## Characterization of a new rice glutelin gene *GluD-1* expressed in the starchy endosperm

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## **Supplementary Material**

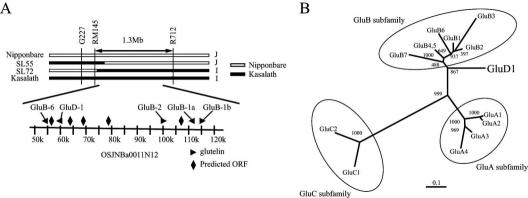
Supplementary Fig. 1. Alignment of rice glutelin genes used for drawing a phylogenetic tree.

Supplementary Fig. 2. Mapping of glutelin a4 gene and a phyllogenetic tree of rice glutelins.

Supplementary Fig. 3. Alignment of *GluD-1* cDNAs among cultivars Nipponbare, Wataribune 2, Kasalath and Nona Bokra.

Supplementary Fig. 4. Alignment of GluD-1 among cultivars Nipponbare, Wataribune 2, Kasalath and Nona Bokra.

		$\downarrow$
GluA1 GluA2	1	MASINRPIVEFTVCLFLLCNGSLAQQLLGQSTSQWQSSRRGSPRECRFDRLQAFEPIRSVRSQAGTTEFFDVSNE-QFQCTGVSVVRRVIEPRGLLLPMASINRPIVEFTVCLFLLCDGSLAQQLLGQSTSQWQSSRRGSPRECRFDRLQAFEPIRSVRSQAGTTEFFDVSNE-LFQCTGVSVVRRVIEPRGLLLPMAIIKPPIVFSVVCLFLLCNGSLAQLES-QSTSQWQSSRRGSPRECRFDRLQAFEPIRTVRSQAGTTEFFDVSNE-LFQCTGVFVVRRVIEPRGLLLPIAIIKFPVVFSAICLFLLCHGSLAQFLS-QSTSQWQSSRRGNPRECRFDFLQAFKPIRTVRSQADTTEVIDISK-LFQCTGVFVVRRVIEPRGLLLPVASSVFSRFSIIYFGVLLLCHGSMAQLFNPSTNPW-SPRQGSFRECRFDRLQAFEPLRKVRSEAGVTEYFDEKNE-LFQCTGTFVIRRVIQPQGLLVPVAITIFSRFSIIYFGAMLLQGSMAQLFNPSTNPW-SPRQGSFRECRFDRLQAFEPLRKVRSEAGVTEYFDEKNE-LFQCTGTFVIRRVIQPQGLLVPVAITIFSRFSIIYFGVLLUCHGSMAQLFNPSTNPW-SPRQGSFRECRFDRLQAFEPLRKVRSEAGVTEYFDEKNE-LFQCTGTFVIRRVIQPQGLLVPVAITIFSRLSIIYFGVLLUCHGSMAQLFDPATNOWOTHORGSFRECRFDRLQAFEPLRKVRSEAGVTEYFDEKNE-QFQCTGTFVIRRVIQPQGLLVPVAITIFSRLSIIYFGVLLUCHGSMAQLFDPATNOWOTHORGSFRECRFBRLQAFEPLRNVRSEAGVTEYFDEKNE-QFQCTGTFVIRRVIQPQGLLVPVAITISFRLSIIYFGVLLUCHGSMAQLFDPATNOWOTHORGSFRECRFBRLQAFEPLDNVRSEAGVTEYFDEKNE-QFQCTGTFVIRRVIEPQGLLVP
GluA3	1	MATIKFPIVES.VCLFLLCNGSLAQLLS-QSTSQWQSSRGSPRECRFDRLQAFEPIRTVRSQAGTTEFFDVSNE-LFQCTGVFVVRRVIEPRGLLLP
GluA4 GluB1a/b	1	IAITKFPVVFSATCLFLLCHGSLAQFIIS-QSTSQWQSSHRQNPRECRFDHLQAFKPTRTVRSQADTTEVVDTSNK-LFQCTGVFVVRRVTEPRGLLLP VASSVFSRFSITYFQVLLLCHGSMAQLFNPSTNPWHSPRQGSFRECRFDRLQAFEPLRKVRSEAGVTEYFDEKNE-LFQCTGTFVTRRVTQPQGLLVP
GluB2 GluB3	1	VAITTIFSRFSITYFGAYLLLQGSMAQLFNPSTNPWISPRQGSFRECRFDRLQAFEPLRKVRSEAGVTEYFDEKNE-LFQCTGTFVTRRVTQPQGLLVP
GluB4/5	1	VAITIAFSRLSTYFGVLLLCHGSMAQLFGPNVNPWHNPRQGGFRECRFDRLQAFEPLRRVRSEAGVTEYFDEKNE-QFQCTGTFVTRRVIEPQGLLVP
GluB6 GluB7	1	MATITAT SREST CFCVLLLCHGSMAQTESLGINPWONPROGGSRECREDRLQAFEPLRKVRHEAGVTEYFDEKNE-QFQCTGTLVIRRITEPQGLLLP
GluC1 GluC2	1	MASMSTILLPLCLG.LLFFQVSMAQFSFGGSPLQSPRGFRGDQDSRHQCRFFHLTALEATHQQRSEAGFTEY)NIEARNEFRGAGVSVRRLVVESKGLVLP MASMSTIVPLCLS.LLFFQVSIAQFSFGGGPLYSSRGFRGDSVSQHQCRFFHLAALKVTHRDRSEADFIEYYNTEVRNEFRGAGVSVRRLVIESRGLALP
GluD1	1	mattitellesclealillaplesogydawes-rogasrocrfdrloafeplrkvrseagdteyfderne-ofroagyfytrrvtepoglyvp
GluA1 GluA2	98 98	HYTNGASLVYIIQGRGITGPTFPGCPESYQQQFQQSGQAQLTESQSQSQKFKDEHQKIHRFRQGDVIALPAGVAHW <mark>G</mark> YNDGEVPVVAIYVTDLNN <mark>G</mark> AN HYTNGASLVYIIQGRGITGPTFPGCPETYQQQFQQSGQAQLTESQSQSHKFKDEHQKIHRFRQGDVIALPAGVAHW <mark>G</mark> YNDGEVPVVAIYVTDINN <mark>G</mark> AN
GluA3	97	HYSNGATLVYVIQGRGITGPTFPGCPETYQQQFQQSEQDQQLEGQSQSHKFRDEHQKIHRFQQGDVVALPAGVAHWCYNDGDAPIVAIYVTDIYNSAN
GluA4 GluB1a/b	97 97	RYTNIPGVVYIIQGRG <mark>S</mark> MGLTFPGCPATYQQQFQQFSSQGQSQSQKFRDEHQKIHQFRQGDIVALPAGVAHWFYNDGD <mark>A</mark> PIVAVYVYDVNNNAN
GluB2 GluB3	97 97	RYSNTPGLVYIIQGRGSMGLTFPGCPATYQQQFQQFSSQGOSQSQKFRDEHQKIHQFRQGDVVALPAGVAHWFYNDGDASVVALYVYDINNSAN RYTNTLSWYYIIQGRGTMGLTFLGCPANY-QQFQQFSPQWQSESQKFRGEHQKIYQFRQGDIIPLPAGVAHWFYNDGDAPVVTIIYVYDINNRAN
GluB4/5	97	RYSNTPGMYYIIQGRGSMGLTFPGCPATYQQQFQQFLPEGQSQSQKFRDEHQKIHQFRQGDIVALPAGVAHWFYNEGDAPVVALYVFDLNNNAN RY <mark>ANTPG</mark> MYYIIQGRGSMGLTFPGCPATYQQQS <mark>QQFLFQGESQSQKF<mark>T</mark>IDEHQKIHQFRQGDIV<mark>Y</mark>LPTTGVAHWFYNDGDTPVVALYVYDINNSAN</mark>
GluB6 GluB7	97	RYSNTPGLVYIIQGTGVLGLTFPGCPATYQKQFRHFGLEGGSQRQGKKLRDENQKIHQFRQGDVVALPSGIPHWFYNEGDTPVVALFVFDVNNNAN
GluC1 GluC2	101 101	VYANAHKILYIIOGHGVFGMALPGCPETFQSVOYAFEOSSTOKLSDEHQOLHKFRQGDVIAVPAGVAHWLYNNGDSPMVAFLVIDFGNNAN
GluD1	90	RYSNTPALAYIIQGKGYVGLTFPGCPATHQQQFQLEEQRQSDQAHKFRDEHQKIHEFRQGDVVALPASVAHWFYNGGDTPAVVVYVYDIKSFAN
GluA1 GluA2	196 196	QLDPRQRDFLLAGNKRNP-QAYRREVEERSQNIFSGFSTELLSEALGYSSQVARQLQCONDQRGEIVRVEHGLSLLQPYASLQEQEQQVQSRERY QLDPRQRDFLLAGNKRNP-QAYRREVEEWSQNIFSGFSTELLSEAFGISNQVARQLQCONDQRGEIVRVERGLSLLQPYASLQEQEQQAQSREHY
GluA3		
GluA4 GluB1a/b	191	QLEPRQKEFLLAGNNNRAQQQQVYGSSIEQHS-QQNIFSGFGYEMLSEALGINAVAAKRLQSQNDQRGETIHVKNGLQLLKPTLTQQQEQAQAQDQY
GluB2 GluB3	191 190	QLEPRQKEFLLAGNNNRVQQYYGSSIEQHS-SQNIFNGFGTELLSEALGINTVAAKRLQSONDQRGEIVHYKNGLQLLKPTLTQQQEQAQAQY -VEPRQKEFLLAANNNRVQQYYGSSIAEEP-RQNIFNRIGVEQLSEALGINTVAAKRPQSONDQRGEITVDGLYPA/FKGRKVRLIPRNTREW
GluB4/5	191	QLEPRQKEFLLAGNNNREQQMYGRSIEQHS-GQNIFSGFNNELLSEALGVNALVAKRLQGQNDQRGEIIRVKNGLKLLRPAFAQQQEQAQQQQEQAQQ
GluB6 GluB7	191 193	QLEPRHREFLLAGKNNRVQQYYGRSIQQHS-GQNIFNGFSVEPLSEALNINTVTTKRLQSQNDQRGEIIHVK\GLQLLKPTLTQRQEQEQAQY QLEPRQKEFLLAGNNIEQQYSNPSINKHS-GQNIFNGFNTKLLSEALGYNIEVTKRLQSQNDRRGDIIRVK\GLRLTKPTITQQQEQTQDQY QLDPKRREFFLAGKPRSSWQQQSYSYQTE <mark>G</mark> LSRNQNIFAGFSPDLLSEALSVSKQTYLRLQGLSDPRGAIIRVE\GLQALQPSLQVEPYKEEQTQAYLPT
GluC1 GluC2	201 192	QLDPKRREFFLAGKPRSSWQQQSGSYQTEQLSRNQNIFAGFSPDLLSEALSVSKQTVLRLQGLSDPRGATIRVENGLQALQPSLQVEPVKEEQTQAYLPT QLDPIPREFFLAGKP-TSWQQEQYSYQAEQQSDNQNIFAGFNPDLLGEALGVSRQTAMRLQELNDQRGVIIRVAQGLQALHPSFQTEQVQEEQSQE
GluD1		QLEPRQKEFLLAGNNQRGQQTEFFSTFQHS-GQNTFSGFNTEVLSEALGTNTEASKRLQSQNDQRGDTTRVKHGLQLLKPTLTTQRQE
GluA1	291	QEGQYQQSQYGSGCSNGLDETFCTLRVR <mark>Q</mark> NIDNPNRADTYNPRAGRVTNLNTQXFPIL <mark>S</mark> LVQMSA <mark>V</mark> KVNLYQNALLSPFWNINAHSVYYTTQGRARVQ
GluA2 GluA3		QEGGYQQSQYGSGCPNGLDETFCTMRVRQNIDNPNRADTYNPRAGRYTNLNSQNFPILNLVQMSAVKVNLYQNALLSPFWNINAHSIVYITQGRAQVQ GQTQYQQKQLQGSCSNGLDETFCTMRVRQNIDNPNLADTYNPRAGRITYLNGQKFPILNLVQMSAVKVNLYQNALLSPFWNINAHSVYYITQGRARVQ
GluA4 GluB1a/b	287	QQVQYSERQQTSSRWNGLEENFCTIKVRVNIENPSRADSYNPRAGRITSVNSQKFPILNLIQMSATRVNLYQNAILSPFWNVNAHSLVYMIQGRSRVQ
GluB2	283	Q <mark>EVQYSEQQQT</mark> SSRWNGLEENFCTIKARVNIENPSRADSYNPRAGRISSVNSQKFPILNLIQMSATRVNLYQNAILSPFWNVNAHSLVYM <mark>I</mark> QG <mark>Q</mark> SRVQ
GluB3 GluB4/5	288	flra, dkdfytgsgpq y <mark>g</mark> vqysgeqopstronglden <mark>f</mark> ctikarlnienbshadtynpragritrlnsokfpilnlvolsatrvnlyonatlspfwnynahslvyivogharvo
GluB6 GluB7	283 284	QEVQYSEKPQTSSRWNGLEENLCTIKTRLNIENPSRADSYDPRAGRITSLDSQKFPILNIIQMSATRVNLYQNAILTPFWNVNAHSLMYVIRGRARVQ QQIQYHREQRSTSKYNGLDENFCAIRARLNIENPNHADTYNPRAGRITNLNSQKFSILNLYQMSATRVNLYQNAILSPFWNINAHSLVYTIQGRARVQ
GluC1 GluC2	301	QCIQYHREQRSTSKYNGLDENFCATRARINIENPNHADTYNPRAGRITNLNSQKF <mark>S</mark> LLNLVQMSATRVNLYQNAILSPFWNINAHSLVYTIQGRARVQ KQLQPTWLRSGGACGQQNVLDEIMCAFKLRKNIDNPQSSDIFNPHGGRITRANSQNFPILNIIQMSATRIVLQNNALLTPHNTVNAHTVMYVTAGQGHIQ
GluD1	270	QQQQPTWSGRGCAQNNGLDEIKCAFKLSKNINNAQSTDIFNPRGGRITRANS- EHRQYQQVQYREGQYNGLDENFCTIKARVNIENBSRADYYNPRAGRITLLNNQKFPILNLIGNGAARVNLYQNALLSPFWNINAHSVVYTIIQGSVRVQ
GluA1	389	VVMNNGKTVFNGELRRGQLLIIPQHYAVVKKAQREGCAYIAFKTNPNS VSHLAGKSSIFRALPNDVLANAYRISREEAQRLKHNRGDEFGAFTPIQYKS VVNNNGKTVFNGELRRGQLLIVPQHYVVVKKAQREGCAYIAFKTNPNS VSHLAGKSSIFRALPTDVLANAYRISREEAQRLKHNRGDEFGAFTPLQYKS
GluA2 GluA3 GluA4	389 388	VVVNNGKTYFNGELRRGQLLIYPOHYVVKKAQREGCAYLAFKTNYNSKYSHLAGKSSIFRALFIDVLANAYRISREEAQRUKINRODEFGAFTPLQYKS VVMNMGKTYFDGELRRGQLLIIPQHHVYLKKAQREGCSYLALKTNPDS/VSHMAGKNSIFRALFDDVVANAYRISREEARRUKHNRGDELGYFTPSHAYK
GluB1a/b GluB2	385 381	VVSN EGKTVFDGVLRPGQLLIIPQHYAVLKKAEREGCQYIAIKTNANAFVSHLAGKNSVFRALPVDVVANAYRISREQARSLKNNRGEEHGAFTPRFQQQ VVSN EGKTVFDGVLRPGQLLIIPQHYAVLKKAEREGCQYIAIKTNANAFVSHLAGKNSVFRALPVDVVANAYRISREQARSIKNNRGEEHGAFTPRFQQQ
GluB3 GluB4/5		
GluB6	381	VVSNFGKTVFDGYLRPEQLLIIPQNYVVLKKAQHEGGGYIA <mark>IN</mark> TNAMAFYSHLAGVDSVFHALPVDVIANAYCISREEARRLKNNRGDEYGPFPPRLQQQ
GluB7 GluC1	582 401	VVSNLGKTVFNGVLRPGQLLIIPQHYVVLKKAEHEGCQYISFKTNANSYVSHLAGKNSIFRAMPVDVIANAYRISREQARSLKNNRGEELGAFTPRYQQQ VVSNFGKTVFDGVLRPEQLLIIPQNYVVLKKAQHEGCQYIAINTNANAFVSHLAGVDSVFHALPVDVIANAYCISREEARRLKNNRGDEYGPFPRLQQQ VVSNHGKAVFNGVLRPGQLLIIPQNYAVMKKAELEGFQFIAFKTNPNAMYNHIAGKNSVLRAMPVDVIANAYRISRQEARSLKNNRGEEIGAFTPRYQQQ VVDHRGRSVFDGELHQQQILLIPQNFAVVVKARREGFAMYSFKTNHNAVDSQIAGKASILRALPVDVVANAYRISREDGRHVKFNRGDEMAVFAPRRGPQ
GluC2 GluD1		VAN <mark>Y</mark> QGRSVFNGVLHQGQLLIIPQNHAVIKKAEHNGCQYVAIKTISDPTVSWVAGKNSILLRALPVDVIANAYRISRDEARRLKNNRADEIGPFTPRFPQK
GluA1		YQDV <mark>I</mark> NAAESS
GluA2 GluA3		YQDVMVAESS
GluA4		
GluB1a/b GluB2		YYPGLSNESESETSE YYPG <mark>I</mark> SNESESETSE
GluB3 GluB4/5	486	TTLG SNESENEASE
GluB6	481	IYPEFSNESKGETSE
GluB7 GluC1		KIHQEYSNPNESETQEVI Q <mark>Y</mark> AE <mark>N</mark> QINEK
GluC2 GluD1	468	SQRG QFLTEGLSLIGM-
		_



Nipponbare		ATGGCAACTACTACTCTATTGTCTTCCTGTCCTCTGTGCTCTTCTTTGGCTCCGCTCTTTAGCCAAGGTGTAGATGCATGGGAAAGCCGACAAGGGGCTTCCAGGCAGTGCAGATTT
Wataribune2 Kasalath	1	G
NonaBokra		6
Nonaboki a	1	
Nipponbare	121	GATAGGTTACAAGCATTTGAGCCCCTAAGAAAGGTACGATCGGAAGCTGGGGACACAGAGTACTTTGATGAGAGAAATGAGCAGTTTCGATGCGCTGGTGTCTTTGTCATTCGGCGCGCTG
Wataribune2	121	<u>T</u>
Kasalath	121	Ç
NonaBokra	121	СТТ
Nipponbare	241	ATTGAGCCACAAGGCCTTGTGGTGCCTCGATACTCGAACACTCCTGCTCTAGCCTACATAATCCAAGGAAAAGGTTACGTAGGATTGACTTTTCCTGGTTGCCCAGCAACACCCAACAA
Wataribune2		
Kasalath	241	g
NonaBokra	241	
Nipponbare	361	CAATTCCAACTATTTGAACAAAGACAGAGCGACCAAGCTCATAAGTTTAGAGATGAGCACCAGGAGATTCACGAATTTAGGCAAGGGGATGTTGTTGCACTTCCGGCTAGTGTTGCACAT
Wataribune2		
Kasalath		AA
NonaBokra	361	A
Nipponbare	481	TGGTTCTACAATGGTGGTGATACACCGGCTGTTGTTGTTCTATGTTTATGACATAAAAAGTTTTGCTAATCAGCTTGAACCAAGGCAGAAGGAGTTTTTATTAGCTGGTAACAACCAGAGA
Wataribune2	481	
Kasalath		AA
NonaBokra	481	AA
Nipponbare	601	GGGCAACAAATATTTGAACATTCCATCTTTCAACACTCTGGACAAAATATATTTAGTGGGTTCAATACTGAGGTACTTAGCGAGGCCCTTGGAATAAACACGGAGGCTTCCAAGAGGCTC
Wataribune2		
Kasalath	601	<u> </u>
NonaBokra	601	G
Nipponbare	721	CAAAGTCAAAATGACCAAAGGGGAGATATCATTCGAGTGAAGCACGGGCTTCAATTGTTGAAACCCACATTAACACAACGACAGGAAGAACATCGTCAATATCAACAAGTCCAGTATCGT
Wataribune2		
Kasalath NonaBokra	721	
Nonabokra	721	
Nipponbare		GAAGGACAATATAATGGATTGGACGAGAATTTCTGTACAATAAAGGCAAGGGTAAACATTGAAAATCCTAGCCGCGCTGACTACTACAACCCTCGTGCTGGAAGGATAACCCTTCTTAAC
Wataribune2		
Kasalath NonaBokra	8/11	CAAAAAA
nonaboki a	011	
Nipponbare		AACCAAAAGTTCCCTATTCTCAACCTTATTGGAATGGGTGCTGCAAGAGTAAACTTATACCAGAATGCTCTTCTCTCACCCTTCTGGAACATTAATGCCCATAGTGTAGTGTATATCATC
Wataribune2 Kasalath		C
NonaBokra		C
		CAAGGAAGTGTGCGAGTACAGGTTGCCAATAATCAAGGAAGATCTGTGTTTAATGGTGTACTTCATCAGGGGCAACTATTAATCATACCACAAAACCATGCCGTCATTAAGAAAGCCGAG
		. C. A
		CAAG
Nipponbare	1 201	CACAATGGGTGCCAGTATGTCGCAATAAAGACAATTTCGGACCCTACGGTGAGTTGGGTTGCTTGGAAAGAACTCCATATTACGTGCATTGCCTGTAGATGTTATTGCCAATGCTTATCGT
		CACAATIGGT GCCAGTATOT GCCAATAAAGACAATT TCGGACCCTACGGT GAGT TGGT TG
Kasalath	1201	G
NonaBokra	1201	G
Nipponbare	1321	ATCTCGAGGGATGAAGCCCGACGTCTAAAGAATAATAGGGCAGATGAGATTGGCCCTTTTACTCCTCGTTTCCCCCAGAAGAGCCAGCGGGGTTACCAGTTCCTAACTGAAGGCCTCTCT
		A
Kasalath	1321	GAAA
NonaBokra	1321	
Nipponbare	1441	TTAATCGGCATGTAA
		Than Education
NonaBokra	1441	

Nipponbare Wataribune2 Kasalath Nona Bokra	1 MATTTSLLSSCLCALLLAPLFSQGVDAWESRQGASRQCRFDRLQAFEPLRKVRSEAGDTE         1
Nipponbare Wataribune2 Kasalath Nona Bokra	61 YFDERNEQFRCAGVFVIRRVIEPQGLVVPRYSNTPALAYIIQGKGYVGLTFPGCPATHQQ 61
Nipponbare Wataribune2 Kasalath Nona Bokra	121 QFQLFEQRQSDQAHKFRDEHQKIHEFRQGDVVALPASVAHWFYNGGDTPAVVVYVYDIKS 121
Nipponbare Wataribune2 Kasalath Nona Bokra	181 FANQLEPRQKEFLLAGNNQRGQQIFEHSIFQHSGQNIFSGFNTEVLSEALGINTEASKRL 181
Nipponbare Wataribune2 Kasalath Nona Bokra	241 QSQNDQRGDIIRVKHGLQLLKPTLTQRQEEHRQYQQVQYREGQYNGLDENFCTIKARVNI 241
Nipponbare Wataribune2 Kasalath Nona Bokra	301 ENPSRADYYNPRAGRITLLNNQKFPILNLIGMGAARVNLYQNALLSPFWNINAHSVVYII 301
Nipponbare Wataribune2 Kasalath Nona Bokra	361 QGSVRVQVANNQGRSVFNGVLHQGQLLIIPQNHAVIKKAEHNGCQYVAIKTISDPTVSWV 361
Nipponbare Wataribune2 Kasalath Nona Bokra	421 AGKNSILRALPVDVIANAYRISRDEARRLKNNRADEIGPFTPRFPQKSQRGYQFLTEGLS 421
Nipponbare Wataribune2 Kasalath Nona Bokra	481 LIGM 481 481