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**History Earliest work contributions on EST’s, transcriptome, Assemblies, Annotations, Microbiome. 2000-2012. Pierce’s Disease and Glassy-winged Sharpshooter, National program.**

**HOMVIT\_0.1.**

**Funding USDA, ARS, Fort Pierce, FL. Lead Researcher :**

**Wayne B. Hunter,** USDA, ARS, U.S. Horticultural Research Laboratory, Subtropical Insects research unit. Fort Pierce, FL 34945. Genome Center Lab. (HOMVIT), Colonies, Collections, EST’s, Libraries, sequencing, annotations. Pierce’s Disease and glassy-winged sharpshooter national project 2000-2012**.**  Leafhopper cultures, sample preparation and submissions RNA/gDNA, EST sequencing, Transcriptome, sequence and protein submission NCBI, and Baylor College of Medicine databases.

**Shannon Johnson,** Los Alamos National Laboratory, BioScience Division B-11, PO Box 1663 M888, Los Alamos, NM 87545 (HOVIT). Libraries, Sequencing, Assembly, Submission NCBI and Baylor College.

**Stephen Richards**, Baylor College of Medicine, i5K Arthropod Genomics, and Baylor College of Medicine, Human Genome Sequencing Center, Houston, TX 77030 , USA. Assembly (HOMVIT).

Adelaide Rhodes, Ph.D., Center for Genome Research and Biocomputing, Oregon State University, OR. Sequence Blast analyses, proteins.

Adam English, Baylor College of Medicine, i5K Arthropod Genomics, and Baylor College of Medicine, Human Genome Sequencing Center, Houston, TX 77030 , USA. Assembly (HOMVIT).

Paul Davis, Dept. Biology, University of Nebraska at Omaha, Omaha, Nebraska 68182, USA (HOVIT) microbiome, transcript assembly.

Matthew K. Christenson, Dept. Biology, University of Nebraska at Omaha, Omaha, Nebraska 68182, USA, microbiome, transcript assembly (HOVIT).

Phat Dang, USDA,ARS, (HOMVIT), EST’s, libraries, sequencing, assembly.

Laura Hunnicutt, USDA,ARS, (HOMVIT), EST’s, libraries, sequencing, assembly, annotations.

Catherine S. Katsar, USDA, ARS, Fort Pierce, FL. EST’s, Transcripts, Libraries, assembly.

Scot E Dowd PhD, MR DNA, 503 Clovis Rd, Shallowater, TX 79363, Assembly, assembly.

Justin Reese, Reese Consulting, LTD. 2920 Sawtooth Circle, Alpharetta, GA 30022. USA. Assemblies, Transcriptome.

Justin MacCarthy, Reese Consulting, LTD. 2920 Sawtooth Circle, Alpharetta, GA 30022. USA. Assemblies and Transcriptome.

Stacy Ciufo, NIH/NLM/NCBI, Genome Project Coordinator, Washington, DC. (HOVIT/DIACI)

Blake Bextine, University of Texas at Tyler, TX.

Elaine A. Backus, USDA, ARS, Parlier, CA (2006)

Habibi, J. USDA, ARS, Parlier, CA (2006)

Shatter, Robert, USDA,ARS, Fort Pierce, FL. (2006)

Gary Puterka, USDA, ARS, 2005, Field sample collections of leafhoppers.

Mike Reinke, USDA, ARS, 2005, Field sample collections of Leafhoppers.

Heather Costa, “University of Riverside, CA. 2005”.

Xiomara Sinisterra, USDA, ARS, Fort Pierce, FL.

Russell F. Mizell, III. University of Florida, Quincy, FL.

Tobin Northfield, University of Florida, Quincy, FL.

Charles Powell, University of Florida, Fort Pierce, FL.

Jerry Mozoruk, USDA,ARS, Fort Pierce, FL

Tim Crouch, Justin Summerlin, Networks and Operations, University of Texas at Tyler, TX.

Glassy-winged Sharpshooter ESTs, transcripts, proteins,

1. Hunter, WB. **2003**. Published 427 pages. Data Set: Glassy-winged Sharpshooter, Expressed Sequence Tags, ESTs, Adult *Homalodisca coagulata* (Hemiptera). CF194966-CF195393. NCBI.
2. Hunter WB, Dang PM, Puterka G, Shatters RG, McKenzie CL, Sinisterra XH. **2005**. 5th Instar Glassy-winged Sharpshooter *Homalodisca vitripennis*, (Hemiptera) DN195890-DN203579, 3,921 mRNA seqs. NCBI. A high quality EST with at least 200 contiguous bases at Trace Tuner score of 20 or better. Construction by Laura Hunnicutt,USDA,ARS, U.S. Horticultural Res.Lab, Ft.Pierce, FL, USA. Submission USDA-ARS, Wayne Hunter, Phat Dang, USDA, ARS; 2005-02-25.
3. Hunter, W.B., Backus, E.A., Hunnicutt, L.E., Habibi, J., Dang, P.M. **2006**. Salivary gland gene expression in glassy-winged sharpshooter, *Homalodisca vitripennis* (syn. *H. coagulata*) (Hemiptera: Cicadellidae). Accession numbers: EG368539.1-EG372472.1. GenBank NCBI.
4. Hunter, WB, Backus, E, Hunnicutt, L, Habibi, J, Dang, P. **2006**. Midgut gene expression in glassy-winged sharpshooter, *Homalodisca vitripennis* (Hemiptera), 3,933 seqs. EG368538-EG365118. NCBI.
5. Hunter, WB. 2007. Genomic Sequencing, Discovery, and Characterization of Viral Pathogens in Glassy-winged Sharpshooters (*Homalodisca vitripennis*: Hemiptera: Cicadellidae) . Proceedings of the **2007** Pierce’s Disease Research Symposium. Dec. 12-14, **2007**, San Diego, CA, pp. 17-21.
6. Hunter, W.B., Bextine, BR., Johnson, S., Shunsheng, H., et al., International Leafhopper Genome Consortium, **2012** and **2014**. Glassy-winged sharpshooter, HOVIT\_ *Homalodisca vitripennis*, Draft genome 0.1. Originally USDA (Hunter) Los Alamos National Lab, LANL (Shannon Johnson), HGSC, Baylor (Stephen Richards), Then in 2014 all data resubmitted into NCBI for their Pipeline (**Improved draft 1.0. 2014\_i5K\_NCBI**).

**Closely related Sharpshooter Leafhoppers for Comparative Transcriptome/EST’s:**

1. Hunter W.B, Mizell RF, III, Tipping C, Dang PM, Hunnicutt LE. 2005. Adult sharpshooter leafhopper *Oncometopia nigricans*, (Hemiptera: Cicadellidae), DR755012-DR759538. 4,527 mRNA. NCBI.
2. Hunter, WB, Hunnicutt, L, Wistrom, C, Purcell, A. 2006. Proteins expressed in Blue-green sharpshooter, *Graphocephala atropunctata* (Hemiptera). DQ445499-DQ445542. NCBI.
3. Hunter, WB, Hunnicutt, LE, Wistrom, CM, Purcell, AH. 2007. Gene expression in adult blue-green sharpshooters, *Graphocephala atropunctata* (Signoret) (Hemiptera: Cicadellidae). 6,481 sequences. EH655849-EH662332. NCBI.

**Assembly statistics**

* [Primary Assembly](https://www.ncbi.nlm.nih.gov/assembly/GCA_000696855.1#st_Primary-Assembly)

| **Molecule** | **Total Length** | **Scaffold Count** | **UngappedLength** | **ScaffoldN50** | **SpannedGaps** | **UnspannedGaps** |
| --- | --- | --- | --- | --- | --- | --- |
| unplaced | 2,246,365,390 | 61,370 | 1,324,906,634 | 915,377 | 450,679 |  |

**Hvit\_1.0**

Organism name:

[Homalodisca vitripennis (glassy-winged sharpshooter)](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=197043&lvl=3&lin=f&keep=1&srchmode=1&unlock)

Isolate:

HVIT.00

Sex: pooled males and females

BioSample: [SAMN02728788](https://www.ncbi.nlm.nih.gov/biosample/SAMN02728788/)

Submitter: The i5k Initiative

Date: 2014/06/05

Assembly level: Scaffold

Genome representation: full

RefSeq category: representative genome

GenBank assembly accession: GCA\_000696855.1 (latest)

RefSeq assembly accession: n/a

RefSeq assembly and GenBank assembly identical: n/a

WGS Project: [JJNS01](https://www.ncbi.nlm.nih.gov/nuccore/JJNS00000000.1/)

Assembly method: AllPaths LG v. 35218; Atlas Link v. 1.0; Atlas GapFill v. 2.2

Genome coverage: 68.3x

Sequencing technology: Illumina

IDs: 187951 [UID] 1138168 [GenBank]

**See** [**Genome**](https://www.ncbi.nlm.nih.gov/genome/?term=txid197043%5borgn%5d) **Information for *Homalodisca vitripennis***

**History** [**(Show revision history)**](https://www.ncbi.nlm.nih.gov/assembly/GCA_000696855.1)

| **GenBank AssemblyAccession** |  | **RefSeq AssemblyAccession** | **AssemblyName** | **AssemblyLevel** | **Status** |
| --- | --- | --- | --- | --- | --- |
| [**GCA\_000696855.1**](https://www.ncbi.nlm.nih.gov/assembly/187951/) | **n/a** | **n/a** | [**Hvit\_1.0**](https://www.ncbi.nlm.nih.gov/assembly/GCA_000696855.1/) | **Scaffold** | **Latest GenBank** |

**Global statistics**

|  |  |
| --- | --- |
| Total sequence length | 2,246,365,390 |
| Total assembly gap length | 921,458,756 |
| Gaps between scaffolds | 0 |
| Number of scaffolds | 61,370 |
| Scaffold N50 | 915,377 |
| Scaffold L50 | 541 |
| Number of contigs | 512,049 |
| Contig N50 | 4,857 |
| Contig L50 | 62,703 |
| Total number of chromosomes and plasmids | 0 |

**Supplemental Content**

**Access the data**

* Download the GenBank assembly
* [BLAST search the assembly](https://blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastSearch&PROG_DEF=blastn&BLAST_SPEC=Assembly&ASSEMBLY_NAME=GCA_000696855.1)
* Download the full sequence report
* Download the statistics report

**Assembly Information**

* [Assembly Help](https://www.ncbi.nlm.nih.gov/assembly/help/)
* [Assembly Basics](https://www.ncbi.nlm.nih.gov/assembly/basics/)
* [NCBI Assembly Data Model](https://www.ncbi.nlm.nih.gov/assembly/model/)

**Related Information**

[BioProject](https://www.ncbi.nlm.nih.gov/bioproject?LinkName=assembly_bioproject&from_uid=187951)

BioProject [BioSample](https://www.ncbi.nlm.nih.gov/biosample?LinkName=assembly_biosample&from_uid=187951) BioSample [Genome](https://www.ncbi.nlm.nih.gov/genome?LinkName=assembly_genome&from_uid=187951) **Related Genome records GENE**

* [Assembly Definition](https://www.ncbi.nlm.nih.gov/assembly/GCA_000696855.1#def)
* [Assembly Statistics](https://www.ncbi.nlm.nih.gov/assembly/GCA_000696855.1#st)

**Global assembly definition**

**Download the full sequence report**

**Click on the table row to see sequence details in the table to the right**

| **Assembly Unit Name** |
| --- |
| **Assembly Unit Name** |
| **Primary Assembly** |

The primary assembly unit does not have any assembled chromosomes or linkage groups.
Please download the full sequence report for information on the scaffolds.