|  |
| --- |
| Table 1: Functional classification of transcripts from *Culex tarsalis* |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Class** | **Total Number of Contigs** | **% total** | **Number of contigs overexpressed in the salivary glands** | **% Total** |
| Secreted | 2,753 | 11.11 | 366 | 54.79 |
| Unknown | 3,256 | 13.14 | 131 | 19.61 |
| Unknown, conserved | 4,095 | 16.53 | 48 | 7.19 |
| Transposable element | 486 | 1.96 | 23 | 3.44 |
| Immunity | 394 | 1.59 | 15 | 2.25 |
| Protein modification machinery | 666 | 2.69 | 14 | 2.10 |
| Metabolism, nucleotide | 278 | 1.12 | 13 | 1.95 |
| Transporters/storage | 1,059 | 4.27 | 12 | 1.80 |
| Metabolism, carbohydrate | 471 | 1.90 | 11 | 1.65 |
| Extracellular matrix/cell adhesion | 443 | 1.79 | 11 | 1.65 |
| Signal transduction | 2,711 | 10.94 | 7 | 1.05 |
| Metabolism, lipid | 762 | 3.08 | 5 | 0.75 |
| Metabolism, energy | 658 | 2.66 | 3 | 0.45 |
| Metabolism, amino acid | 327 | 1.32 | 3 | 0.45 |
| Transcription machinery | 1,577 | 6.37 | 2 | 0.30 |
| Proteasome machinery | 614 | 2.48 | 1 | 0.15 |
| Protein synthesis machinery | 488 | 1.97 | 1 | 0.15 |
| Transcription factor | 350 | 1.41 | 1 | 0.15 |
| Viral | 15 | 0.06 | 1 | 0.15 |
| Protein export machinery | 1,017 | 4.11 | 0 | 0.00 |
| Cytoskeletal | 815 | 3.29 | 0 | 0.00 |
| Nuclear regulation | 806 | 3.25 | 0 | 0.00 |
| Oxidant metabolism/detoxification | 393 | 1.59 | 0 | 0.00 |
| Metabolism, intermediate | 115 | 0.46 | 0 | 0.00 |
| Nuclear export | 95 | 0.38 | 0 | 0.00 |
| Signal transduction, apoptosis  | 77 | 0.31 | 0 | 0.00 |
| Storage | 51 | 0.21 | 0 | 0.00 |
|  |  |  |  |  |
| Total | 24,772 | 100 | 668 | 100 |

Table 2: Classification of transcripts 10 x overexpressed in female SG when contrasted with male SG, from a subset of transcripts enriched in the SG as compared to carcasses of both sexes.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Class** | **Number of contigs** | **Average RPKM female SG** | **Average RPKM male SG** | **Ratio Female / male** | **Average RPKM female carcass** | **Average RPKM male carcass** |
| **Putative secreted** |  |  |  |  |  |  |
| **Enzymes** |  |  |  |  |  |  |
| Apyrase \* | 7 | 184.44 | 0.19 | 985.82 | 0.12 | 0.13 |
| Adenosine deaminase | 2 | 280.98 | 0.50 | 560.28 | 0.75 | 2.69 |
| Endonuclease | 2 | 399.55 | 0.48 | 839.11 | 0.30 | 1.23 |
| Hyaluronidase \* | 3 | 193.89 | 0.15 | 1,326.69 | 0.08 | 0.09 |
| Sphingomyelinase \* | 5 | 416.28 | 0.36 | 1,150.09 | 0.35 | 0.40 |
| Serine protease | 1 | 1,109.21 | 2.77 | 400.43 | 0.63 | 1.03 |
| **Protease inhibitors** |  |  |  |  |  |  |
| Serpins | 1 | 618.31 | 0.59 | 1,039.77 | 0.41 | 0.40 |
| **Ubiquitous protein families** |  |  |  |  |  |  |
| Antigen 5 family | 3 | 3,323.33 | 2.70 | 1,229.73 | 2.85 | 3.22 |
| **Mosquito specific families** |  |  |  |  |  |  |
| D7 protein family | 19 | 5,956.98 | 4.36 | 1,366.88 | 3.93 | 4.47 |
| Aegyptin/30kDa antigen family | 5 | 3,273.15 | 3.87 | 845.19 | 2.85 | 3.88 |
| 10-14 kDa family - also in Corethrella \* | 6 | 4,844.78 | 22.07 | 219.53 | 3.60 | 4.22 |
| 20.2 kDa family - Culex and Corethrella \* | 4 | 278.51 | 7.34 | 37.95 | 0.30 | 0.27 |
| 62/34 kDa culicine family  | 11 | 287.72 | 0.34 | 851.31 | 0.22 | 0.19 |
| gSG5 family \* | 4 | 394.11 | 0.27 | 1,466.63 | 0.33 | 0.34 |
| gSG8 family \* | 4 | 155.17 | 1.14 | 136.05 | 0.10 | 0.14 |
| Hyp37 \* | 6 | 1,478.03 | 0.99 | 1,495.81 | 0.88 | 1.30 |
| SGS1 family | 8 | 60.21 | 0.10 | 627.36 | 0.52 | 0.22 |
| 16.7 kDa/WRP family | 70 | 2,260.61 | 1.90 | 1,187.89 | 1.53 | 1.86 |
| 4.2 kDa peptide | 5 | 1,697.78 | 1.61 | 1,052.29 | 0.67 | 1.10 |
| 9.7 kDa family | 19 | 603.36 | 0.59 | 1,019.43 | 0.42 | 0.48 |
| Basic tail protein \* | 1 | 1,085.96 | 1.79 | 606.43 | 1.09 | 1.02 |
| Mucins | 5 | 658.27 | 0.89 | 741.70 | 0.68 | 1.17 |
| Proline rich salivary peptide \* | 4 | 212.57 | 0.22 | 972.77 | 0.62 | 0.32 |
| Unknown secreted proteins | 23 | 191.37 | 6.05 | 31.65 | 0.38 | 0.96 |
| **Putative Housekeeping** |  |  |  |  |  |  |
| Extracellular matrix | 21 | 39.52 | 0.55 | 72.15 | 0.04 | 0.15 |
| Amino acid metabolism | 1 | 322.89 | 20.41 | 15.82 | 7.27 | 33.60 |
| Protein modification | 5 | 36.80 | 0.29 | 126.50 | 0.02 | 2.26 |
| Signal transduction | 3 | 14.98 | 0.17 | 87.36 | 0.80 | 1.07 |
| Transporters | 7 | 158.03 | 8.17 | 19.34 | 1.99 | 5.26 |
| Unknown conserved | 22 | 2,259.62 | 2.13 | 1,059.58 | 1.37 | 1.75 |
| Unknown | 47 | 77.88 | 0.73 | 106.28 | 0.51 | 0.98 |
| **Transposable elements** | 8 | 14.44 | 0.11 | 126.70 | 0.09 | 0.12 |
|  |  |  |  |  |  |  |
| **Total or average** | 332 | 1,027.77 | 2.93 | 681.39 | 1.12 | 2.38 |

 \* Not found on previous limited *C. tarsalis* sialotranscriptome (Calvo et al., 2010).

Table 3: Classification of transcripts overexpressed nearly equal in both male and female salivary glands

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Class** | **Number of contigs** | **Average RPKM female SG** | **Average RPKM male SG** | **Ratio Female/male** | **Average RPKM female carcass** | **Average RPKM male carcass** |
| **Putative secreted** |  |  |  |  |  |  |
| **Enzymes** |  |  |  |  |  |  |
| Apyrase/5' nucleotidase | 1 | 7.70 | 8.01 | 0.96 | 0.27 | 1.19 |
| Endonuclease | 13 | 897.19 | 526.00 | 1.71 | 0.46 | 0.63 |
| Lipases | 6 | 195.12 | 316.89 | 0.62 | 0.23 | 0.79 |
| Chitinase | 1 | 20.18 | 24.74 | 0.82 | 0.07 | 0.49 |
| Amylase/Maltase | 4 | 18,428.54 | 27,652.44 | 0.67 | 23.00 | 37.39 |
| Chitinase | 4 | 3,309.88 | 3,223.10 | 1.03 | 3.11 | 4.92 |
| Serine proteases | 14 | 157.37 | 242.60 | 0.65 | 0.74 | 0.91 |
| **Protease inhibitors** |  |  |  |  |  |  |
| TIL domain | 4 | 265.82 | 624.71 | 0.43 | 0.23 | 0.17 |
| Thyroglobulin repeats | 1 | 8.24 | 1.70 | 4.85 | 0.50 | 0.36 |
| **Antimicrobial peptides/Immunity** |  |  |  |  |  |  |
| Gambicin | 2 | 1,226.23 | 1,226.93 | 1.00 | 35.75 | 163.29 |
| H rich peptides | 2 | 40,934.49 | 105,148.02 | 0.39 | 58.42 | 55.73 |
| C-type lectins | 6 | 1,843.81 | 2,834.35 | 0.65 | 6.82 | 50.30 |
| Fred domain containing proteins | 7 | 527.70 | 217.05 | 2.43 | 15.29 | 12.63 |
| Gram negative binding protein | 3 | 634.77 | 883.67 | 0.72 | 1.18 | 1.89 |
| **Ubiquitous protein families** |  |  |  |  |  |  |
| Nematocera mucin I family | 11 | 5,102.16 | 12,243.32 | 0.42 | 5.77 | 6.01 |
| Mucin II superfamily | 5 | 441.98 | 656.03 | 0.67 | 0.52 | 0.71 |
| Perithrophin-like | 4 | 1,120.15 | 265.03 | 4.23 | 65.96 | 1.91 |
| Orphan mucins | 10 | 78.16 | 125.33 | 0.62 | 0.14 | 0.14 |
| Antigen 5 related | 6 | 1,167.20 | 2,437.53 | 0.48 | 1.21 | 1.77 |
| **Nematocera protein families** |  |  |  |  |  |  |
| 23.5 kDa culicine family | 2 | 369.03 | 140.17 | 2.63 | 0.32 | 0.50 |
| 56 kDa mosquito family | 4 | 7,550.37 | 7,165.22 | 1.05 | 5.67 | 6.66 |
| 41 kDa culicine family  | 1 | 1,122.98 | 708.71 | 1.58 | 0.94 | 1.10 |
| 30.5 kDa culicine protein family | 6 | 1,693.44 | 4,198.73 | 0.40 | 2.32 | 2.36 |
| hyp10 hyp12 anopheline family | 3 | 8,589.98 | 15,849.59 | 0.54 | 12.11 | 12.14 |
| W rich peptides of culicines | 7 | 2,548.26 | 4,070.01 | 0.63 | 2.72 | 2.96 |
| 6.8 kDa culicine family | 3 | 755.70 | 1,352.77 | 0.56 | 0.45 | 0.81 |
| Novel 6-8 kDa family | 5 | 1,911.70 | 1,089.59 | 1.75 | 0.90 | 1.22 |
| Culicoides epididymal protein | 1 | 2.83 | 8.49 | 0.33 | 0.00 | 0.00 |
| **Conserved secreted proteins** | 4 | 4,579.51 | 9,838.11 | 0.47 | 5.40 | 4.82 |
| **Novel secreted proteins** | 14 | 4,915.41 | 8,994.77 | 0.55 | 10.83 | 14.91 |
| **Putative housekeeping** |  |  |  |  |  |  |
| Extracellular matrix | 5 | 26.66 | 3.92 | 6.80 | 0.03 | 0.02 |
| Amino acid metabolism | 1 | 7,257.57 | 15,697.46 | 0.46 | 30.72 | 23.18 |
| Energy metabolism | 1 | 14,724.35 | 17,802.51 | 0.83 | 85.81 | 158.25 |
| Lipid metabolism | 1 | 16.21 | 4.89 | 3.32 | 1.55 | 0.25 |
| Protein modification | 3 | 3,755.52 | 6,665.16 | 0.56 | 30.18 | 26.82 |
| Protein synthesis machinery | 1 | 642.13 | 381.94 | 1.68 | 15.82 | 15.47 |
| Signal transduction | 4 | 92.66 | 223.95 | 0.41 | 1.43 | 5.13 |
| Transcription factor | 1 | 171.97 | 497.85 | 0.35 | 21.53 | 25.36 |
| Transcription machinery | 1 | 339.90 | 193.03 | 1.76 | 17.25 | 14.76 |
| Transporters and channels | 6 | 126.19 | 123.48 | 1.02 | 6.89 | 8.98 |
| Unknown conserved | 5 | 51.63 | 48.25 | 1.07 | 0.19 | 2.95 |
| Unkown conserved membrane protein | 4 | 7.81 | 6.31 | 1.24 | 0.29 | 1.14 |
| Unknown product | 32 | 1,026.63 | 2,244.85 | 0.46 | 2.42 | 3.55 |
| **Transposable element** | 6 | 218.84 | 692.20 | 0.32 | 7.28 | 21.76 |
|  |  |  |  |  |  |  |
| **Total or average** | 225 | 3,156.00 | 5,833.17 | 1.23 | 10.97 | 15.83 |

Table 4: Classification of transcripts overexpressed in the adult male salivary glands

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Class** | **Number of contigs** | **Average RPKM female SG** | **Average RPKM****male SG**  | **Ratio male / female** | **Average RPKM female carcass** | **Average RPKM male carcass** |
| **Putative secreted proteins** | 6 | 81.58 | 2,048.36 | 25.11 | 38.33 | 58.66 |
| **Putative housekeeping** |  |  |  |  |  |  |
| Immunity | 2 | 73.94 | 4,568.98 | 61.79 | 30.66 | 79.20 |
| Amino acid metabolism | 1 | 134.47 | 7,135.76 | 53.07 | 70.81 | 158.03 |
| Energy metabolism | 2 | 299.63 | 12,949.26 | 43.22 | 193.63 | 383.32 |
| Lipid metabolism | 1 | 50.26 | 1,330.44 | 26.47 | 21.93 | 56.11 |
| Nucleotide metabolism | 2 | 130.09 | 7,529.86 | 57.88 | 120.23 | 154.98 |
| Proteasome machinery | 1 | 277.29 | 11,976.76 | 43.19 | 133.50 | 269.72 |
| Signal transduction | 1 | 115.04 | 6,111.54 | 53.12 | 51.55 | 116.54 |
| Transporters and channels | 1 | 783.64 | 48,431.45 | 61.80 | 314.03 | 801.90 |
| Unknown conserved | 6 | 7.14 | 267.77 | 37.51 | 2.08 | 6.22 |
| Unknown product | 11 | 5.96 | 133.36 | 22.39 | 0.87 | 1.89 |
| **Viral product** | 1 | 0.21 | 6.38 | 30.64 | 0.19 | 0.24 |
| **Transposable element** | 9 | 18.47 | 595.47 | 32.24 | 3.85 | 10.38 |
|  |  |  |  |  |  |  |
| **Total or average** | 44 | 152.13 | 7,929.64 | 42.19 | 75.51 | 161.32 |

Calvo, E., Sanchez-Vargas, I., Favreau, A.J., Barbian, K.D., Pham, V.M., Olson, K.E., Ribeiro, J.M., 2010. An insight into the sialotranscriptome of the West Nile mosquito vector, *Culex tarsalis*. BMC genomics 11, 51.