Supplementary Data 1

**Phylogenomics resolves the root of hexapods: Protura are sister to all other hexapods**

Du *et al*

**RESULTS**

**Phylogenetic Signal**

We conducted several tests to discriminate between the four hypotheses of hexapod relationships. We subjected every gene from the four matrices to the Approximately Unbiased (AU), Weighted Kishino-Hasegawa (WKH), and Weighted Shimodaira-Hasegawa (WSH) tests to compute the distribution of gene tree supports (i.e., the gene-wise likelihood score). In all matrices, hypothesis H2 had the highest number of gene tree supports, and hypothesis H4 had the lowest. Hypotheses H1 and H3 had similar numbers and ratios of gene tree supports, albeit the consistent genes (Matrix1-con and Matrix2-con) lent more support to H3 than H1 (Supplementary Table S1; Supplementary Fig. S1a). We furthermore compared the site-wise likelihood scores for the four hypothesised topologies. For Matrix1 and Matrix2, a distinctly greater number of sites supported H4 than any of the other three hypotheses (Supplementary Table S2; Supplementary Fig. S1b). For Matrix2-con, the highest supported topology was H4 followed by H3 (Supplementary Fig. S1b).

We detected potentially confounding signal using four-cluster likelihood mapping (FcLM) with all four matrices, and evaluated which hypothesis (unrooted trees) was predominantly supported by these quartets: T1 (Collembola + Diplura) and (Protura + Insecta); T2 (Collembola + Insecta) and (Diplura + Protura); T3 (Collembola + Protura) and (Diplura + Insecta). The majority of quartets placing Protura plus Collembola were sister group to a clade comprising Diplura + Insecta, i.e., topology T3 favoured, which corresponding to the hypothesis H2 (Supplementary Fig. S2; but with no significant support (FcLM range from 44.4% to 51.8%)).

In order to examine three gene properties, evolutionary rate, DVMC, and treeness, we compared the ASTRAL topologies from our original matrix (only after trimming for 75% completeness) and those obtained after filtering based on these properties. The resulting topologies were the same (Supplementary Fig. S3); all supported ‘Collembola-first’ (H1). The results shows that evolutionary rate, DVMC, and treeness were not strongly correlated with phylogenetic signal.

**METHOD DETAILS**

**Effect of gene properties on the recovered topologies**

Three properties of each analysed gene were measured. The evolutionary rate of sequencesS1 was estimated with a custom script (loci\_filtering\_alignment-based.sh) which was used to calculate the values of average pairwise identity in PhyKIT. Lower values are indicative of slowly evolving genes suitable for resolving ancient divergences. We further quantified the genic deviation from the assumptions of a molecular clock using PhyKIT. Lower DVMC are indicative of a lower degree of violation of the molecular clock assumption and are hence presumably more desirable for phylogenomic analysis. Treeness describes the signal-to-noise ratio in a phylogeny, whereby higher values of treeness are thought to be desirableS2 for phylogenetic inference. A custom script (loci\_filtering\_tree-based.sh) was used to calculate these values. By comparing ASTRAL topologies of the original matrix (only after trimming for 75% completeness) to topologies derived from analyses of genes that are slow-evolving (average pairwise identity lower than 0.5), don’t violate the molecular clock assumption (DVMC values lower than 1.0) and display high treeness (values greater than 0.2), we investigated the effect of these gene properties on the recovered topology.

**Four-cluster likelihood mapping**

To infer the strength of phylogenetic signals with the competing phylogenetic hypotheses and to assess the stability of our phylogeny, the four-cluster likelihood mapping (FcLM) approachS3 was applied to all four matrices in IQ-TREE. The FcLM analyses were conducted under the LG+PMSF(C60) model (H3\_guide-tree). The nexus file containing the four taxon clusters (1, Protura [two species]; 2, Diplura [five species]; 3, Collembola [seven species]; and 4, Insecta [31 species]) is available from GitHub: https://github.com/xtmtd/Phylogenomics/tree/main/basal\_hexapods.

**Site-wise and gene-wise likelihood analyses**

In addition to the sCF values, the site-wise likelihood scores for all four hypotheses from each matrix were calculated, to obtain the number of sites supporting each hypothesis and site log-likelihood scores (Δ|lnL|). Furthermore, we performed a gene-wise likelihood analysis for every gene in each matrix using the AU, WKH, and WSH tests under model EX\_EHO+F+R4 in IQ-TREE. Genes not present in one of the three basal hexapod groups were excluded in PhyKIT using the prune tree function. The genes in each matrix with the highest *p*-value in the AU test were extracted, to count the number of genes supporting each hypothesis. Then, a coalescent-based phylogenetic analysis with the MSC model and default parameters was conducted using these gene trees in ASTRAL. The custom scripts or commands for the site-wise and gene-wise likelihood analyses used in this study are available at GitHub https://github.com/xtmtd/Phylogenomics/tree/main/basal\_hexapods/scripts.

**Supplemental References**

S1. Zhang, J. & Yang, J. R. Determinants of the rate of protein sequence evolution. *Nat. Rev. Genet.* **16**, 409–420 (2015).

S2. Liu, L. et al. Genomic evidence reveals a radiation of placental mammals uninterrupted by the KPg boundary. *Proc. Natl. Acad. Sci. USA* **114**, E7282–E7290 (2017).

S3. Strimmer, K. & von Haeseler, A. Likelihood-mapping: A simple method to visualize phylogenetic. *Proc. Natl. Acad. Sci. USA* **94**, 6815–6819 (1997).



**Supplementary Fig. S1** The gene-wise and site-wise likelihood analyses from four hypotheses for every gene in each matrix. (a) Gene-wise likelihood which detect distribution of gene tree support. The counts of genes from each hypothesis of four matrices (left), and the proportion of genes from each hypothesis of four matrices (right). (b) Site-wise likelihood which detect distribution of sites support. The counts of sites from each hypothesis of four matrices (left), and the proportion of sites from each hypothesis of four matrices (right).



**Supplementary Fig. S2** Four-cluster Likelihood Mapping (FcLM). Voronoi cells are areas, in which quartets show predominant or maximal support for either of the three topologies T1, T2, T3, or in which quartets show ambiguous support T12, T13, T23, and T\*. Voronoi cell corresponding to T1: quartets show support for (Collembola + Diplura) – (Protura + Insecta); Voronoi cell corresponding to T2: quartets show support for (Collembola + Insecta) – (Diplura + Protura); Voronoi cell corresponding to T3: quartets show support for (Collembola + Protura) – (Diplura + Insecta); Voronoi cells corresponding to T12, T13, T23 do not show clear support for T1, T2, and T3; in T\* all topologies are equally likely. (a) FcLM of Matrix1. (b) FcLM of Matrix1-con. (c) FcLM of Matrix2. (d) FcLM of Matrix2-con.



**Supplementary Fig. S3** Phylogenetic trees analyzed by using ASTRAL with (a) original matrix (only after trimming of 75% completeness, remaining 956 genes), (b) filtering of evolutionary rate of sequences (remaining 543 genes), (c) filtering of DVMC (remaining 808 genes), and (d) filtering of treeness (remaining 312 genes).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **BUSCO\_id** | **Hypothesis** | | | |
|  | **Matrix1** | **Matrix1-con** | **Matrix2** | **Matrix2-con** |
| 1 | 100070at6656 | H4 | - | H4 | - |
| 2 | 100136at6656 | H3 | H3 | - | - |
| 3 | 100216at6656 | H2 | H2 | H2 | H2 |
| 4 | 100227at6656 | H1 | - | H1 | - |
| 5 | 100296at6656 | H3 | H3 | H3 | H3 |
| 6 | 100612at6656 | H3 | H3 | - | - |
| 7 | 100664at6656 | H1 | - | H1 | - |
| 8 | 100673at6656 | H4 | H4 | - | - |
| 9 | 100760at6656 | H1 | H1 | H1 | H1 |
| 10 | 101349at6656 | H3 | H3 | H3 | H3 |
| 11 | 101359at6656 | H1 | H1 | H1 | H1 |
| 12 | 101491at6656 | missing | missing | missing | missing |
| 13 | 101531at6656 | H4 | - | - | - |
| 14 | 101621at6656 | H3 | - | - | - |
| 15 | 101727at6656 | H3 | - | - | - |
| 16 | 101761at6656 | H4 | H4 | - | - |
| 17 | 101767at6656 | H4 | H4 | H4 | H4 |
| 18 | 101829at6656 | H2 | H2 | H2 | H2 |
| 19 | 102321at6656 | H2 | H2 | H2 | H2 |
| 20 | 102770at6656 | H2 | - | - | - |
| 21 | 103125at6656 | H1 | - | H1 | - |
| 22 | 103207at6656 | H1 | - | H1 | - |
| 23 | 103479at6656 | H1 | H1 | H1 | H1 |
| 24 | 103590at6656 | H1 | - | H1 | - |
| 25 | 103747at6656 | H2 | - | H2 | - |
| 26 | 103752at6656 | H1 | H1 | H1 | H1 |
| 27 | 103908at6656 | H2 | - | H2 | - |
| 28 | 103914at6656 | H1 | - | H1 | - |
| 29 | 104063at6656 | H3 | H3 | H3 | H3 |
| 30 | 104122at6656 | H3 | H3 | - | - |
| 31 | 104410at6656 | H2 | - | H2 | - |
| 32 | 104595at6656 | H2 | H2 | - | - |
| 33 | 104604at6656 | H4 | H4 | H4 | H4 |
| 34 | 104769at6656 | H1 | H1 | H1 | H1 |
| 35 | 104898at6656 | H1 | H1 | - | - |
| 36 | 105000at6656 | H2 | H2 | - | - |
| 37 | 105170at6656 | H1 | - | H1 | - |
| 38 | 105364at6656 | H3 | - | H3 | - |
| 39 | 105457at6656 | H3 | H3 | H3 | H3 |
| 40 | 105771at6656 | H4 | H4 | - | - |
| 41 | 105887at6656 | H2 | H2 | - | - |
| 42 | 106116at6656 | H2 | - | - | - |
| 43 | 106126at6656 | H3 | - | - | - |
| 44 | 106466at6656 | H3 | H3 | - | - |
| 45 | 106470at6656 | H3 | - | H3 | - |
| 46 | 106634at6656 | H1 | - | H1 | - |
| 47 | 106639at6656 | H1 | - | - | - |
| 48 | 106788at6656 | H2 | - | H2 | - |
| 49 | 106988at6656 | H2 | H2 | H2 | H2 |
| 50 | 107030at6656 | H1 | - | H1 | - |
| 51 | 107139at6656 | H2 | H2 | H2 | H2 |
| 52 | 107226at6656 | H1 | H1 | - | - |
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| 54 | 107453at6656 | H2 | - | H2 | - |
| 55 | 107615at6656 | H2 | H2 | H2 | H2 |
| 56 | 107802at6656 | H4 | - | - | - |
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| 58 | 108162at6656 | H1 | H1 | H1 | H1 |
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| 62 | 108702at6656 | H2 | H2 | H2 | H2 |
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| 64 | 108808at6656 | H2 | H2 | H2 | H2 |
| 65 | 109131at6656 | H2 | H2 | - | - |
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| 67 | 109325at6656 | H3 | H3 | H3 | H3 |
| 68 | 109444at6656 | H1 | - | H1 | - |
| 69 | 109484at6656 | H3 | H3 | - | - |
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| 71 | 109664at6656 | H3 | - | - | - |
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| 77 | 110504at6656 | H2 | H2 | H2 | H2 |
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| 80 | 111153at6656 | H4 | - | H4 | - |
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| 207 | 130514at6656 | H3 | H3 | H3 | H3 |
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| 216 | 131642at6656 | H3 | - | - | - |
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| 223 | 133329at6656 | H4 | - | - | - |
| 224 | 133362at6656 | H1 | H1 | - | - |
| 225 | 133422at6656 | H3 | - | H3 | - |
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| 227 | 133735at6656 | H1 | - | H1 | - |
| 228 | 133949at6656 | H2 | H2 | H2 | H2 |
| 229 | 134209at6656 | H1 | - | H1 | - |
| 230 | 134216at6656 | H4 | H4 | H4 | H4 |
| 231 | 134673at6656 | H2 | - | H2 | - |
| 232 | 134708at6656 | H4 | - | H4 | - |
| 233 | 134776at6656 | H2 | H2 | - | - |
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| 235 | 134853at6656 | H4 | - | H4 | - |
| 236 | 134865at6656 | missing | missing | missing | missing |
| 237 | 134885at6656 | H2 | H2 | H2 | H2 |
| 238 | 135107at6656 | H1 | - | - | - |
| 239 | 135123at6656 | H2 | - | - | - |
| 240 | 135203at6656 | H2 | - | - | - |
| 241 | 135204at6656 | H2 | H2 | - | - |
| 242 | 135215at6656 | H2 | H2 | H2 | H2 |
| 243 | 135357at6656 | H1 | - | - | - |
| 244 | 135373at6656 | H4 | H4 | - | - |
| 245 | 135526at6656 | H1 | - | - | - |
| 246 | 135676at6656 | missing | missing | missing | missing |
| 247 | 135690at6656 | H1 | H1 | H1 | H1 |
| 248 | 135764at6656 | H1 | H1 | H1 | H1 |
| 249 | 135859at6656 | H3 | H3 | - | - |
| 250 | 135975at6656 | H2 | - | H2 | - |
| 251 | 135994at6656 | H2 | H2 | - | - |
| 252 | 136055at6656 | H1 | H1 | - | - |
| 253 | 136095at6656 | H3 | - | H3 | - |
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| 255 | 136224at6656 | H2 | H2 | - | - |
| 256 | 136365at6656 | H4 | H4 | - | - |
| 257 | 137197at6656 | H2 | - | H2 | - |
| 258 | 137202at6656 | H2 | H2 | H2 | H2 |
| 259 | 137334at6656 | H3 | - | - | - |
| 260 | 137338at6656 | H1 | H1 | - | - |
| 261 | 13736at6656 | H2 | H2 | H2 | H2 |
| 262 | 137422at6656 | H3 | H3 | - | - |
| 263 | 137609at6656 | H3 | H3 | H3 | H3 |
| 264 | 137688at6656 | H3 | - | - | - |
| 265 | 138243at6656 | H3 | H3 | H3 | H3 |
| 266 | 138271at6656 | H3 | - | - | - |
| 267 | 13833at6656 | H4 | H4 | H4 | H4 |
| 268 | 138379at6656 | H1 | - | H1 | - |
| 269 | 138401at6656 | H3 | H3 | - | - |
| 270 | 138502at6656 | H1 | H1 | H1 | H1 |
| 271 | 138553at6656 | H2 | H2 | - | - |
| 272 | 13858at6656 | H2 | H2 | H2 | H2 |
| 273 | 138659at6656 | H1 | H1 | - | - |
| 274 | 138684at6656 | H4 | H4 | - | - |
| 275 | 138937at6656 | H2 | H2 | - | - |
| 276 | 139217at6656 | H1 | H1 | - | - |
| 277 | 13934at6656 | H2 | - | H2 | - |
| 278 | 139553at6656 | H4 | - | H4 | - |
| 279 | 139834at6656 | H3 | H3 | - | - |
| 280 | 140076at6656 | H3 | H3 | - | - |
| 281 | 140197at6656 | H3 | H3 | - | - |
| 282 | 140198at6656 | H4 | H4 | - | - |
| 283 | 140403at6656 | H2 | - | - | - |
| 284 | 140461at6656 | H2 | - | H2 | - |
| 285 | 140693at6656 | H2 | - | - | - |
| 286 | 140874at6656 | H2 | H2 | - | - |
| 287 | 140903at6656 | H1 | H1 | - | - |
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| 289 | 141031at6656 | H4 | H4 | H4 | H4 |
| 290 | 141163at6656 | H1 | H1 | H1 | H1 |
| 291 | 141166at6656 | H2 | - | - | - |
| 292 | 141298at6656 | H1 | - | - | - |
| 293 | 141804at6656 | H1 | H1 | H1 | H1 |
| 294 | 141859at6656 | H1 | - | - | - |
| 295 | 141916at6656 | H1 | - | - | - |
| 296 | 142388at6656 | H1 | - | - | - |
| 297 | 142415at6656 | H1 | - | - | - |
| 298 | 142522at6656 | H1 | H1 | H1 | H1 |
| 299 | 142613at6656 | H4 | H4 | H4 | H4 |
| 300 | 142661at6656 | H1 | H1 | H1 | H1 |
| 301 | 142833at6656 | H2 | H2 | H2 | H2 |
| 302 | 143154at6656 | H4 | H4 | - | - |
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| 305 | 143489at6656 | H4 | - | - | - |
| 306 | 143709at6656 | H3 | H3 | H3 | H3 |
| 307 | 143812at6656 | H1 | H1 | H1 | H1 |
| 308 | 143930at6656 | H2 | - | H2 | - |
| 309 | 144337at6656 | H4 | H4 | - | - |
| 310 | 14447at6656 | H2 | H2 | H2 | H2 |
| 311 | 144652at6656 | H2 | H2 | - | - |
| 312 | 144836at6656 | H2 | - | - | - |
| 313 | 144851at6656 | H3 | H3 | H3 | H3 |
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| 316 | 145443at6656 | missing | missing | missing | missing |
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| 319 | 145996at6656 | H2 | H2 | - | - |
| 320 | 146007at6656 | H1 | H1 | H1 | H1 |
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| 322 | 146383at6656 | H1 | H1 | - | - |
| 323 | 146600at6656 | H2 | H2 | H2 | H2 |
| 324 | 146920at6656 | H2 | - | - | - |
| 325 | 147002at6656 | H4 | - | H4 | - |
| 326 | 147025at6656 | H3 | - | - | - |
| 327 | 147322at6656 | H3 | - | - | - |
| 328 | 147657at6656 | H3 | - | - | - |
| 329 | 147891at6656 | H3 | H3 | H3 | H3 |
| 330 | 147980at6656 | H1 | - | H1 | - |
| 331 | 148619at6656 | H3 | H3 | - | - |
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| 340 | 149973at6656 | H3 | - | - | - |
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| 346 | 150479at6656 | H2 | - | - | - |
| 347 | 150583at6656 | H3 | - | - | - |
| 348 | 150765at6656 | H1 | H1 | - | - |
| 349 | 151102at6656 | H4 | H4 | - | - |
| 350 | 151111at6656 | H4 | H4 | - | - |
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| 353 | 151642at6656 | H2 | H2 | H2 | H2 |
| 354 | 151658at6656 | H1 | H1 | H1 | H1 |
| 355 | 15200at6656 | H2 | H2 | H2 | H2 |
| 356 | 152032at6656 | H2 | - | - | - |
| 357 | 152402at6656 | H4 | H4 | - | - |
| 358 | 152534at6656 | H2 | H2 | - | - |
| 359 | 153155at6656 | H3 | - | - | - |
| 360 | 153232at6656 | H1 | H1 | - | - |
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| 362 | 153693at6656 | H2 | H2 | - | - |
| 363 | 153873at6656 | H3 | - | H3 | - |
| 364 | 154133at6656 | H3 | H3 | - | - |
| 365 | 154507at6656 | H3 | H3 | - | - |
| 366 | 155285at6656 | H3 | H3 | - | - |
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| 378 | 159420at6656 | H1 | H1 | H1 | H1 |
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| 380 | 160675at6656 | H4 | H4 | - | - |
| 381 | 160705at6656 | H2 | H2 | - | - |
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| 385 | 162594at6656 | H1 | H1 | - | - |
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| 394 | 166479at6656 | H3 | H3 | - | - |
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| 406 | 19289at6656 | H4 | H4 | H4 | H4 |
| 407 | 20935at6656 | H2 | - | - | - |
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| 409 | 21191at6656 | H4 | H4 | H4 | H4 |
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| 413 | 22611at6656 | missing | missing | missing | missing |
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| 415 | 23917at6656 | H4 | H4 | H4 | H4 |
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| 417 | 26653at6656 | H2 | H2 | H2 | H2 |
| 418 | 26734at6656 | H1 | - | H1 | - |
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| 424 | 28519at6656 | H2 | H2 | H2 | H2 |
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| 427 | 29365at6656 | H4 | H4 | H4 | H4 |
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| 429 | 29744at6656 | H1 | - | H1 | - |
| 430 | 30184at6656 | H2 | - | H2 | - |
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| 432 | 30512at6656 | H2 | H2 | H2 | H2 |
| 433 | 30526at6656 | H3 | H3 | H3 | H3 |
| 434 | 30642at6656 | H1 | H1 | H1 | H1 |
| 435 | 30822at6656 | H3 | H3 | H3 | H3 |
| 436 | 31119at6656 | H4 | H4 | H4 | H4 |
| 437 | 31333at6656 | H2 | - | H2 | - |
| 438 | 31480at6656 | H2 | - | H2 | - |
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| 450 | 36387at6656 | H3 | - | H3 | - |
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| 457 | 38303at6656 | H3 | H3 | H3 | H3 |
| 458 | 38819at6656 | H3 | - | H3 | - |
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| 474 | 42842at6656 | H1 | H2 | H2 | H2 |
| 475 | 42929at6656 | H2 | - | H1 | - |
| 476 | 42943at6656 | H1 | - | H2 | - |
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| 487 | 44504at6656 | H4 | H1 | - | - |
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| 583 | 63924at6656 | H2 | - | H4 | - |
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| 656 | 78921at6656 | H3 | - | - | - |
| 657 | 78947at6656 | H3 | - | H1 | - |
| 658 | 78968at6656 | H1 | H3 | H3 | H3 |
| 659 | 79241at6656 | H3 | H3 | H3 | H3 |
| 660 | 79915at6656 | H3 | - | - | - |
| 661 | 80067at6656 | H3 | H4 | H4 | H4 |
| 662 | 80294at6656 | H4 | - | H1 | - |
| 663 | 80317at6656 | H1 | H1 | H1 | H1 |
| 664 | 80689at6656 | H1 | - | H3 | - |
| 665 | 80693at6656 | H3 | H2 | H2 | H2 |
| 666 | 80948at6656 | H2 | H4 | - | - |
| 667 | 81292at6656 | missing | missing | missing | missing |
| 668 | 81307at6656 | H4 | H3 | - | - |
| 669 | 81650at6656 | H3 | H2 | H2 | H2 |
| 670 | 81703at6656 | H2 | H1 | H1 | H1 |
| 671 | 81708at6656 | H1 | H4 | H4 | H4 |
| 672 | 81919at6656 | missing | missing | missing | missing |
| 673 | 81950at6656 | H4 | H4 | - | - |
| 674 | 83102at6656 | H4 | H1 | H1 | H1 |
| 675 | 83164at6656 | H1 | H2 | H2 | H2 |
| 676 | 83303at6656 | H2 | H2 | H2 | H2 |
| 677 | 83350at6656 | H2 | H3 | H3 | H3 |
| 678 | 83376at6656 | H3 | H1 | H1 | H1 |
| 679 | 83613at6656 | H1 | - | - | - |
| 680 | 83755at6656 | H1 | - | H3 | - |
| 681 | 84097at6656 | H3 | H2 | H2 | H2 |
| 682 | 84149at6656 | H2 | - | - | - |
| 683 | 84422at6656 | H2 | - | - | - |
| 684 | 84576at6656 | H2 | H2 | - | - |
| 685 | 84819at6656 | H2 | H4 | H4 | H4 |
| 686 | 85103at6656 | H4 | - | H3 | - |
| 687 | 85509at6656 | H3 | - | H1 | - |
| 688 | 85680at6656 | H1 | H1 | - | - |
| 689 | 85810at6656 | H1 | H3 | H3 | H3 |
| 690 | 86318at6656 | H2 | - | H2 | - |
| 691 | 86488at6656 | H3 | - | H3 | - |
| 692 | 86654at6656 | H4 | H4 | H4 | H4 |
| 693 | 86715at6656 | H2 | H2 | - | - |
| 694 | 86889at6656 | H2 | H2 | - | - |
| 695 | 87014at6656 | H4 | H4 | - | - |
| 696 | 87089at6656 | H3 | - | - | - |
| 697 | 87114at6656 | H2 | - | H2 | - |
| 698 | 87139at6656 | H2 | - | H2 | - |
| 699 | 87142at6656 | H3 | - | H3 | - |
| 700 | 87527at6656 | H2 | - | - | - |
| 701 | 87575at6656 | H3 | - | H3 | - |
| 702 | 87695at6656 | H3 | - | H3 | - |
| 703 | 87728at6656 | H3 | H3 | - | - |
| 704 | 87910at6656 | H1 | H1 | H1 | H1 |
| 705 | 87928at6656 | H2 | - | H2 | - |
| 706 | 87933at6656 | H4 | - | H4 | - |
| 707 | 88051at6656 | H4 | H4 | H4 | H4 |
| 708 | 88711at6656 | H4 | - | H4 | - |
| 709 | 89064at6656 | H2 | H2 | - | - |
| 710 | 8913at6656 | H2 | - | H2 | - |
| 711 | 89677at6656 | H1 | - | H1 | - |
| 712 | 89713at6656 | H1 | - | H1 | - |
| 713 | 89810at6656 | missing | missing | missing | missing |
| 714 | 89840at6656 | H4 | H4 | H4 | H4 |
| 715 | 89864at6656 | H1 | H1 | H1 | H1 |
| 716 | 90126at6656 | H2 | H2 | - | - |
| 717 | 90322at6656 | H2 | - | H2 | - |
| 718 | 90580at6656 | H3 | H3 | - | - |
| 719 | 90600at6656 | H3 | H3 | H3 | H3 |
| 720 | 90822at6656 | H3 | - | H3 | - |
| 721 | 90928at6656 | H2 | - | H2 | - |
| 722 | 90931at6656 | H2 | - | - | - |
| 723 | 91002at6656 | H1 | - | H1 | - |
| 724 | 91005at6656 | H2 | - | H2 | - |
| 725 | 91022at6656 | H1 | - | H1 | - |
| 726 | 91313at6656 | H1 | H1 | - | - |
| 727 | 91418at6656 | missing | missing | missing | missing |
| 728 | 91933at6656 | H2 | H2 | H2 | H2 |
| 729 | 92167at6656 | H4 | H4 | - | - |
| 730 | 92184at6656 | H1 | H1 | H1 | H1 |
| 731 | 92420at6656 | H1 | - | H1 | - |
| 732 | 92576at6656 | H2 | - | H2 | - |
| 733 | 92854at6656 | H1 | - | H1 | - |
| 734 | 93061at6656 | H4 | H4 | - | - |
| 735 | 93085at6656 | H4 | H4 | - | - |
| 736 | 93152at6656 | H1 | - | H1 | - |
| 737 | 93168at6656 | H4 | H4 | H4 | H4 |
| 738 | 93408at6656 | H2 | - | H2 | - |
| 739 | 93432at6656 | H2 | H2 | H2 | H2 |
| 740 | 93483at6656 | H3 | H3 | H3 | H3 |
| 741 | 93507at6656 | H3 | - | H3 | - |
| 742 | 93535at6656 | H3 | - | H3 | - |
| 743 | 93797at6656 | H4 | H4 | H4 | H4 |
| 744 | 94054at6656 | H1 | - | H1 | - |
| 745 | 94238at6656 | H4 | - | H4 | - |
| 746 | 94263at6656 | H4 | H4 | H4 | H4 |
| 747 | 94304at6656 | H3 | - | H3 | - |
| 748 | 94473at6656 | H3 | H3 | H3 | H3 |
| 749 | 94476at6656 | H1 | H1 | H1 | H1 |
| 750 | 94842at6656 | H2 | - | H2 | - |
| 751 | 94878at6656 | H1 | H1 | - | - |
| 752 | 95028at6656 | H2 | H2 | H2 | H2 |
| 753 | 95089at6656 | H4 | H4 | H4 | H4 |
| 754 | 95294at6656 | H2 | H2 | H2 | H2 |
| 755 | 95524at6656 | H2 | - | H2 | - |
| 756 | 96251at6656 | H2 | H2 | H2 | H2 |
| 757 | 96444at6656 | H2 | - | H2 | - |
| 758 | 96569at6656 | H2 | - | H2 | - |
| 759 | 96592at6656 | H2 | H2 | - | - |
| 760 | 96601at6656 | H3 | - | - | - |
| 761 | 96956at6656 | H1 | H1 | H1 | H1 |
| 762 | 96971at6656 | H1 | - | - | - |
| 763 | 97225at6656 | H2 | - | H2 | - |
| 764 | 97492at6656 | H4 | H4 | - | - |
| 765 | 97763at6656 | H1 | H1 | - | - |
| 766 | 97865at6656 | H1 | - | - | - |
| 767 | 98066at6656 | H2 | - | H2 | - |
| 768 | 98620at6656 | H2 | - | - | - |
| 769 | 98755at6656 | H4 | H4 | H4 | H4 |
| 770 | 98821at6656 | H4 | - | H4 | - |
| 771 | 98845at6656 | H1 | H1 | - | - |
| 772 | 98927at6656 | H1 | - | - | - |
| 773 | 98948at6656 | H2 | H2 | - | - |
| 774 | 99204at6656 | H1 | - | H1 | - |
| 775 | 99270at6656 | H4 | H4 | H4 | H4 |
| 776 | 99307at6656 | H1 | - | H1 | - |
| 777 | 99377at6656 | H3 | H3 | - | - |
| 778 | 99519at6656 | H1 | H1 | H1 | H1 |
| 779 | 99625at6656 | H1 | H1 | H1 | H1 |
| 780 | 99998at6656 | missing | missing | missing | missing |
|  | H1 | 191 | 105 | 123 | 66 |
|  | H2 | 240 | 138 | 152 | 86 |
|  | H3 | 183 | 117 | 117 | 77 |
|  | H4 | 126 | 83 | 83 | 52 |
|  | totally | 740 | 443 | 475 | 281 |

Note: The loci with one of the three basal hexapods (Collembola, Protura and Diplura) complete lacking were marked by yellow. These loci were not used for analysis.

**Supplementary Table S1** Comparison of tree topologies for every gene under four matrices using the approximately unbiased (AU), weighted Kishino-Hasegawa (WKH), and weighted Shimodaira-Hasegawa (WSH) tests. H1: Collembola + (Protura + (Diplura + Insecta)); H2: (Collembola + Protura) + (Diplura + Insecta); H3: Protura + ((Collembola + Diplura) + Insecta); H4: (Protura + (Collembola + Diplura)) + Insecta.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Hypothesis** | **Site-likelihood scores** | | | |
| **Matrix1** | **Matrix1-con** | **Matrix2** | **Matrix2-con** |
| H1 | 87,910 | 39,094 | 57,942 | 29,872 |
| H2 | 75,415 | 64,324 | 67,523 | 30,926 |
| H3 | 59,504 | 29,410 | 33,268 | 37,595 |
| H4 | 119,423 | 69,068 | 96,362 | 51,510 |

**Supplementary Table S2** The site-wise likelihood scores for all four hypotheses from each matrix.