論文 / 著書情報
Article / Book Information

題目(和文)	染色体進化の統合的理解に向けた鱗翅目昆虫の比較ゲノム解析
Title(English)	Comparative genomic analysis of Lepidoptera for an integrated understanding of chromosomal evolution
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出典(和文)	学位:博士(理学), 学位授与機関:東京科学大学, 報告番号:甲第241号, 授与年月日:2025年3月26日, 学位の種別:課程博士, 審査員:伊藤 武彦,本郷 裕一,立花 和則,二階堂 雅人,山田 拓司
Citation(English)	Degree:Doctor (Science), Conferring organization: Institute of Science Tokyo, Report number:甲第241号, Conferred date:2025/3/26, Degree Type:Course doctor, Examiner:,,,,
学位種別(和文)	博士論文
Category(English)	Doctoral Thesis
種別(和文)	要約
Type(English)	Outline

令和６年度 博士論文

染色体進化の統合的理解に向けた鱗翅目昆虫の比較ゲノム解析

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論文要約

本論文は「染色体進化の統合的理解に向けた鱗翅目昆虫の比較ゲノム解析(Comparative genomic analysis of Lepidoptera for an integrated understanding of chromosomal evolution)」と題し、鱗翅目昆虫における染色体進化のメカニズムを解明するために行った一連の研究成果をまとめたものであり、全四章より構成されている。

第一章「序論」では、本研究の対象である鱗翅目昆虫について、種の多様性や核型の多様性の特徴、さらには染色体の分裂・融合といった進化的観点からも見られる特徴を紹介している。続いて、鱗翅目のゲノム解析が進む中で明らかになった染色体長や核型変化が進化に与える影響、ならびに性染色体である Z 染色体の特異性について詳述すると共に、従来の研究で提唱された Faster-Z 仮説と Slower-Z 仮説の 2 つの仮説が混在している現状を整理した上でその解明の意義を論じている。さらに、本研究の主題として、「染色体長がゲノム進化に与える影響の解明」と「Faster-Z 仮説の包括的検証」を設定し、染色体進化の多面的なメカニズムを探ることの重要性を述べている。

第二章「オオスカシバの染色体比較ゲノム解析」では、スズメガ科の昆虫オオスカシバゲノムを対象に、染色体長が進化動態に与える影響についての研究成果を述べている。オオスカシバのゲノムは、鱗翅目のモデル生物であるタバコスズメガやカイコと異なる核型を持つため、染色体融合の変遷および、融合に伴う染色体長変化がゲノム進化に与える影響の解明に適したモデルである。本研究では、これまで未解読であった本種の染色体レベルの全ゲノムアセンブルを構築し、近縁種との比較ゲノム解析を行うことで、短い染色体ほど種間で配列分化が速く、種内多様性が高いこと、さらにはリピート配列の割合が増加することを明らかにした。この結果は、短い染色体では変異頻度が高く、ゲノム配列の適応進化を促進する可能性を示唆している。また、染色体融合によって染色体長が増加すると、リピート配列の蓄積や進化速度が変化することも確認され、「染色体長」が進化特性を規定する主要因の一つであると述べている。

第三章「鱗翅目 46 種における Z 染色体の進化解析」では、46 種の鱗翅目ゲノムデータを用いた解析を通じて、性染色体である Z 染色体の進化的特性についての解析結果を述べている。本研究では、これまで少ない種の遺伝子領域に限定されていた Faster-Z 仮説の検証を、46 種の全ゲノム配列に解析対象を広げることで、遺伝子の有無による偏りなく評価することを可能とした。加えて、構造変異（SV）も考慮に入れ解析を行った。まず、全ゲノム配列の比較により Z 染色体は常染色体に比べて急速な配列分化を示し、鱗翅目全般で Faster-Z 仮説を支持する結果が得られた。さらに、シンテニー（遺伝子の順序）解析によりゲノム構造比較を行ったところ、Z 染色体上では染色体再編成の頻度も高いことが明らかとなった。この急速な配列分化の基盤となるメカニズムを解明するため、リファレンスゲノムの相同染色体配列である Alternate haplotype 配列を活用する新たな解析手法を導入し、二倍体ハプロタイプ間の構造変異および一塩基変異（SNV）の検出を行ったところ、Z 染色体

全体で低い遺伝的多様性が観察された。これは Z 染色体の有効集団サイズが小さいことから、遺伝的浮動の影響が顕著であり、進化速度の加速に寄与していることが理由であると考えられる。また、変異の割合について SV と SNV を比較したところ、Z 染色体では SV に起因する変異の割合が SNV の 19.4 倍と、全染色体中で最も高い値を示した。この結果から、遺伝的浮動による SV の蓄積が Faster-Z の大きな要因である可能性が示された。これらの成果は、従来議論されてきた Faster-Z 仮説を支持するとともに、新たな進化メカニズムを提示するものであると述べている。

第四章「総論」では、短い染色体や Z 染色体特有の進化動態を総括している。本研究を通じて、短い染色体が種間・種内で高い多様性を維持しており、新規遺伝子の獲得や適応進化に貢献している可能性を示唆するとともに、染色体融合がゲノム進化特性に与える影響を明らかにした。また Z 染色体については、配列分化の加速化、染色体再編成の頻発といった常染色体と異なる特異的な進化動態が確認され、特に逆位による Faster-Z の促進が示唆された。さらに、有効集団サイズの小ささが遺伝的浮動を引き起こし、それが進化速度の違いに寄与しているという新たな知見を提供したと論じている。

参考文献

[1] Van Nieukerken E, Kaila L, Kitching I, KRISTENSEN N, Lees D, MINET J, et al. Order Lepidoptera Linnaeus, 1758. In: Zhang, Z.-Q. (Ed.) Animal biodiversity: An outline of higher-level classification and survey of taxonomic richness. Zootaxa 2011;3148:212–21. https://doi.org/10.11646/zootaxa.3148.1.41.

[2] Mita K, Kasahara M, Sasaki S, Nagayasu Y, Yamada T, Kanamori H, et al. The Genome Sequence of Silkworm, *Bombyx mori*. DNA Research 2004;11:27–35. https://doi.org/10.1093/dnares/11.1.27.

[3] Dasmahapatra KK, Walters JR, Briscoe AD, Davey JW, Whibley A, Nadeau NJ, et al. Butterfly genome reveals promiscuous exchange of mimicry adaptations among species. Nature 2012;487:94–8. https://doi.org/10.1038/nature11041.

[4] Kunte K, Zhang W, Tenger-Trolander A, Palmer DH, Martin A, Reed RD, et al. doublesex is a mimicry supergene. Nature 2014;507:229–32. https://doi.org/10.1038/nature13112.

[5] Nishikawa H, Iijima T, Kajitani R, Yamaguchi J, Ando T, Suzuki Y, et al. A genetic mechanism for female-limited Batesian mimicry in Papilio butterfly. Nat Genet 2015;47:405–9. https://doi.org/10.1038/ng.3241.

[6] Lewis JJ, van der Burg KRL, Mazo-Vargas A, Reed RD. ChIP-Seq-Annotated *Heliconius erato* Genome Highlights Patterns of *cis*-Regulatory Evolution in Lepidoptera. Cell Reports 2016;16:2855–63. https://doi.org/10.1016/j.celrep.2016.08.042.

[7] Ferguson L, Marlétaz F, Carter J-M, Taylor WR, Gibbs M, Breuker CJ, et al. Ancient Expansion of the Hox Cluster in Lepidoptera Generated Four Homeobox Genes Implicated in Extra-Embryonic Tissue Formation. PLOS Genetics 2014;10:e1004698. https://doi.org/10.1371/journal.pgen.1004698.

[8] Johnson SD, Moré M, Amorim FW, Haber WA, Frankie GW, Stanley DA, et al. The long and the short of it: a global analysis of hawkmoth pollination niches and interaction networks. Functional Ecology 2017;31:101–15. https://doi.org/10.1111/1365-2435.12753.

[9] Akiyama T, Uchiyama H, Yajima S, Arikawa K, Terai Y. Parallel evolution of opsin visual pigments in hawkmoths by tuning of spectral sensitivities during transition from a nocturnal to a diurnal ecology. Journal of Experimental Biology 2022;225:jeb244541. https://doi.org/10.1242/jeb.244541.

[10] Wenger AM, Peluso P, Rowell WJ, Chang P-C, Hall RJ, Concepcion GT, et al. Accurate circular consensus long-read sequencing improves variant detection and

assembly of a human genome. Nat Biotechnol 2019;37:1155–62. https://doi.org/10.1038/s41587-019-0217-9.

[11] Lieberman-Aiden E, van Berkum NL, Williams L, Imakaev M, Ragoczy T, Telling A, et al. Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. Science 2009;326:289–93. https://doi.org/10.1126/science.1181369.

[12] Lewin HA, Robinson GE, Kress WJ, Baker WJ, Coddington J, Crandall KA, et al. Earth BioGenome Project: Sequencing life for the future of life. Proceedings of the National Academy of Sciences 2018;115:4325–33. https://doi.org/10.1073/pnas.1720115115.

[13] Rhie A, McCarthy SA, Fedrigo O, Damas J, Formenti G, Koren S, et al. Towards complete and error-free genome assemblies of all vertebrate species. Nature 2021;592:737–46. https://doi.org/10.1038/s41586-021-03451-0.

[14] The Darwin Tree of Life Project Consortium. Sequence locally, think globally: The Darwin Tree of Life Project. Proceedings of the National Academy of Sciences 2022;119:e2115642118. https://doi.org/10.1073/pnas.2115642118.

[15] Mulhair PO, Crowley L, Boyes DH, Harper A, Lewis OT, Consortium DT of L, et al. Diversity, duplication, and genomic organization of homeobox genes in Lepidoptera. Genome Res 2023;33:32–44. https://doi.org/10.1101/gr.277118.122.

[16] Wright CJ, Stevens L, Mackintosh A, Lawniczak M, Blaxter M. Comparative genomics reveals the dynamics of chromosome evolution in Lepidoptera. Nat Ecol Evol 2024;8:777–90. https://doi.org/10.1038/s41559-024-02329-4.

[17] d'Alençon E, Sezutsu H, Legeai F, Permal E, Bernard-Samain S, Gimenez S, et al. Extensive synteny conservation of holocentric chromosomes in Lepidoptera despite high rates of local genome rearrangements. Proceedings of the National Academy of Sciences 2010;107:7680–5. https://doi.org/10.1073/pnas.0910413107.

[18] Dam MHV, Cabras AA, Henderson JB, Rominger AJ, Estrada CP, Omer AD, et al. The Easter Egg Weevil (*Pachyrhynchus*) genome reveals syntenic patterns in Coleoptera across 200 million years of evolution. PLOS Genetics 2021;17:e1009745. https://doi.org/10.1371/journal.pgen.1009745.

[19] de Vos JM, Augustijnen H, Bätscher L, Lucek K. Speciation through chromosomal fusion and fission in Lepidoptera. Philosophical Transactions of the Royal Society B: Biological Sciences 2020;375:20190539. https://doi.org/10.1098/rstb.2019.0539.

[20] Lukhtanov VA, Dincă V, Friberg M, Šíchová J, Olofsson M, Vila R, et al. Versatility of multivalent orientation, inverted meiosis, and rescued fitness in holocentric chromosomal hybrids. Proceedings of the National Academy of Sciences

2018;115:E9610–9. https://doi.org/10.1073/pnas.1802610115.

[21] Marec F, Tothová A, Sahara K, Traut W. Meiotic pairing of sex chromosome fragments and its relation to atypical transmission of a sex-linked marker in Ephestia kuehniella (Insecta: Lepidoptera). Heredity 2001;87:659–71. https://doi.org/10.1046/j.1365-2540.2001.00958.x.

[22] Charlesworth B, Coyne JA, Barton NH. The Relative Rates of Evolution of Sex Chromosomes and Autosomes. The American Naturalist 1987;130:113–46. https://doi.org/10.1086/284701.

[23] Vicoso B, Charlesworth B. Evolution on the X chromosome: unusual patterns and processes. Nat Rev Genet 2006;7:645–53. https://doi.org/10.1038/nrg1914.

[24] Mank JE, Nam K, Ellegren H. Faster-Z Evolution Is Predominantly Due to Genetic Drift. Molecular Biology and Evolution 2010;27:661–70. https://doi.org/10.1093/molbev/msp282.

[25] Wright AE, Harrison PW, Zimmer F, Montgomery SH, Pointer MA, Mank JE. Variation in promiscuity and sexual selection drives avian rate of Faster-Z evolution. Molecular Ecology 2015;24:1218–35. https://doi.org/10.1111/mec.13113.

[26] Zhang G, Li C, Li Q, Li B, Larkin DM, Lee C, et al. Comparative genomics reveals insights into avian genome evolution and adaptation. Science 2014;346:1311–20. https://doi.org/10.1126/science.1251385.

[27] Mongue AJ, Hansen ME, Walters JR. Support for faster and more adaptive Z chromosome evolution in two divergent lepidopteran lineages*. Evolution 2022;76:332–45. https://doi.org/10.1111/evo.14341.

[28] Sackton TB, Corbett-Detig RB, Nagaraju J, Vaishna L, Arunkumar KP, Hartl DL. POSITIVE SELECTION DRIVES FASTER-Z EVOLUTION IN SILKMOTHS. Evolution 2014;68:2331–42. https://doi.org/10.1111/evo.12449.

[29] Pinharanda A, Rousselle M, Martin SH, Hanly JJ, Davey JW, Kumar S, et al. Sexually dimorphic gene expression and transcriptome evolution provide mixed evidence for a fast‐Z effect in Heliconius. Journal of Evolutionary Biology 2019;32:194–204. https://doi.org/10.1111/jeb.13410.

[30] Rousselle M, Faivre N, Ballenghien M, Galtier N, Nabholz B. Hemizygosity Enhances Purifying Selection: Lack of Fast-Z Evolution in Two Satyrine Butterflies. Genome Biology and Evolution 2016;8:3108–19. https://doi.org/10.1093/gbe/evw214.

[31] Godfrey RK, Britton SE, Mishra S, Goldberg JK, Kawahara AY. A high-quality, long-read genome assembly of the whitelined sphinx moth (Lepidoptera: Sphingidae: Hyles lineata) shows highly conserved melanin synthesis pathway genes. G3 Genes|Genomes|Genetics 2023;13:jkad090.

https://doi.org/10.1093/g3journal/jkad090.

[32] Hundsdoerfer AK, Schell T, Patzold F, Wright CJ, Yoshido A, Marec F, et al. High-quality haploid genomes corroborate 29 chromosomes and highly conserved synteny of genes in Hyles hawkmoths (Lepidoptera: Sphingidae). BMC Genomics 2023;24:443. https://doi.org/10.1186/s12864-023-09506-y.

[33] Kanost MR, Arrese EL, Cao X, Chen Y-R, Chellapilla S, Goldsmith MR, et al. Multifaceted biological insights from a draft genome sequence of the tobacco hornworm moth, *Manduca sexta*. Insect Biochemistry and Molecular Biology 2016;76:118–47. https://doi.org/10.1016/j.ibmb.2016.07.005.

[34] Pippel M, Jebb D, Patzold F, Winkler S, Vogel H, Myers G, et al. A highly contiguous genome assembly of the bat hawkmoth *Hyles vespertilio* (Lepidoptera: Sphingidae). GigaScience 2020;9. https://doi.org/10.1093/gigascience/giaa001.

[35] Yan M, Su B-S, Huang Y-X, Xu Z-B, Jiang Z-H, Wang X. Chromosome-level Genome Assembly of Theretra japonica (Lepidoptera: Sphingidae). Sci Data 2024;11:770. https://doi.org/10.1038/s41597-024-03500-z.

[36] Yan Y, Zhao K, Yang L, Liu N, Xu Y, Gai J, et al. Chromosome-level genome assembly and annotation of Clanis bilineata tsingtauica Mell (Lepidoptera: Sphingidae). Sci Data 2024;11:1062. https://doi.org/10.1038/s41597-024-03853-5.

[37] *Cephonodes hylas* Linnaeus, 1771 in GBIF Secretariat (2021). GBIF Backbone Taxonomy. Checklist dataset https://doi.org/10.15468/39omei accessed via GBIF.org on 2022-07-13. n.d.

[38] Crowe TJ. Coffee pests in Africa. Coffee: Growing, Processing, Sustainable Production A Guidebook for Growers, Processors, Traders and Researchers 2009:425–62.

[39] Puttick GM, Bowers MD. Effect of qualitative and quantitative variation in allelochemicals on a generalist insect: Iridoid glycosides and the southern armyworm. J Chem Ecol 1988;14:335–51. https://doi.org/10.1007/BF01022550.

[40] Yoshida A, Motoyama M, Kosaku A, Miyamoto K. Antireflective Nanoprotuberance Array in the Transparent Wing of a Hawkmoth, *Cephonodes hylas*. Jzoo 1997;14:737–41. https://doi.org/10.2108/zsj.14.737.

[41] Yoshida A, Kato Y, Takahashi H, Kodama R. Programmed Scale Detachment in the Wing of the Pellucid Hawk Moth, *Cephonodes hylas*: Novel Scale Morphology, Scale Detachment Mechanism, and Wing Transparency. Jzoo 2021;38:427–35. https://doi.org/10.2108/zs210031.

[42] Hill J, Rastas P, Hornett EA, Neethiraj R, Clark N, Morehouse N, et al. Unprecedented reorganization of holocentric chromosomes provides insights into the

enigma of lepidopteran chromosome evolution. Science Advances 2019;5:eaau3648. https://doi.org/10.1126/sciadv.aau3648.

[43] Guerrero RF, Kirkpatrick M. Local Adaptation and the Evolution of Chromosome Fusions. Evolution 2014;68:2747–56. https://doi.org/10.1111/evo.12481.

[44] Liu Z, Roesti M, Marques D, Hiltbrunner M, Saladin V, Peichel CL. Chromosomal Fusions Facilitate Adaptation to Divergent Environments in Threespine Stickleback. Molecular Biology and Evolution 2022;39:msab358. https://doi.org/10.1093/molbev/msab358.

[45] Mackintosh A, Vila R, Laetsch DR, Hayward A, Martin SH, Lohse K. Chromosome Fissions and Fusions Act as Barriers to Gene Flow between Brenthis Fritillary Butterflies. Molecular Biology and Evolution 2023;40:msad043. https://doi.org/10.1093/molbev/msad043.

[46] Lukhtanov VA, Dincă V, Friberg M, Vila R, Wiklund C. Incomplete Sterility of Chromosomal Hybrids: Implications for Karyotype Evolution and Homoploid Hybrid Speciation. Frontiers in Genetics 2020;11.

[47] Cicconardi F, Lewis JJ, Martin SH, Reed RD, Danko CG, Montgomery SH. Chromosome Fusion Affects Genetic Diversity and Evolutionary Turnover of Functional Loci but Consistently Depends on Chromosome Size. Molecular Biology and Evolution 2021;38:4449–62. https://doi.org/10.1093/molbev/msab185.

[48] Fischer HM, Wheat CW, Heckel DG, Vogel H. Evolutionary Origins of a Novel Host Plant Detoxification Gene in Butterflies. Molecular Biology and Evolution 2008;25:809–20. https://doi.org/10.1093/molbev/msn014.

[49] Engsontia P, Sangket U, Chotigeat W, Satasook C. Molecular Evolution of the Odorant and Gustatory Receptor Genes in Lepidopteran Insects: Implications for Their Adaptation and Speciation. J Mol Evol 2014;79:21–39. https://doi.org/10.1007/s00239-014-9633-0.

[50] Chen W, Yang X, Tetreau G, Song X, Coutu C, Hegedus D, et al. A high-quality chromosome-level genome assembly of a generalist herbivore, *Trichoplusia ni*. Molecular Ecology Resources 2019;19:485–96. https://doi.org/10.1111/1755-0998.12966.

[51] Gouin A, Bretaudeau A, Nam K, Gimenez S, Aury J-M, Duvic B, et al. Two genomes of highly polyphagous lepidopteran pests (*Spodoptera frugiperda*, Noctuidae) with different host-plant ranges. Sci Rep 2017;7:11816. https://doi.org/10.1038/s41598-017-10461-4.

[52] Marçais G, Kingsford C. A fast, lock-free approach for efficient parallel counting of occurrences of k-mers. Bioinformatics 2011;27:764–70.

https://doi.org/10.1093/bioinformatics/btr011.

[53] Ranallo-Benavidez TR, Jaron KS, Schatz MC. GenomeScope 2.0 and Smudgeplot for reference-free profiling of polyploid genomes. Nat Commun 2020;11:1432. https://doi.org/10.1038/s41467-020-14998-3.

[54] Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, Phillippy AM. Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. Genome Res 2017;27:722–36. https://doi.org/10.1101/gr.215087.116.

[55] Li H. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM 2013. https://doi.org/10.48550/arXiv.1303.3997.

[56] Walker BJ, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, et al. Pilon: An Integrated Tool for Comprehensive Microbial Variant Detection and Genome Assembly Improvement. PLOS ONE 2014;9:e112963. https://doi.org/10.1371/journal.pone.0112963.

[57] Guan D, McCarthy SA, Wood J, Howe K, Wang Y, Durbin R. Identifying and removing haplotypic duplication in primary genome assemblies. Bioinformatics 2020;36:2896–8. https://doi.org/10.1093/bioinformatics/btaa025.

[58] Jin J-J, Yu W-B, Yang J-B, Song Y, dePamphilis CW, Yi T-S, et al. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biology 2020;21:241. https://doi.org/10.1186/s13059-020-02154-5.

[59] Durand NC, Shamim MS, Machol I, Rao SSP, Huntley MH, Lander ES, et al. Juicer Provides a One-Click System for Analyzing Loop-Resolution Hi-C Experiments. Cels 2016;3:95–8. https://doi.org/10.1016/j.cels.2016.07.002.

[60] Dudchenko O, Batra SS, Omer AD, Nyquist SK, Hoeger M, Durand NC, et al. De novo assembly of the *Aedes aegypti* genome using Hi-C yields chromosome-length scaffolds. Science 2017;356:92–5. https://doi.org/10.1126/science.aal3327.

[61] Durand NC, Robinson JT, Shamim MS, Machol I, Mesirov JP, Lander ES, et al. Juicebox Provides a Visualization System for Hi-C Contact Maps with Unlimited Zoom. Cell Systems 2016;3:99–101. https://doi.org/10.1016/j.cels.2015.07.012.

[62] Rhie A, Walenz BP, Koren S, Phillippy AM. Merqury: reference-free quality, completeness, and phasing assessment for genome assemblies. Genome Biology 2020;21:245. https://doi.org/10.1186/s13059-020-02134-9.

[63] Manni M, Berkeley MR, Seppey M, Simão FA, Zdobnov EM. BUSCO Update: Novel and Streamlined Workflows along with Broader and Deeper Phylogenetic Coverage for Scoring of Eukaryotic, Prokaryotic, and Viral Genomes. Molecular Biology and Evolution 2021;38:4647–54. https://doi.org/10.1093/molbev/msab199.

[64] Flynn JM, Hubley R, Goubert C, Rosen J, Clark AG, Feschotte C, et al.

RepeatModeler2 for automated genomic discovery of transposable element families. PNAS 2020;117:9451–7. https://doi.org/10.1073/pnas.1921046117.

[65] Smit A, Hubley R, Green P. RepeatMasker Open-4.0 2015.

[66] Krzywinski M, Schein J, Birol İ, Connors J, Gascoyne R, Horsman D, et al. Circos: An information aesthetic for comparative genomics. Genome Res 2009;19:1639–45. https://doi.org/10.1101/gr.092759.109.

[67] Hao Z, Lv D, Ge Y, Shi J, Weijers D, Yu G, et al. RIdeogram: drawing SVG graphics to visualize and map genome-wide data on the idiograms. PeerJ Comput Sci 2020;6:e251. https://doi.org/10.7717/peerj-cs.251.

[68] Taniguchi T, Okuno M, Shinoda T, Kobayashi F, Takahashi K, Yuasa H, et al. GINGER: an integrated method for high-accuracy prediction of gene structure in higher eukaryotes at the gene and exon level. DNA Research 2023;30:dsad017. https://doi.org/10.1093/dnares/dsad017.

[69] Gotoh O. A space-efficient and accurate method for mapping and aligning cDNA sequences onto genomic sequence. Nucleic Acids Research 2008;36:2630–8. https://doi.org/10.1093/nar/gkn105.

[70] Grabherr MG, Haas BJ, Yassour M, Levin JZ, Thompson DA, Amit I, et al. Full-length transcriptome assembly from RNA-Seq data without a reference genome. Nat Biotechnol 2011;29:644–52. https://doi.org/10.1038/nbt.1883.

[71] Schulz MH, Zerbino DR, Vingron M, Birney E. Oases: robust de novo RNA-seq assembly across the dynamic range of expression levels. Bioinformatics 2012;28:1086–92. https://doi.org/10.1093/bioinformatics/bts094.

[72] Fu L, Niu B, Zhu Z, Wu S, Li W. CD-HIT: accelerated for clustering the next-generation sequencing data. Bioinformatics 2012;28:3150–2. https://doi.org/10.1093/bioinformatics/bts565.

[73] Wu TD, Watanabe CK. GMAP: a genomic mapping and alignment program for mRNA and EST sequences. Bioinformatics 2005;21:1859–75. https://doi.org/10.1093/bioinformatics/bti310.

[74] Kim D, Paggi JM, Park C, Bennett C, Salzberg SL. Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. Nat Biotechnol 2019;37:907–15. https://doi.org/10.1038/s41587-019-0201-4.

[75] Kovaka S, Zimin AV, Pertea GM, Razaghi R, Salzberg SL, Pertea M. Transcriptome assembly from long-read RNA-seq alignments with StringTie2. Genome Biology 2019;20:278. https://doi.org/10.1186/s13059-019-1910-1.

[76] Stanke M, Waack S. Gene prediction with a hidden Markov model and a new intron submodel. Bioinformatics 2003;19:ii215–25.

https://doi.org/10.1093/bioinformatics/btg1080.

[77] Korf I. Gene finding in novel genomes. BMC Bioinformatics 2004;5:59. https://doi.org/10.1186/1471-2105-5-59.

[78] Nawrocki EP, Eddy SR. Infernal 1.1: 100-fold faster RNA homology searches. Bioinformatics 2013;29:2933–5. https://doi.org/10.1093/bioinformatics/btt509.

[79] Kalvari I, Nawrocki EP, Ontiveros-Palacios N, Argasinska J, Lamkiewicz K, Marz M, et al. Rfam 14: expanded coverage of metagenomic, viral and microRNA families. Nucleic Acids Research 2021;49:D192–200. https://doi.org/10.1093/nar/gkaa1047.

[80] Chan PP, Lin BY, Mak AJ, Lowe TM. tRNAscan-SE 2.0: improved detection and functional classification of transfer RNA genes. Nucleic Acids Research 2021;49:9077–96. https://doi.org/10.1093/nar/gkab688.

[81] Larkin A, Marygold SJ, Antonazzo G, Attrill H, dos Santos G, Garapati PV, et al. FlyBase: updates to the *Drosophila melanogaster* knowledge base. Nucleic Acids Research 2021;49:D899–907. https://doi.org/10.1093/nar/gkaa1026.

[82] The UniProt Consortium. UniProt: the universal protein knowledgebase in 2021. Nucleic Acids Research 2021;49:D480–9. https://doi.org/10.1093/nar/gkaa1100.

[83] Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K, et al. BLAST+: architecture and applications. BMC Bioinformatics 2009;10:421. https://doi.org/10.1186/1471-2105-10-421.

[84] Buchfink B, Reuter K, Drost H-G. Sensitive protein alignments at tree-of-life scale using DIAMOND. Nat Methods 2021;18:366–8. https://doi.org/10.1038/s41592-021-01101-x.

[85] Jones P, Binns D, Chang H-Y, Fraser M, Li W, McAnulla C, et al. InterProScan 5: genome-scale protein function classification. Bioinformatics 2014;30:1236–40. https://doi.org/10.1093/bioinformatics/btu031.

[86] Li H. Minimap2: pairwise alignment for nucleotide sequences. Bioinformatics 2018;34:3094–100. https://doi.org/10.1093/bioinformatics/bty191.

[87] Cosentino S, Iwasaki W. SonicParanoid: fast, accurate and easy orthology inference. Bioinformatics 2019;35:149–51. https://doi.org/10.1093/bioinformatics/bty631.

[88] Katoh K, Standley DM. MAFFT Multiple Sequence Alignment Software Version 7: Improvements in Performance and Usability. Molecular Biology and Evolution 2013;30:772–80. https://doi.org/10.1093/molbev/mst010.

[89] Capella-Gutiérrez S, Silla-Martínez JM, Gabaldón T. trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics 2009;25:1972–3. https://doi.org/10.1093/bioinformatics/btp348.

[90] Yang Z. PAML 4: Phylogenetic Analysis by Maximum Likelihood. Molecular Biology

and Evolution 2007;24:1586–91. https://doi.org/10.1093/molbev/msm088.

[91] Wang Y, Tang H, DeBarry JD, Tan X, Li J, Wang X, et al. MCScanX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. Nucleic Acids Research 2012;40:e49. https://doi.org/10.1093/nar/gkr1293.

[92] Levy Karin E, Mirdita M, Söding J. MetaEuk—sensitive, high-throughput gene discovery, and annotation for large-scale eukaryotic metagenomics. Microbiome 2020;8:48. https://doi.org/10.1186/s40168-020-00808-x.

[93] Höök L, Näsvall K, Vila R, Wiklund C, Backström N. High-density linkage maps and chromosome level genome assemblies unveil direction and frequency of extensive structural rearrangements in wood white butterflies (Leptidea spp.). Chromosome Res 2023;31:2. https://doi.org/10.1007/s10577-023-09713-z.

[94] Dobin A, Davis CA, Schlesinger F, Drenkow J, Zaleski C, Jha S, et al. STAR: ultrafast universal RNA-seq aligner. Bioinformatics 2013;29:15–21. https://doi.org/10.1093/bioinformatics/bts635.

[95] Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology 2014;15:550. https://doi.org/10.1186/s13059-014-0550-8.

[96] Alexa A, Rahnenfuhrer J. topGO: Enrichment Analysis for Gene Ontology. 2020.

[97] Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, et al. IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. Molecular Biology and Evolution 2020;37:1530–4. https://doi.org/10.1093/molbev/msaa015.

[98] Zhang J, Sun B, Zhang X. [Miocene insects and spiders from Shanwang, Shandong.] 1994.

[99] Durden CJ, Rose H. Butterflies from the middle Eocene: the earliest occurrence of fossil Papilionoidea (Lepidoptera). Texas Memorial Museum, The University of Texas at Austin; 1978.

[100] Kawahara AY, Plotkin D, Espeland M, Meusemann K, Toussaint EFA, Donath A, et al. Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. Proceedings of the National Academy of Sciences 2019;116:22657–63. https://doi.org/10.1073/pnas.1907847116.

[101] Mendes FK, Vanderpool D, Fulton B, Hahn MW. CAFE 5 models variation in evolutionary rates among gene families. Bioinformatics 2020;36:5516–8. https://doi.org/10.1093/bioinformatics/btaa1022.

[102] Gilchrist CLM, Chooi Y-H. clinker & clustermap.js: automatic generation of gene cluster comparison figures. Bioinformatics 2021;37:2473–5.

https://doi.org/10.1093/bioinformatics/btab007.

[103] Sondhi Y, Ellis EA, Bybee SM, Theobald JC, Kawahara AY. Light environment drives evolution of color vision genes in butterflies and moths. Commun Biol 2021;4:1–11. https://doi.org/10.1038/s42003-021-01688-z.

[104] Kosakovsky Pond SL, Poon AFY, Velazquez R, Weaver S, Hepler NL, Murrell B, et al. HyPhy 2.5—A Customizable Platform for Evolutionary Hypothesis Testing Using Phylogenies. Molecular Biology and Evolution 2020;37:295–9. https://doi.org/10.1093/molbev/msz197.

[105] Kosakovsky Pond SL, Wisotsky SR, Escalante A, Magalis BR, Weaver S. Contrast-FEL—A Test for Differences in Selective Pressures at Individual Sites among Clades and Sets of Branches. Molecular Biology and Evolution 2021;38:1184–98. https://doi.org/10.1093/molbev/msaa263.

[106] Kawahara AY, Plotkin D, Espeland M, Meusemann K, Toussaint EFA, Donath A, et al. Data from: Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths 2019:3374815981 bytes. https://doi.org/10.5061/DRYAD.J477B40.

[107] Ioannidou ZS, Theodoropoulou MC, Papandreou NC, Willis JH, Hamodrakas SJ. CutProtFam-Pred: Detection and classification of putative structural cuticular proteins from sequence alone, based on profile Hidden Markov Models. Insect Biochemistry and Molecular Biology 2014;52:51–9. https://doi.org/10.1016/j.ibmb.2014.06.004.

[108] Mohanty PK, Nayak B. Chromosome numbers of some Indian moths. Genetica 1983;61:147–9. https://doi.org/10.1007/BF00123225.

[109] Ahola V, Lehtonen R, Somervuo P, Salmela L, Koskinen P, Rastas P, et al. The Glanville fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. Nat Commun 2014;5:4737. https://doi.org/10.1038/ncomms5737.

[110] Kawahara AY, Mignault AA, Regier JC, Kitching IJ, Mitter C. Phylogeny and Biogeography of Hawkmoths (Lepidoptera: Sphingidae): Evidence from Five Nuclear Genes. PLOS ONE 2009;4:e5719. https://doi.org/10.1371/journal.pone.0005719.

[111] Liu J, Chen Z, Xiao Y, Asano T, Li S, Peng L, et al. Lepidopteran wing scales contain abundant cross-linked film-forming histidine-rich cuticular proteins. Commun Biol 2021;4:1–10. https://doi.org/10.1038/s42003-021-01996-4.

[112] Kimura A, Go AC, Markow T, Ranz JM. Evidence of Nonrandom Patterns of Functional Chromosome Organization in Danaus plexippus. Genome Biology and Evolution 2024;16:evae054. https://doi.org/10.1093/gbe/evae054.

[113] Davey JW, Chouteau M, Barker SL, Maroja L, Baxter SW, Simpson F, et al. Major Improvements to the Heliconius melpomene Genome Assembly Used to Confirm 10 Chromosome Fusion Events in 6 Million Years of Butterfly Evolution. G3 Genes|Genomes|Genetics 2016;6:695–708. https://doi.org/10.1534/g3.115.023655.

[114] Halldorsson BV, Palsson G, Stefansson OA, Jonsson H, Hardarson MT, Eggertsson HP, et al. Characterizing mutagenic effects of recombination through a sequence-level genetic map. Science 2019;363:eaau1043. https://doi.org/10.1126/science.aau1043.

[115] Breeschoten T, van der Linden CFH, Ros VID, Schranz ME, Simon S. Expanding the Menu: Are Polyphagy and Gene Family Expansions Linked across Lepidoptera? Genome Biology and Evolution 2022;14:evab283. https://doi.org/10.1093/gbe/evab283.

[116] Vega FE, Brown SM, Chen H, Shen E, Nair MB, Ceja-Navarro JA, et al. Draft genome of the most devastating insect pest of coffee worldwide: the coffee berry borer, *Hypothenemus hampei*. Sci Rep 2015;5:12525. https://doi.org/10.1038/srep12525.

[117] Srinivasan A, Giri A, Gupta V. Structural and functional diversities in lepidopteran serine proteases. Cellular and Molecular Biology Letters 2006;11:132–54. https://doi.org/doi:10.2478/s11658-006-0012-8.

[118] Feuda R, Marlétaz F, Bentley MA, Holland PWH. Conservation, Duplication, and Divergence of Five Opsin Genes in Insect Evolution. Genome Biology and Evolution 2016;8:579–87. https://doi.org/10.1093/gbe/evw015.

[119] Macias-Muñoz A, Rangel Olguin AG, Briscoe AD. Evolution of Phototransduction Genes in Lepidoptera. Genome Biology and Evolution 2019;11:2107–24. https://doi.org/10.1093/gbe/evz150.

[120] Chen X, Wang Z, Zhang C, Hu J, Lu Y, Zhou H, et al. Unraveling the complex evolutionary history of lepidopteran chromosomes through ancestral chromosome reconstruction and novel chromosome nomenclature. BMC Biol 2023;21:265. https://doi.org/10.1186/s12915-023-01762-4.

[121] Höök L, Vila R, Wiklund C, Backström N. Temporal dynamics of faster neo-Z evolution in butterflies. Evolution 2024:qpae082. https://doi.org/10.1093/evolut/qpae082.

[122] Auton A, Abecasis GR, Altshuler DM, Durbin RM, Abecasis GR, Bentley DR, et al. A global reference for human genetic variation. Nature 2015;526:68–74. https://doi.org/10.1038/nature15393.

[123] Hämälä T, Wafula EK, Guiltinan MJ, Ralph PE, dePamphilis CW, Tiffin P. Genomic

structural variants constrain and facilitate adaptation in natural populations of Theobroma cacao, the chocolate tree. Proceedings of the National Academy of Sciences 2021;118:e2102914118. https://doi.org/10.1073/pnas.2102914118.

[124] Mérot C, Oomen RA, Tigano A, Wellenreuther M. A Roadmap for Understanding the Evolutionary Significance of Structural Genomic Variation. Trends in Ecology & Evolution 2020;35:561–72. https://doi.org/10.1016/j.tree.2020.03.002.

[125] Kirkpatrick M, Barton N. Chromosome Inversions, Local Adaptation and Speciation. Genetics 2006;173:419–34. https://doi.org/10.1534/genetics.105.047985.

[126] Navarro A, Barton NH. ACCUMULATING POSTZYGOTIC ISOLATION GENES IN PARAPATRY: A NEW TWIST ON CHROMOSOMAL SPECIATION. Evolution 2003;57:447–59. https://doi.org/10.1111/j.0014-3820.2003.tb01537.x.

[127] Faria R, Johannesson K, Butlin RK, Westram AM. Evolving Inversions. Trends in Ecology & Evolution 2019;34:239–48. https://doi.org/10.1016/j.tree.2018.12.005.

[128] Zhang L, Reifová R, Halenková Z, Gompert Z. How Important Are Structural Variants for Speciation? Genes 2021;12:1084. https://doi.org/10.3390/genes12071084.

[129] Bhutkar A, Schaeffer SW, Russo SM, Xu M, Smith TF, Gelbart WM. Chromosomal Rearrangement Inferred From Comparisons of 12 Drosophila Genomes. Genetics 2008;179:1657–80. https://doi.org/10.1534/genetics.107.086108.

[130] López Villavicencio M, Ledamoisel J, Poloni R, Lopez-Roques C, Debat V, Llaurens V. Increased evolutionary rate in the Z-chromosome of sympatric and allopatric species of Morpho butterflies. Genome Biology and Evolution 2024:evae227. https://doi.org/10.1093/gbe/evae227.

[131] Pazhenkova EA, Lukhtanov VA. Whole-Genome Analysis Reveals the Dynamic Evolution of Holocentric Chromosomes in Satyrine Butterflies. Genes 2023;14:437. https://doi.org/10.3390/genes14020437.

[132] Cheng H, Concepcion GT, Feng X, Zhang H, Li H. Haplotype-resolved de novo assembly using phased assembly graphs with hifiasm. Nat Methods 2021;18:170–5. https://doi.org/10.1038/s41592-020-01056-5.

[133] Chin C-S, Peluso P, Sedlazeck FJ, Nattestad M, Concepcion GT, Clum A, et al. Phased diploid genome assembly with single-molecule real-time sequencing. Nat Methods 2016;13:1050–4. https://doi.org/10.1038/nmeth.4035.

[134] Nurk S, Walenz BP, Rhie A, Vollger MR, Logsdon GA, Grothe R, et al. HiCanu: accurate assembly of segmental duplications, satellites, and allelic variants from high-fidelity long reads. Genome Res 2020;30:1291–305. https://doi.org/10.1101/gr.263566.120.

[135] Ondov BD, Treangen TJ, Melsted P, Mallonee AB, Bergman NH, Koren S, et al. Mash: fast genome and metagenome distance estimation using MinHash. Genome Biology 2016;17:132. https://doi.org/10.1186/s13059-016-0997-x.

[136] Lovell JT, Sreedasyam A, Schranz ME, Wilson M, Carlson JW, Harkess A, et al. GENESPACE tracks regions of interest and gene copy number variation across multiple genomes. eLife 2022;11:e78526. https://doi.org/10.7554/eLife.78526.

[137] Huerta-Cepas J, Serra F, Bork P. ETE 3: Reconstruction, Analysis, and Visualization of Phylogenomic Data. Molecular Biology and Evolution 2016;33:1635–8. https://doi.org/10.1093/molbev/msw046.

[138] Ebert P, Audano PA, Zhu Q, Rodriguez-Martin B, Porubsky D, Bonder MJ, et al. Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science 2021;372:eabf7117. https://doi.org/10.1126/science.abf7117.

[139] Quinlan AR, Hall IM. BEDTools: a flexible suite of utilities for comparing genomic features. Bioinformatics 2010;26:841–2. https://doi.org/10.1093/bioinformatics/btq033.

[140] Cingolani P, Platts A, Wang LL, Coon M, Nguyen T, Wang L, et al. A program for annotating and predicting the effects of single nucleotide polymorphisms, SnpEff: SNPs in the genome of Drosophila melanogaster strain w1118; iso-2; iso-3. Fly 2012;6:80–92. https://doi.org/10.4161/fly.19695.

[141] Schield DR, Scordato ESC, Smith CCR, Carter JK, Cherkaoui SI, Gombobaatar S, et al. Sex-linked genetic diversity and differentiation in a globally distributed avian species complex. Molecular Ecology 2021;30:2313–32. https://doi.org/10.1111/mec.15885.

[142] Catanach A, Crowhurst R, Deng C, David C, Bernatchez L, Wellenreuther M. The genomic pool of standing structural variation outnumbers single nucleotide polymorphism by threefold in the marine teleost Chrysophrys auratus. Molecular Ecology 2019;28:1210–23. https://doi.org/10.1111/mec.15051.

[143] Leffler EM, Bullaughey K, Matute DR, Meyer WK, Ségurel L, Venkat A, et al. Revisiting an Old Riddle: What Determines Genetic Diversity Levels within Species? PLOS Biology 2012;10:e1001388. https://doi.org/10.1371/journal.pbio.1001388.

[144] Lupski JR. Structural variation mutagenesis of the human genome: Impact on disease and evolution. Environmental and Molecular Mutagenesis 2015;56:419–36. https://doi.org/10.1002/em.21943.

[145] Tolman ER, Beatty CD, Bush J, Kohli MK, Frandsen PB, Gosnell JS, et al. Exploring chromosome evolution in 250 million year old groups of dragonflies and damselflies (Insecta:Odonata). Molecular Ecology 2023;32:5785–97.

https://doi.org/10.1111/mec.17147.

[146] Yoshida Y, Shaikhutdinov N, Kozlova O, Itoh M, Tagami M, Murata M, et al. High quality genome assembly of the anhydrobiotic midge provides insights on a single chromosome-based emergence of extreme desiccation tolerance. NAR Genomics and Bioinformatics 2022;4:lqac029. https://doi.org/10.1093/nargab/lqac029.

[147] Microchromosomes are building blocks of bird, reptile, and mammal chromosomes | PNAS n.d. https://www.pnas.org/doi/full/10.1073/pnas.2112494118 (accessed January 13, 2025).

[148] Megens H-J, Crooijmans RP, Bastiaansen JW, Kerstens HH, Coster A, Jalving R, et al. Comparison of linkage disequilibrium and haplotype diversity on macro- and microchromosomes in chicken. BMC Genetics 2009;10:86. https://doi.org/10.1186/1471-2156-10-86.

[149] Axelsson E, Webster MT, Smith NGC, Burt DW, Ellegren H. Comparison of the chicken and turkey genomes reveals a higher rate of nucleotide divergence on microchromosomes than macrochromosomes. Genome Res 2005;15:120–5. https://doi.org/10.1101/gr.3021305.

[150] Divergent sensory and immune gene evolution in sea turtles with contrasting demographic and life histories | PNAS n.d. https://www.pnas.org/doi/10.1073/pnas.2201076120 (accessed January 13, 2025).

論文要旨

鱗翅目は、約16万種が知られるチョウやガの仲間の昆虫であり、その高い多様性から進化学および生態学研究のモデルとして注目されている。近年、DNA配列解析技術の進展に伴い、鱗翅目のゲノム解析が盛んに行われ、多くの種でゲノム情報が解読されている。鱗翅目の特徴の一つに、ホロセントリック染色体を持つことが挙げられ、この特徴により染色体の融合や分裂が比較的頻繁に起こることが報告されている。融合や分裂に起因する染色体長の変化は、組換え頻度や遺伝的連鎖の性質を変化させ、ゲノム進化に影響を及ぼす可能性がある。しかし、染色体長の変化が遺伝子の機能や進化速度に与える影響については、十分に検証されていない。また、長さだけではなく染色体の種類によって進化のパターンが異なる可能性もある。例えば、鱗翅目の性染色体であるZ染色体では、Z染色体上の遺伝子が常染色体上の遺伝子よりも速く進化する「Faster-Z仮説」が提唱されている。しかし、鱗翅目ではFaster-Z仮説と対立するSlower-Z仮説の両方が報告されており、統一的な結論には至っていない。さらに、これまでの研究は主に遺伝子領域の塩基置換に焦点を当てており、非コード領域やゲノム構造変化の影響については十分に検討されていない。以上の課題を解決するため、本研究では「染色体長がゲノム進化に与える影響の解明」および「Faster-Z仮説の包括的検証」を目的として一連の解析を行った。

はじめに、スズメガ科のオオスカシバ (*Cephonodes hylas*) の全ゲノム配列を決定した。本種はモデル生物であるタバコスズメガやカイコと近縁でありながら異なる核型を持ち、鱗翅目の染色体進化研究に適した材料である。解析の結果、29本の染色体に対応する高い連続性を持つアセンブルを得て、遺伝子の網羅性を示すBUSCO解析でも高い完成度が確認された。さらに、近縁種との比較ゲノム解析を行ったところ、短い染色体ほど種間での配列分化が速く、種内多様性が高いことに加え、リピート配列の割合が増加することが明らかになった。この結果は、短い染色体では変異頻度が高く、ゲノム配列の適応進化が促進される可能性を示唆している。次に、構築したゲノム配列を用いて、近縁種であるタバコスズメガとの比較ゲノム解析を実施した。オオスカシバが29本の染色体を持つのに対し、タバコスズメガは28本の染色体を持つ。この違いは染色体融合に起因し、タバコスズメガの28番染色体がオオスカシバの3番および27番染色体に対応することが明らかになった。また、染色体融合による染色体長の増加に伴い、リピート配列の蓄積や進化速度の変化も確認され、「染色体長」が進化特性を規定する主要因の一つであることが示された。

次に、鱗翅目46種の公開ゲノムデータを用いて、Z染色体と常染色体の種間比較を実施し、多様な系統におけるZ染色体の進化的特性を、全ゲノムレベルで明らかにすることを試みた。加えて、構造変異 (SV) も考慮に入れて解析を行った。全ゲノム配列の比較により、Z染色体は常染色体に比べて急速な配列分化を示し、鱗翅目全般でFaster-Z仮説を支持する結果が得られた。さらに、シンテニー解析によりゲノム構造を比較したところ、Z染色体上では染色体再編成の頻度も高いことが明らかになった。この急速な配列分化の基盤となる

メカニズムを解明するため、リファレンスゲノムの相同染色体配列である Alternate haplotype 配列を活用する新たな解析手法を導入し、二倍体ハプロタイプ間の構造変異および一塩基変異 (SNV) の検出を行った。その結果、Z 染色体全体で低い遺伝的多様性が観察された。これは Z 染色体の有効集団サイズが小さいため、遺伝的浮動の影響が顕著であり、進化速度の加速に寄与していると考えられる。また、SV と SNV の割合を比較したところ、Z 染色体では SV に起因する変異の割合が SNV の 19.4 倍と、全染色体中で最も高い値を示した。この結果から、遺伝的浮動による SV の蓄積が Faster-Z の大きな要因である可能性が示された。

本研究を通じて、短い染色体が種間・種内で高い多様性を維持し、新規遺伝子の獲得や適応進化に貢献している可能性が示唆された。また、染色体融合がゲノム進化特性に与える影響が明らかになった。さらに、Z 染色体に関しては、配列分化の加速化、染色体再編成の頻発といった常染色体とは異なる特異的な進化動態が確認され、特に逆位による Faster-Z の促進が示唆された。加えて、有効集団サイズの小ささが遺伝的浮動を引き起こし、それが進化速度の違いに寄与しているという新たな進化メカニズムを提示した。