Characterization of microtubule associated protein tau isoforms and Alzheimer's disease-like pathology in normal sheep (*Ovis aries*) - relevance to their potential as a model of Alzheimer's disease.

Authors: Emma S. Davies[a], Russell M. Morphew[a], David Cutress[a], A. Jennifer Morton[b], Sebastian McBride[a]

[a] Department of Life Sciences, Aberystwyth University, Aberystwyth, Wales.

[b] Department of Physiology, Development and Neuroscience, University of Cambridge, Cambridge, UK

Correspondence: sdm@aber.ac.uk, +44 (0) 1970 621633, Institute of Biological, Environmental and Rural Sciences, Aberystwyth University, Aberystwyth, Wales.

Email: Emma S. Davies; esd5@aber.ac.uk, Russel M. Morphew; rom@aber.ac.uk, David Cutress; djc25@aber.ac.uk, A. Jennifer Morton; ajm41@cam.ac.uk, Sebastian McBride; sdm@aber.ac.uk

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Human MAEPRQEFEVMEDHA-GTYGLGDRKDQGGYTMHQDQEGDTDAGLKESPLQ    49
Mouse MADPRQEFDTMEDHA-GDYTLL----------QDQEGDMDHGLKESPPQ    38
Sheep MAEPRQEFDVMEDHAQGDYTL----------QDHEGDMEPGLKESPLQ    38

Human TPTEDGSEEPGSETSDAKSTPTAEDVTAPLVDEGAPGKQAAAQPHTEIPE    99
Mouse PPADDGAEEPGSETSDAKSTPTAEDVTAPLVDERAPDKQAAAQPHTEIPE    88
Sheep TPADDGSEEPGSETSDAKSTPTAEDATAPLVDEGALGEQAAAQAPTEIPE    88

Human GTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGK-   148
Mouse GITAEEAGIGDTPNQEDQAAGHVTQARVASK--DRTGNDEKKAKGADGKT   136
Sheep GTTAEEAGIGDTSNLEDQAAGHVTQARMVSKGKDGTGPDDKKAKGADGKP   138

Human -TKIATPRGAAPPGQKGQANATRIPAKTPPAPKTPPSSGEPPKSGDRSGY   197
Mouse GAKIATPRGAASPAQKGTSNATRIPAKTTPSPKTPPGSGEPPKSGERSGY   186
Sheep GTKIATPRGAAPPGQKGQANATRIPAKTTPTPKTSPGTGESGKSGDRSGY   188

Human SSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSSAKSRLQTAP   247
Mouse SSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSASKSRLQTAP   236
Sheep SSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSAAKSRLQAAP   238

Human VPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNI   297
Mouse VPMPDLKNVRSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNI   286
Sheep GPMPDLKNVKSKIGSTENLKHQPGGGKVQIINKKLDLSNVQSKCGSKDNI   288

Human KHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFK   347
Mouse KHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFK   336
Sheep KHVPGGGSVQIVYKPVDLSKVTSKCGSLGNIHHKPGGGQVEVKSEKLDFK   338

Human DRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSP   397
Mouse DRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSP   386
Sheep DRVQSKIGSLDNITHVPGGGNKKIETHKLTFRENAKAKTDHGAEIVYKSP   388

Human VVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL         441
Mouse VVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL         430
Sheep VVSGDTSPRHLSNVSSTGSIDMVDSPQLATLADEVSASLAKQGL         432
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Fig. S5 Multiple amino acid alignment of the longest human (NP_005901.2), murine (NP_001033698.1) and ovine (XP_027830182.1) tau protein sequences. Amino acids unique to the sheep are highlighted in bold red type. Major phosphorylation sites identified in humans are indicated by bold purple type. Conserved KXGS motifs which can be phosphorylated my multiple kinases are indicated by bold black type. Conserved PGGG sequences which facilitate the formation of type II β-turns and β-hairpin structures are indicated by bold blue type.