Microarray data on the comparison of transcript expression between normal and Pt-Delta RNAi embryos in the common house spider Parasteatoda tepidariorum

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ABSTRACT

We conducted a custom microarray experiment to detect the differences in the transcript expression levels between untreated (normal) and Pt-Delta-RNAi embryos at late stage 6 in the common house spider Parasteatoda tepidariorum. The array probes were designed based on accumulated EST and cDNA sequences. The microarray dataset has been deposited in the Gene Expression Omnibus (GEO) Database at the National Center for Biotechnology Information (NCBI) under the accession GSE113064. The expression of the transcripts selected based on the detected differences was examined in embryos by whole-mount in situ hybridization.

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1. Data

Transcript expression was compared between untreated (normal) and Pt-Delta RNAi-treated (Pt-Delta RNAi) embryos at late stage 6 using a Combimatrix custom microarray in 12K format (Fig. 1), which was designed based on the accumulated Parasteatoda tepidariorum EST and cDNA sequences. The microarray dataset deposited in the GEO Database at NCBI under the accession GSE113064. https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE113064

The image data have been deposited in the Mendeley Data repository. https://doi.org/10.17632/r79vg2ctr2.3.

The dataset is useful for identifying the candidate genes whose expression is regulated by Delta-Notch signaling in P. tepidariorum embryos.

The dataset is useful for identifying the genes whose expression marks specific cell types or regions of P. tepidariorum embryos.

The dataset is useful for investigating the gene regulatory networks in the embryonic development of spider.

Fig. 1. Flowchart of the microarray experiment.
ratio of \([Pt-Delta \text{RNAi}] / [\text{normal}]\) for each array spot (Sample: GSM3095654). Values of the \([Pt-Delta \text{RNAi}] / [\text{normal}]\) ratio from control probes are shown in Table 1. EST clones that showed the ratio of \([Pt-Delta \text{RNAi}] / [\text{normal}]\) of <0.6 for at least one array probe are listed together with their details in Table 2. Whole-mount in situ hybridizations (WISHs) of stage 5–8 embryos showing expression of the transcripts related to these EST clones are displayed in Fig. 2. The original images, including high-magnification images showing the transcript expression patterns and nuclear stains, are available in a data repository [1].

2. Experimental design, materials and methods

The primary objective of this experiment was to identify the genes whose expression might be affected by parental RNA interference (pRNAi) against \(Pt-Delta\) in \(P. tepidariorum\) embryos [2]. Flow of the microarray experiment is schematically shown in Fig. 1.

2.1. Custom microarray design

40-mer oligonucleotide probes were designed based on the accumulated \(P. tepidariorum\) EST and cDNA sequences [2,3] using OligoArray 2.1 [4] and embedded in a custom microarray (CombiMatrix CustomArray 12K, CustomArray, Inc.). There were single or multiple probes designed from each EST or cDNA sequence. Four or three spot replicates of control probes (Table 1) were included to validate the experiment. The details of the microarray design, including the probe sequences, are available from the GEO database (GPL24882).

| EST/cDNA clone | Gene product | Spot position numbers in MAa | Sequence accession | AUGUSTUS gene modelb | NCBI GenID | Ratio (mean ± s.d.)c |
|---------------|--------------|-----------------------------|--------------------|----------------------|------------|---------------------|
| At_eW_003_D02 | alpha-catenin | 1719/4149/8989/11508         | AB433907 g13984    | LOC107439705         | 0.880 ± 0.039 |
| At_eW_003_D02 | alpha-catenin | 623/6036/6733/11968         | AB433907 g13984    | LOC107439705         | 0.950 ± 0.265 |
| eS7_003_G08  | elongation factor 1-alpha | 1697/2124/4972 | AB433908 g27264 | LOC107441347 | 1.163 ± 0.040 |
| eS7_003_G08  | elongation factor 1-alpha | 6130/9614/11011 | AB433908 g27264 | LOC107441347 | 1.061 ± 0.072 |
| eS7_SB_037_C01| histone H3    | 565/1580/1610/4874          | AB433909 g1955     | LOC107447866         | 0.965 ± 0.074 |
| eS7_SB_037_C01| histone H3    | 946/6236/6382/9005          | AB433909 g1955     | LOC107447866         | 0.834 ± 0.085 |
| At_O091      | Delta         | 3003/6080/9491/10203        | AB287420 g25248    | LOC107456255         | 1.022 ± 0.099 |
| At_O091      | Delta         | 3364/10373/10432/12130      | AB287420 g25248    | LOC107456255         | 1.164 ± 0.212 |
| At_OO34      | caudal        | 4150/6419/9162/12485        | AB096075 g12643    | LOC107437910         | 0.379 ± 0.068 |
| At_OO34      | caudal        | 6936/8225/8588/10344        | AB096075 g12643    | LOC107437910         | 0.355 ± 0.026 |
| At_OO35      | caudal        | 3904/4818/8215/10264        | AB096075 g12643    | LOC107437910         | 0.150 ± 0.009 |
| At_OO45      | twist         | 6351/7485/7754/9334         | AB167807 g14287    | LOC107440133         | 1.464 ± 0.098 |
| At_OO45      | twist         | 1481/3243/73/4544/10872     | AB167807 g14287    | LOC107440133         | 1.058 ± 0.074 |
| At_OO46      | twist         | 2538/3783/7509/8625         | AB167807 g14287    | LOC107440133         | 1.070 ± 0.095 |
| At_OO29      | hedgehog      | 3925/5404/11012/11143       | AB125742 g4322     | LOC107451809         | 0.436 ± 0.037 |
| At_OO29      | hedgehog      | 432/865/4950               | AB125742 g4322     | LOC107451809         | 0.623 ± 0.102 |
| At_OO30      | hedgehog      | 2406/4772/4947/7704         | AB125742 g4322     | LOC107451809         | 0.905 ± 0.053 |
| At_OO32      | orthodenticle | 1941/5594/10660/11559       | AB096074 g9172     | LOC107457189         | 0.298 ± 0.040 |
| At_OO32      | orthodenticle | 838/3555/8545/9265          | AB096074 g9172     | LOC107457189         | 0.878 ± 0.155 |
| At_OO71      | odd-paired    | 6865/9525/9551/11052        | AB605264 g12202    | LOC107437305         | 0.716 ± 0.023 |
| At_OO71      | odd-paired    | 347/3228/4356/10492         | AB605264 g12202    | LOC107437305         | 1.021 ± 0.161 |

a Two or three 40-mer oligonucleotide sequences were designed from each EST/cDNA sequence for the microarray (MA). The spot position numbers in MA link the data in this report and those deposited in the GEO database.

b AUGUSTUS gene models (aug3) were described by Schwager et al. (2017) [6].

c The average value based on four or three spot replicates in a MA.
Table 2
List of EST clones selected based on the [Pt-Delta RNAi]/[normal] ratio (<0.6) in the microarray analysis.

| EST clone | Spot position number in MA | Sequence accession | AUGUSTUS gene modelb | NCBI GeneId | Ratio | WISH probe | Exp. | cm, cumulus mesenchymal cells) and/or specific patterns (ptn, patterned) as revealed by WISH. |
|-----------|---------------------------|--------------------|----------------------|-------------|-------|-----------|------|--------------------------------------------------|
| At_eW_000_A15 | 10599 | FY216311 g9542 | LOC107437620 | 0.597 | At_eW_000_A15+ | end |
| eS7_SB_035_H06 | 7990 | FY380468 g9542 | LOC107437620 | 0.550 | eS7_SB_035_H06+ | ect (ptn) |
| At_eW_000_E06 | 8245 | FY216397 g15506 | LOC107449884 | 0.453 | At_eW_000_E06+ | ect (ptn) |
| At_eW_000_J22 | 11227 | FY216533 g15506 | LOC107449884 | 0.506 | At_eW_000_J22+ | ect (ptn) |
| At_eW_000_J22 | 9441 | FY216533 g15506 | LOC107449884 | 0.519 | At_eW_000_J22+ | ect (ptn) |
| At_eW_002_J21 | 4632 | FY217255 g6063 | LOC107445132 | 0.580 | At_eW_002_J21+ | ect (ptn) |
| At_eW_007_I04 | 6439 | FY218925 g18068 | LOC107444715 | 0.498 | At_eW_007_I04+ | ect (ptn) |
| eS7_008_B04 | 11074 | FY378225 g8636 | LOC107456533 | 0.579 | eS7_SB_001_H07+ | end ex |
| eS7_008_B04 | 11074 | FY378225 g15296 | LOC107441456 | 0.553 | eS7_SB_008_B12+ | cm |
| eS7_008_B04 | 9585 | FY378241 g11817 | LOC107436785 | 0.524 | eS7_SB_008_D04+ | cm |
| eS7_008_G06 | 11640 | FY380468 g5924 | LOC107445132 | 0.535 | eS7_SB_008_GO6+ | cm |
| eS7_008_B10 | 12337 | FY380468 g18790 | LOC107445841 | 0.565 | eS7_SB_008_B10+ | end |
| eS7_008_B10 | 7166 | FY380468 g18790 | LOC107445841 | 0.535 | eS7_SB_008_B10+ | end |
| eS7_SB_009_A02 | 12357 | FY380468 g5847 | LOC107456289 | 0.493 | eS7_SB_009_A02+ | end |
| eS7_SB_028_A08 | 8536 | FY380468 g4630 | LOC107455614 | 0.536 | eS7_SB_045_H12+ | end |

n/a, not applicable.

a The spot position numbers in the microarray (MA) link the data in this report and those deposited in the GEO database.

b AUGUSTUS gene models (aug3) were described by Schwager et al. (2017) [6].

c EST clone used for the synthesis of RNA probes for whole-mount in situ hybridization (WISH). In some cases, a different EST clone including the MA probe sequence was used for WISH. The WISH data from EST clones indicated by asterisks are displayed in Fig. 1.

d Expression in specific cell types (end, endoderm; ex, extraembryonic tissue; mes, mesoderm; ect, ectoderm; cm, cumulus mesenchymal cells) and/or specific patterns (ptn, patterned) as revealed by WISH.
Fig. 2. Staining of stage 5–8 embryos for selected transcripts by WISH.
2.2. Microarray analysis

A mated female was injected with approximately 1.5 μl of Pt-Delta dsRNA solution (2 μg/μl) 4 times at 2–3 days intervals. Embryos derived from an egg sac produced by the female one day before (normal) and 25 days after (Pt-Delta RNAi) the first injection of Pt-Delta dsRNA were used for RNA extraction. The total RNA was extracted from approximately 250 embryos at late stage 6 using MagExtractor (Toyobo). The RNA integrity was examined with an Agilent Bioanalyzer 2100. cRNA labeled with Cy3 or Cy5 was prepared from 2 μg of total RNA using RNA Transcript SureLABEL Core Kit (Takara). The cRNA probes were hybridized to microarray using Hybridization buffer (5X SSC, 0.1% SDS, 10% formamide) at 42 °C for 16–20 h. The microarray slide was scanned using a GenePix 4000B Scanner (Molecular Devices). There were no biological replicates. The obtained image was analyzed using an Array-Pro Analyzer ver. 4.5 (Media Cybernetics, Inc.). The quantitative data were subjected to Loess normalization. The ratio of the normalized intensity values ([Pt-Delta RNAi]/[normal]) for each probe was calculated. The probes for alpha-catenin (GB_ACC: AB433907; GI: LOC107439705), elongation factor 1-alpha (GB_ACC: AB433908; GI: LOC107441347), and histone H3 (GB_ACC: AB433909; GI, LOC107447866) served as negative controls, and the probes for a homolog of Drosophila caudal, Pt-cad (GB_ACC: AB096075; GI: LOC107437910) [2], served as positive controls to validate the experiment (Table 1).

2.3. Embryo staining

EST clones that were selected based on the [Pt-Delta RNAi]/[normal] ratio (<0.6) were used for the synthesis of Digoxigenin-labeled RNA probes for WISH. Normal embryos at stages 5–8 were stained by WISH as described [5]. They were counter-stained with 4’,6-diamidino-2-phenylindole for visualization of the nuclei. The stained embryos were photographed using a stereomicroscope (SZX12, Olympus) equipped with a color CCD camera (C7780-10, Hamamatsu Photonics) and examined using a fluorescence microscope (Axiophot 2, Zeiss).

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Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

[1] H. Oda, Y. Akiyama-Oda, Data for: microarray data on the comparison of transcript expression between normal and Pt-Delta RNAi embryos in the common house spider Parasteatoda tepidariorum, Mendeley Data (2019) v3, https://dx.doi.org/10.17632/r79vg2ctr2.3.

[2] H. Oda, O. Nishimura, Y. Hirao, H. Tarui, K. Agata, Y. Akiyama-Oda, Progressive activation of Delta-Notch signaling from around the blastopore is required to set up a functional caudal lobe in the spider Achaearanea tepidariorum, Development 134 (2007) 2195–2205, https://doi.org/10.1242/dev.004598.

[3] M. Kanayama, Y. Akiyama-Oda, O. Nishimura, H. Tarui, K. Agata, H. Oda, Travelling and splitting of a wave of hedgehog expression involved in spider-head segmentation, Nat. Commun. 2 (2011) 500. https://doi.org/10.1038/ncomms1510.

[4] J.M. Rouillard, M. Zuker, E. Gulari, OligoArray 2.0: design of oligonucleotide probes for DNA microarrays using a thermodynamic approach, Nucleic Acids Res. 31 (2003) 3057–3062.

[5] Y. Akiyama-Oda, H. Oda, Early patterning of the spider embryo: a cluster of mesenchymal cells at the cumulus produces Dpp signals received by germ disc epithelial cells, Development 130 (2003) 1735–1747. https://dx.doi.org/10.1242/dev.00390.
[6] E.E. Schwager, P.P. Sharma, T. Clarke, D.J. Leite, T. Wierschin, M. Pechmann, Y. Akiyama-Oda, L. Esposito, J. Bechsgaard, T. Bilde, A.D. Buffry, H. Chao, H. Dinh, H. Doddapaneni, S. Dugan, C. Eibner, C.G. Extavour, P. Funch, J. Garb, L.B. Gonzalez, V.L. Gonzalez, S. Griffiths-Jones, Y. Han, C. Hayashi, M. Hilbrant, D.S.T. Hughes, R. Janssen, S.I. Lee, I. Maeso, S.C. Murali, D.M. Muzny, R. Nunes da Fonseca, C.L.B. Paese, J. Qu, M. Ronshaugen, C. Schomburg, A. Schonauer, A. Stollewerk, M. Torres-Oliva, N. Turetzek, B. Vanthournout, J.H. Werren, C. Wolff, K.C. Worley, G. Bucher, R.A. Gibbs, J. Coddington, H. Oda, M. Stanke, N.A. Ayoub, N.M. Prpic, J.F. Flot, N. Posnien, S. Richards, A.P. McGregor, The house spider genome reveals an ancient whole-genome duplication during arachnid evolution, BMC Biol. 15 (2017) 62. https://doi.org/10.1186/s12915-017-0399-x.