SUPPLEMENTARY DATA

Fig. 1. Sequence alignment of the human and mouse hyaluronidases Hyal-1-Hyal-4, PH-20, and Phyal1

The conserved identical amino acid residues are shaded as by black color whereas homologous residues by grey. The human Hyal sequences are designated as *_h and mouse ones by *_m. The clear homology of all proteins is evident.

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Hyal2_h     1 ------------------------MRAGPGPTVTLALVLAVAW----AMELKPTAPPIFTGRPFVVAWDVPTQDCGPRLK
Hyal2_m     1 ------------------------MRAGLGPIITLALVLEVAW----AGELKPKPPPIFTGRPFVVAWNVPTQECAPRHK
PH20_h      1 -----------MGVLKFKHIFFRSFVKSSGVSQIVFTFLLIPC----CLTLNFRAPPVIPNVAFLWAWNAPSEFCLGKFD
PH20_m      1 -----------MGELRFKHLFWGSFVESGGTFQTVLIFLLIPC----SLTVDYRAAPILSNTTFLWIWNVPTERCVGNVN
Hyal1_h     1 ----------------------------MAAHLLPICALFLTL----LDMAQGFRGPLLPNRPFTTVWNANTQWCLERHG
Hyal1_m     1 MLGLTQHAQKVWRMKPFSPEVSPGSSPATAGHLLRISTLFLTL----LELAQVCRGSVVSNRPFITVWNGDTHWCLTEYG
Hyal4_h     1 ----------------MKVLSEGQLKLCVVQPVHLTSWLLIFFILKSISCLKPARLPIYQRKPFIAAWNAPTDQCLIKYN
Hyal4_m     1 ----------------MQLLPEGQLRLCVFQPVHLTSGLLILFILKSISSLKPARLPVYQRKPFIAAWNAPTDLCLIKYN
Hyalp1_h    1 ---------------------------MCNPWVAWLGVLPLFILL-TQAALKPAMPPVIKSQPFNIFWAAPTMYCMPSFN
Hyalp1_m    1 ---------------------------MFIQWVTQLGELVLFVLLVAPAALKPAMPPVIKDHPFNVFWAAPTLFCKDHFN
Hyal3_h     1 ------------------------------MTTQLGPALVLGV---ALCLGCGQPLPQVPERPFSVLWNVPSAHCEARFG
Hyal3_m     1 ------------------------------MIMHLGLMMVVGL---TLCLMHGQALLQVPEHPFSVVWNVPSARCKAHFG

Hyal2_h    53 VPLDLNAFDVQASPNEGFVNQNITIFYRDRLGLYPRFDSA-GRSVHGGVPQNVSLWAHRKMLQKRVEHYIRTQESAGLAV
Hyal2_m    53 VPLDLRAFDVKATPNEGFFNQNITTFYYDRLGLYPRFDAA-GTSVHGGVPQNGSLCAHLPMLKESVERYIQTQEPGGLAV
PH20_h     66 EPLDMSLFSFIGSPRINATGQGVTIFYVDRLGYYPYIDSITGVTVNGGIPQKISLQDHLDKAKKDITFYM-PVDNLGMAV
PH20_m     66 DPIDLSFFSLIGSPRKTATGQPVTLFYVDRLGLYPHIDANQAEHY-GGIPQRGDYQAHLRKAKTDIEHYI-PDDKLGLAI
Hyal1_h    49 VDVDVSVFDVVANPGQTFRGPDMTIFYSSQLGTYPYYTPT-GEPVFGGLPQNASLIAHLARTFQDILAAIPAPDFSGLAV
Hyal1_m    77 VDVDVSVFDVVANKEQSFQGSNMTIFYREELGTYPYYTPT-GEPVFGGLPQNASLVTHLAHTFQDIKAAMPEPDFSGLAV
Hyal4_h    65 LRLNLKMFPVIGSPLAKARGQNVTIFYVNRLGYYPWYTSQ-GVPINGGLPQNISLQVHLEKADQDINYYIPAEDFSGLAV
Hyal4_m    65 LTLNLKVFQMVGSPRLKDRGQNVVIFYANRLGYYPWYTSE-GVPINGGLPQNTSLQVHLKGAGQDINYYIPSENFSGLAV
Hyalp1_h   53 VDINLQVFNIISNPLETQSGSKIAIFYPNELGYYPYLSQD-GKSFNGGIPQNVSLSEHLRKTADDIGEGVPWWRSEELVV
Hyalp1_m   54 VNMNLQVFNIIPNPFETQSGSTITVFYPKELGYYPYFSED-GTSFYGGIPQKVNLSEHLRKSAGDIADAVTLWRSEGLAV
Hyal3_h    48 VHLPLNALGIIANRGQHFHGQNMTIFYKNQLGLYPYFGPR-GTAHNGGIPQALPLDRHLALAAYQIHHSL-RPGFAGPAV
Hyal3_m    48 VHLPLDALGIVANHGQHFHGQNISIFYKNQFGLYPYFGPR-GTAHNGGIPQAVSLDEHLARAAHQILHSL-GSSFAGLAV

Hyal2_h   132 IDWEDWRPVWVRNWQ-DKDVYRRLSRQLVASRHPDWPPDRIVKQAQYEFEFAAQQFMLETLRYVKAVRPRHLWGFYLFPD
Hyal2_m   132 IDWEEWRPVWVRNWQ-EKDVYRQSSRQLVASRHPDWPSDRVMKQAQYEFEFAARQFMLNTLRLRQGSQTQHLWGFYLFPD
PH20_h    145 IDWEEWRPTWARNWK-PKDVYKNRSIELVQQQNVQLSLTEATEKAKQEFEKAGKDFLVETIKLGKLLRPNHLWGYYLFPD
PH20_m    144 IDWEEWRPTWLRNWK-PKDNYRNKSIELVQSTNPGLSITRATQKAIQQLEEAGRKFMEGTLHLGKFLRPNQLWGYYLFPD
Hyal1_h   128 IDWEAWRPRWAFNWD-TKDIYRQRSRALVQAQHPDWPAPQVEAVAQDQFQGAARAWMAGTLQLGQALRPRGLWGFYGFPD
Hyal1_m   156 IDWEAWRPRWAFNWD-SKDIYRQRSMELVQAEHPDWPETLVEAAAKNQFQEAAEAWMAGTLQLGQVLRPRGLWGYYGFPD
Hyal4_h   144 IDWEYWRPQWARNWN-SKDVYRQKSRKLISDMGKNVSATDIEYLAKVTFEESAKAFMKETIKLGIKSRPKGLWGYYLYPD
Hyal4_m   144 IDWEYWRPQWARNWN-TKDIYRQKSRTLISDMKENISAADIEYSAKATFEKSAKAFMEETIKLGSKSRPKGLWGYYLYPD
Hyalp1_h  132 IDWESWKPQWDRNQG-SRIIYKNHSLAFTRNKHPYWSEMKVETVAREEFENAGKNFMNITLTLALEMRPKCLWGFYLYPD
Hyalp1_m  133 IDWEGWRPQWDRNWG-SRMIYKNHSLAFTRHHHPDWAETKVRTAAQKEFENAGRSFMNVTLTLALEMRPKRLWGFYLYPD
Hyal3_h   126 LDWEEWCPLWAGNWG-RRRAYQAASWAWAQQVFPDLDPQEQLYKAYTGFEQAARALMEDTLRVAQALRPHGLWGFYHYPA
Hyal3_m   126 LDWEEWYPLWAGNWGPHRQVYLAASWVWTQQMFPGLDPQEQLHKAHTSFEQAARALMEYTLQLGRTLRPSGLWGFYRYPA

Hyal2_h   211 CYNHD--YVQNWESYTGRCPDVEVARNDQLAWLWAESTALFPSVYLDETLASALHGRNFVSFRVQEALRVARTHHANHA-
Hyal2_m   211 CYNHD--YVQNWESYTGRCPDVEVARNDQLAWLWAESTALP-SVYLDETLASSVHSRNFVRFGGREALRVAHTHHANHA-
PH20_h    224 CYNHH--Y--KKPGYNGSCFNVEIKRNDDLSWLWNESTALYPSIYLNTQ-QSPVAATLYVRNRVREAIRVSKIPDAKSP-
PH20_m    223 CYNNK--F--QDPKYDGQCPAVEKKRNDNLKWLWKASTGLYPSVYLKKDLKSNRQATLYVRYRVVEAIRVSKVGNASDP-
Hyal1_h   207 CYNYD--FL--SPNYTGQCPSGIRAQNDQLGWLWGQSRALYPSIYMPAVLEGTGKSQMYVQHRVAEAFRVA--VAAGDPN
Hyal1_m   235 CYNND--FL--SLNYTRQCPVFVRDQNDQLGWLWNQSYALYPSIYLPAALMGTEKSQMYVRHRVQEALRVA--IVSRDPH
Hyal4_h   223 CHNYN--V--YAPNYSGSCPEDEVLRNNELSWLWNSSAALYPSICVWKSLGDSENILRFSKFRVHESMRIS--TMTSHDY
Hyal4_m   223 CHNYN--V--YATNYTGSCPEEEVLRNNDLSWLWNSSTALYPAVSIRKSFADSENTLHFSRFRVRESLRIS--TMTSQDY
Hyalp1_h  211 CYNYDYRI--NPETYTGNCPNXXXXXXXXXXWLWEKSAALYPSIHLDKILKSSLNALKFVHYRVREAMRVA--EMARHDY
Hyalp1_m  212 CYNYDYRI--NPEFYTGSCPDDEIPRNDQLMWLWEKSAALYPSIYLSKILKSNLNALKFVHPRVREALRVA--EMARKDY
Hyal3_h   205 CGNG---WHSMASNYTGRCHAATLARNTQLHWLWAASSALFPSIYLPPR-LPPAHHQAFVRHRLEEAFRVA--LVGHRH-
Hyal3_m   206 CGNG---WHKMASNYTGHCHAAITTRNTQLRWLWAASSALFPSIYLPPR-LPLAYRQAFVRHRLEEAFRVA--LLEHSH-

Hyal2_h   288 -LPVYVFTRPTYSR--CTGL---SEMDLISTIGESAALGAAGVILWGDAGYTTSTETCQYLKDYLTRLLVPYVVNVSWAT
Hyal2_m   287 -LPVYVFTRPTYTRG-LTGL---SQVDLISTIGESAALGSAGVIFWGDSEDASSMETCQYLKNYLTQLLVPYIVNVSWAT
PH20_h    298 -LPVFAYTRIVFTDQVLKFL---SQDELVYTFGETVALGASGIVIWGTLSIMRSMKSCLLLDNYMETILNPYIINVTLAA
PH20_m    298 -VPIFVYIRLVFTDRTSEYL---LEDDLVNTIGEIVALGTSGIIIWDAMSLAQRAAGCPILHKYMQTTLNPYIVNVTLAA
Hyal1_h   281 -LPVLPYVQIFYDT-TNHFL---PLDELEHSLGESAAQGAAGVVLWVSWENTRTKESCQAIKEYMDTTLGPFILNVTSGA
Hyal1_m   309 -VPVMPYVQIFYEM-TDYLL---PLEELEHSLGESAAQGVAGAVLWLSSDKTSTKESCQAIKAYMDSTLGPFIVNVTSAA
Hyal4_h   297 ALPVFVYTRLGY---RDEPLFFLSKQDLVSTIGESAALGAAGIVIWGDMNLTASKANCTKVKQFVSSDLGSYIANVTRAA
Hyal4_m   297 ALPVFVYTQLGY---KEEPLLFPFKQDLISTIGESAALGAAGIVVWGDMNLTSSEENCTKVNRFVNSDFGSYIINVTRAA
Hyalp1_h  287 VLPVFIFSRPPYLH-STEAL---SQVDLVHAIGESAALGAAGVILWGGYEYS-ASENCLSVQQSIRGPLGHYAVNVTSAA
Hyalp1_m  288 VLPVFIFSRPPYLQ-SIEAL---SEEDLVHTIGESAALGAAGIILWGGYEYSDTKETCLSVRQTVHGLLGPYVLNVTSAA
Hyal3_h   278 PLPVLAYVRLTH-RRSGRFL---SQDDLVQSIGVSAALGAAGVVLWGDLSLSSSEEECWHLHDYLVDTLGPYVINVTRAA
Hyal3_m   279 PLPVLAYSRLTH-RSSGRFL---SLDDLMQTIGVSAALGTAGVVLWGDLSFSSSEEKCWRLHDYLVGTLGPYVINVTKAA

Hyal2_h   362 QYCSRAQCHGHG--CVPGNPSASTFLHL--STNSFRLVPGHAPGEPQLRPVGELSWADIDHLQTHFRCQCYLGWSGEQCQ
Hyal2_m   362 QYCSWTQCHGHGR-CVRRNPSVNTFLHL--NASSFRLVPGHTPSEPQLRPEGQLSERDRQLPEKHFRCQCYLGWGGEQCQ
PH20_h    374 KMCSQVLCQEQGV-CIRKNWNSSDYLHL--NPDNFAIQLEKG---GKFTVRGKPTLEDLEQFSEKFYCSCYSTLSCKEKA
PH20_m    374 KMCSQTLCNEKGM-CSRRKESSDVYLHL--NPSHPDIMLTET---GKYEVLGNPRVGDLEYFSEHFKCSCFSRMTCKETS
Hyal1_h   356 LLCSQALCSGHGR-CVRRTSHPKALLLL--NPASFSIQLTPG--GGPLSLRGALSLEDQAQMAVEFKCRCYPGWQAPWCE
Hyal1_m   384 LLCSEALCSGHGR-CVRHPSYPEALLTL--NPASFSIELTHD--GRPPSLKGTLSLKDRAQMAMKFRCRCYRGWRGKWCD
Hyal4_h   374 EVCSLHLCRNNGR-CIRKMWNAPSYLHL--NPASYHIEASED---GEFTVKGKASDTDLAVMADTFSCHCYQGYEGADCR
Hyal4_m   374 EVSSRHLCKNNGR-CVRKTWKAAHYLHL--NPASYHIEASED---GEFIVRGRASDTDLAVMAENFLCHCYEGYEGADCR
Hyalp1_h  362 KLCSQSLCNNHGR-VPEKHLSPPSICICL-KAVVRNMYXNKS---PRFIISENNKQKTITDMKNGFVCHCYYGWHQPSCH
Hyalp1_m  364 KLCSQNLCNSHGR-CVRKTPESSPYLHMP-EDSHKNYVSKKG---FRFVIPSPSKLKTIMNMKNGFVCHCYYGWHGDSCR
Hyal3_h   354 MACSHQRCHGHGRCARRDPGQMEAFLHLWPDGSLGDWKSFSC---HCYWGWAGPTCQEPRPGPKEAV-------------
Hyal3_m   355 MACSHQRCHGHGRCARKDPGQMEAFLHLQPDDSLGAWNSFRC---RCYSGWAGPTCLEPKP-------------------

Hyal2_h   438 WDHRQAAGGANEAWAGSHLTSLLALAALAFTWTL-----------------------------------
Hyal2_m   439 RNYKGAAGNASRAWAGSHLTSLLGLVAVALTWTL-----------------------------------
PH20_h    448 DVKDTDAVDVCIADGVCIDAFLKP-P---METEEPQIFYNASPS---TLSATMFIVSILFLIISSVASL
PH20_m    448 DVKNVQDVNVCVGDNVCIKAKVEPNPAFYLLPGKSLLFMTTLGHVLYHLPQDIPVFPRKTLVSTP----
Hyal1_h   431 RKSMW----------------------------------------------------------------
Hyal1_m   459 KRGM-----------------------------------------------------------------
Hyal4_h   448 EIKTADGCSGVSPSPGSLMTLCLLLLASYRSIQL-----------------------------------
Hyal4_m   448 EMTEASGPSGLSLSSSSVITLCLLVLAGYQSIQL-----------------------------------
Hyalp1_h  437 D-HSSDLLRVMNKAPTINFNLLVFLIMASSVILLKKILALTTMPIFS----------------------
Hyalp1_m  439 S-HSPMLQK--NKAPASGLNSAVIVGMALFVILNN----YFPIPYYNGNFSLKPLKRREIIFL------
Hyal3_h       ---------------------------------------------------------------------
Hyal3_m       ---------------------------------------------------------------------
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