

Supplementary Materials: Combined Venom Gland Transcriptomic and Venom Peptidomic Analysis of the Predatory Ant *Odontomachus monticola*

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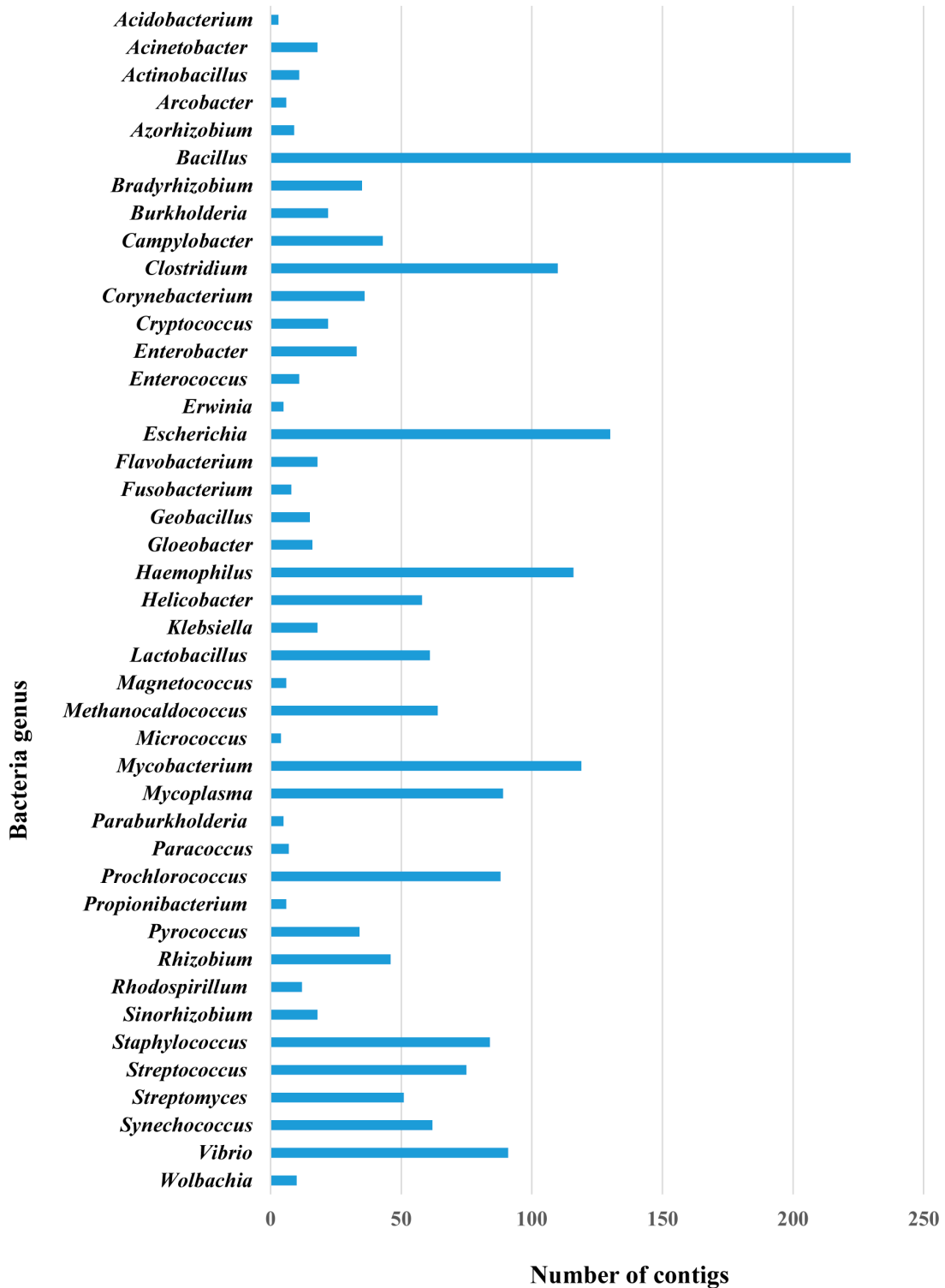


Figure S1. Number of contigs derived from various bacterial genera.

Table S1. Other toxin-like peptides and proteins.

| The putative toxin name | Contig ID | ACC number | Length (bp) | Reads | Identity with corresponding ortholog | Potential function |
|--------------------------------------|------------------|------------|-------------|-------|--|---|
| Venom allergen 1 (PLA ₁) | Om11857_c0_g1_i2 | FX985511 | 1637 | 1668 | <i>Ooceraea biroi</i> Phospholipase A ₁ (EZA56721.1) 53.0% | Venom diffusion Tissue damage Allergy |
| Venom allergen 2 | Om26417_c0_g1_i1 | FX985512 | 707 | 48 | <i>Solenopsis geminata</i> venom allergen 4 (Q9NH75.1) 26.9% <i>Dinoponera quadriceps</i> uncharacterized protein (XP_014487550.1) 46.8% | Allergy |
| Venom allergen 3 | Om7646_c0_g1_i1 | FX985513 | 994 | 1945 | <i>Dinoponera quadriceps</i> venom allergen 3-like (XP_014469499.1) 60.6% | Allergy |
| Venom allergen 4 | Om27249_c0_g1_i1 | FX985514 | 692 | 423 | <i>Solenopsis invicta</i> Venom allergen 4 (XP_011172701.1) 24.8% <i>Dinoponera quadriceps</i> uncharacterized protein (XP_014487550.1) 36.8% | Allergy |
| Venom acid phosphatase 1 | Om3982_c1_g1_i1 | FX985517 | 705 | 73 | <i>Ooceraea biroi</i> Venom phosphatase A1 (EZA56721.1) 53.6% | |
| Venom acid phosphatase 2 | Om13241_c0_g1_i2 | FX985518 | 773 | 95 | <i>Harpegnathos saltator</i> venom acid phosphatase Acph-1 (XP_011144396.1) 72.4% | Allergy |
| Venom acid phosphatase 3 | Om8247_c0_g2_i1 | FX985519 | 2526 | 1543 | <i>Harpegnathos saltator</i> venom acid phosphatase Acph-1 (XP_011149152.2) 68.3% | |
| Venom serine protease 1 | Om8957_c0_g1_i1 | FX985522 | 1625 | 2434 | <i>Harpegnathos saltator</i> venom serine protease Bi-VSP (XP_011142320.1) 82.4% | |
| Venom serine protease 2 | Om7503_c0_g1_i1 | FX985523 | 1483 | 1416 | <i>Dinoponera quadriceps</i> venom protease-like (XP_014477083.1) 62.8% | Venom diffusion Tissue damage |
| Venom serine protease 3 | Om13129_c3_g1_i3 | FX985524 | 3750 | 810 | <i>Harpegnathos saltator</i> serine protease snake-like (XP_011142690.1) 79.5% | |
| Venom serine protease 4 | Om10669_c0_g1_i1 | FX985525 | 3565 | 78 | <i>Harpegnathos saltator</i> serine protease snake (EFN89361.1) 75.1% | |
| Waprin-like 1 | Om9947_c0_g4_i1 | FX985515 | 1034 | 852 | <i>Dinoponera quadriceps</i> waprin-Thr1-like (XP_014487667.1) 85.6% | Not classified (Protease Inhibitor) |
| Waprin-like 2 | Om5029_c0_g2_i1 | FX985516 | 1486 | 573 | <i>Dinoponera quadriceps</i> waprin-Phi1-like (XP_014487661.1) 87.3% | |
| VEGF | Om8718_c0_g1_i1 | FX985521 | 3797 | 1781 | <i>Habropoda laboriosa</i> VEGF-like protein (KOC69027.1) 48.4% <i>Harpegnathos saltator</i> uncharacterized protein (XP_019698417.1) 64.7% | Venom diffusion |
| Phospholipase D1 | Om8739_c0_g1_i2 | FX985534 | 3359 | 536 | <i>Harpegnathos saltator</i> phospholipase D1 (XP_019701186.1) 91.1% | Venom diffusion |
| Kazal Protease Inhibitor | Om10389_c0_g1_i1 | FX985520 | 819 | 727 | <i>Drosophila busckii</i> Kaz1-ORFB (ALC43924.1) 51.9% <i>Harpegnathos saltator</i> uncharacterized protein (XP_011137886.1) 77.1% | Not classified (Protease Inhibitor) |

| | | | | | | |
|--------------------------------|------------------|----------|------|------|---|-------------------------------------|
| Kunitz type protease inhibitor | Om26503_c0_g1_i1 | FX985536 | 543 | 716 | <i>Vollenhovia emeryi</i> kunitz-type serine protease inhibitor (XP_011873052.1) 52.5% | Not classified (Protease Inhibitor) |
| Venom metalloproteinase 1 | Om13234_c6_g1_i8 | FX985526 | 3368 | 142 | <i>Harpegnathos saltator</i> ADAM with thrombospondin motifs (XP_011152782.1) 95.8% | |
| Matrix metalloproteinase 2 | Om13249_c2_g1_i2 | FX985527 | 3610 | 105 | <i>Harpegnathos saltator</i> MMP-2 (XP_011138596.1) 87.8% | |
| Matrix metalloproteinase 14 | Om12910_c3_g1_i1 | FX985528 | 4848 | 79 | <i>Dinoponera quadriceps</i> MMP-14 isoform X3 (XP_014475594.1) 93.8% | Venom diffusion Tissue damage |
| ADAM 12 | Om12161_c0_g1_i2 | FX985529 | 5791 | 126 | <i>Harpegnathos saltator</i> ADAM 19 (XP_011140269.2) 86.6% | |
| ADAM TS 7 | Om480_c0_g1_i1 | FX985530 | 3684 | 127 | <i>Dinoponera quadriceps</i> ADAM with thrombospondin motifs 7-like (XP_014473812.1) 94.2% | |
| ADAM1 10 | Om10140_c0_g1_i2 | FX985531 | 3355 | 113 | <i>Harpegnathos saltator</i> ADAM 10 (XP_011153168.1) 96.4% | |
| Secapin | Om3630_c0_g1_i1 | FX985535 | 994 | 465 | <i>Camponotus floridanus</i> Secapin (AEM44798.1) 67.5% <i>Dinoponera quadriceps</i> uncharacterized protein (XP_014488812.1) 70.6% | Allergy |
| Carboxypeptidase | Om9464_c0_g1_i1 | FX985537 | 2025 | 2618 | <i>Harpegnathos saltator</i> venom serine carboxypeptidase (XP_011143619.1) 84.1% | Allergy |
| Venom carboxylesterase 1 | Om13001_c0_g1_i2 | FX985532 | 2862 | 4017 | <i>Harpegnathos saltator</i> venom carboxylesterase-6-like (XP_011149322.1) 78.2% | |
| Venom carboxylesterase 2 | Om21361_c0_g1_i1 | FX985533 | 1842 | 1457 | <i>Harpegnathos saltator</i> venom Esterase FE4 (EFN85480.1) 76.0% <i>Dinoponera quadriceps</i> venom carboxylesterase-6-like (XP_014477483.1) 70.9% | Allergy |

Potential function was followed by classification of dos Santos *et al* [25]. *O. monticola* toxin-like peptides and their orthologues were aligned by the John-Hein method in Lasergene 12 (DNASTAR, Madison, WI, USA).

Table S2. Alignments of pilosulin-like peptide 1, 2, and 3 amino acid sequences from peptidomic and transcriptomic analyses.

| Peptide Name | Retention time | Observed/Theoretical molecular mass | Amino acid sequence |
|--------------|----------------|--|--|
| | 8.15 | 787.423 | GLLDWVGK |
| | 8.55 | 1291.677 | KVMDWLKDKM-NH ₂ |
| | 9.08 | 1163.582 | VMDWLKDKM-NH ₂ |
| | 11.86 | 2077.083 | GLLDWVGKKVMDWLKDKM-NH ₂ |
| | 12.75 | 2061.090 | GLLDWVGKKVMDWLKDKM-NH ₂ |
| PLP1 | | 2061.090 | GLLDWVGKKVMDWLKDKM-NH ₂ |
| | 9.21 | 793.412 | GWGSLFK |
| | 9.40 | 894.458 | GWGSLFKT |
| | 9.54 | 1309.685 | GWGSLFKTVGKM |
| | 10.95 | 1991.142 | GWGSLFKTVGKMLAKAAVK |
| PLP2 | | 3361.753 | GWGSIFKTVGKMIAKAAVKAAPEAISAMASQNE |
| | 8.75 | 1776.795 | EAAANAAASEALSAMASQNE |
| | 11.08 | 2319.098 | KTALEAANAAASEALSAMASQNE |
| PLP3 | | 4229.336 | KIKWGKIFKGGKLIKTALEAANAAASEALSAMASQNEK |