (including antixenosis and antibiosis) to the yellow rice stem borer (<i>Scirpophaga incertulas</i>)	Female stem borers consistently preferred the abaxial leaf surface for laying egg masses. In antixenosis testing, the landrace Kanowit was significantly more preferred for oviposition, suggesting its susceptibility to the pest. Antibiosis resistance toward the eggs and larvae was absent	Female stem borers consistently preferred the abaxial leaf surface for laying egg masses. In antixenosis testing, the landrace Kanowit was significantly more preferred for oviposition, suggesting its susceptibility to the pest. Antibiosis resistance toward the eggs and larvae was absent	Yellow Rice Stem Borer (<i>S. incertulas</i>); 12 Sarawak paddy landraces	Antixenosis resistance (oviposition site preference), antibiosis resistance (larvae length/survival)	Sarawak, Malaysia (Kampung Skuduk-Chupak)

Table 2 (continued)

Theme	Title	Objective summary	Key finding summary	Materials used	Traits studied	Country
Plant physiology & Structural adaptation	Cardinal temperatures for germination of Sarawak traditional rice (Luing & Nori 2023)	The focus of the study was on analysing and referencing data related to cardinal temperatures and thermal time for germination of Sarawak traditional rice	Both Bario Sederhana and Biris rice landraces germinate best between 27.5–35 °C, with an optimum around 33 °C. Germination slows below 15 °C and above 37.5 °C and stops near 43.5 °C. Biris performs slightly better at lower temperatures, while Bario Sederhana shows greater thermal resilience within the optimal range	Seeds of two traditional rice landraces: Bario Sederhana and Biris	Germination (quantification), cardinal temperatures, thermal time	Sarawak, Malaysia (Serian district)
	Low variation in anatomical characters of lowland and upland rice from Sarawak, Malaysian Borneo (Sylvester Embuas et al. 2025)	The objective was to characterise and document the variations in anatomical traits of leaf, midrib and the root of 22 lowland and 22 upland rice accessions	While both lowland and upland rice shared the same fundamental anatomical structure in the leaf, midrib, and root, upland rice accessions showed significantly advantageous drought-adaptive traits. Specifically, upland rice accessions had larger root diameters, larger stele diameters, and higher stomatal density on the adaxial surface	44 rice accessions (22 lowland, 22 upland); Leaf, midrib, and root tissues; 4 SSR markers used for selection	Anatomical traits (e.g., stomatal density, root diameter, stele diameter, midrib width)	Sarawak, Malaysian Borneo (North-Western region)
Viral disease & Molecular epidemiology	Molecular characterization of rice tungro bacilliform virus isolated from Bario, Sarawak (Sum & Yee 2018)	The study's implied objective, based on the title, was to conduct the molecular characterization of rice tungro bacilliform virus isolated from Bario, Sarawak	Phylogenetic analysis successfully documented the genetic relationships between rice tungro bacilliform virus (RTBV) isolates from Bario, Sarawak, and other South Asian and Southeast Asian isolates	Two primary isolates of RTBV; partial coat protein (CP) gene sequence	Molecular characterization, genetic relationships (phylogenetic analysis), sequence identity	Bario, Sarawak, Malaysia

Table 2 (continued)

Theme	Title	Objective summary	Key finding summary	Materials used	Traits studied	Country
Germplasm characterization & Biodiversity documentation	Rice tungro disease in Sarawak past and present status (Chong et al. 2015)	The main objective was to monitor the severity of Rice Tungro Disease (RTD) epidemics in Sarawak since its first report in 2012	Rice Tungro Bacilliform Virus (RTBV) was confirmed to be present in samples from multiple Sarawak divisions surveyed in 2013 and 2014, including Miri (Bario and Pa'lungan), Sibul, Samarahan, and Sri Aman. Rice Tungro Spherical Virus (RTSV) was also detected in Miri samples	Infected field rice samples; Focus on RTBV and RTSV viruses	Severity of Rice Tungro Disease (RTD) epidemics; Viral presence confirmed by PCR	Sarawak, Malaysia (Miri, Sibul, Samarahan, Sri Aman divisions)
	Glimpses of bornean biodiversity (Yeo et al. 2018a, b)	The study was presented as the first step towards plant variety registration for rice of Sarawak	Morphological characteristics showed variation among the collected rice accessions, with notable differences observed in traits like grain colour and seed shape. For example, "Arang" accessions had black grains and linear shape, while "Bario (Bintung)" accessions had yellow grains and oblong shape	19 rice accessions collected from Kampung Lebor, Serian	Morphological characteristics: grain colour, seed shape, seed length	Sarawak, Malaysia
	Preliminary characterisation of lowland and upland rice from Sarawak, Malaysian Borneo (Clifton et al. 2024)	The objective was to characterise the morphological traits of 22 lowland and 22 upland rice accessions from the North-Western region of Sarawak	Lowland rice accessions had significantly higher average Plant Height (PH) than upland rice accessions. Cluster analysis demonstrated that the primary factor separating the accessions into two main clusters was the presence/absence of secondary branching (SB) of the panicle	44 rice accessions (22 lowland, 22 upland); SSR markers used for pre-selection	22 morphological traits (9 qualitative, 13 quantitative). Examples: Plant Height (PH), panicle type (PT), secondary branching (SB), seed/grain characteristics	Sarawak, Malaysian Borneo (North-Western region)

Table 2 (continued)

Theme	Title	Objective summary	Key finding summary	Materials used	Traits studied	Country
Microbial ecology	Genotype and organ effect on the occupancy of phyllosphere prokaryotes in different rice landraces (Yeo et al. 2022)	The study aimed to characterize the relationship between rice genotype and plant organ (leaf blade and stem) effects on the occupancy and diversity of associated prokaryotes	Both rice genotype (landrace) and plant organ (leaf blade vs. stem) were found to significantly affect the occupancy and diversity of associated prokaryotes. Significant differences in alpha diversity indices were noted between the leaf blade and rice stem samples	Two-month-old seedlings of three Sarawak landraces (Bajong, Bario, Bubok); Leaf blades and stems; 16S rDNA amplicon sequencing	Occupancy and diversity of associated prokaryotes, alpha and beta diversity indices (Shannon's, Bray-Curtis, etc.)	Sarawak, Malaysia
Agronomy & Nutrient management	Yield Performance and nutrient uptake of red rice cultivar (MRM 16) at different NPK fertilizer rates (Masni & Wasli 2019)	The objectives were to evaluate the yield and yield components of red rice at different fertilizer rates and to determine the nutrient uptake of red rice cultivated at different fertilizer rates	Grain yield did not significantly increase when NPK fertilizer was applied above the lowest tested rate (T2: 60N 35P 40 K). There was a strong positive relationship between grain yield and the total aboveground uptake of Nitrogen, Phosphorus, and Potassium across all treatments. The intermediate rate (T2) was suggested as the most economical choice	Red Rice cultivar (MRM 16); Bijat soil; NPK fertilizer applied at four rates (T1–T4)	Grain yield, yield components; Nutrient uptake (N, P, K)	Sarawak, Malaysia (Bijat soil)
Plant tissue culture & Regeneration	Callus induction and plant regeneration of Sarawak rice cultivar Biris (Libin et al. 2012)	The objective was to study the establishment methods for callus induction and plant regeneration of the Sarawak rice cultivar Biris	The highest frequency of callus induction (97.5%) was achieved using 2.0 mg/L 2, 4-D (T2 treatment). The combination of 2.0 mg/L NAA + 1.0 mg/L Kn (T3) resulted in the highest frequency of root formation (55.6%)	Sarawak rice cultivar Biris; Culture media (e.g., 2, 4-D, NAA + Kn)	Callus induction frequency, root formation frequency	Sarawak, Malaysia

Table 2 (continued)

Theme	Title	Objective summary	Key finding summary	Materials used	Traits studied	Country
Natural product-based disease control	Antifungal properties of <i>Elephantopus scaber</i> L. (Asteraceae) against crop pathogenic fungi (Hussin et al. 2016)	The aim was to determine the effect of antimicrobial properties of <i>Elephantopus scaber</i> L. against six crop pathogenic fungi	The crude methanolic extract of <i>E. scaber</i> successfully obtained did not show a significant inhibitory effect on fungal growth at low concentrations (1% and 5%). Potential compounds like saponins, stigmasterol, lupeol, luteolin, and alkaloids are proposed as candidates for retarding the growth of <i>Colletotrichum</i> sp., <i>Fusarium solani</i> , and <i>P. oryzae</i>	Crude methanolic extract of <i>Elephantopus scaber</i> L.; Six crop pathogenic fungi (implied)	Antifungal/antimicrobial properties, inhibition of fungal growth	Not specified in excerpts

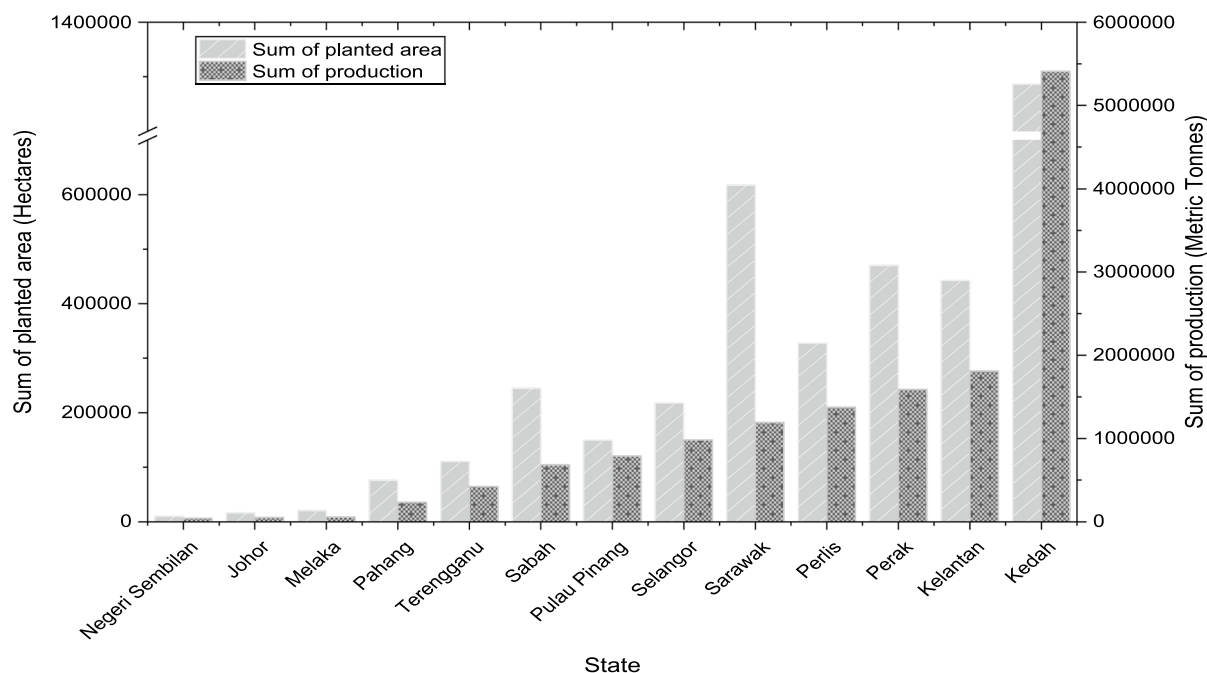


Fig. 1 The sum of production area (hectares) and sum of rice production (metric tonnes) of each state from year 2017 to year 2022

Titles and abstracts were first screened to exclude investigations that (i) did not involve Sarawak rice material or agro-ecosystems, (ii) focused solely on generic Malaysian or international cultivars without clear relevance to Sarawak, or (iii) were purely methodological without biological or agronomic interpretation. Full texts were then assessed for eligibility. We prioritised research providing primary data on Sarawak landraces (e.g. agronomic performance, stress tolerance, anatomical traits, grain quality, genetic diversity, pathogen or insect interactions) as well as reviews or reports that synthesised these aspects. Purely descriptive news articles and non-traceable sources were excluded. Where multiple publications reported overlapping results from the same dataset, we cited the most complete or recent source and cross-referenced earlier work where appropriate.

Sarawak's rice landraces

Major landraces

Sarawak is home to a diverse collection of rice cultivars, with many unique landraces passed down

through generations within local communities. These are often referred to as heirloom, specialty, or traditional rice. There are hundreds of rice landraces cultivated by the local farmers, including the three Geographical Indication (GI) registered local rice landraces of Sarawak are Bario (Kelabit Highland), Biris (Simunjang) and Bajong (Lubok Nibong) (Omar et al. 2022). Bario is a type of upland rice with yield around 2.5–4.0 ton/ha (Jabatan Pertanian Sarawak, n.d. 2025), Biris is predominantly a rainfed lowland rice cultivar with reported 2,190 kg/ha, while Bajong with yield 2.5–3.5 t/ha is primarily grown in rainfed lowland, but also adapted to the upland environment (Nori et al. 2009; Teo 2008, 2010). Other well-known rice landraces are Rotan (Wai), Adan, Bario Sederhana, Mamut, Chelum, Merah, Bubuk, Pandan, Keladi, Lemak, Udang and many more (Omar et al. 2022). The geographical distribution of these landraces across Sarawak in Fig. 2. Rice landraces in Sarawak can be classified into at least six distinct genetic clusters based on microsatellite marker analysis, reflecting substantial genetic diversity among local cultivars (Lee et al. 2011). This diversity provides a valuable resource for breeding programs, offering a broad genetic base to develop cultivars with

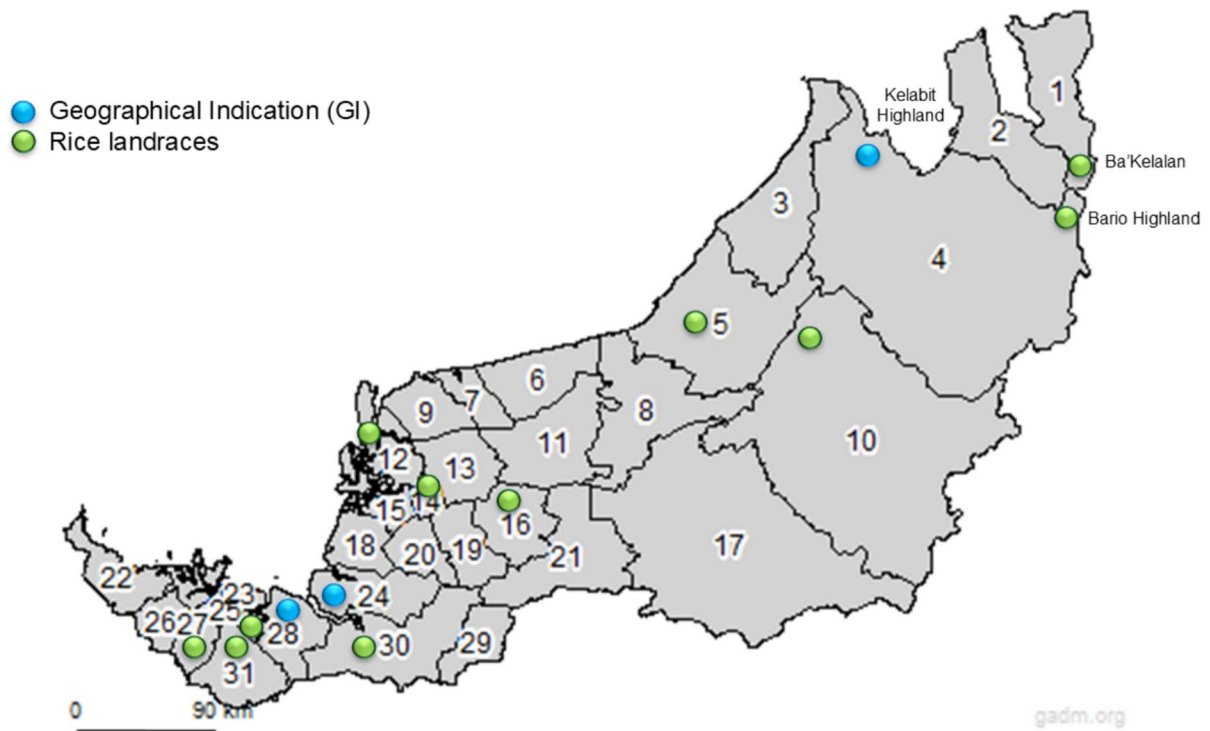


Fig. 2 Regional distribution of key Sarawak rice landraces. Locations represent reported cultivation sites at the district scale. Data points are approximate and signify the presences of specific cultivars as identified through the literature review with each number corresponding to the following districts: (1) Lawas (2) Limbang (3) Miri (4) Marudi (5) Bintulu (6) Mukah (7) Dalat (8) Tatau (9) Matu (10) Belaga (11) Selangau (12) Daro (13) Sibu (14) Meradong (15) Sarikei (16) Kanowit (17) Kapit (18) Saratok (19) Julau (20) Pakan (21) Song (22) Lundu (23) Asajaya (24) Betong (25) Samarahan (26) Bau (27)

Kuching (28) Simunjan (29) Lubok Antu (30) Sri Aman (31) Serian. Geographical Indication are Bario from Kelabit Highland, Biris from Simunjan and Bajong from Betong. Other main cultivated landraces included Mamut and Bubuk from Sri Aman, Adan from Ba'Kelalan and Bario Highland, Padi Hitam or Chelum from Serian, Kuching, Sri Aman, Kota Samarahan, Betong, Bau. Base administrative boundaries were obtained from GADM (<https://gadm.org/>) and plotted for illustrative purposes. Data points represent the presence of specific landraces and are not precise geolocations

improved stress tolerance, yield potential, and adaptability. Of particular interest, the Biris cultivar forms a genetically distant cluster with MR219, the modern rice cultivar, indicating unique alleles that could be harnessed to enhance hybrid vigour and resilience in future breeding efforts (Lee et al. 2011). Although the Sarawak rice landraces share similar morphological characteristics throughout development, their adaptation to different environments distinguishes them agronomically. Representative images of these landraces from germination to maturity are shown in Fig. 3.

Indigenous cultivation practices

According to Sah et al. (2024), Sungai Asap, at Bakun, Belaga is one of the hill paddy planting sites of the Kenyah ethnic group, where nearly 70% of the community are full-time hill paddy farmers, although some have shifted to small-scale oil palm cultivation for higher income. Their hill paddy system follows traditional shifting cultivation, beginning with site selection, manual clearing, drying, and controlled burning, followed by group planting, hand weeding, and harvest about six months later, with grain stored in elevated huts for protection (Robin et al. 2023). Irrigation relies entirely on natural water sources such as rivers and rainfall. Farmers receive fertiliser subsidies from the Sarawak Department of Agriculture

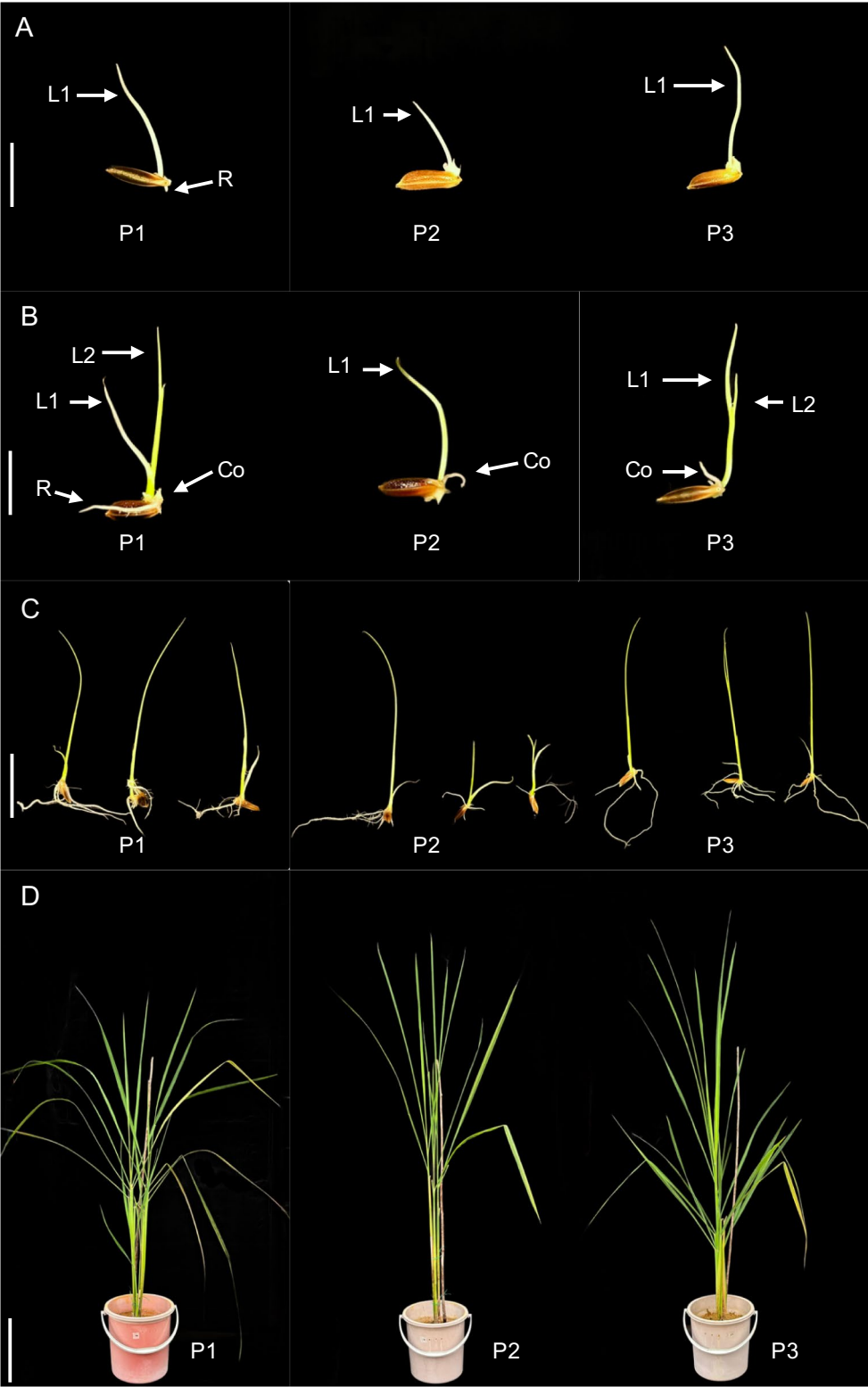


Fig. 3 Morphologies of the rice landrace at the germination stage and the vegetative stage. P1 and P3 have a faster germination rate (1 day) compared to L2 (2 days). **A** Seedlings of 3 days after sowing (DAS). Scale bar=1 cm. **B** Seedlings of 5 DAS. Scale bar=2 cm. **C** Seedlings of 10 DAS. Scale bar=5 cm. **D** Rice plants 4.5 months after sowing. Scale bar=27 cm. P1=Paddy Hitam Wangi, P2=Paddy Bario Merah, P3=Paddy Mamut, R=Root, Co=Coleoptile, L1=Primary leaf, L2=Secondary leaf

but must cover the cost of pesticides and herbicides themselves, adding to overall production expenses (Sah et al. 2024).

In the study by Sah et al. (2024), 13 landraces were collected from two locations in Sungai Asap, Lebu' Kulit and Lepo' Badeng, with assistance from local farmers who typically grow four to five landraces together in a single plot. The landraces included Padi Kerawing, Padi Kerawing Timai, Padi Kerawing Mempat, Padi Abeng, Padi Abeng 2, Padi Abeng 3, Padi Kabeng, Padi Iban, Padi Pasir, Padi Alik, Padi Pulut Sepakau-07, Padi Pulut Sepakau-11 and Padi Lejang. Molecular characterization revealed two main genetic clusters, with some landraces closely related but most showing high genetic variability.

Pigmented rice and cultural use

Pigmented rice landraces highlight one of the unique diversities of Sarawak's local rice, with Bario rice alone exhibiting yellow, red, and black cultivars (Fig. 4). Red, brown and black rice are determined by the concentration of anthocyanin inside the rice. Anthocyanins, major flavonoid compounds in rice, have garnered attention for their multifunctional health-promoting properties. Their strong antioxidant activity arises from their structural ability to scavenge reactive oxygen species (ROS), thereby protecting cells from oxidative stress and lipid peroxidation. This antioxidant capacity is notably higher in pigmented rice landraces, with black rice showing a clear advantage (Palungwachira et al. 2019). When comparing bran color, the total anthocyanin content (TAC) decreased in the following order: purple (2874.0 CGE/100 g), black (1884.0 CGE/100 g), red (8.78 CGE/100 g), and brown (3.09 CGE/100 g), where CGE denotes cyanidin-3-O-glucoside equivalent (Goufo & Trindade 2014). Beyond their antioxidant activity, anthocyanins exhibit significant anti-inflammatory effects, support wound healing, exhibit

anti-ageing, and modulate key signalling pathways that promote cell survival and tissue repair (Goufo & Trindade 2014; Palungwachira et al. 2019). Collectively, the bioactivity of anthocyanins highlights their potential not only as therapeutic agents but also as valuable targets for the development of health-oriented rice cultivars. In some indigenous communities, red or black rice cultivars are reserved for ceremonial use or as postpartum tonics, underscoring both their cultural and nutritional value (Sharifah Zalhura et al. 2016).

Traits of interest for breeding

Abiotic stress tolerance

Global climate change is projected to increase the risk of drought events by up to 30% by the end of this century. In Malaysia, prolonged dry seasons and droughts are occurring more frequently and with greater severity, alongside episodes of heavy rainfall and flooding (Solaymani 2023). Each 1% increase in temperature is estimated to reduce rice production by 7–21% (Ariff 2016), with potential yield reductions of up to 31.3% leading to substantial losses in farmers' gross income (Vaghefi et al. 2016).

Sarawak upland rice landraces often possess larger root and stele diameters, traits that enhance axial conductance and water uptake efficiency under water-limited conditions (Table 1). Higher stomatal density on the adaxial leaf surface may further support water-use regulation during fluctuating environmental conditions (Sylvester Embuas et al. 2025). Upland cultivars such as Nabawan, Tenom, and Sintok from East Malaysia have shown moderate drought tolerance at the seedling stage, with minimal reductions in shoot and root growth under water stress (Omar et al. 2022). *OsRC12* gene is associated drought stress tolerant in rice, as overexpression of *OsRC12-5* was observed when rice plants treated with 10% polyethylene glycol (Li et al. 2014). Elevated expression of the *OsRC12* gene family in Bajong rice has been linked to improved drought resistance; when cloned into other rice mutants, *OsRC12* expression enhanced ion transport and stress tolerance (Yeo 2016), suggesting unique physiological and molecular adaptations in Sarawak cultivars.

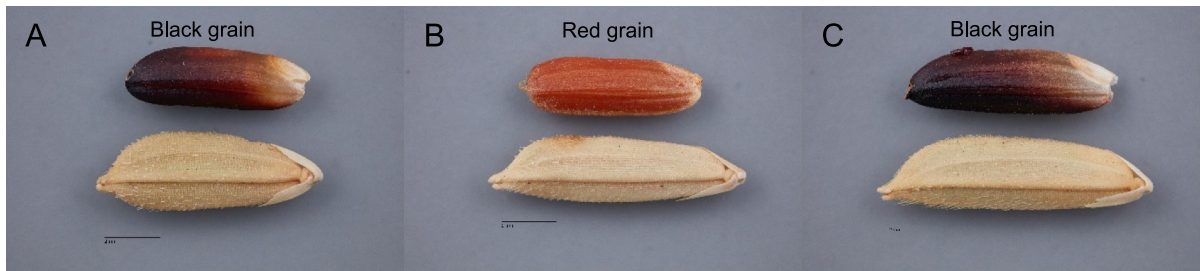


Fig. 4 The husked (Top) and unhusked (Bottom) seeds of Sarawak's pigmented rice landraces with black grain and red grain. **A** Paddy Hitam Wangi (Black grain). **B** Paddy Bario Merah (Red grain). **C** Paddy Mamut (Black grain)

Salinity tolerance

Bajong also demonstrates strong salinity tolerance through complementary physiological and molecular mechanisms. These include limiting sodium accumulation, elevating calcium (Ca^{2+}) levels after salt exposure, and maintaining effective stomatal regulation. Calcineurin B-like proteins (CBLs) Interacting Protein Kinases (CIPKs) is group of protein associated with the Ca^{2+} signalling pathway in plants (Luan 2009). In the study of Xiang et al. (2007), the transgene plants with OsCIPK03, OsCIPK12 and OsCIPK15 shown significant greater abiotic resistant toward cold, drought and salt stress, respectively. Elevated antioxidant enzyme activity suggests an ability to mitigate oxidative stress, while the upregulation of stress-related genes such as CIPK1 and CIPK11 indicates active molecular signalling under saline conditions (Yeo 2016). Biris, a rainfed lowland rice, exhibits exceptional salinity tolerance, outperforming Bajong, MR219, and Bario at the seedling stage in relative water content, germination rate, and radicle and plumule growth under saline stress. Although Biris accumulates high sodium (Na^+), it maintains a relatively low K^+/Na^+ ratio, suggesting a distinctive ionic regulation strategy (Yeo et al. 2018a, b).

Temperature and multi-stress tolerance

Biris also displays high thermotolerance, with a 95% germination rate within two days at 40 °C, likely reflecting its adaptation to the hot lowlands of Simunjan (Luing & Nori 2023). In addition, it can withstand both drought and flooding, reinforcing its potential in multi-stress-resilient breeding.

Landraces from the Kelabit Highlands, such as Bario, Bario Sederhana, and Adan, are adapted to water-limited environments, indicating inherent drought tolerance (Yeo 2016). Bario Sederhana also demonstrates cold tolerance, with the ability to germinate at 12.5–15 °C, consistent with the highlands' average temperatures of 19–22 °C (Luing & Nori 2023). However, both Bario and Bario Sederhana are relatively sensitive to salinity, performing less well than MR219, Biris, and Bajong. Adan rice, in contrast, has shown high productivity in wet rice systems in Ba'Kelalan, suggesting adaptation to specific local agroecosystems (Omar et al. 2022).

The abiotic stress adaptations found in Sarawak rice landraces, ranging from drought and salinity resilience to thermal adaptability and multi-stress tolerance, make them valuable genetic resources for breeding climate-resilient rice cultivars. These traits, shaped by diverse agroecological conditions, can contribute to yield stability and environmental adaptability in modern cultivars. Strategic incorporation of these genetic resources into breeding programs will be critical for sustaining rice production under increasing climatic uncertainties.

Biotic stress resistance

Sarawak rice landraces also harbour valuable traits for biotic stress resistance, offering natural defence mechanisms against major pests and diseases. These genetic resistances are critical for reducing yield losses, lowering chemical inputs, and ensuring sustainable rice production under pest and disease pressure. Yellow stem borer (YSB) is a serious biotic stress that significantly reduces rice yield and grain quality in Malaysia and across Asia (Abdullah

& Mokhtar 2024). In Malaysia, brown planthoppers (*Nilaparvata lugens*) outbreaks have caused yield losses of up to 25% (approx. 870 kg/ha), with severe infestations in Asia reaching as high as 60% (Heong 2009). Yellow stem borer infestations have been linked to yield losses ranging from 20 to 70% (Sharma et al. 2018). Developing pest-resistant or tolerant cultivars reduces reliance on chemical pesticides, enhances yield stability, and supports ecological farming practices by minimizing environmental harm and promoting agroecosystem balance.

According to Hamsein et al. (2020), YSB exhibited a stronger oviposition preference for older plants or those approaching the heading to flowering stage in six rice landraces. In a non-choice study involving Bajong, Bubok, and Bario, the number and size of egg masses were similar, indicating the absence of strong antixenosis resistance or only a weak level in these three landraces (Cheok et al. 2019). In contrast, a choice experiment involving 12 Sarawak paddy landraces revealed that Kanowit was more frequently selected for oviposition by *Scirpophaga incertulas*, highlighting its susceptibility (Ling et al. 2020).

Additionally, in choice experiments, YSB demonstrated a marked preference for laying eggs on the abaxial leaf surface (Hamsein et al. 2020; Ling et al. 2020), whereas no significant oviposition surface preference was observed under non-choice conditions with *S. incertulas* (Cheok et al. 2019). The landraces (Padi Adan, Padi Merawi, Padi Hitam) with low number of egg mass may possess antixenosis traits that can be exploited in breeding to reduce attraction to YSB, minimise yield losses and reduce pesticide dependence (Ling et al. 2020).

Rice blast, caused by *Pyricularia oryzae* (syn. *Magnaporthe oryzae*), is a major biotic disease globally and in Sarawak, with yield losses in Malaysia potentially reaching 50% (Klaubauf et al. 2014; Husin et al. 2020). Its resistance often follows the gene-for-gene interaction model proposed by Flor (1971), where specific rice resistance (R) genes recognize corresponding avirulence (Avr) genes in the pathogen, triggering a defence response. A primary control strategy involves integrating R genes into susceptible cultivars to confer resistance. However, the high genetic diversity, mutation rate, and recombination capacity of *P. oryzae* enable rapid pathogen evolution, frequently causing resistance breakdown and

posing an ongoing challenge for breeders (Scheuermann et al. 2012).

In the study by Lai et al. (2019), four Sarawak rice landraces, namely Padi Semanggang, Padi Perintah, Padi Rendah, and Padi Bubuk were identified with resistance to *Pyricularia oryzae*. These landraces showed resistance to the B2PG isolate of *P. oryzae* obtained from the Serian division, characterized by immune reactions or the presence of only brown specks (lesion types 0–2). These phenotypes suggest the possible presence of qualitative resistance genes (R-genes). In contrast, landraces such as Padi Entangor and Padi Hitam exhibited moderate resistance (lesion types 3–4), which may reflect weak qualitative resistance or the operation of polygenic quantitative resistance mechanisms.

In the study by Yeo et al. (2024) on *AvrPiz-t* gene diversity in *P. oryzae*, multiple haplotypes with distinct mutations were identified and pathogenicity assays revealed that the Merah landrace exhibited resistance to the Malaysian isolate POS17, suggesting the presence of a corresponding R-gene. Similarly, Rafael et al. (2025) conducted a pathogenicity test for the *AvrPi-54 H1* gene from the *P. oryzae* and reported that the Merah landrace exhibited resistance toward the POS17 isolate of *P. oryzae* from the Kanowit region, suggesting that it may carry an R-gene that is recognised by the *Avr*-gene in that isolate. Collectively, these findings indicate that the Merah landrace represents a strong candidate for targeted resistance breeding against diverse *P. oryzae* populations.

Sylvester Embuas et al. (2025) observed the presence of dumbbell-shaped silica cells in rice leaf epidermis of all 44 landraces, including Padi Bario, Padi Bajong, Padi Chelum, Padi Pandan and Padi Kanowit. Higher silica accumulation in plant tissues is associated with increased resistance to fungal pathogens, such rice blast and insect pests. This anatomical trait warrants further investigation to elucidate its potential role in conferring resistance among Sarawak rice landraces. The double silica-cuticle layer also acts as a mechanical barrier reduces transpiration and enhance water usage efficiency.

Rice Tungro Disease (RTD) is a major constraint to rice production in Southeast Asia, caused by the combined infection of rice tungro bacilliform virus (RTBV) and rice tungro spherical virus (RTSV), with the green leafhopper (*Nephotettix virescens*) as the vector (Hull 1996). The first confirmed report of

RTD in Sarawak was in 2012, when field surveys and molecular detection identified its presence across five divisions: Kuching, Samarahan, Sarikei, Sibuan, and Miri (Chong et al. 2015). By 2013 and 2014, disease incidence had declined substantially, with no reported cases in all seven administrative divisions except for Bario and Pa'lungan in the Miri division. This shift in distribution suggested localized persistence rather than widespread transmission. PCR diagnostics, which demonstrated a detection sensitivity up to 10^4 times greater than ELISA for RTBV, confirmed these field observations at the molecular level. The persistence of RTD in Bario and Pa'lungan was linked to agronomic practices such as staggered planting and the retention of ratoon crops during the off-season, both of which maintain reservoirs for the virus and vector populations, thereby promoting sustained virus–vector–host interactions. In contrast, lower planting intensity in other divisions likely disrupted these cycles, contributing to the decline in RTD incidence elsewhere (Chong et al. 2015).

Building on the identification of Bario as a persistent hotspot, Sum and Yee (2018) conducted the first molecular characterization of RTBV isolates from Sarawak, focusing on samples collected from Bario in 2012 and 2013. Sequencing of the partial coat protein gene revealed that the two isolates fell into distinct phylogenetic sub-clusters: MQ 2012–11-Bario grouped closely with Malaysian (Serdang) and Thai isolates, whereas MQ 2013–5-Bario was more closely related to isolates from the Philippines. Their intra-pair nucleotide identity of 93.9% indicates moderate genetic diversity, likely reflecting dynamic viral evolution under local environmental conditions and vector-mediated selection pressures. This genetic heterogeneity suggests that multiple RTBV variants co-circulate in Bario, a factor that could complicate control strategies (Sum & Yee 2018). The integration of epidemiological surveillance with molecular data provides a more complete understanding of RTD dynamics in Sarawak, highlighting both the need for site-specific management strategies in persistent hotspots and the value of these genetic references for future diagnostic development, epidemiological modelling, and breeding programs aimed at enhancing tungro resistance in locally adapted rice cultivars.

Grain quality and aroma

Sarawak's traditional rice landraces are widely recognized for their distinct aromatic traits and vibrant pigmentation. They also exhibited specific grain characteristics. These attributes not only make them appealing as specialty products but also render them valuable genetic resources for rice improvement (Omar et al. 2022). Among the distinguishing traits, aromatic properties stand out prominently. Cultivars such as Bario, Bajong, and traditional cultivars like Rotan (Wai) are recognized for their pleasant aroma and fragrance, contributing significantly to the region's aromatic (Libin et al. 2012; Yeo 2016; Abd Hamid et al. 2022; Luong & Nori 2023; Lam et al. 2025). Biris rice, which gained popularity in the early 1980s, is especially noted for its particularly strong aroma and sustained market demand (Libin et al. 2012; Yeo 2016; Luong & Nori 2023). Investigations have shown that rice with medium amylose content typically expresses stronger aromatic traits than high-amylose cultivars, which may partially explain consumer preference (Saragih et al. 2019). Due to these sensory qualities, aromatic rice cultivars often command higher prices in local and niche markets (Jasim Aljumaili et al. 2018).

Colour is a distinctive feature of Sarawak's rice landraces, often associated with health-beneficial properties. For instance, Bajong is a fragrant rice with a distinctive dark purple grain, while Bario rice is known to exist in several pigmented forms, including white (Bario Adan Halus), brown (Bario Tuan), black (Bario Chelum), and red (Bario Merah Sederhana) (Ronie et al. 2022; Lam et al. 2025). Grain colour is determined by the pigment concentrated in the rice bran layer, with red and black rice being rich in anthocyanins and proanthocyanidins, respectively (Ronie et al. 2022). These pigmented rice types are valued for their antioxidant capacity and are often marketed as functional or health-enhancing foods (Masni & Wasli 2019). Numerous investigations support the health benefits of pigmented rice, which tends to contain higher levels of phenolic compounds and anthocyanins known for their antioxidant, anti-inflammatory, hypoglycaemic, and anticancer activities (Tian et al. 2004; Deng et al. 2013; Palungwachira et al. 2019). The combination effect of nutritional advantages and their rarity in the market, pigmented rice cultivars are attracting growing interest in biofortification

initiatives and specialty-market breeding programs. YF53 is a hybrid rice from white and black rice as to improve the yield and antioxidant properties in rice (Zhang et al. 2015). Additionally, the intact bran layer in pigmented rice contributes to their higher crude fat, ash, and fibre content compared to non-pigmented types (Maulani et al. 2019; Ronie et al. 2022). Notably, Black Adan rice from North and East Borneo has demonstrated the highest levels of protein, fat, and calories among the cultivars studied, whereas White Mayas was most preferred in terms of colour appeal (Saragih et al. 2019). These pigmented landraces represent an untapped reservoir of genetic traits for developing functional rice with enhanced nutritional profiles.

Beyond aroma and colour, Sarawak landraces exhibit a diverse array of grain quality traits that influence their culinary and nutritional value. Bario rice is characterized by its soft texture, fine elongated grains, and delicate mouthfeel after cooking, while Biris rice similarly possesses a soft, cooked texture (Wong et al. 2009; Luing & Nori 2023). The high amylose content in Bario rice flour, ranging from 26.67 to 36.52%, is advantageous in enhancing loaf volume for gluten-free baking applications (Ronie et al. 2022). In terms of grain shape, Bario rice is recognized for its slender grain morphology, while Biris is classified as a long slender type with an average grain length of 6.88 mm, width of 2.47 mm, and a length-to-width ratio of 3:10. It also exhibits low chalkiness, a desirable quality trait (Libin et al. 2012; Ronie et al. 2022; Luing & Nori 2023). Other cultivars, such as Adan and Mayas, are distinguished by their smaller, finer grains, which are often preferred in niche markets (Saragih et al. 2019). Consistent with broader market preferences, Malaysian consumers generally favour long-grain types (Abdul Hadi et al. 2012).

Nutritionally, these landraces offer several benefits that align with health-conscious consumer trends. Bario rice, for instance, has a moderate glycemic index (GI), making it suitable for individuals managing blood glucose levels, diabetes, or cardiovascular conditions (Omar et al. 2022; Ronie et al. 2022; Luing & Nori 2023). Bajong, especially in its unpolished form, has been found to possess a low GI, further enhancing its appeal as a functional food (Lam et al. 2025). Bario Sederhana stands out for its high protein and low-fat content, with Bario rice flour offering a reliable protein source ranging between

6.89% and 9.43% (Omar et al. 2022; Ronie et al. 2022; Luing & Nori 2023). Bajong has also demonstrated promising health-promoting effects due to its rich amino acid profile, including tryptophan and glycine, as well as high phenolic and flavonoid content, contributing to its antimicrobial properties (Lam et al. 2025). Furthermore, extracts from Biris seedlings have shown antioxidant potential, suggesting potential alongside anticancer therapies. The antioxidant potential of other Sarawak cultivars, including Bajong, Bubok, and Bario, also points to their potential for pharmaceutical or nutraceutical development (Yeo 2016; Lam et al. 2025). Additionally, some local cultivars such as Udang Halus and Silah have shown high concentrations of γ -oryzanol, a bioactive compound relevant to health and commercial nutraceuticals, particularly after extended germination (Kiing et al. 2009).

Sarawak's traditional rice landraces, estimated at around 300 types, form a valuable yet underutilised genetic reservoir for breeding and sustainable agriculture (Omar et al. 2022). They are genetically distinct from modern cultivars such as MR219, with heirloom cultivars like Bajong, Biris, and Adan clustering separately (Lee et al. 2011). Many remain informally named and lack formal characterization, raising the risk of genetic erosion through unintended cross-breeding. While yields are generally lower than those of commercial cultivars, these landraces thrive in low-input, traditional systems, showing resilience and adaptability. Their conservation, documentation, and official recognition are essential to safeguard genetic diversity and enhance future food security (Ab Razak et al. 2020).

Past and current status of rice breeding and research

Malaysia has a robust national rice breeding program focused on enhancing yield and resilience in diverse agro-ecological zones. However, the rich and unique genetic diversity present within Sarawak's rice landraces germplasm has received comparatively less attention in national initiatives, representing a significant missed opportunity for targeted trait improvement. According to the DOA (2024), the ministry had established a zone to sustain and protect the genetic purity of several rice landraces germplasm, namely

Bario (Bario Highlands), Adan (Ba'Kelalan), Biris (Lubok Punggor, Samarahan), Bajong (Lubok Nibong, Betong), Wai and Saga (Daro), and Mamut (Sri Aman).

A series of recent research initiatives conducted by Universiti Malaysia Sarawak (UNIMAS) has significantly advanced our understanding of rice cultivation, pest and disease management, and genetic diversity in Sarawak (Table 2). These efforts span diverse scientific areas, including biofungicide development, pathogen characterization, germplasm documentation, insect resistance screening, and risk management in rice farming.

Formal breeding programs and institutional initiatives

Recent initiatives in hybrid rice development in Sarawak include a collaboration between Universiti Malaysia Sarawak (UNIMAS) and Onemas Agriculture Sdn. Bhd. to establish a field research laboratory at Onemas's experimental station in Sungai Padi, Bintarong. The laboratory is intended to support trials of Honglian-type (HL-type) hybrid rice, alongside associated work on precision agronomy, soil and plant nutrition, and pest and disease management. In an initial planting of four HL-type hybrid cultivars imported from China, Onemas reported grain yields of up to 11.08 t ha⁻¹, with grain-setting rates of 94.46% and a crop duration of approximately 88 (Ho et al. 2024). These early results suggest that HL-type hybrids can perform competitively under local conditions; however, multi-season and multi-location trials are still required to evaluate yield stability, input requirements and farmer acceptability. This collaboration illustrates how public–private partnerships can be used to assess the relevance of external hybrid technologies in Sarawak, rather than serving as a fully established breeding pathway at this stage.

Farmer-led selection and indigenous practices

Most farmers in Sarawak rely on indigenous knowledge and experience for rice cultivation, often follow traditional, non-systematic approach (Sang et al. 2018). Heirloom paddy cultivars are typically grown from seeds inherited over several generations or shared among communities (Hanafi et al. 2009; Omar et al. 2022; Abd Hamid et al. 2022). Traditional practices such as planting diverse landraces in

close proximity and exchanging seeds across farm families, villages, or regions can lead to occasional seed impurity (Abd Hamid et al. 2022; Clifton et al. 2024). However, these same practices are also central to maintaining and enriching the genetic diversity of Sarawak's rice (Wong et al. 2009).

Over generations, this continuous cycle of seed exchange and farmer-led selection guided by environmental adaptation and cultural preferences has shaped genetically and phenotypically distinct landraces. For example, cultivars such as Bario Sederhana and Biris, which were sourced from farmers' fields in the Serian District, have become recognized as distinct rice landraces due to their localized adaptation and unique traits (Luig & Nori 2023).

The Iban community in Sarawak, a major rice-farming group, practices self-sustaining paddy farming primarily for household consumption, with surplus sold at local markets. This involves a constant shifting cultivation system within their own land (Daniel et al. 2015). Within a single longhouse community, different types of paddies are meticulously preserved and cultivated for specific cultural, culinary, or seasonal purposes, highlighting the considerable genetic diversity maintained through traditional knowledge and localized selection (Omar et al. 2022).

Molecular and genomic research

Understanding the genetic makeup and variability of local pathogens is critical for designing effective resistance breeding strategies and diagnostic tools. A foundational study by Lai et al. (2019) successfully isolated key avirulence (*Avr*) genes, namely *AvrPiz-t*, *Avr-Pik*, *Avr-Pi54*, and *Avr-Pita1*, from a local Sarawak fungal isolate. The study found that these genes possessed known functional motifs and structural similarities with global strains, thereby highlighting the potential of local isolates resistance breeding. Building upon these findings, subsequent research has provided more detailed insights into the genetic evolution of these specific genes. A study by Yeo et al. (2024), focused on the *AvrPiz-t* gene. Their research reported eight novel haplotypes and identified trends of directional selection. This finding provides additional evidence of the evolving pathogenicity of the fungus and reinforces the complexity of its interaction with specific rice hosts. In a parallel investigation, Rafael

et al. (2025) performed a sequence analysis of the *AvrPi-54* gene, which revealed six novel haplotypes under positive selection. The identification of these haplotypes under positive selection provides strong evidence of the pathogen's ongoing adaptation and diverse virulence, which has significant implications for developing and deploying resistant rice cultivars. Together, these investigations demonstrate a clear and evolving picture of the rice blast pathogen in Sarawak. The initial characterization of key *Avr* genes has been followed by more in-depth genetic analyses, collectively revealing a highly diverse and adaptive pathogen population that poses a continuous challenge for rice breeders.

Yeo et al. (2025) analyzed 44 upland and lowland landraces using 39 SSR markers and identified eight polymorphic loci with high discriminatory power, with RM257 showing the highest polymorphic information content. Despite this, overall genetic divergence between populations was low, and most genetic variation occurred within populations rather than among them. SSR-based clustering revealed that genetic groupings did not correspond to geographic origin, ecotype, or farmer-assigned cultivar names, indicating seed mixing and limitations of traditional classification systems. In contrast, *Maturase-K* barcoding grouped all Sarawak accessions into a single cluster based on shared AA genome type, reflecting the conserved nature and limited resolving power of this marker. Collectively, these findings indicate that Sarawak rice landraces harbour narrow but structured genetic diversity, underscoring the need for conserving existing variation and adopting higher-resolution genomic tools, such as SNP-based approaches, to support effective resistance breeding.

To support pathogen monitoring and laboratory diagnosis, foundational research has profiled the morphological and physiological diversity of *P. oryzae* from multiple rice growing regions in Sarawak. Twelve isolates from Miri, Serian, Kuching, and Sri Aman showed wide variability in colony appearance, pigmentation, and growth across different media, suggesting genetic diversity and varied pathogenic potential (Hussin. et al. 2020). A broader study involving 14 isolates cultured on seven media types determined that oatmeal agar (OMA) best promoted sporulation, while potato dextrose agar (PDA) supported superior growth, offering practical

guidance for fungal isolation and sporulation assays (Rafael et al. 2023). Together, these investigations demonstrate a clear and evolving picture of the rice blast pathogen in Sarawak. The initial characterization of key *Avr* genes has been followed by more in-depth genetic analyses, collectively revealing a highly diverse and adaptive pathogen population that poses a continuous challenge for rice breeders.

Phenotypic traits, resistance, and farming context of landraces

Genetic research on Sarawak's rice cultivars only began in 2006. Despite Sarawak's recognised biodiversity, characterization of its rice germplasm remains limited (Lee et al. 2011; Omar et al. 2022). Similarly, there is a lack of scientific research on the nutritional value and physicochemical properties of Bario rice flour (Ronie et al. 2022).

Scientific evidence on disease and pest resistance remains limited. Resistance characterization of Sarawak landraces against major pathogens like *Pyricularia oryzae* (rice blast) and insect pests is still considered limited. To date, there is also no documentation of bacteria associated with local landraces, indicating an untapped area for future metagenomic research. However, some work has been initiated, such as the molecular characterization of rice tungro bacilliform virus (RTBV) isolates from Bario, which provided the first genetic insight into local virus strains (Sum & Yee 2018).

On the germplasm front, comprehensive phenotyping of 44 lowland and upland rice landraces revealed important morphological and anatomical differences, including traits related to drought adaptation (e.g., root and stele diameter) and phenolic content, which are critical for trait-targeted breeding (Clifton et al. 2024). Supporting this, a localized study in Kampung Lebor documented 19 unique landraces with a wide range of grain sizes, shapes, and colours, and flagged challenges in naming conventions and seed purity, urging the need for systematic landrace documentation (Yeo et al. 2018a, b).

The germination behavior of rice landraces has been clarified through a study on two traditional cultivars, Bario Sederhana and Biris. They were both found to have a base temperature of 10 °C, an optimum between 32 to 33 °C, and distinct thermal time requirements, providing quantified data previously

missing for these Sarawak cultivars (Luing & Nori 2023).

Hossen and Nori (2023) reported the photoperiodic responses of the Sarawak rice landrace Bario Sederhana under controlled day lengths of 8, 9, 10, 11, and 12h. The shortest time to heading was recorded at 10h (70.8 days), whereas both shorter and longer day lengths delayed reproductive development, with the longest delay observed at 12h (132.6 days). The study determined the base photoperiod for flowering to be 7.4h, the optimum at 10h, and the maximum at 14.8h. Extended day lengths of 11–12h significantly enhanced panicle length, spikelet number per panicle, and the proportion of filled spikelets, resulting in the highest grain weight (1.4 g per panicle) at 12h. These findings confirm the pronounced photoperiod sensitivity of Bario Sederhana, which requires approximately five months to reach maturity under Sarawak's near-constant 12h day length, with implications for resource allocation and crop management in traditional farming systems.

Natural compounds have shown promise in disease control. A significant finding is the antifungal potential of *Elephantopus scaber* extract, where a 15% methanol crude concentration inhibited the mycelial growth of *Colletotrichum* sp., *Fusarium solani*, and *Piricularia oryzae* (Hussin et al. 2016). This highlights the plant's potential for biofungicide development.

Lee et al., (2014) provided the first integrated analysis of how genotype, grain morphology, and locality influence phytate content and phytase activity in Sarawak's Bario rice. This is a promising nutritional aspect, as phytate can limit mineral bioavailability while also offering health benefits, and its breakdown depends on phytase activity. The study found that phytate content was mainly shaped by locality factors (cropping and fertilization), whereas phytase activity was strongly linked to intrinsic traits, with rounded grain types and the 'Tuan' cultivar (genotype L) showing the highest activity. By identifying these determinant factors, the research established a foundation for breeding and selection programs aimed at enhancing nutrient bioavailability in this culturally and economically important rice.

Investigations on plant–microbe interactions have also revealed that the diversity and composition of phyllosphere prokaryotes in rice are more strongly influenced by plant organs (leaf vs. stem) than by host

genotype. This suggests that organ-specific factors play a key role in microbial assembly, with implications for understanding endophytic behavior in rice (Yeo et al. 2022).

In the realm of insect resistance, a non-choice study on the yellow rice stemborer (*Scirpophaga incertulas*) demonstrated no significant differences in oviposition preference among Bajong, Bubok and Bario, though females preferred laying eggs on leaves rather than stems (Cheok et al. 2019). A follow-up screening of 12 landraces uncovered significant variation in oviposition preference (antixenosis) but found no clear antibiosis resistance in larval development, suggesting limited resistance mechanisms in the tested landraces (Ling et al. 2020).

Kevin et al. (2007) conducted a preliminary trial to evaluate the growth and nutrient uptake of the highland rice landrace Bario on lowland Bekenu series acid soils under nitrogen and potassium fertilization. Urea (46% N) and muriate of potash (60% K₂O) were applied at recommended rates, and plant performance was compared with unfertilized controls. Fertilization significantly increased plant height, panicle number, and concentrations of N, K, Mg, and Na in both soil and plant stems, although no significant difference was observed in root or stem dry weights or root nutrient uptake. Nitrogen and potassium use efficiencies were low, at 9.90% and 4.23%, respectively, attributed to low nutrient recovery under submerged conditions and the inherently low organic matter of Bekenu soils. Soil pH increased significantly with fertilization, likely due to urea application. The findings suggest that Bario rice can grow in lowland conditions but with poor efficiency in inorganic nutrient use, highlighting the need for integrated organic–inorganic fertilization strategies to improve performance while maintaining the crop's traditional quality attributes.

Finally, risk and safety considerations in rice farming were tackled using an enhanced fuzzy Failure Mode and Effects Analysis (FMEA) approach. The study identified critical occupational health risks, especially chemical misuse and musculoskeletal disorders, during Sarawak's rice production phases, offering a structured risk assessment model that could enhance both productivity and safety in the region (Sang et al. 2018).

While molecular and genomic approaches have provided deep insight into the genetic makeup of

Sarawak's landraces, the sustainability of these resources also depends heavily on how they are managed, conserved, and passed down within local communities. Although important agronomic and quality traits, such as abiotic stress tolerance, disease resistance, and specialty grain characteristics, have been documented in these landraces, many remain characterized primarily at the phenotypic level. The lack of extensive genotypic validation and marker trait association research limit their immediate utility in molecular breeding, thereby highlighting the need for integrative genomic characterization. This underscores the importance of on-farm conservation and indigenous knowledge systems.

Across the reported traits, validation strength varies substantially. To clarify the translational progression from phenotypic observation to breeding confirmation, traits are categorized into three levels of evidence (Table 3).

Genetic conservation and challenges

Ex-situ and in-situ conservation efforts

The gene bank at the Agriculture Research Centre in Semongok has played a pivotal role in conserving rice genetic resources in Sarawak. Since beginning its conservation efforts in 1963 with an initial collection of 305 rice accessions, the repository has expanded steadily through systematic collection missions, farmer contributions, and research collaborations (Bordoni & Hodgkin 2015). According to the Department of Agriculture Sarawak, the gene bank now holds a total of 2011 rice accessions, which include both local and imported cultivars (Clifton et al. 2024). This expansion reflects the state's commitment to preserving rice biodiversity and safeguarding valuable genetic materials for future breeding and research efforts.

While Sarawak has many rice landraces, efforts to properly conserve their genetic resources remain insufficient. Abd Hamid et al. (2022) reported that seed sharing among friends is common (60.71%), whereas the use of high-quality seedlings from government agencies is below 10%.

Threats to genetic purity and identity

The genetic purity of rice cultivars has gradually declined due to several factors, but primarily to farmers' farming practices. One of the key contributors to this genetic erosion is the traditional farming practice of cultivating multiple landraces simultaneously in the same or adjacent plots without physical barriers. This setup facilitates natural cross-pollination among cultivars and unintended varietal mixtures in farmers' seed lots. Although such practices can enhance genetic diversity within the field, they also lead to a gradual erosion of individual cultivars' purity (Clifton et al. 2024).

Another compounding factor is the deeply embedded culture of seed exchange within and between villages. While this exchange promotes genetic diversity by introducing new genotypes into the local gene pool, it can also lead to a dilution of the original genetic makeup of specific cultivars over time (Wong et al. 2009; Lee et al. 2011).

The challenge of maintaining genetic purity is further complicated by the inconsistent naming practice from the farmers. In most traditional rice-growing communities, landraces are identified and named by farmers based on morphological characteristics or cultural significance. However, such farmer-derived nomenclature often lacks consistency and objectivity. Investigations report genetically distinct cultivars sharing the same name, morphologically similar cultivars being named differently. For instance, "Bario Lowland" landraces collected from Meradong and Serian were found to be genetically distinct despite sharing the same name (Wong et al. 2009). The same issue was reported, as the Selasih landraces collected from Betong and Bintulu were classified into clusters II and V, respectively (Lee et al. 2011). These inconsistencies are often the result of synonymy (different names for genetically similar cultivars) and homonymy (the same name for genetically distinct cultivars), both of which contribute to confusion during collection and conservation efforts (Yeo et al. 2018a, b; Clifton et al. 2024).

Beyond naming inconsistencies, continuous cultivation over many generations under varying ecological and agronomic conditions can also drive genetic drift within landraces. Differences in climate, soil type, farming practices, and selection pressures exerted by farmers can cause a cultivar to diverge

Table 3 Summary of reported abiotic, biotic, quality, and yield-related traits in local rice landraces, organized into three levels of evidence: phenotypic observation (Level 1), molecular or genetic support (Level 2), and breeding validation (Level 3)

Trait domain	Trait	Level 1: Phenotypic evidence	Level 2: Marker/gene/QTL support	Level 3: Breeding validation
Abiotic stress	Drought	Nabawan, Tenom, Sintok: Moderate seedling-stage tolerance with minimal growth reduction (Omar et al. 2022)	Bajong: Associated with elevated expression of <i>OsRC12</i> gene family (Yeo et al. 2018a, b)	None documented
	Salinity	Biris: Superior germination and radicle growth under salt stress (Yeo et al. 2018a, b)	Bajong: Linked to upregulation of <i>CIPK1</i> and <i>CIPK11</i> <i>rrcc</i> (B, P. H. Yeo 2016)	None documented
	Heat	Biris: High thermotolerance (95% germination at 40 °C) (Luig & Nori 2023)	No molecular validation reported	None documented
	Cold	Bario Sederhana: Germination at 12.5–15 °C (Luig & Nori 2023)	No molecular validation reported	None documented
Biotic stress	Rice blast	Padi Semanggang, Padi Perintah, Padi Rendah, Padi Bubuk: Type 0–2 lesion resistance in seedling assays (Lai et al. 2019)	Merah: Resistance associated with candidate R-genes recognized by <i>AvrPi54</i> and <i>AvrPi2-t</i> haplotypes (Yeo et al. 2024; Rafael et al. 2025)	None documented
	Stem borer	Padi Adan, Padi Merawi, Padi Hitam: Antixenosis traits (low egg mass counts) (Ling et al. 2020)	No molecular validation reported	None documented
Quality traits	Sensory/physical	Biris: Low chalkiness, long slender grain (Libin et al. 2012; Luig & Nori 2023); Bario and Bario Sederhana: Soft cooked texture and slender grain type (Luig & Nori 2023)	Limited molecular characterization	None documented
Breeding status	Yield/stability	Landraces identified as improvement targets (e.g., Bubok, Bali, Mamut) (Razak et al. 2018)	No genomic selection frameworks reported	No improved lines with multi-location field validation

As shown, most traits remain at Level 1 or Level 2, highlighting the need for field-based breeding validation.

from its original genetic makeup. Over time, this local adaptation makes it harder to recognize the cultivar's original identity (Lee et al. 2011). Such patterns have been observed in highland communities such as the Kenyah of Belaga, where traditional heirloom cultivars show extensive genetic variation despite being maintained under similar cultural names. Many accessions have been found to carry unique genotypes, reflecting cumulative effects of genetic drift and farmer-driven selection (Sah et al. 2024).

To address the challenges in maintaining genetic purity, molecular marker technologies have become essential tools for assessing genetic diversity, identifying cultivars, and evaluating seed purity. Unlike morphological traits, these markers offer more reliable results, being unaffected by environmental or growth conditions and can be applied even at the seedling stage (Amom & Nongdam 2017). Such methods are also important for protecting intellectual property rights and preserving the genetic integrity of rice cultivars.

Although community-led conservation and traditional knowledge play a pivotal role in safeguarding rice genetic diversity, these efforts face multiple systemic constraints. From fragmented documentation systems to limited research investment, a complex set of challenges continues to hinder the effective integration and use of Sarawak's landraces. The following section examines these multifaceted limitations in greater depth.

Limitations

This section explores the structural and institutional bottlenecks that limit the integration of Sarawak's rice landrace diversity into mainstream breeding and conservation frameworks.

The Malaysian Agricultural Research and Development Institute (MARDI) plays a central role in introducing high-yielding seed cultivars such as MR219, a commercial lowland indica cultivar known for shorter planting durations (105–112 days) and improved yields potential (6–8 t/ha) (Hashim et al. 2015; Dorairaj & Govender 2023). MARDI also maintains a national rice gene bank, which includes approximately 1000 accessions from Sarawak. However, many of these have limited trait information (less than 25%) available (Omar et al. 2022).

Despite the genetic value of upland rice, research in this area remains limited, largely due to the perception of low yield potential. This perception persists despite the crop's desirable traits and commercialization potential under good management (Hanafi et al. 2009). Moreover, there is a recognized need for site-specific production guidelines, particularly for red rice, indicating an absence of structured breeding programs for these local types (Masni & Wasli 2019).

To understand the root causes of this underutilization, it is essential to examine the broader institutional and funding landscape that underpins rice research and development in Sarawak.

Institutional and funding constraints

Research and development (R&D) focused on indigenous crops in East Malaysia remains underfunded. There is a strong need for increased research grants and incentives to support institutions, universities, and private entities in exploring and utilizing underutilized rice genetic resources (Omar et al. 2022). Rice production in Sarawak still depends heavily on manual labor with minimal automation or mechanization (Sang et al. 2018). Infrastructure issues such as poor irrigation, unpredictable weather, and limited fertilizer access contribute to low yields. High transportation costs for agricultural supplies in remote and upland areas further constrain productivity (Abd Hamid et al. 2022).

Low participation from private companies further compounds this limitation. Investment in indigenous rice landraces breeding and conservation is often perceived as high-risk due to lower immediate profitability, longer breeding cycles, and uncertain market demand compared to commercial high-yield cultivars (Mahmood 2006). In addition, the absence of clear benefit-sharing mechanisms or intellectual property frameworks for indigenous landraces may discourage corporate involvement (Nijar 2012). In addition to financial and infrastructural limitations, institutional fragmentation in research collaboration further restricts the effective integration of landraces into national breeding programs.

Research and collaboration gaps

There is limited long-term collaboration between universities, the Department of Agriculture (DOA),

and national breeding bodies like MARDI. This institutional fragmentation impedes the coordinated documentation and utilization of agro-morphological and genetic traits and slows integration of Sarawak landraces into national breeding pipelines. While MARDI and DOA Sarawak support research by providing accessions and facilities (Jasim Aljumaili et al. 2018; Sarif et al. 2020), their roles are not yet fully integrated, and collaborative frameworks remain underdeveloped (Omar et al. 2022). There is a call for DOA to formally recognize Sarawak's unique landraces and work more closely with research institutions to establish robust varietal development initiatives. These collaboration gaps also have downstream effects on field-level activities, particularly in the classification, naming, and maintenance of genetic purity among local cultivars.

Cultivar characterization and seed system challenges

A persistent issue in Sarawak is the lack of standardized naming and classification of landraces. The same cultivar may be known by different names across communities. Conversely, different cultivars may be known by a shared name. This informal and overlapping nomenclature system, compounded by close-proximity planting, on-field crossing, and farmer selection practices leads to challenges in maintaining varietal purity (Omar et al. 2022; Clifton et al. 2024). In addition, comprehensive phenotypic characterization remains incomplete for many non-GI landraces, limiting reliable comparison and documentation. The absence of systematic evaluation using standardized frameworks, such as the IRRI Standard Evaluation System (SES) (Irri, 2013), further constrains consistent trait assessment and cross-study comparability. Without formal recognition and systematic agro-morphological and molecular characterization, these unique genetic resources are at risk of erosion. Even where unique landraces are recognized at the community level, the absence of supportive policy and market structures presents another significant barrier to their broader use and commercialization.

Policy and market barriers

Current regulations and policies do not adequately distinguish between commercial high-yielding rice and traditional, high-value landraces. This poses

challenges for branding, certification, and export of specialty rice. One proposal is to establish rice biodiversity centres in Sarawak that preserve both dried and living landrace collections. These centres could assist in characterization, seed banking (e.g., with MARDI and IRRI), and certification processes such as expanding on the Bario Rice Certification Scheme (BRCS). Policy reforms could also support export licensing and facilitate access to niche markets, both domestically and internationally (Omar et al. 2022).

Genetic and agronomic constraints

Despite their valuable genetic diversity, the utilization of Sarawak rice landraces in breeding programs presents several practical constraints. Many lowland landraces exhibit tall plant architecture, increasing lodging susceptibility under high-input or mechanized production systems. For instance, Bali 1, Bali 2, and Bali 3 have culm heights ranging from 156.52 to 172.60 cm (Razak et al. 2018), while Kanowit (170.1 cm) (Clifton et al. 2024) and Mamut (150.77 cm) (Yeo et al. 2018a, b) also display substantially taller stature compared with modern semi-dwarf cultivars. In addition, several landraces are characterized by long maturity duration. Kanowit requires approximately 120 days to heading and 151 days to flowering, and Bario Sederhana may take up to five months to reach maturity (Table 1), compared with 105–112 days for the modern cultivar MR219 (Hashim et al. 2015). This results in a longer breeding cycle when local landraces are selected as the parent line. Photoperiod sensitivity further restricts their adaptability. Bario Sederhana, for example, heads at 70.8 days under a 10h photoperiod but is delayed to 132.6 days under a 12h day length, limiting planting flexibility and double-cropping potential (Hossen & Nori 2023).

Moreover, the use of rice landraces as donor parents may increase the risk of linkage drag, whereby undesirable traits are co-inherited with target alleles due to tight genetic linkage. In Sarawak rice landraces, traits such as tall stature or late maturity may therefore be introgressed alongside favourable resistance genes, particularly when crossed with elite semi-dwarf cultivars. To date, no genetic mapping or quantitative trait locus (QTL) analyses have been conducted in Sarawak rice landraces to directly quantify linkage drag; therefore, it remains a plausible

breeding constraint. Future breeding efforts integrating molecular mapping, high-resolution genotyping, and marker-assisted selection will be essential to assess and minimize unwanted genomic segments while retaining desirable alleles. This is consistent with the limited progression of reported traits beyond phenotypic or molecular characterization (Table 3)."

Opportunities for future breeding programs

Participatory plant breeding (PPB)

Participatory Plant Breeding (PPB) is a collaborative crop improvement model that actively involves farmers and other stakeholders in all major stages of a breeding program, including setting priorities, selecting parents, and evaluating progenies (Sperling et al. 2001; Ceccarelli & Grando 2020, 2022). Unlike conventional breeding, which is often centralized and scientist-led, PPB is grounded in the principle that co-decision-making among farmers, researchers, and institutions leads to more relevant and sustainable varietal outcomes (Ceccarelli & Grando 2020).

PPB differs from Participatory Variety Selection (PVS), where farmers only participate in the evaluation of finished breeding lines. While PVS is easier to implement and useful for rapid feedback, it risks excluding farmer input at earlier, critical stages (Burman et al. 2018; Ceccarelli & Grando 2020). In contrast, PPB is decentralized and iterative, allowing farmers to evaluate breeding material under local conditions as early as the F₃ generation (Colley et al. 2021). Two broad institutional models of PPB exist. In formal-led PPB, researchers manage the program while integrating farmer input at structured stages, often aligning with formal seed systems and cultivar release protocols. In farmer-led PPB, farmers define breeding goals, manage selection, and lead dissemination, with researchers acting as facilitators (Sperling et al. 2001).

PPB has been applied in over 69 countries across 47 crop species, including rice, where it is especially prominent due to the crop's diversity and socio-cultural importance. Notably, the participatory release of the Jethobudho landrace in Nepal demonstrates the model's success (Ceccarelli & Grando 2020). PPB consistently results in cultivars with higher adoption rates, better adaptability, and increased farmer

satisfaction. Farmer-selected lines often outperform conventional ones or provide additional locally valued traits, contributing to genetic diversity and system resilience (Ceccarelli & Grando 2020, 2022).

The approach also empowers communities through shared decision-making, enhances gender inclusivity, and supports organic and low-input systems. Its flexibility makes it a strong candidate for climate-resilient breeding, as decentralized trials expose germplasm to diverse and shifting environmental pressures (Ceccarelli & Grando 2022). Community engagement in PPB is multidimensional. Farmers contribute to setting breeding priorities, selecting germplasm (local or exotic), conducting on-farm evaluations and even making crosses. They provide practical insights into traits like grain quality, pest resistance and taste, ensuring varietal outputs meet user needs (Sperling et al. 2001). Farmer organizations, cooperatives, and local seed networks also play vital roles in seed multiplication, popularization and dissemination further embedding PPB within local systems. Degrees of participation vary from consultative (feedback-based) to collegial (farmer-led programs). While full collegial models are rare, they offer the greatest potential for decentralized innovation. Importantly, PPB is not defined merely by farmers providing land or labour; genuine participation requires shared authority in decision-making (Sperling et al. 2001).

In the context of Sarawak, characterized by agroecological complexity and rich indigenous knowledge, PPB offers a promising, context-specific strategy for rice breeding (Table 2). This approach integrates collaborative selection with advanced biotechnological tools within a holistic landrace-based breeding framework for climate-resilient rice improvement (Fig. 5).

Marker-assisted and genomic selection

Trait-targeted breeding using molecular markers

Molecular markers are powerful tools for accelerating trait introgression and improving breeding efficiency. In Sarawak SSRs (Simple Sequence Repeats) and SNPs (Single Nucleotide Polymorphisms) markers have been applied to characterize the genetic diversity of local landraces. SSRs are highly polymorphic, reproducible, and co-dominant, making them suitable for assessing genetic relationships and guiding association mapping (Wong et al. 2009; Lee et al. 2011;

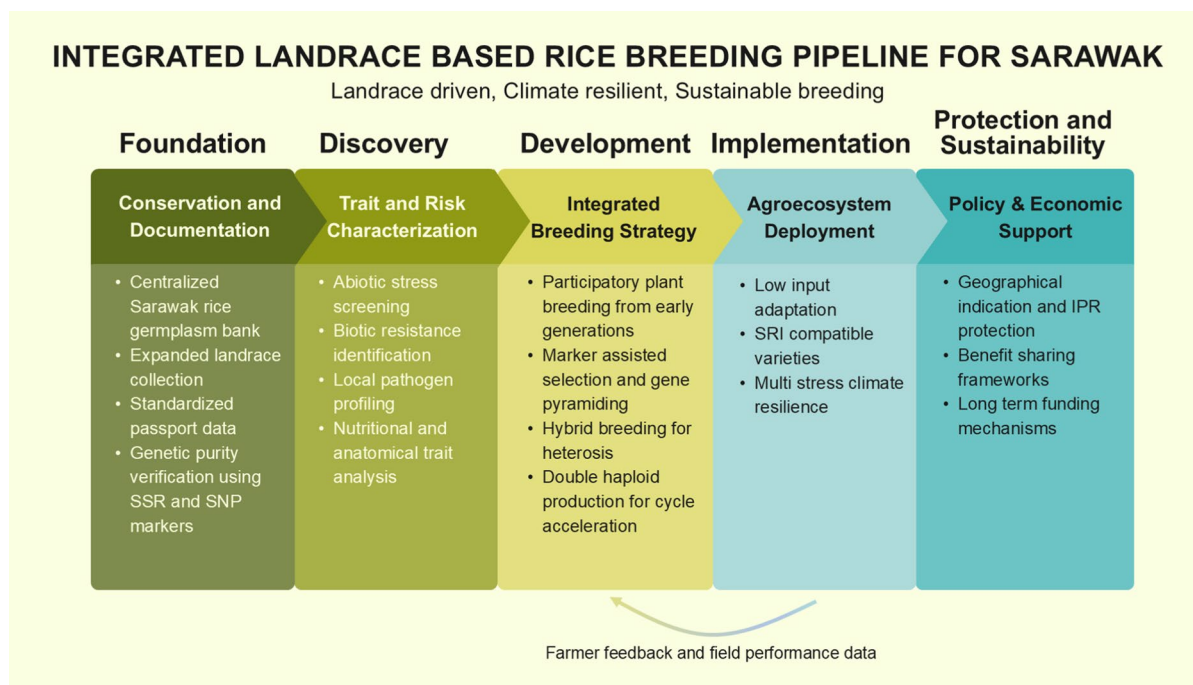


Fig. 5 Conceptual landrace-based breeding pipeline for climate-resilient rice improvement in Sarawak

Jasim Aljumaili et al. 2018; Sarif et al. 2020). SNP markers, enhanced by next-generation sequencing (NGS) platforms, offer high throughput and low error rates (Ab Razak et al. 2020).

Aroma, a key trait influencing marketability, has been genetically profiled using SSRs in aromatic rice from Sarawak (Jasim Aljumaili et al. 2018). Bajong and Biris have both shown potential for drought and salt tolerance. In Bajong, transcriptomic analyses via RNA-Seq revealed secondary metabolite pathways linked to salinity tolerance (Yeo 2016; Lam et al. 2025). Biris, meanwhile, maintained high germination under saline conditions, an important trait for areas with irregular water access.

In addition to abiotic stress tolerance, several Sarawak landraces also exhibit resistance to major rice diseases and pests. Sarawak landraces show resistance to blast (*Pyricularia oryzae*) and stem borers. Cultivars such as Padi Semanggang, Padi Perintah, Padi Rendah, and Padi Bubuk resist blast isolates like *B2PG* (Rafael et al. 2025). Novel *AvrPi-54* and *AvrPiz-t* haplotypes in local *P. oryzae* isolates provide valuable data for resistance breeding (Cheok et al. 2019; Lai et al. 2019; Rafael et al. 2025).

Accelerating breeding cycles and reducing linkage drag

Marker-assisted selection (MAS) has emerged as one of the most effective tools in modern rice breeding, offering advantages in speed, accuracy, biosafety, and consistency over traditional phenotypic selection (Jena & Mackill 2008). By enabling precise introgression of desirable QTLs and genes into elite lines, MAS reduces the risk of linkage drag, which can compromise grain quality or yield (Simon et al. 2023). SSR-based fingerprinting facilitates accurate identification of accessions and maintains varietal purity, ensuring that elite lines remain true-to-type (Wong et al. 2009; Razak et al. 2018).

Integration of high-throughput genotyping, genome-wide association studies (GWAS), and functional genomics accelerates the discovery of causal genes for target traits. To optimize local breeding pipelines, breeder-friendly, allele-specific markers are essential for rapidly deploying stress resistance into elite Sarawak cultivars (Simon et al. 2023).

Beyond accelerating trait introgression, a particularly powerful MAS application is gene pyramiding. Multiple resistance or tolerance genes (or QTLs) are

combined into a single cultivar to provide durable, broad-spectrum protection against biotic and abiotic stresses (Joshi & Nayak, 2010). For example, in rice blast resistance breeding, Xia et al. (2019) used marker-assisted backcross breeding (MABB) to develop monogenic lines, two-gene pyramids (e.g., Pi46 + Pi2, Pi46 + Pita, Pi2 + Pita), and a three-gene pyramid (Pi2 + Pi46 + Pita) within a common background. While multi-gene pyramids offered broader resistance, the three-gene combination also resulted in yield penalties, highlighting the need for strategic trait stacking and careful trade-off analysis (Xia et al. 2019).

For Sarawak's rice sector, where breeding programs must address multiple stressors in complex agroecological systems MAS offers a unique capacity to integrate diverse local landrace traits while maintaining yield stability and grain quality. When combined with participatory approaches, MAS can deliver cultivars that are both scientifically robust and farmer accepted.

Gene editing as a future tool

CRISPR-Cas gene editing technologies present an emerging alternative to conventional breeding, enabling precise modifications in elite genetic backgrounds while bypassing the need for donor crosses and eliminating linkage drag (Simon et al. 2023). This capability is particularly valuable in resource-limited contexts like Sarawak, where access to multi-location trials or large backcross populations may be constrained. In rice, CRISPR-Cas9 has been applied to enhance both yield potential and stress resilience. For yield improvement, knockouts of *GS3* (grain size), *DEP1* (panicle architecture), *IPA1* (plant architecture), and *Gn1a* (grain number per panicle) in the Zhonghua 11 cultivar have produced larger grains, more flowers per panicle, and overall yield gains (Rengasamy et al. 2024). For abiotic stress tolerance, knockout of the *OsSAP* (*Oryza sativa* Senescence-Associated Protein) gene altered antioxidant defences and improved drought tolerance, while also influencing yield-related traits under water-limited conditions (Park et al. 2022). Structural improvement for yield stability has also been achieved through editing of *SD1* (Semi-Dwarf1) and *DEP1*, generating semi-dwarf rice lines with enhanced lodging resistance and more stable yields (Hu et al. 2019).

Despite its precision and potential, CRISPR implementation in Sarawak will depend on Malaysia's regulatory framework and public acceptance. In the near term, marker-assisted selection (MAS) remains the more accessible option, supported by established laboratory capacity, lower regulatory barriers, and strong integration within existing breeding pipelines. Ultimately, while genetic tools such as CRISPR can rapidly deliver improved traits, their success will hinge on ensuring that new cultivars remain compatible with Sarawak's predominantly low-input farming systems.

Integration with sustainable farming systems

Breeding for low-input and organic conditions

Traditional Sarawak rice landraces are inherently suited to low-input environments, favored by farmers for their pest resilience and adaptability to unploughed, rainfed conditions (Dorairaj & Govender 2023). Despite their lower yield potential, these landraces thrive without irrigation or chemical inputs and are often grown in mixed systems where fertilizer is shared across crops leading to suboptimal nutrient availability for rice.

To support these traditional farming systems, breeding programs should focus on enhancing performance under organic or low-input conditions. The System of Rice Intensification (SRI), adopted in highland areas such as Ba'kelalan, has demonstrated improved yields by optimizing spacing, nutrient use and water management. Yields and productivity under SRI are almost double those achieved with conventional methods in many Asian rice-growing regions (Aris & Fatah 2019). In addition, SRI practices can reduce water usage by 20–50% and lower greenhouse gas emissions by 65–73% (Thakur et al. 2016). Developing cultivars specifically adapted to SRI or other agroecological systems could improve both sustainability and farmer acceptance.

Climate resilience for upland and flood-prone environments

Climate variability is a major constraint in Sarawak rice production, with challenges including high temperatures during anthesis, water scarcity and flooding.

These stressors reduce yield through decreased pollen viability and poor grain filling.

Sarawak's diverse landraces offer unique adaptive traits. Tall cultivars such as DV107, Tidong Tambunan and Padi Randau exhibit elongation traits beneficial for flood-prone lowlands. Meanwhile, Biris and Bajong also exhibit early-stage salt tolerance, making them candidates for breeding in water-stressed or saline environments. Understanding the biochemical and physiological markers of these adaptations will be key to developing resilient cultivars.

Genetic improvement for biotic stress resistance, especially via host resistance, is the most cost-effective and sustainable strategy for ensuring yield stability. Integrating these traits into climate-resilient cultivars through MAS or participatory breeding will enhance the viability of rice cultivation in marginal, upland or environmentally sensitive areas.

Given the complexity of combining multiple adaptive traits such as submergence tolerance, salt tolerance and drought resilience, marker-assisted selection (MAS) offers the most practical and efficient approach for integrating these traits into elite Sarawak lines. MAS enables precise tracking of target alleles from donor landraces, minimizes linkage drag, and shortens breeding cycles compared to conventional methods. For example, tall flood-tolerant lines could be crossed with salt-tolerant lines, with MAS applied to ensure retention of both tolerance genes in the progeny. The resulting pyramided cultivars would deliver enhanced climate resilience while maintaining yield stability, making MAS the most suitable primary strategy for this objective in the current Sarawak breeding context.

Implications for research, policy and practice

Addressing key limitations

Mathew et al. (2025) highlighted Kampung Skuduk and Kampung Chupak in Siburan as two of the few locations in Sarawak where wet paddy is cultivated twice annually. Most farmers with access to paddy land in these villages also practise agroforestry, with around 60% citing food security as their primary motivation and about 30% identifying supplementary income as an additional benefit. These communities therefore illustrate how rice production, agroforestry

and livelihood objectives can be combined, and provide one example of how productivity gains might be pursued alongside more diversified and sustainable land use.

Institutional and funding constraints

Rice research and development in Sarawak has been affected by fragmented and short-term funding, which limits sustained trait characterization, breeding cycles and on-farm evaluation. Addressing these constraints is likely to require more predictable and coordinated support from public agencies, research institutions and private partners. In the short term (approximately one–two years), one possible mechanism would be to create a dedicated funding window focused on indigenous rice R&D, with competitive grants available to universities, research institutes and agri-tech enterprises. Such a window could draw on state allocations, federal agricultural programs and relevant international biodiversity or food-security schemes. Clear benefit-sharing and intellectual-property arrangements, aligned with the Nagoya Protocol, would help to ensure that both farming communities and private investors are fairly recognized.

Over the medium term (three–five years), additional instruments could include risk-sharing schemes in which the government co-invests in early breeding stages or underwrites part of the cost of field trials, together with support for mechanization hubs that provide shared planting, harvesting and milling services. Improvements in rural roads and irrigation infrastructure in major production zones could further reduce transaction and transport costs, lower post-harvest losses and enhance yield potential. While the specific mix of instruments will depend on local policy priorities and budget constraints, these examples illustrate the types of coordinated investments that could improve the enabling environment for the use of Sarawak rice landraces in breeding and production.

In the long term (beyond five years), the R&D fund could evolve into a sustainable endowment to protect research continuity from political or budgetary fluctuations. Mechanization hubs could be expanded into regional value-adding centres, integrating milling, branding, and packaging operations to help farmers capture a greater share of market value. Finally, with production capacity and quality standards in place, Sarawak could develop export-oriented branding for

premium indigenous rice cultivars, building an additional revenue stream for rural communities while strengthening the state's agricultural identity in global markets.

Research and collaboration gaps

A coordinated Sarawak rice germplasm bank could provide a shared platform linking the Department of Agriculture (DOA), MARDI, universities and private breeders. By centralising seed accessions and associated passport data, such a facility would allow stakeholders to work from verified genetic materials, reduce duplication of effort and improve comparability of data across investigations. Formal collaboration agreements could specify shared responsibilities for collection, characterization and maintenance, while also defining transparent rules for access and use. In this way, a common germplasm platform could help to integrate Sarawak landraces more systematically into national breeding pipelines and support long-term cooperation in research, training and capacity building, rather than isolated, institution-specific initiatives. In line with this objective, a Sarawak rice gene bank initiative has planned to support the systematic collection and characterization of under-documented landraces, including Padi Bubuk, Padi Chelum, Padi Mamut, Padi Merah, and Padi Wai. The program aims to generate standardized agronomic datasets to facilitate future breeding and conservation efforts.

The effectiveness of any germplasm bank would depend heavily on the quality of its passport data. At present, Sarawak's landraces are only sparsely recorded, with much of the information on their origins, traits and uses dispersed across reports or retained in farmer knowledge. This lack of centralised, standardized documentation makes it difficult for breeders to identify accessions with specific adaptive traits, while genetic erosion remains a concern as traditional cultivation declines. A germplasm bank that assembles passport data on collection location, associated farmers, agro-ecological context and notable phenotypic traits would help convert fragmented records into a structured and searchable database (Vaughan 1991; FOA 2014; Jamora & Ramaiah 2022). Such documentation would make it easier to target traits such as the salinity tolerance associated with Biris or the drought resilience of upland Sarawak

cultivars for use in crossing programs (Jackson 1997; Cai et al. 2025).

Beyond direct breeding applications, a well-documented germplasm bank would also support research on disease and stress resistance. Vasudevan et al. (2014), for example, screened 4,246 geographically diverse rice accessions from 13 major rice-growing countries for blast resistance and were able to annotate useful resistance traits. Applying similar approaches in Sarawak and explicitly linking seed accessions to research on *Pyricularia oryzae* and other major pathogens, could accelerate the identification of pest- and disease-resistant materials. In addition, a curated germplasm collection linked to passport and ethnobotanical information would help safeguard cultural heritage by recording indigenous cultivar names and associated traditional knowledge, thereby supporting recognition and benefit-sharing for local communities (Wang et al. 2024).

In summary, a Sarawak rice germplasm bank equipped with robust passport data has the potential to help secure genetic diversity, strengthen breeding and research capacity, and contribute to the conservation of the cultural and ecological legacy associated with local rice cultivars. Collectively, these functions could support longer-term objectives related to food security and agricultural resilience in the state.

Intellectual property rights and geographical indications

Policies on intellectual property rights (IPR) for local cultivars, particularly through Geographical Indications (GIs), can play an important role in linking agricultural resilience with rural livelihoods. Protecting local cultivars can provide economic incentives for farmers while contributing to food security by helping to maintain diverse food sources shaped by regional ecological conditions (Manap et al. 2007; Fahmi et al. 2023). GIs, as one form of IPR, identify agricultural products whose quality or reputation is associated with their geographical origin (Moor & Aziz 2011; Gautam et al. 2012). In Malaysia, such products are protected under the Geographical Indications Act 2000, which covers distinctive community-based cultivars including Bario, Biris and Bajong rice in Sarawak (Moor & Aziz 2011; Omar et al. 2022). GI registration can add commercial value, support

premium branding and facilitate access to niche, higher-value markets (Manap et al. 2007).

IPR instruments are also relevant from the perspective of traditional knowledge and long-term stewardship. Farmers, local communities and indigenous peoples have maintained many of these cultivars over generations, and legal recognition of their contributions can help to protect both genetic resources and associated knowledge (Gautam et al. 2012; Andersen & Winge, 2017; Fahmi et al. 2023). In Malaysia, the Protection of New Plant Varieties Act 2004 (PNPVA 2004) complements the GI system by providing a sui generis framework intended to encourage the development of superior cultivars while recognizing the role of farmers and communities (Manap et al. 2007; Moor & Aziz 2011). This approach is broadly consistent with the Third National Agricultural Policy (NAP3), which emphasizes biodiversity conservation, regulates access to genetic resources and promotes the domestication and use of valuable species (Moor & Aziz 2011).

Sui generis systems adopted in countries such as India and Malaysia seek to balance breeders' rights with farmers' rights (Moor & Aziz 2011; Gautam et al. 2012). They often protect, to varying degrees, the ability of farmers to save, use, exchange and sell farm-saved seed for non-commercial purposes (Moor & Aziz 2011; Andersen & Winge, 2017). In some frameworks, farmers and communities can register traditional cultivars, sometimes with reduced or waived fees, which provides formal recognition of their role as innovators and custodians of agrobiodiversity (Manap et al. 2007; Gautam et al. 2012).

An effective IPR framework in the context of rice landraces is likely to be most robust when combined with fair and equitable benefit-sharing mechanisms. Such mechanisms can help ensure that both breeders and farming communities participate in decision-making on the conservation and sustainable use of plant genetic resources and share in any resulting benefits (Gautam et al. 2012; Andersen & Winge, 2017). This type of legal infrastructure not only supports farmers' rights but can also facilitate participatory varietal improvement, which is particularly relevant where hybrid rice breeding and other innovation pathways depend on close interaction between scientists and local knowledge holders.

Plant tissue culture and hybrid breeding

Plant tissue culture in rice breeding

Plant tissue culture is widely used in rice improvement as a platform for in vitro selection under defined conditions. By exposing callus or other tissues to specific abiotic stresses in the laboratory, breeders can screen for tolerance to factors such as drought or salinity with reduced environmental noise at early developmental stages (Sahu et al. 2023). For example, Biswas et al. (2002) showed that callus regeneration declined at higher polyethylene glycol (PEG) concentrations and, in the process, identified the C 14–8 line, an indigenous rice cultivar from Bays Island, India, with strong drought tolerance.

Anther culture provides a related approach to accelerating selection by generating double-haploid (DH) or dihaploid plants within one or two generations, rather than the five to six generations typically required in conventional breeding (Ingle et al. 2023). By fixing segregating loci in a single generation, DH production enables earlier and more efficient identification of superior genotypes, potentially lowering both time and cost per selected line (Purwoko et al. 2010; Prigge et al. 2012) technology has already led to several commercially grown rice cultivars in countries such as India, China, South Korea, the Philippines, Argentina and Hungary, illustrating its utility as a mainstream breeding tool (Samantaray et al. 2021).

Although most published DH and in vitro selection work has focused on non-Sarawak germplasm, the same approaches could, in principle, be applied to Sarawak landraces to capture complex traits such as combined drought–salinity tolerance, grain quality and pigment-related nutritional properties in a more systematic way.

Hybrid rice breeding

Hybrid breeding exploits heterosis, where crosses between genetically diverse parents produce offspring with improved performance for traits such as biomass, growth rate and fertility (Birchler et al. 2010; Longin et al. 2012). Hybrid rice frequently show yield advantages, enhanced tolerance to abiotic stresses, stronger resistance to pests and diseases, and facilitate the stacking of dominant traits within single cultivars. A

recent example is the iS1000 hybrid, which achieved 17.06 t ha⁻¹ and showed improved resistance to bacterial blight and rice blast (He et al. 2022). From a commercial perspective, hybrids also tend to support continued seed production because inbreeding depression in later generations (e.g. F₂) encourages farmers to replace seed regularly (Longin et al. 2012; Paril et al. 2024).

The substantial genetic divergence documented among Sarawak rice landraces suggests that they could serve as useful parental pools for hybrid breeding programs. Greater genetic distance between parental lines is often associated with stronger heterosis, providing a broader set of gene combinations, masking deleterious recessive alleles, and enabling complementation among favourable loci, such as higher yields, faster development, and greater biomass (Tomkowiak et al. 2020; Farinati et al. 2023). Hybrids derived from parents with contrasting adaptations, for example, upland, drought-tolerant landraces crossed with high-yielding lowland types, may carry a wider range of alleles for tolerance to drought, salinity, temperature extremes and biotic stresses (Salgotra & Chauhan 2023). In environments where climate variability is increasing, such diversified hybrid backgrounds could contribute to more stable performance, particularly if combined with participatory testing in the target production systems. Further research is exploring the identification of fertility restorer (Rf) genes from selected landraces for application in cytoplasmic male sterility (CMS) hybrid rice breeding systems.

Feasibility of molecular breeding implementation in Sarawak

The successful translation of molecular breeding strategies into practical varietal development depends on local infrastructure, technical expertise, and sustained institutional support. In Sarawak, molecular research on rice has primarily focused on SSR-based diversity assessment and basic genotyping (Wong et al. 2009; H. H. Lee et al. 2011; Anisuzzaman et al. 2022; F. K. S. Yeo et al. 2025), reflecting the availability of PCR-based laboratory facilities and conventional marker analysis. However, high-throughput SNP genotyping platforms, large-scale next-generation sequencing infrastructure, and gene-editing systems such as

CRISPR-Cas9 are not yet fully established locally and often require external collaboration.

Several implementation barriers currently limit the deployment of advanced molecular breeding technologies. These include incomplete phenotypic databases for local landraces, limited integration between germplasm conservation and formal breeding programs, restricted funding for long-term genomic selection pipelines, and insufficient large-scale field validation systems. In addition, the absence of centralized germplasm characterization data reduces the efficiency of marker-assisted selection and allele mining efforts.

A phased implementation strategy is therefore more realistic than immediate adoption of high-end genomic platforms. In the short term, emphasis can be placed on systematic phenotyping and the use of SSR and low-density SNP panels for pre-breeding and parental selection. Medium-term priorities include establishing a centralized Sarawak rice gene bank database, strengthening collaboration with national institutions for high-throughput genotyping services, and building technical capacity in bioinformatics and quantitative genetics. In the longer term, investment in genomic selection frameworks and gene-editing capabilities may enable precision improvement of locally adapted landraces. Such a staged approach aligns technological ambition with institutional readiness, ensuring that molecular breeding strategies are both scientifically robust and practically achievable within the Sarawak context.

Conclusion

Sarawak's indigenous rice landraces constitute a distinctive reservoir of genetic diversity that has been shaped by long-term farmer management across contrasting agro-ecological zones. The literature reviewed here documents adaptive traits related to drought and salinity tolerance, temperature and multi-stress resilience, resistance or reduced susceptibility to key pests and diseases, and a wide spectrum of grain quality, pigment and nutritional attributes. Together, these characteristics indicate clear potential breeding value for climate-resilient, nutritionally enhanced and market-differentiated rice cultivars.

At the same time, several gaps are evident. Many landraces remain incompletely characterized at phenotypic and molecular levels; documentation and

passport data are fragmented across investigations; and links between on-farm management, ex situ collections and formal breeding pipelines are still limited. Strengthening both in situ and ex situ conservation (gene bank), improving traceability of accessions, and clarifying genetic relationships among landraces and between landraces and modern cultivars would provide a stronger foundation for future use.

A range of breeding tools is now available to translate these resources into improved cultivars, including double haploid production, in vitro selection, conventional and hybrid breeding, and participatory approaches that integrate farmer preferences from early generations onward. In parallel, policy instruments such as Geographical Indications (GI) and plant variety protection frameworks can help ensure that economic benefits and recognition flow back to farming communities that have maintained these landraces, while also supporting responsible access and benefit-sharing.

Overall, the evidence indicates that Sarawak's rice landraces remain underutilized, yet they represent strategic genetic assets with substantial potential for breeding, conservation, and value-addition. With systematic integration of genetic, agronomic, socio-economic, and policy research, these locally important cultivars can be progressively elevated into nationally and even globally relevant genetic resources, strengthening regional food security and contributing to broader efforts to conserve crop diversity under increasingly variable climatic conditions. Crucially, conserving and improving these landraces goes beyond documenting diversity, it supports rural livelihoods and cultural heritage while delivering practical benefits to smallholder farmers through higher-yielding, climate-resilient cultivars that can improve income stability. At the same time, it reinforces Malaysia's rice self-sufficiency and safeguards a valuable pool of adaptive traits for future breeding programs, ensuring long-term resilience for both local food systems and regional agricultural development.

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Declarations

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