

Species	Order	Resource	Tissue Origin	# reads	# bp	# contigs/transcripts/ unigenes/gene models	References
<i>Limulus polyphemus</i>	Xiphosura	genome	adult third walking leg, larvae	1,700,000,000	N/A	N/A	[1]
<i>Rhipicephalus (Boophilus) microplus</i>	Acari	BAC library	N/A	3,072	136,474,000	24	[2]
<i>Rhipicephalus (Boophilus) microplus</i>	Acari	EST library	eggs, larvae, nymphs, adults, dissected adult organs	42,512	N/A	13,643	[3,4]
<i>Rhipicephalus appendiculatus</i>	Acari	EST library	salivary gland	18,422	626,000	7,359	[5]
<i>Ixodes scapularis</i>	Acari	genome	N/A	N/A	1,388,472,180	24,925	[6,7]
<i>Tetranychus urticae</i>	Acari	genome	embryos	N/A	~10,000,000,000	18,414	[8]
<i>Mesobuthus martensii</i>	Scorpiones	BAC library	male testis	46,080	46,080,000,000	N/A	[9]
<i>Mesobuthus martensii</i>	Scorpiones	genome	male adult muscle tissues of the pedipalp and metasoma	1,634,795,503	1,128,500,000	32,016	[10]
<i>Loxosceles laeta</i>	Araneae	EST library	venom gland	3,008	N/A	1,357	[11]
<i>Citharischius crawshayi</i>	Araneae	EST library	venom gland	282	N/A	44	[12]
<i>Acanthoscurria gomesiana</i>	Araneae	EST library	hemocytes	7,584	N/A	3,723	[13]
<i>Aphonopelma sp.</i>	Araneae	EST library	leg muscles of adults	2,507	N/A	305	[14]
<i>Chilobrachys jingzhao</i>	Araneae	EST library	venom gland	788	N/A	356	[15]
<i>Ornithoctonus huwena</i>	Araneae	EST library	venom gland	468	N/A	89	[16]
<i>Lycosa singoriensis</i>	Araneae	EST library	venom gland	833	N/A	331	[17]
<i>Dolomedes mizhoanus</i>	Araneae	EST library	venom gland	356	N/A	N/A	[18]
<i>Gasteracantha cancriformis</i>	Araneae	454 Transcriptome	spinning gland of adult females	52,399	14,339,651	25,663	[19]
<i>Actinopus spp.</i>	Araneae	454 Transcriptome	spinning gland of adult females	34,496	8,087,280	18,257	[19]
<i>Stegodyphus lineatus</i>	Araneae	454 Transcriptome	adult	457675	165,220,675	8,944	[20]
<i>Stegodyphus tentoriicola</i>	Araneae	454 Transcriptome	adult	459,994	157,317,948	6,094	[20]
<i>Stegodyphus mimosarum</i>	Araneae	454 Transcriptome	adult	542,510	175,230,730	5,893	[20]
<i>Theridion grallator</i>	Araneae	Illumina Transcriptome	adult females	239,263,493	N/A	104,481	[21]
<i>Theridion californicum</i>	Araneae	Illumina Transcriptome	adult females	250,930,772	N/A	128,391	[21]
<i>Trittame loki</i>	Araneae	454 Transcriptome	female venom glands	N/A	N/A	4,711	[22]
<i>Latrodectus tredecimguttatus</i>	Araneae	Illumina Transcriptome	venom glands	27,605,467	2,484,492,030	34,334	[23]
<i>Latrodectus hesperus</i>	Araneae	Illumina Tag sequencing	female major ampullate silk glands and cephalothorax	25,857,032	N/A	200,603 unique tags	[24]
<i>Latrodectus hesperus</i>	Araneae	Illumina Transcriptome	silk glands, cephalothorax, seven pairs of venom glands	149,000,000	N/A	103,365	[25]

<i>Gasteracantha arcuata</i>	Araneae	Illumina Transcriptome	adults	23,370,495	4,674,099,000	54,871	[26]
<i>Nasoonaria sinensis</i>	Araneae	Illumina Transcriptome	adults	25,346,489	5,069,297,800	101,855	[26]
<i>Gasteracantha hasselti</i>	Araneae	Illumina Transcriptome	adults	16,416,304	3,283,260,800	75,455	[26]
<i>Stegodyphus mimosarum</i>	Araneae	genome	adults	N/A	~2,550,000,000	27,235	[27]
<i>Acanthoscurria geniculata</i>	Araneae	genome	adults	N/A	~6,000,000,000	~70,000	[27]
<i>Parasteatoda tepidariorum</i>	Araneae	EST library	embryos	24,360	16,537,059	N/A	[28,29], this study
<i>Parasteatoda tepidariorum</i>	Araneae	454 Transcriptome	embryos (stages 1-13)	1,040,006	639,294,706	21,959 isotigs	this study
<i>Parasteatoda tepidariorum</i>	Araneae	Illumina Transcriptome	embryos (stages 1-14)	332,245,126	33,556,757,726	N/A	this study
<i>Parasteatoda tepidariorum</i>	Araneae	Illumina Transcriptome	nymphs, larvae, adult female, adult male	292,831,388	29,575,970,188	N/A	this study
<i>Parasteatoda tepidariorum</i>	Araneae	Combined assembly	embryos, nymphs, larvae, adults	625,219,691	61,839,406,064	41,766 unique BLAST hits	this study

References

1. Nossa CW, Havlak P, Yue J-X, Lv J, Vincent KY, et al. (2014) Joint assembly and genetic mapping of the Atlantic horseshoe crab genome reveals ancient whole genome duplication. *GigaScience* 3: 9. doi:10.1186/2047-217X-3-9.
2. Moolhuijzen PM, Lew-Tabor AE, Morgan JAT, Valle MR, Peterson DG, et al. (2011) The complexity of *Rhipicephalus (Boophilus) microplus* genome characterised through detailed analysis of two BAC clones. *BMC Res Notes* 4: 254. doi:10.1186/1756-0500-4-254.
3. Wang M, Guerrero FD, Pertea G, Nene VM (2007) Global comparative analysis of ESTs from the southern cattle tick, *Rhipicephalus (Boophilus) microplus*. *BMC Genomics* 8: 368. doi:10.1186/1471-2164-8-368.
4. Guerrero FD, Miller RJ, Rousseau M-E, Sunkara S, Quackenbush J, et al. (2005) BmiGI: a database of cDNAs expressed in *Boophilus microplus*, the tropical/southern cattle tick. *Insect Biochem Mol Biol* 35: 585–595. doi:10.1016/j.ibmb.2005.01.020.
5. Nene V, Lee D, Kang'a S, Skilton R, Shah T, et al. (2004) Genes transcribed in the salivary glands of female *Rhipicephalus appendiculatus* ticks infected with *Theileria parva*. *Insect Biochem Mol Biol* 34: 1117–1128. doi:10.1016/j.ibmb.2004.07.002.

6. Hill CA, Wikel SK (2005) The *Ixodes scapularis* Genome Project: an opportunity for advancing tick research. *Trends Parasitol* 21: 151–153. doi:10.1016/j.pt.2005.02.004.
7. Vectorbase (n.d.). Available: <http://www.vectorbase.org>.
8. Grbić M, Leeuwen TV, Clark RM, Rombauts S, Rouzé P, et al. (2011) The genome of *Tetranychus urticae* reveals herbivorous pest adaptations. *Nature* 479: 487–492. doi:10.1038/nature10640.
9. Li S, Ma Y, Jang S, Wu Y, Liu H, et al. (2009) A HindIII BAC library construction of *Mesobuthus martensii* Karsch (Scorpiones:Buthidae): An important genetic resource for comparative genomics and phylogenetic analysis. *Genes Genet Syst* 84: 417–424. doi:10.1266/ggs.84.417.
10. Cao Z, Yu Y, Wu Y, Hao P, Di Z, et al. (2013) The genome of *Mesobuthus martensii* reveals a unique adaptation model of arthropods. *Nat Commun* 4. Available: <http://www.nature.com/ncomms/2013/131015/ncomms3602/full/ncomms3602.html>. Accessed 12 November 2013.
11. Fernandes-Pedrosa M de F, Junqueira-de-Azevedo I de L, Gonçalves-de-Andrade RM, Kobashi LS, Almeida DD, et al. (2008) Transcriptome analysis of *Loxosceles laeta* (Araneae, Sicariidae) spider venomous gland using expressed sequence tags. *BMC Genomics* 9: 279. doi:10.1186/1471-2164-9-279.
12. Diego-García E, Peigneur S, Waelkens E, Debaveye S, Tytgat J (2010) Venom components from *Citharischius crawshayi* spider (Family Theraphosidae): exploring transcriptome, venomics, and function. *Cell Mol Life Sci* 67: 2799–2813. doi:10.1007/s00018-010-0359-x.
13. Lorenzini DM, Silva Jr PI da, Soares MB, Arruda P, Setubal J, et al. (2006) Discovery of immune-related genes expressed in hemocytes of the tarantula spider *Acanthoscurria gomesiana*. *Dev Comp Immunol* 30: 545–556. doi:10.1016/j.dci.2005.09.001.
14. Zhu J, Sun Y, Zhao F-Q, Yu J, Craig R, et al. (2009) Analysis of tarantula skeletal muscle protein sequences and identification of transcriptional isoforms. *BMC Genomics* 10: 117. doi:10.1186/1471-2164-10-117.
15. Chen J, Zhao L, Jiang L, Meng E, Zhang Y, et al. (2008) Transcriptome analysis revealed novel possible venom components and cellular processes of the tarantula *Chilobrachys jingzhao* venom gland. *Toxicon Off J Int Soc Toxinology* 52: 794–806. doi:10.1016/j.toxicon.2008.08.003.
16. Jiang L, Peng L, Chen J, Zhang Y, Xiong X, et al. (2008) Molecular diversification based on analysis of expressed sequence tags from the venom glands of the Chinese bird spider *Ornithoctonus huwena*. *Toxicon Off J Int Soc Toxinology* 51: 1479–1489. doi:10.1016/j.toxicon.2008.03.024.
17. Zhang Y, Chen J, Tang X, Wang F, Jiang L, et al. (2010) Transcriptome analysis of the venom glands of the Chinese wolf spider *Lycosa singoriensis*. *Zool Jena Ger* 113: 10–18. doi:10.1016/j.zool.2009.04.001.

18. Jiang L, Liu C, Duan Z, Deng M, Tang X, et al. (2013) Transcriptome analysis of venom glands from a single fishing spider *Dolomedes mizhoanus*. *Toxicon* 73: 23–32. doi:10.1016/j.toxicon.2013.07.005.
19. Prosdocimi F, Bittencourt D, da Silva FR, Kirst M, Motta PC, et al. (2011) Spinning Gland Transcriptomics from Two Main Clades of Spiders (Order: Araneae) - Insights on Their Molecular, Anatomical and Behavioral Evolution. *PLoS ONE* 6: e21634. doi:10.1371/journal.pone.0021634.
20. Mattila TM, Bechsgaard JS, Hansen TT, Schierup MH, Bilde T (2012) Orthologous genes identified by transcriptome sequencing in the spider genus *Stegodyphus*. *BMC Genomics* 13: 70. doi:10.1186/1471-2164-13-70.
21. Croucher PJ, Brewer MS, Winchell CJ, Oxford GS, Gillespie RG (2013) De novo characterization of the gene-rich transcriptomes of two color-polymorphic spiders, *Theridion grallator* and *T. californicum* (Araneae: Theridiidae), with special reference to pigment genes. *BMC Genomics* 14: 862. doi:10.1186/1471-2164-14-862.
22. Undheim EAB, Sunagar K, Herzig V, Kely L, Low DHW, et al. (2013) A Proteomics and Transcriptomics Investigation of the Venom from the Barychelid Spider *Trittame loki* (Brush-Foot Trapdoor). *Toxins* 5: 2488–2503. doi:10.3390/toxins5122488.
23. He Q, Duan Z, Yu Y, Liu Z, Liu Z, et al. (2013) The Venom Gland Transcriptome of *Latrodectus tredecimguttatus* Revealed by Deep Sequencing and cDNA Library Analysis. *PLoS ONE* 8: e81357. doi:10.1371/journal.pone.0081357.
24. Lane AK, Hayashi CY, Whitworth GB, Ayoub NA (2013) Complex gene expression in the dragline silk producing glands of the Western black widow (*Latrodectus hesperus*). *BMC Genomics* 14: 846. doi:10.1186/1471-2164-14-846.
25. Clarke TH, Garb JE, Hayashi CY, Haney RA, Lancaster AK, et al. (2014) Multi-tissue transcriptomics of the black widow spider reveals expansions, co-options, and functional processes of the silk gland gene toolkit. *BMC Genomics* 15: 365. doi:10.1186/1471-2164-15-365.
26. Zhao Y-J, Zeng Y, Chen L, Dong Y, Wang W (2013) Analysis of transcriptomes of three orb-web spider species reveals gene profiles involved in silk and toxin. *Insect Sci*: n/a–n/a. doi:10.1111/1744-7917.12068.
27. Sanggaard KW, Bechsgaard JS, Fang X, Duan J, Dyrland TF, et al. (2014) Spider genomes provide insight into composition and evolution of venom and silk. *Nat Commun* 5. Available: <http://www.nature.com/ncomms/2014/140506/ncomms4765/full/ncomms4765.html>. Accessed 9 July 2014.
28. Kanayama M, Akiyama-Oda Y, Nishimura O, Tarui H, Agata K, et al. (2011) Travelling and splitting of a wave of hedgehog expression involved in spider-head segmentation. *Nat Commun* 2: 500. doi:10.1038/ncomms1510.

29. Oda H, Nishimura O, Hirao Y, Tarui H, Agata K, et al. (2007) Progressive activation of Delta-Notch signaling from around the blastopore is required to set up a functional caudal lobe in the spider *Achaearanea tepidariorum*. *Dev Camb Engl* 134: 2195–2205. doi:10.1242/dev.004598.