Roles of Major Facilitator Superfamily Transporters in Phosphate Response in Drosophila

Clemens Bergwitz, Matthew D. Rasmussen, Charles DeRobertis, Mark J. Wee, Sumi Sinha, Hway H. Chen, Joanne Huang, Norbert Perrimon

Supporting Information

Figure S1.
P-element and deficiency stocks for MFS13 (l(2)01810, FBgn0010497). The insertion sites of the P-elements obtained from flybase (www.flybase.org) is shown in A, the location of available chromosome 2 deficiency mutants surrounding the genetic locus and including FBgn0010497 is shown in B. qRT-PCR to confirm complete loss of MFS13 transcripts in P{PZ}l(2)0181001810/Df(2L)BSC826 (11076/27900) or P{PZ}l(2)0181001810/Df(2L)BSC323 (11076/24348) adult flies when compared to heterozygous stocks and wild-type flies (CTRL) (C).
doi:10.1371/journal.pone.0031730.s001

Figure S2.
Sequence comparison between ph84 and MFS transporters expressed in S2R+ cells. A: Global alignment. Amino acid sequence identity in % between the sequence shown in column and row (alignment length in brackets). B: Local alignment. Amino acid sequence identity in % between sequence shown in column and row (alignment length in brackets). C: Clustal W alignment of fly transporters expressed in S2R+ cells along with Pho84 using Jalview (http://www.jalview.org/download.html).
doi:10.1371/journal.pone.0031730.s002

Figure S3.
FlyAtlas tissue distribution of MFS10 (FBgn0030452) and MFS13 (FBgn0010497). Using FlyAtlas [47](http://flyatlas.org/) mRNA expression of MFS10, and MFS13 (encoded by FBgn0030452, FBgn0010497, respectively) is shown for various larval and adult fly tissues.
doi:10.1371/journal.pone.0031730.s003

Figure S4.
Phosphonoformic acid and sevelamer impair larval development. Yellow white flies were cultured on standard medium at 25°C. This medium was supplemented with 30 mM sodium-phosphate (pH6.0)(P30), 1 mM phosphonoformic acid (PFA), or 0.5% sevelamer (Sev) or in combinations thereof. Number of larvae emerged from the medium over time are shown.
doi:10.1371/journal.pone.0031730.s004

Table S1.
Primer sequences used for dsRNA synthesis, cRNA synthesis and qRT-PCR. Primer sequences are displayed 5′ to 3′ and include the T7-RNA-polymerase promotor when used to generate PCR templates for dsRNA or cRNA sythesis.
doi:10.1371/journal.pone.0031730.s005

Table S2.
Tables of all blast hits S. cerevisiae vs. D. melanogaster (S2.1), D. melanogaster vs. D. melanogaster (S2.2), D. melanogaster vs. human (S2.3) with the following format. 1. Query ID (Ensembl). 2. Subject ID (Ensembl). 3. % identity between query and subject, 4. alignment length between query

and subject, 5. mismatches between query and subject, 6. gap openings between query and subject, 7. query start, 8. query end, 9. subject start, 10. subject end, 11. e-value, 12. bit score. 13. query family ID. 14. subject family ID.
doi:10.1371/journal.pone.0031730.s006

Table S3.
MFS expression in S2R+ cells. Cell-specific RNA expression profiling for S2R+ cells using high-density genome tiling microarrays (next generation RNAseq technology) was obtained from ModENCODE [45], and using Affymetrix Flychip Drosophila expression array technology was obtained from FLIGHT [46]. Expression cut-off's are given in brackets and expressed genes are highlighted in green.

doi:10.1371/journal.pone.0031730.s007

Table S4.
Expression data for Drosophila MFS transporters in S2R+ cells. Cell-specific RNA expression profiling of 17 Drosophila cell lines using high-density genome tiling microarrays (next generation RNAseq technology) was obtained from ModENCODE [45], and using Affymetrix Flychip Drosophila expression array technology was obtained from FLIGHT [46]. Expressed genes are highlighted in green (or blue for modest expression).
doi:10.1371/journal.pone.0031730.s008