

Insights into panicle trait variation and *DUF-640* gene conservation in Indonesian foxtail millets (*Setaria italica*)

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Electronic Supplementary Material (ESM)

The authors are fully responsible for both the content and the formal aspects of the electronic supplementary material. No editorial adjustments were made.

Table S1. Source of the sequences for phylogenetic tree construction

GenBank accession number	Species	Total score	Coverage (%)	E value	Similarity (%)	Sequence length (aa)
XPR33401.1	<i>Setaria italica</i> cv. ICERI-5					214
XPR33402.1	<i>Setaria italica</i> cv. ICERI-6					214
XPR33403.1	<i>Setaria italica</i> cv. ICERI-7					214
XPR33404.1	<i>Setaria italica</i> cv. Botok-4					214
XPR33405.1	<i>Setaria italica</i> cv. Mauliru-2					214
XPR33406.1	<i>Setaria italica</i> cv. Botok-10					211
XPR33407.1	<i>Setaria italica</i> cv. NTB-1					207
XPR33408.1	<i>Setaria italica</i> cv. Buru					214
XPR33409.1	<i>Setaria italica</i> cv. Hambapraing					196
RCV42509.1	<i>Setaria italica</i> cv. Yugu1	399	98	1.0×10^{-139}	96.21	207
XP_034571411.1	<i>Setaria viridis</i>	434	100	4.00×10^{-153}	100.00	214
XP_021311543.1	<i>Sorghum bicolor</i>	387	100	3.00×10^{-134}	89.33	223
XP_039831029.1	<i>Panicum virgatum</i>	328	100	4.00×10^{-111}	90.23	212
XP_025795635.1	<i>Panicum hallii</i>	320	100	5.00×10^{-108}	90.78	215
XP_037418735.1	<i>Triticum dicoccoides</i>	285	100	3.00×10^{-94}	79.07	206
XP_044324749.1	<i>Triticum aestivum</i>	284	100	6.00×10^{-94}	78.60	206
XP_062200265.1	<i>Phragmites australis</i>	282	100	4.00×10^{-93}	85.51	205
XP_044958408.1	<i>Hordeum vulgare</i> subsp. <i>vulgare</i>	262	100	2.00×10^{-85}	75.23	206
XP_003571880.1	<i>Brachypodium distachyon</i>	260	88	2.00×10^{-84}	79.47	207
PWZ41807.1	<i>Zea mays</i>	256	81	4.00×10^{-83}	79.77	198
XP_047045063.1	<i>Lolium rigidum</i>	253	91	6.00×10^{-82}	77.95	204
XP_051218273.1	<i>Lolium perenne</i>	247	92	2.00×10^{-79}	74.62	203
XP_052134976.1	<i>Oryza glaberrima</i>	244	75	4.00×10^{-78}	88.75	208
XP_040384270.1	<i>Oryza brachyantha</i>	244	78	4.00×10^{-78}	82.08	216
NP_001411433.1	<i>Oryza sativa</i> Japonica	244	75	4.00×10^{-78}	86.25	204

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Table S2. Analysis of variance of whole panicle architecture traits of eight Indonesian foxtail millet genotypes

Traits	Source of variation	df	Sum of square	Mean square	P-value	CV (%)
Panicle density (PD) ¹	genotypes	7	2.795	0.399	< 0.0001**	5.40
	blocks	2	0.005	0.002	0.918 ^{ns}	
	error	14	0.384	0.027		
	total	23	3.184			
Primary branch number (PBN) ²	genotypes	7	0.438	0.063	< 0.0001**	6.49
	blocks	2	0.003	0.002	0.482 ^{ns}	
	error	14	0.028	0.002		
	total	23	0.469			
Panicle length (PL)	genotypes	7	604.923	86.418	< 0.0001**	11.56
	blocks	2	10.192	5.096	0.382 ^{ns}	
	error	14	69.158	4.940		
	total	23	684.273			
Grain number per panicle (GNP) ²	genotypes	7	1.005	0.144	0.0002**	3.50
	blocks	2	0.151	0.075	0.024*	
	error	14	0.214	0.015		
	total	23	1.369			
Grain density per panicle (GDP) ²	genotypes	7	0.702	0.100	< 0.0001**	4.04
	blocks	2	0.104	0.052	0.012*	
	error	14	0.117	0.008		
	total	23	0.922			

df – degrees of freedom; CV – coefficient of variation; *, **significant at the $\alpha = 5\%$, 1% ; ^{ns}not significant ($P > 0.05$); ANOVA analysis for randomized complete block design (RCBD); ¹the data were transformed using the formula $\sqrt{x + 0.5}$; ²the data were transformed using the formula $\text{LOG}_{10}(X)$

Table S3. Analysis of variance for segmented panicle architecture traits in eight Indonesian foxtail millet genotypes

Traits	Source of variation	df	Sum of squares	Mean square	F-value	P-value	CV (%)
Primary branch length (PBL)	genotype	7	2.422	0.346	21.620	< 0.0001**	4.36
	panicle zones (within genotypes)	16	10.168	0.636	39.720	< 0.0001**	
	error	48	0.768	0.016			
	total	71	13.358				
Primary branch diameter (PBD)	genotype	7	23.160	3.309	12.340	< 0.0001**	7.49
	panicle zones (within genotypes)	16	58.151	3.635	13.550	< 0.0001**	
	error	48	12.871	0.268			
	total	71	94.182				
Primary branch number (PBN) ¹	genotype	7	1.096	0.157	64.970	< 0.0001**	2.94
	panicle zones (within genotypes)	16	3.313	0.207	85.920	< 0.0001**	
	error	48	0.116	0.002			
	total	71	4.524				
Grain number (GN) ²	genotype	7	14.250	2.036	15.000	< 0.0001**	5.27
	panicle zones (within genotypes)	16	3.681	0.230	1.700	0.0805 ^{ns}	
	error	48	6.514	0.136			
	total	71	24.445				
Grain density (GD) ²	genotype	7	1.862	0.266	15.690	< 0.0001**	5.80
	panicle zones (within genotypes)	16	0.687	0.043	2.530	0.0067**	
	error	48	0.814	0.017			
	total	71	3.363				

df – degrees of freedom; CV – coefficient of variation; *, **significant at the $\alpha = 5\%$, 1% ; ^{ns}not significant ($P > 0.05$); ANOVA analysis for Nested design; ¹the data were transformed using the formula $\sqrt{x + 0.5}$; ²the data were transformed using the formula $\text{LOG}_{10}(X)$

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Table S4. Independent *t*-test results identifying discriminant panicle traits among two foxtail millet clusters

Traits	Cluster	Independent <i>t</i> -test	
		Mean	<i>P</i> ($T \leq t$)
Panicle density (PD)	I	10.03	0.123
	II	7.40	
Primary branch number (PBN)	I	194.99	0.042*
	II	121.24	
Panicle length (PL)	I	20.57	0.403
	II	17.00	
Grain number per panicle (GNP)	I	4 979.98	0.015*
	II	2 136.14	
Grain density per panicle (GDP)	I	244.97	0.018*
	II	124.79	
Primary branch length of upper zone (PBL-U)	I	5.72	0.754
	II	5.38	
Primary branch length of middle zone (PBL-M)	I	7.84	0.719
	II	8.15	
Primary branch length of lower zone (PBL-L)	I	10.35	0.314
	II	11.48	
Primary branch diameter of upper zone (PBD-U)	I	5.76	0.518
	II	6.04	
Primary branch diameter of middle zone (PBD-M)	I	6.69	0.137
	II	7.35	
Primary branch diameter of lower zone (PBD-L)	I	7.69	0.266
	II	8.38	
Primary branch number of upper zone (PBN-U)	I	108.31	0.099
	II	63.60	
Primary branch number of middle zone (PBN-M)	I	56.38	0.033*
	II	34.73	
Primary branch number of lower zone (PBN-L)	I	30.38	0.281
	II	22.83	
Grain number of upper zone (GN-U)	I	2 083.74	0.036*
	II	680.47	
Grain number of middle zone (GN-M)	I	1 633.79	0.010**
	II	735.42	
Grain number of lower zone (GN-L)	I	1 262.45	0.086
	II	720.26	
Grain density of upper zone (GD-U)	I	290.28	0.049*
	II	118.02	
Grain density of middle zone (GD-M)	I	245.35	0.012*
	II	129.78	
Grain density of lower zone (GD-L)	I	199.27	0.119
	II	126.59	

*, ***P* < 0.05, 0.01 (based on independent *t*-test)

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Table S5. Comparative analysis of SNP between the reference genotype (Yugu1) and 1 844 world-wide foxtail millet germplasms using *Setaria*-db

Chr	Position	Region	Reference allele (Yugu1)	Alternate allele	Type	Variant type	MAF	MIS
9	16 558 319	protein coding	G	T	SNP	synonymous	0.21	0.02
9	16 558 481	protein coding	C	T	SNP	synonymous	0.06	0.01

Chr – chromosome; MAF – minor allele frequency; MIS – missense; available at: <http://111.203.21.71:8000/multi-omics/variation.html> (accessed Sept 24, 2025)

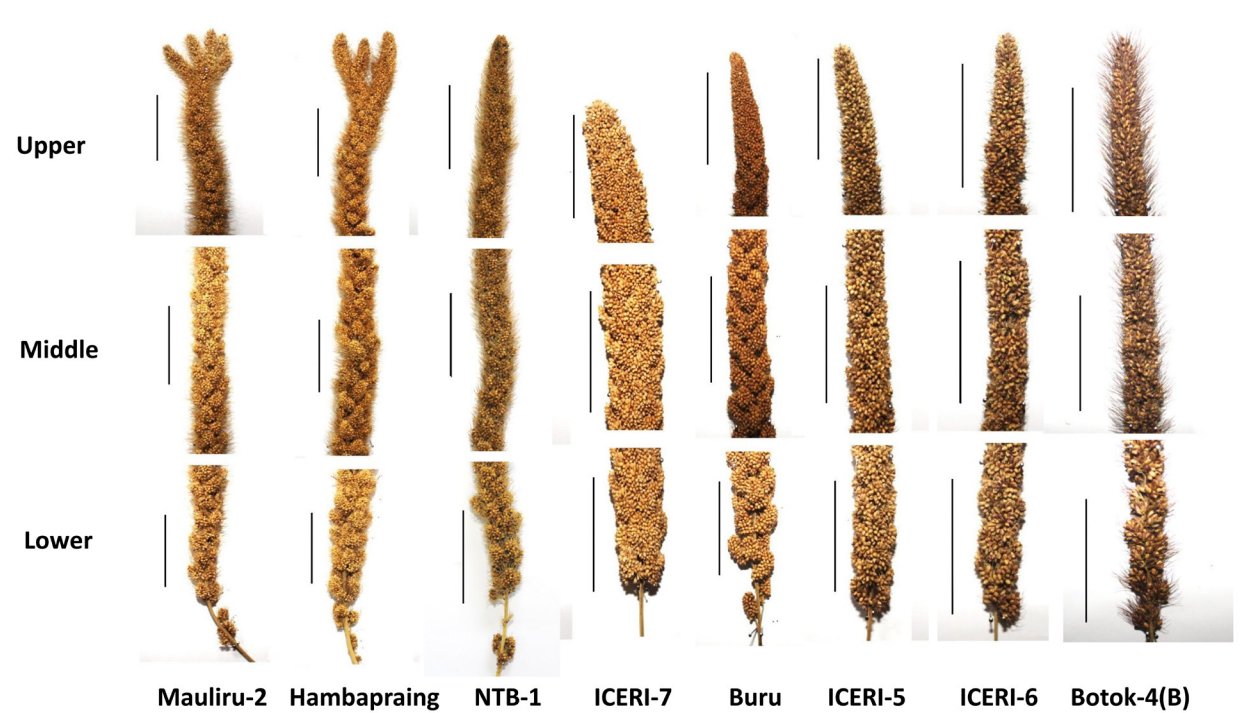


Figure S1. Variation in panicle architecture among eight Indonesian foxtail millet genotypes across three spatial panicle zones (upper, middle, and lower)
scale bar – 4 cm

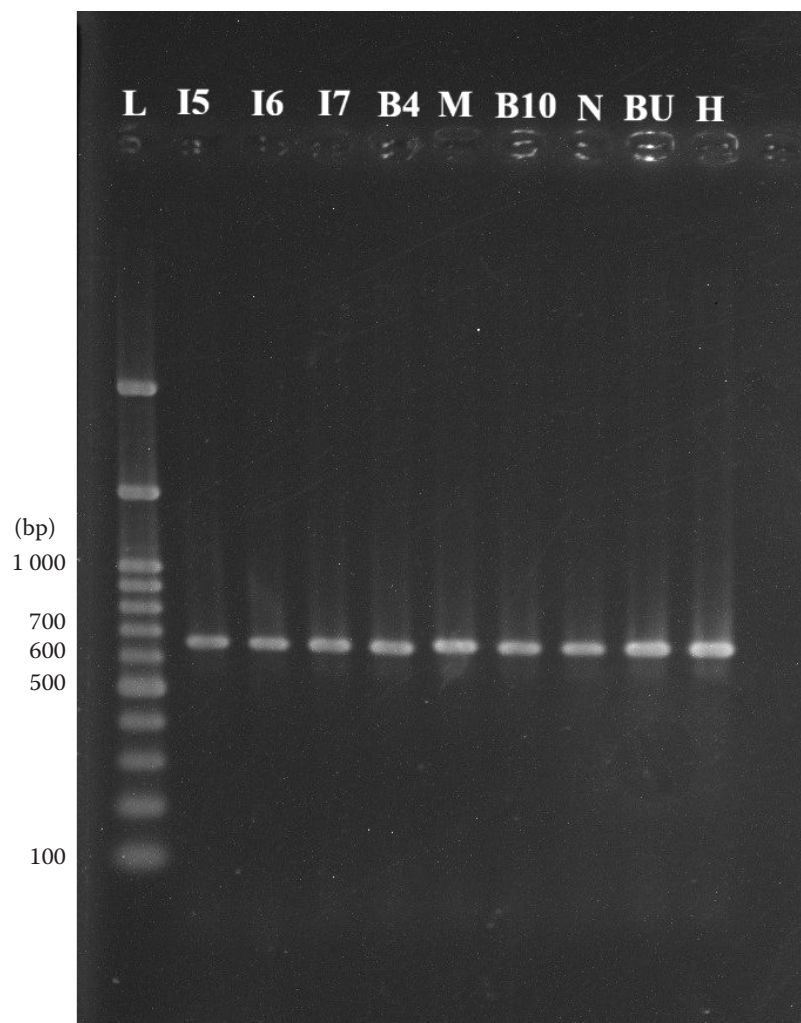
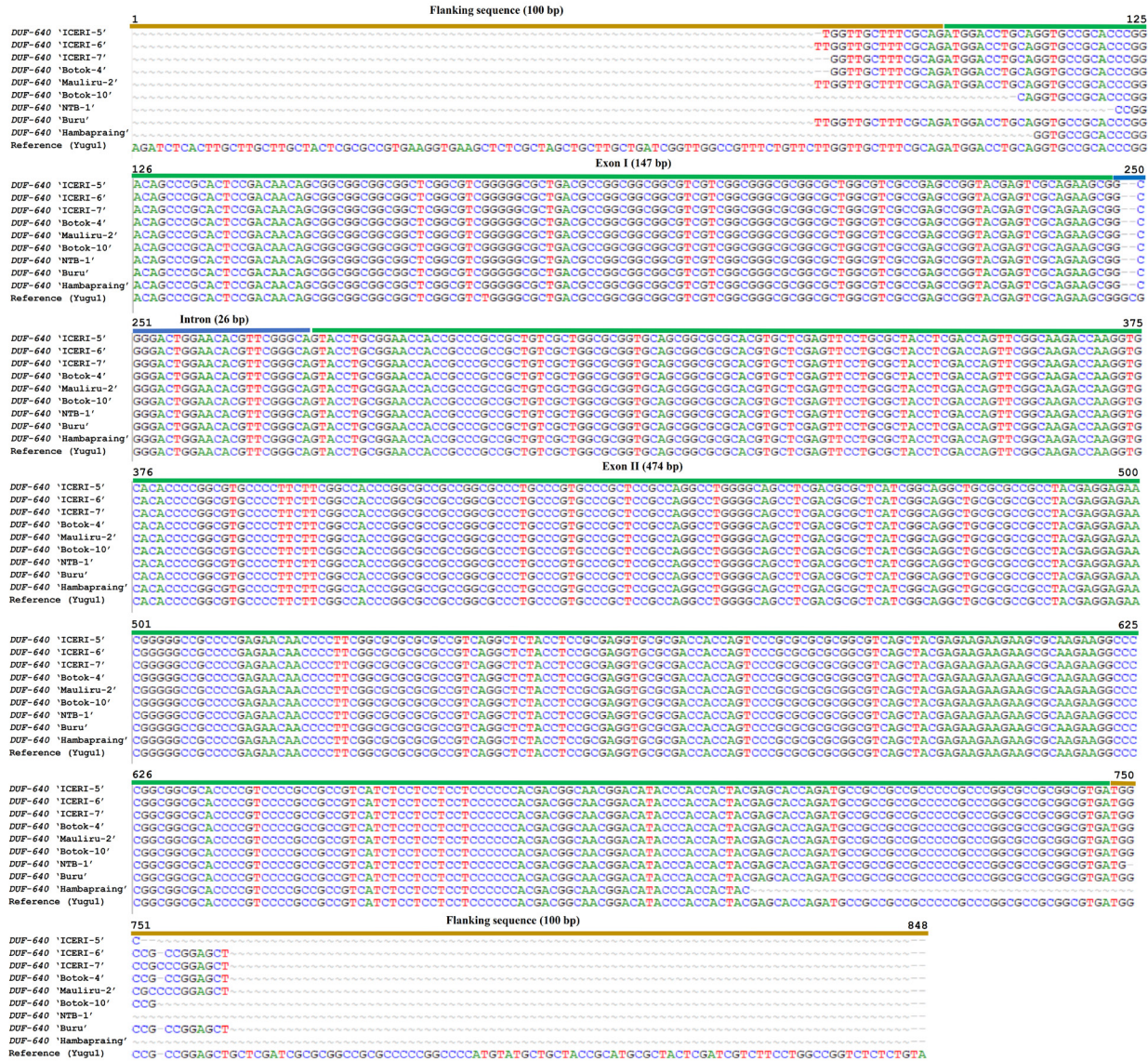


Figure S2. Electropherogram displaying the PCR amplification visuals of the *DUF-640* gene fragments in Indonesian foxtail millet genotypes

I5 – ICERI-5; I6 – ICERI-6; I7 – ICERI-7; B4 – Boto-4; M – Mauliru-2; B10 – Boto-10; N – NTB-1; BU – Buru; H – Hambapraing

(A)



(B)

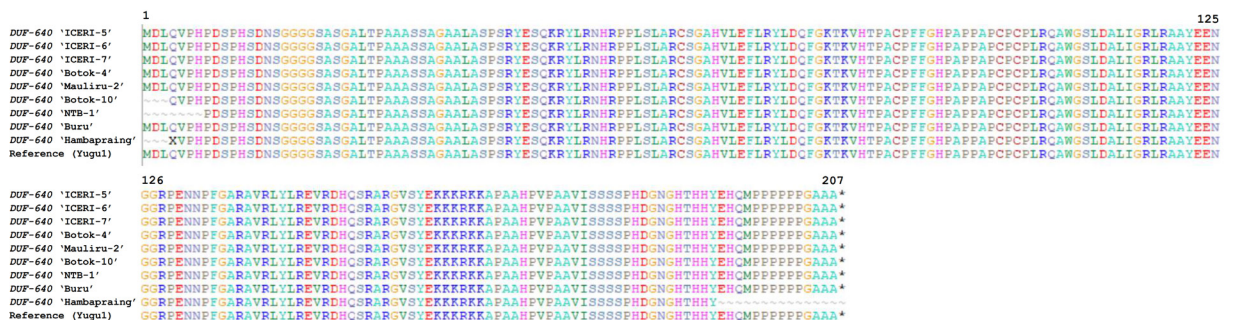


Figure S3. Comparative multiple sequence alignment of Indonesian foxtail millet genotypes with reference genotype (Yugu1): the alignment of nucleotide sequences (A), the amino acid sequence alignment (B)