

Table S1

List of the full mouse matrisome used in the comparison was downloaded from the [The Matrisome Project](#). The genes are ordered in columns by division, category, gene symbol, gene name, synonym, MGI_IDs, UniProt_IDs, Refseq_IDs and notes.

Table S2

List of all GAG related genes used in the comparison. The genes are ordered by category and organized in column by gene symbol, gene name and gene function.

Table S3

FW = flank wound

The excel file shows the results of our own analysis with the microarray performed by Monaghan (2012). Column A is Affymetrix gene ID, column B contains the gene expression value on day 7, column C contains the gene expression value on day 0. Column D contains the calculated fold change of day 7 compared to day 0. Column E = P-value and column F = FDR P-value. Column G and H display the gene symbol (human) and associated gene name.

Table S4

Sheet 1. 'Matrisome d7 vs d14'

Column A contains the gene symbols of the mouse matrisome master list and column B the associated gene names. The remaining columns display the matrisome categories; collagens (C-F), ECM glycoproteins (I-M), proteoglycans (O-T), ECM affiliated genes (V-AA), secreted factors (AC-AH) and regulators (AJ-AN). Each set of columns is organized as follows: gene symbol – gene name – fold change on day 7 – gene symbol – gene name – fold change on day 14. Only genes with $P < 0.05$ were used for matching.

Sheet 2. 'GAG genes day 7 vs d14'

Column A contains the GAG subgroup name and the gene symbols, column B displays the gene name and column C displays the function of the encoded protein. Column D-G display the fold change and adjusted P-value for day 7 (D-E) and day 14 (F-G). Only genes with $P < 0.05$ were used for matching.

Table S5

Sheet 1. 'matrisome and GAG matches'

Column A (gene symbol) and column D (fold change) were extracted from S1. The remaining columns are clustered per matrisome or GAG category: column F-H = collagens, J-L = ECM glycoproteins, N-P = proteoglycans, R-T = ECM affiliated, V-X = secreted factors, Z-AB = regulators, AE-AG = preparation of linkage region, AI-AK = glycosaminoglycan chain polymerization, AM-AO = glycosaminoglycan chain modification and AQ-AS = glycosaminoglycan chain degradation. All categories are organized by: gene symbol – gene name – fold change (of the matching gene). N/A indicates no match was found in the dataset.

Table S6

Sheet 1. 'Brant vs Monaghan match'

Column A-C contain the matrisome and GAG matches identified in *Acomys* skin wounds on day 7. Column A = gene symbol, column B = gene name, column C = fold change. The matrisome and GAG categories are divided by rows: row 2-32 = collagens, row 35-142 = ECM glycoproteins, row 145-162 = proteoglycans, row 165-251 = ECM affiliated, row 254-412 = secreted factors, row 415-552 = regulators, row 556-567 = glycosaminoglycan chain modification. Column E-G displays the matrisome and GAG matches identified in *Axolotl* skin wounds on day 7 (column E = gene symbol, column F = gene name, column G = fold change on day 7). Row H displays whether a match was found in the *Acomys* list using the VLOOKUP function, the fold change is present when a gene matched and N/A indicates the gene was not present.

Table S7

Sheet 1. 'Raw data acomys'

Contains the extracted raw data for *Acomys* only from the Gawriluk et al. dataset. Column A = gene symbol, column B = sequence ID, columns C-F = fold change on day 5, 10, 15 and 20.

Sheet 2. 'Matrisome matches'

Column A (gene symbol) and B (gene name) display the matrisome list used for the gene extraction. The following columns contain the matrisome genes identified in the dataset, organized per category: column D-H = collagens, J-N = ECM glycoproteins, P-T = proteoglycans, V-Z = ECM affiliated, AB-AF = secreted factors, AH-AL = regulators. All categories are organized by gene symbol – gene name – day 5 fold change – day 10 fold change – day 15 fold change.

Sheet 3. 'GAG matches'

Column A-D contains the raw data (also see sheet 1). Columns G-K contain the GAG genes extracted from the dataset: column G = gene symbol, column H = gene function, column I-K = fold change on day 5 – 10 – 15. The four categories of GAG genes are divided over the rows: row 1-10 = preparation of linkage region, row 12-26 = glycosaminoglycan chain polymerization, row 28-61 = glycosaminoglycan chain modification, row 63-83 = glycosaminoglycan chain degradation/

Table S8

Sheet 1. 'Fold change calculation'

Column A-F raw data from the Stewart dataset. Column A = gene symbol, column B = raw data timepoint 0, column C = datapoints from column B were converted from 0 to 1. Column D-F = raw data for timepoint 5 – 10 – 14. Column H-K = fold changes for day 5 – 10 – 14 compared to day 0.

Sheet 2. 'Matrisome matches'

Matrisome genes extracted from the data, when fold change = 0-1 the value was converted using $1/FC$. Matrisome categories are ordered by columns with column A-E = collagens, G-K = ECM glycoproteins, M-Q = proteoglycans, S-W = ECM affiliated, Y-AC = secreted factors, AE-AI = regulators.

All categories are organized by gene symbol – gene name – day 5 fold change – day 10 fold change – day 14 fold change.

Sheet 3. 'GAG matches'

GAG matches extracted from the data, when fold change = 0-1 the value was converted using $-1/FC$. GAG categories are ordered by rows: row 1-4 = preparation of linkage region, 8-18 = glycosaminoglycan chain polymerization, 20-40 = glycosaminoglycan chain modification, 42-58 = glycosaminoglycan chain degradation. All categories are organized by column, column A = gene symbol, column B = gene name, columns C-D-E = fold change on day 5-10-14.

Table S9

Sheet 1. 'Matrisome: Stewart vs Gawriluk'

Columns A-E contain the matrisome matches identified in *Acomys* from the Gawriluk dataset. Column F and G are the gene symbol and gene name, respectively. Column H-J are the fold changes for these genes in Axolotl (Stewart data). In column K-M the fold change of *Acomys* was matched to these genes, in case of N/A no matching gene was present in the *acomys* dataset. The matrisome categories are ordered by rows: row 2-37 = collagens, row 42-184 = ECM glycoproteins, row 187 – 216 = proteoglycans, row 219-317 = ECM affiliated, row 320-500 = secreted factors, row 503-654 = regulators.

Sheet 2. 'GAG: Stewart vs Gawriluk'

Matching GAG genes between Stewart and Gawriluk. GAG gene categories are organized by row: row 1-5 = preparation of linkage region, row 7-17 = glycosaminoglycan chain polymerization, row 19-36 = glycosaminoglycan chain modification, row 38-53 = glycosaminoglycan chain degradation. Categories are organized by columns. Column A = gene symbol, column B = gene name, column C-E = fold change in axolotl, column F-H = fold change in axolotl.