

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

Taiji Kawakatsu, Masayuki P Yamamoto, Sakiko Hirose, Masahiro Yano, and
Fumio Takaiwa

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 phylogenetic 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.

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GluA1 1 --MASINRPVIFVTVCLFLCNGSLAQQLLQGSTISQVSSRRGSPRECFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP
GluA2 1 --MASINRPVIFVTVCLFLCNGSLAQQLLQGSTISQVSSRRGSPRGCFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP
GluA3 1 --MATIKFPVFSVCLFLCNGSLAQQLS-QSTISQVSSRRGSPRECFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP
GluA4 1 --TATIKFPVFSVCLFLCNGSLAQQLS-QSTISQVSSRRGSPRECFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP
GluB1a/b 1 ---MASSVFRSFSIYFCVLLCHGSMALQFNPNPNPWSPROGSPRECFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP
GluB2 1 ---MATITFSRFSIYFCVLLCHGSMALQFNPNPNPWSPROGSPRECFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP
GluB3 1 ---MATVTSQFSIYFCVLLVHDSMAQLFYPTRPNPWSPROGSPRECFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP
GluB4/5 1 ---MATIAFRSISYFCVLLCHGSMALQFNPNPNPWSPROGSPRECFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP
GluB6 1 ---MITSVFRSFSIYFCVLLCNGSMALQFPDPAINQVQHROGSPRECFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP
GluB7 1 ---MATIAFRSISYFCVLLCHGSMALQFSLGNPNWSPROGSPRECFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP
GluC1 1 MASMSIILPLCLGLLFFQVSMQAFSFGGSPLOPRGFRGDDSRHOCRFELTALBATHOQRSEAGTEFFYNI EARNRFRFCAGSVRRLLVIESKGLVLP
GluC2 1 MASVSTVPLCLGLLFFQVSMQAFSFGGSPLOPRGFRGDDSRHOCRFELTALBATHOQRSEAGTEFFYNI EARNRFRFCAGSVRRLLVIESKGLVLP
GluD1 1 ---MATTITLLSSLLCALLLAP----LFSQGDVADES--RQGSAROCFRDLQAFEPTRVRSVSOAGTEFFDVSNB-LFQCTGVSVVRRVIEPRGLLLP

GluA1 98 HYTNASLVYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluA2 98 HYTNASLVYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluA3 98 HYSNGATLVYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluA4 98 HYSNGVTLVYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluB1a/b 98 RYNTNIPGVYIYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluB2 98 RYNTNIPGVYIYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluB3 98 RYNTNIPGVYIYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluB4/5 98 RYNTNIPGVYIYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluB6 98 RYNTNIPGVYIYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluB7 98 RYNTNIPGVYIYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluC1 101 MYANAHKLVYIYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluC2 101 MYANAHKLVYIYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN
GluD1 90 RYNTNIPGVYIYIQGRGITPTFPFGCPETYQQQFQSQGQA--QLTESQSQSKFIDEHQKIHFRQGDVIALPAGVAHWYNDGEPVVAIYYVDINNGAN

GluA1 196 QLDPQRDFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluA2 196 QLDPQRDFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluA3 195 QLDPQRDFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluA4 195 QLDPQRDFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB1a/b 191 QLEPRQKEFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB2 191 QLEPRQKEFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB3 190 QLEPRQKEFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB4/5 191 QLEPRQKEFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB6 191 QLEPRQKEFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB7 193 QLEPRQKEFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluC1 201 QLDPQRDFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluC2 192 QLDPQRDFLLAGNKRNP--QAYRREVEERSQ---NITFSGFSTELLSEALGYSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
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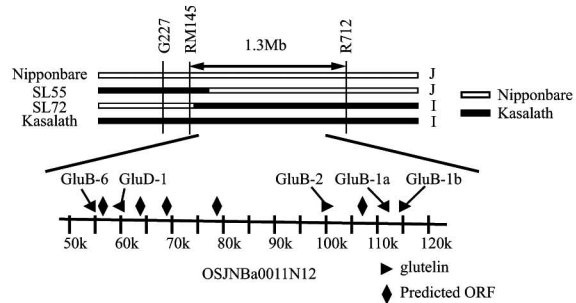
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GluA1 291 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluA2 291 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluA3 290 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
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GluB1a/b 287 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB2 283 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB3 281 FLRAIDKDF---YTSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB4/5 288 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB6 283 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluB7 284 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluC1 301 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluC2 287 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY
GluD1 270 QEGYQQSQ---YGSQVAVRLOQCQNDORGETVIRVEHGLSLLLPYASLQEQEQGVQSRERY

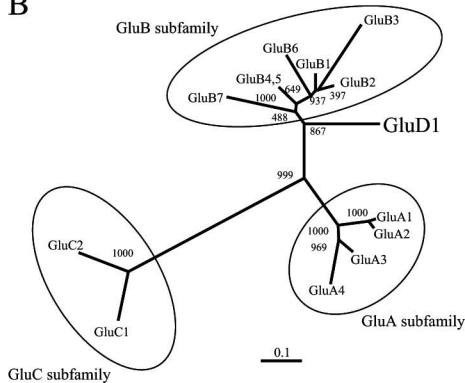
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GluA2 389 VVNNKGTVEFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluA3 388 VVNNKGTVEFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluA4 388 VVNNKGTVEFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluB1a/b 385 VVNSFGKTVFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluB2 381 VVNSFGKTVFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluB3 381 VVNSFGKTVFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluB4/5 386 VVNSFGKTVFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluB6 381 VVNSFGKTVFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluB7 382 VVNSFGKTVFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluC1 401 VVNSFGKTVFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluC2 401 VVNSFGKTVFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS
GluD1 368 VVNSFGKTVFDELRRGQLLIIPOHYVVKKAQREGQYIAFKTNPNVSHLAGKNSIFRALPVDVIANAYRISREAEARLKNRGEDEGFAFTPIQYKS

GluA1 489 YQDVNVAESS-----
GluA2 489 YQDVNVAESS-----
GluA3 488 SYQDISVSA-----
GluA4 488 SYQDISVSA-----
GluB1a/b 485 YYPGDSNESESETSE---
GluB2 481 YYPGDSNESESETSE---
GluB3 481 YYPGDSNESESETSE---
GluB4/5 486 YYPGDSNESESETSE---
GluB6 481 YYPGDSNESESETSE---
GluB7 482 KIHQEYSNPNESETQEVI
GluC1 501 QYAEIQINEK-----
GluC2 501 QYAEIQINEK-----
GluD1 468 SQRGYQLTEGLSLIGM-----

A



B



Nipponbare	1	ATGGCAACTACTACCTCTCTATTGTCTTCCTGTCTCTGTGCTCTTCTCTGGCTCCGCCTTTAGCCAAGGTGTAGATTGCATGGAAAGCCGACAAGGGCTTCCAGGCAGTGCAGATT
Wataribune2	1
Kasalath	1G
NonaBokra	1G
Nipponbare	121	GATAGGTTACAAGCATTGACCCCTAAGAAGGTACGATCGGAAGCTGGGACACAGAGTACTTTGATGAGAGAAATGAGCAGTTTCGATGCCTGGTCTTTGTCTTTCGCGCGTG
Wataribune2	121T
Kasalath	121C
NonaBokra	121C
Nipponbare	241	ATTGAGCCACAAGGCCTTGTGGTGCCTGATACTCGAACACTCTGTCTAGCTACATAATCCAAGGAAAAGGTTACGTAGGATTGACTTTTCTGGTTGCCAGCAACACCAACA
Wataribune2	241
Kasalath	241G
NonaBokra	241
Nipponbare	361	CAATTCCAACTATTGAACAAAGACAGAGCGACCAAGCTCATAAGTTTAGAGATGAGCACAGAAGATTACGAATTTAGGCAAGGGGATGTTGTTGCACTCCGGCTAGTGTGCACAT
Wataribune2	361
Kasalath	361A
NonaBokra	361A
Nipponbare	481	TGGTCTACAATGGTGTGATACCCGGCTGTTGTTGTCTATGTTTATGACATAAAAAAGTTTGCTAATCAGCTTGAACCAAGGCAGAAGGATTTTATTAGCTGGTAACAACACAGAGA
Wataribune2	481
Kasalath	481A
NonaBokra	481A
Nipponbare	601	GGGCAACAAATATTGAACATTCCATCTTCAACACTTGGACAAAATATTTAGTGGGTTCAATACTGAGTACTTAGCAGGCGCTTGAATAAACACGGAGGCTTCCAAGGGCTC
Wataribune2	601
Kasalath	601G
NonaBokra	601G
Nipponbare	721	CAAAGTCAAATGACCAAGGGGAGATATCATTGAGTGAAAGCACGGGCTCAATTTGTTGAAACCCACATTAAACACAACGACAGGAAGAACATCGTCAATATCAACAGTCCAGTATCGT
Wataribune2	721
Kasalath	721CG
NonaBokra	721CG
Nipponbare	841	GAAGGACAATATAATGATTGGACGAGAATTTCTGACAATAAAGGCAAGGTTAAACATTGAAATCTAGCCCGCTGACTACTACAACCTCGTGCTGGAAGGATAACCCCTCTTAAAC
Wataribune2	841
Kasalath	841C
NonaBokra	841C
Nipponbare	961	AACCAAAAGTTCCTATTCTCAACCTTATTGGAATGGTGTGCAAGAGTAAACTTATACAGAATGCTCTTCTCAACCTTCTGGAACATTAAATGCCATAGTGTAGTGATATCATC
Wataribune2	961
Kasalath	961C
NonaBokra	961C
Nipponbare	1081	CAAGGAAGTGTGCGAGTACAGGTTGCCAATAATCAAGGAAGATCTGTGTTAATGGTGACTTCATCAGGGGCAACTTAAATATCATACCAAAAACCATGCCGTCATTAAGAAAGCCGAG
Wataribune2	1081
Kasalath	1081C
NonaBokra	1081C
Nipponbare	1201	CACAATGGTGCCAGTATGTCGCAATAAAGACAATTTGCGACCCTACGGTGAGTTGGGTTGCTGGAAGAACTCCATATTACGTGCATTGCCTGTAGATTGTTGCCAATGCTTATCGT
Wataribune2	1201
Kasalath	1201CC
NonaBokra	1201CC
Nipponbare	1321	ATCTCGAGGGATGAAGCCCGACGCTAAGAATAATAGGCGAGTGAAGTTGCCCTTTTACTCTCGTTCCTCCCAAGAGCCAGCGGGGTACCAGTTCCTAACTGAAGGCCTCTCT
Wataribune2	1321
Kasalath	1321G
NonaBokra	1321G
Nipponbare	1441	TTAATCGGCATGTAA
Wataribune2	1441
Kasalath	1441
NonaBokra	1441

Nipponbare	1	MATTTSLLSCLCALLLAPLFSQGVDAWESRQGASRQCRFDRLQAFEP L R K V R S E A G D T E
Wataribune2	1V..
Kasalath	1E.....A.....V..
Nona Bokra	1E.....A.....V..
Nipponbare	61	YFDERNEQFRCAGVFVIRRVIEPQGLVVP R Y S N T P A L A Y I I Q G K G Y V G L T F P G C P A T H Q Q
Wataribune2	61
Kasalath	61
Nona Bokra	61	...I.....
Nipponbare	121	QFQLFEQRQSDQAHKFRDEHQIHEFRQGDVVALPASVAHWFYNGGDTPAVVVYVYDIKS
Wataribune2	121
Kasalath	121
Nona Bokra	121
Nipponbare	181	FANQLEPRQKEFLLAGNNQRGQQIFEHSIFQHSGQNI F S G F N T E V L S E A L G I N T E A S K R L
Wataribune2	181
Kasalath	181A...
Nona Bokra	181A...
Nipponbare	241	QSQNDQRGDIIRVKHGLQLLKPTLTQRQEEHRQYQQVYREGQYNGLDENFCTIKARVNI
Wataribune2	241
Kasalath	241P.....
Nona Bokra	241P.....
Nipponbare	301	ENPSRADYYNPRAGRITLLNNQKFPILNLI G M G A A R V N L Y Q N A L L S P F W N I N A H S V Y I I
Wataribune2	301
Kasalath	301	...N.....
Nona Bokra	301	...N.....
Nipponbare	361	QGSVRVQVANNQGRSVFNGVLHQQLLIIPQNHAVIKKA E H N G C Q Y V A I K T I S D P T V S W V
Wataribune2	361
Kasalath	361	..AQ.....T..S.....PN.M..R..
Nona Bokra	361	..AQ.....T..S.....PN.M..R..
Nipponbare	421	AGKNSILRALPVDVIANAYRISRDEARRLKNNRADEIGPFTPRFPQKSQRGYQFLTEGLS
Wataribune2	421
Kasalath	421A.....K...
Nona Bokra	421A.....K...
Nipponbare	481	LIGM
Wataribune2	481
Kasalath	481
Nona Bokra	481

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