
「進化の制約と方向性
～微生物から多細胞生物までを貫く表現型進化原理の解明～」

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総計	1, 608, 620, 000 円	1, 237, 400, 000 円	371, 220, 000 円

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計画・倉谷滋

1. Hirasawa, T., Hu, Y., Giles, S., Uesugi, K., Hoshino, M., Manabe, M., and Kuratani, S. (2022). Morphology of Palaeospondylus and its affinity to tetrapod ancestors *Nature* 606, 109-112.
2. Takagi, W., Sugahara, F., Higuchi, S., Kusakabe, R., Pascual-Anaya, J., Sato, I., Oisi, Y., Ogawa, N., Miyanishi, H., Adachi, N., Hyodo, S., and Kuratani, S. (2022). Evolution of thyroid gland and atavistic origin of the lamprey endostyle. *BMC Biol.* 20, 76.
3. Hirasawa, T., Cupello, C., Brito, PM., Yabumoto, Y., Isogai, S., Hoshino, M., Uesugi, K. (2021) Development of the pectoral lobed fin in the Australian lungfish *Neoceratodus forsteri* *Front.Ecol.Evol.* 9, 679633
4. Kusakabe, R., Tanaka, M., and Kuratani, S. (2021). New approaches in chordate and vertebrate evolution and development. *Front. Cell Dev. Biol.* 9, 760366.
5. Sugahara, F., Murakami, Y., Pascual-Anaya, J., and Kuratani, S. (2021). "Genetic Mechanism for the Cyclostome Cerebellar Neurons Reveals Early Evolution of the Vertebrate Cerebellum". *Brain, Behav. Evol.*, 96, 305-317.
6. Higashiyama, H., Koyabu, D., Werneburg, I., Hirasawa, T., Kuratani, S., and Kurihara, H. (2021). Mammalian face as an evolutionary novelty. *Proc. Nat. Acad. Sci. U.S.A.* 118, 44 e2111876118.
7. Sarper, S. E., Hirai, T., Matsuyama, T., Kuratani, S., and Fujimoto, K. (2021). Polymorphism in the symmetries of gastric pouch arrangements in the sea anemone *Diadumene lineata*. *Zool. Lett.* 7, 12
8. Sugahara, F., Pascual-Anaya, J., Kuraku, S., Kuratani, S., & Murakami, Y. (2021b). Genetic mechanism for the cyclostome cerebellar neurons reveals early evolution of the vertebrate cerebellum. In: Special issue; "New approaches in chordate and vertebrate evolution and development". *Front. Cell Dev. Biol.* 9: 1-10.
9. Bakker, M. A. G. de, van der Vos, W., de Jager, K., Yu Chung, W., Willemse, J., Dondorp, E., Spiekman, S. N. F., Yih Chew, K., Jiménez, R., Bickelmann, C., Hirasawa, T., and Kuratani, S., Renfree, M. B., and Richardson, M. K. (2021). Evolutionary tinkering with phalanx development in the bird wing. *Mol. Biol. Evol.* 38, 4222-4237.
10. Fujimoto, S., Yamanaka, K., Tanegashima, C., Nishimura, O., Kuraku, S., Kuratani, S., and Irie, N. (2021). Measuring potential effects of developmental burden associated with the vertebrate notochord. *J. Exp. Zool. Part B Mol. Dev. Evol.* 338, 129-136.
11. Nojiri, T., Wilson, L. A. B., López-Aguirre, C., Tu, V. T., Kuratani, S., Ito, K., Higashiyama, H., Son, N. T., Fukui, D., Sadier, A., Sears, K. E., Endo, H., Kamihori, S., and Koyabu, D. (2021). Embryonic evidence uncovers convergent origins of laryngeal echolocation in bats. *Curr. Biol.* 31, 1-13.
12. Kuroda, S., Adachi, N., Kusakabe, R., and Kuratani, S. (2021). Developmental fates of shark head cavities reveal mesodermal contributions to the tendon progenitor cells for extraocular muscles. *Zool. Lett.* 7, 3
13. Uesaka, M., Kuratani, S., and Irie, N. (2021). The developmental hourglass model and recapitulation: An attempt to integrate the two models. *J. Exp. Zool. B Mol. Dev. Evol.* 338, 9-12.
14. Kuratani, S., Uesaka, M., and Irie, N. (2021). How can recapitulation be reconciled with modern concepts of evolution? *J. Exp. Zool. B Mol. Dev. Evol.* 338, 28-35.
15. Kuratani, S.* (2021). Evo-Devo studies of cyclostomes and origin and evolution of jawed vertebrates. *Curr. Top Dev Biol.* 141, 207-239.
16. Kusakabe, R., Higuchi, S., Tanaka, M., Kadota, M., Nishimura, O., and Kuratani, S. (2020). Novel developmental bases for the evolution of hypobranchial muscles in vertebrates. *BMC Biol.* 18, 120.
17. Uesaka, M., Kuratani, S., Takeda, H., and Irie, N. (2019). Recapitulation-like developmental transitions of chromatin accessibility in vertebrates. *Zool. Lett.* 5, 33.
18. Hirasawa, T., Cantas, A., and Kuratani, S. (2019). Twins at conspicuously different developmental stages in a turtle egg. *Zool. Sci.* 36, 1-4.
19. Higuchi, S., Sugahara, F., Oisi, Y., Pascual Anaya, J., Takagi, W., and Kuratani, S. (2019). Inner ear development in cyclostome and the evolution of vertebrate semicircular canals. *Nature* 565, 347-350

計画・金子邦彦

1. Matsushita, Y., Hatakeyama, T.S., and Kaneko, K. (2022) Dynamical-systems theory of cellular reprogramming. *Phys. Rev. Res.* 4, L022008.
Itao, K., and Kaneko, K. (2022) Emergence of Kinship Structures and Descent Systems: Multi-level Evolutionary Simulation and Empirical Data Analyses. *Proc. Biol. Sci.* 289, 20212641.
2. Takeuchi, N., Mitarai, N., and Kaneko, K. (2022) A scaling law of multilevel evolution: how the balance between within- and among-collective evolution is determined. *Genetics* 220, iyab182
3. Sudo M, and Fujimoto K (2022) Traveling wave of inflammatory response to regulate the expansion or shrinkage of skin erythema. *PLoS One* 10, e0263049.
4. 郷達明, 藤原基洋, 津川暁, 藤本仰一. (2022) 器官の形に種を超えた共通性をもたらす物理. 生物物理62, 7
5. Nishiura, N., Kaneko, K. (2021) Evolution of phenotypic fluctuation under host-parasite interactions. *PLoS*

- Comput. Biol.* 17.11: e1008694.
6. Fujimoto, Y., and Kaneko, K. (2021) Exploitation by asymmetry of information reference in coevolutionary learning in prisoner's dilemma game. *Journal of Physics: Complexity* 2.4: 045007.
 7. Itao, K., and Kaneko, K. (2021) Evolution of family systems and resultant socio-economic structures. *Humanit. Soc. Sci. Commun.* 8.1, 1-11.
 8. Tang, Q-Y., and Kaneko, K. (2021) Dynamics-evolution correspondence in protein structures. *Phys. Rev. Lett.* 127, 098103.
 9. Inoue, M., and Kaneko, K. (2021) Entangled gene regulatory networks with cooperative expression endow robust adaptive responses to unforeseen environmental changes. *Phys. Rev. Research* 3, 033183.
 10. Yamagishi, J. F., Saito, N., and Kaneko, K. (2021) Adaptation of metabolite leakiness leads to symbiotic chemical exchange and to a resilient microbial ecosystem. *PLoS Comput. Biol.* 17: e1009143.
 11. Okubo, K., and Kaneko, K. (2021) Evolution of dominance in gene expression pattern associated with phenotypic robustness. *BMC Ecol Evol.* 21, 110.
 12. Furusawa, C., and Kaneko, K. (2021) Direction and Constraint in Phenotypic Evolution: Dimension Reduction and Global Proportionality in Phenotype Fluctuation and Responses. *Evolutionary Systems Biology* (ed. A. Crombach), 35-58.
 13. Kohsokabe, T., and Kaneko, K. (2021) Dynamical Systems Approach to Evolution-Development Congruence: Revisiting Haeckel's Recapitulation Theory. *J. Exp. Zool B Mol. Dev. Evol.* 338, 62-75.
 14. Sarper SE, Hirai T, Matsuyama Hoyos T, Kuratani S, and Fujimoto K (2021) Polymorphism in the symmetries of gastric pouch arrangements in the sea anemone *Diadumene lineata*. *Zool. Lett.* 7, 12.
 15. Kamamoto, N., Tano, T., Fujimoto, K., and Shimamura, M. (2021) Rotation angle of stem cell division plane controls spiral phyllotaxis in mosses. *J. Plant Res.* 134, 457-473.
 16. Fujiwara, M., Goh, T., Tsugawa, S., Nakajima, K., Fukaki, H., and Fujimoto, K. (2021) Tissue growth constrains root organ outlines into an isometrically scalable shape. *Development* 148: dev196253.
 17. Matsushita, K., Yabunaka, S., and Fujimoto K. (2021) Polarity Fluctuation inhibition by memory in collective cell motion. *J. Physical Soc. Jpn* 90, 054801.
 18. Tang, Q-Y., Hatakeyama, T., and Kaneko, K. (2020) Functional Sensitivity and Mutational Robustness of Proteins. *Phys. Rev. Res.* 2, 033452.
 19. Sakata, A., and Kaneko, K. (2020) Dimensional reduction in evolving spin-glass model: correlation of phenotypic responses to environmental and mutational changes. *Phys. Rev. Lett.* 124, 218101.
 20. Matsushita, Y., and Kaneko, K. (2020) Homeorhesis in Waddington's Landscape by Epigenetic Feedback Regulation. *Phys. Rev. Res.* 2, 023083.
 21. Itao, K., and Kaneko, K. (2020) Reply to Read and Parkin: Our model correctly expresses the ethnographic nature of the cultural incest taboo and kinship structures. *Proc. Natl. Acad. Sci. U. S. A.* 117, 9167-9168.
 22. Tang, Q-Y., and Kaneko, K. (2020) Long-range Correlation in Protein Dynamics: Confirmation by Structural Data and Normal Mode Analysis. *PLoS Comp. Biol.*, 16, e1007670.
 23. Sato, T. U., and Kaneko, K. (2020) Evolutionary dimension reduction in phenotypic space. *Phys. Rev. Res.* 2, 013197
 24. Itao, K., and Kaneko, K. (2020) Evolution of Kinship Structures Driven by Marriage Tie and Competition. *Proc. Natl. Acad. Sci. U. S. A.*, 117, 2378-2384
 25. Yamagishi, J.F. Saito, N., and Kaneko, K. (2020) Advantage of Leakage of Essential Metabolites for Cells. *Phys. Rev. Lett.* 124, 048101.
 26. Himeoka, Y., and Kaneko, K. (2020) Epigenetic Ratchet: Spontaneous Adaptation via Stochastic Gene Expression. *Sci. Rep.*, 10, 459.
 27. Hatakeyama, T.S., and Kaneko, K. (2020) Transition in relaxation paths in allosteric molecules: Enzymatic kinetically constrained model. *Phys. Rev. Res.* 2, 012005(R).
 28. Okuda, S., and Fujimoto, K. (2020) A mechanical instability in planar epithelial monolayers leads to cell extrusion. *Biophys. J.* 10, 2549-2560.
 29. 坪井有寿, 奥田覚, 藤本仰一 (2020) 細胞競合の力学的理諭. 医学のあゆみ 274(5): 537-543.
 30. Takeuchi, N., and Kaneko, K. (2019) The origin of the central dogma through conflicting multilevel selection. *Proc. R. Soc. B*, 286, 20191359.
 31. Fujimoto, Y., and Kaneko, K. (2019) Emergence of Exploitation as Symmetry Breaking in Iterated Prisoner's Dilemma. *Phys. Rev. Res.* 1, 033077.
 32. Nakamura, E., and Kaneko, K. (2019) Statistical Evolutionary Laws in Music Styles. *Sci. Rep.* 9, 15993.
 33. Fujimoto, Y., and Kaneko, K. (2019) Functional Dynamics by Intention Recognition in Iterated Games. *New J. Phys.* 21, 023025.
 34. 金子邦彦, 古澤力 (2019). 適応と進化におけるマクロ現象論 ——表現型変化の低次元拘束と揺らぎ—応答関係. *日本物理学会誌* 74(3), 137 (金子班、古澤班)
 35. Toyokura, K., Goh, T., Shinohara, H., Shinoda, A., Kondo, Y., Okamoto, Y., Uehara, T., Fujimoto, K., Okushima, Y., Ikeyama, Y., Nakajima, K., Mimura, T., Tasaka, M., Matsubayashi, Y. and Fukaki, H. (2019-1). Lateral inhibition by a peptide hormone-receptor cascade during *Arabidopsis* lateral root founder cell formation. *Dev. Cell* 48, 64-75.e5
 36. Inoue, M. and Kaneko, K. (2018-12). Cooperative reliable response from sloppy gene-expression dynamics.

- EPL** 124, 38002.
37. Tsuboi, A., Ohsawa, S., Umetsu, D., Sando, Y., Kuranaga, E., Igaki, T. and Fujimoto, K. (2018-7). Competition for space is controlled by apoptosis-induced change of local epithelial topology. *Curr.Biol.* 28, 2115-2128.
 38. Hemmi, N., Akiyama-Oda, Y., Fujimoto, K. and Oda, H. (2018-5). A quantitative study of the diversity of stripe-forming processes in an arthropod cell-based field undergoing axis formation and growth. *Dev. Biol.*, 437, 84-104
 39. Kaneko, K. and Furusawa, C. Macroscopic Theory for Evolving Biological Systems Akin to Thermodynamics. (2018-5) *Ann. Rev. Biophys* 47, 273-290.
 40. Kohsokabe, T. and Kaneko, K. (2018-4). Boundary-Induced Pattern Formation from Uniform Temporal Oscillation. *Chaos* 28, 45110
 41. Furusawa, C. and Kaneko, K. (2018-4). Formation of Dominant Mode by Evolution in Biological Systems. *Phys. Rev. E* 97, 42410 (金子班、古澤班)
 42. Nakamura, K., Hisanaga, T., Fujimoto, K., Nakajima, K. and Wada, H. (2018-3). Plant-inspired pipettes. *J. R. Soc. Interface* 15, 20170868.
 43. Kitazawa, M. S., and Fujimoto, K. (2018-3). Spiral phyllotaxis underlies constrained variation in Anemone (Ranunculaceae) tepal arrangement. *J. Plant Res.* 131, 459-468.
 44. Takeuchi, N., Hogeweg, P. and Kaneko, K. (2017-11). Conceptualizing the Origin of Life in terms of Evolution. *Phil. Trans. R. Soc. A* 375, 20160346
 45. Mashiko D, Ikawa M and Fujimoto K. (2017-10) Mouse spermatozoa with higher fertilization rates have thinner nuclei. *Peer J.* 5, e3913.
 46. Tsuboi T, #Umetsu D, Kuranaga E and Fujimoto K. (#Co-first) (2017-8) Inference of cell mechanics in heterogeneous epithelial tissue based on multivariate clone shape quantification. *Front. Cell Dev. Biol.* 5, 68.
 47. *Takeuchi, N., Hogeweg, P. and Kaneko, K. (2017-8). The origin of a primordial genome through spontaneous symmetry breaking. *Nat. Commun.* 8, 250.
 48. Ueda, M., Takeuchi, N., and Kaneko, K. (2017-8). Stronger selection can slow down evolution driven by recombination on a smooth fitness landscape. *PLoS ONE* 12, e0183120
 49. Fujimoto, Y., Sagawa, T. and Kaneko, K. (2017-7) Hierarchical prisoner's dilemma in hierarchical game for resource competition. *New J. Phys.* 19, 73008.
 50. Himeoka, Y. and Kaneko, K. (2017-6). Theory for transitions between log and stationary phases: universal laws for lag time. *Phys. Rev. X* 7, 21049.

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1. Uchida, Y., Shigenobu S., Takeda, H., Furusawa, C., and Irie, N. (2022). Potential contribution of intrinsic developmental stability toward body plan conservation. *BMC Biology* 20, 82
2. Leong, JCK*, Uesaka, M., and Irie, N. (2022). Distinguishing Evolutionary Conservation from Derivedness. *Life* 12(3), 440.
3. Fujimoto, K., Nakajima, A., Hori, S., and Irie, N. (2021). Whole embryonic detection of maternal microchimeric cells highlights significant differences in their numbers among individuals. *PLoS ONE* 16, e0261357.
4. Leong, JCK., Li, Y., Uesaka, M., Uchida, U., Omori, A., Hao, M., Wan, W., Dong, Y., RenSi Zhang, Y., Zeng, T., Wang6,F., Chen, L., Wessel, G., Livingston, BT., Bradham, C., Wang, W., and Irie, N. (2021). Derivedness Index for Estimating Degree of Phenotypic Evolution of Embryos: A Study of Comparative Transcriptomic Analyses of Chordates and Echinoderms. *Front. Cell Dev. Biol.* 9:749963.
5. Fujimoto, S., Yamanaka, K., Tanegashima, C., Nishimura, O., Kuraku, S., Kuratani, S., and Irie, N. (2021). Measuring potential effects of the developmental burden associated with the vertebrate notochord. *J. Exp. Zool B Mol. Dev. Evol.*, 338, 129-136.
- Uesaka, M., Kuratani, S., and Irie, N. (2021). The developmental hourglass model and recapitulation: An attempt to integrate the two models. *J. Exp. Zool B Mol. Dev. Evol.*, 338, 76-86.
- Kuratani, S., Uesaka, M., and Irie, N. (2022). How can recapitulation be reconciled with modern concepts of evolution? *J. Exp. Zool B Mol. Dev. Evol.*, 338, 28-35.
- Li, Y., Omori, A., Flores, R., Satterfield, S., Nguyen, C., Ota, T., Tsurugaya, T., Ikuta, T., Ikeo, K., Kikuchi, M., Leong, J., Reich, A., Hao, M., Wan, W., Dong, Y., Ren, Y., Zhang, S., Zeng, T., Uesaka, M., Uchida, Y., Li, X., Shibata, T., Bino, T., Ogawa, K., Shigenobu, S., Kondo, M., Wang, F., Chen, L., Wessel, G., Saiga, H., Cameron, R., Livingston, B., Bradham, C., Wang, W., and Irie, N. (2020). Genomic insights of body plan transitions from bilateral to pentameric symmetry in Echinoderms. *Commun. Biol.* 3,371.
- Hogan, J.D., Keenan, J.L., Luo, L., Hawkins, D.Y., Ibn-Salem, J., Lamba, A., Schatzberg, D., Piacentino, M.L., Zuch, D.T., Core, A.B., Blumberg, C., Timmermann, B., Grau, J.H., Speranza, E., Andrade-Narraway, M.A., Irie, N., Poustka, A.J., and Bradham, C.A. (2020). The developmental transcriptome for Lytechinus variegatus exhibits temporally punctuated gene expression changes. *Dev.Biol.* 460, 139-154.
- Uesaka, M., Kuratani, S., Takeda, H., and Irie, N. (2019). Recapitulation-like developmental transitions of chromatin accessibility in vertebrates. *Zool.Lett.* 5, 33.
- Uchida, U., Uesaka, M., Yamamoto, T., Takeda, H. and Irie, N. (2018). Embryonic lethality is not sufficient to explain hourglass-like conservation of vertebrate embryos. *EvoDevo* 9, 7.

10. Ichikawa, K., Tomioka, S., Suzuki, Y., Nakamura, R., Doi, K., Yoshimura, J., Kumagai, M., Inoue, Y., Uchida, Y., Irie, N., Takeda, H. and Morishita, S. (2017). Centromere evolution and CpG methylation during vertebrate speciation. *Nat. Commun.* 8, 1833.
11. Li, Y., Kikuchi, M., Li, X., Gao, Q., Xiong, Z., Ren, Y., Zhao, R., Mao, B., Kondo, M., Irie, N., and Wang, W. (2017). Weighted gene co-expression network analysis reveals potential genes involved in early metamorphosis process in sea cucumber *Apostichopus japonicus*. *Biochem. Biophys. Res. Commun.* 495, 1395-1402.
12. Hu, H., Uesaka, M., Guo, S., Shimai, K., Lu, TM., Li, F., Fujimoto, S., Ishikawa, M., Liu, S., Sasagawa, Y., Zhang, G., Kuratani, S., Yu, JK., Kusakabe, T.G., Khaitovich, P., Irie, N. (2017). Constrained vertebrate evolution by pleiotropic genes. *Nat. Ecol. Evol.* 1, 1722–1730.

計画・深津武馬

1. Harumoto, T., and Fukatsu, T. (2022). Perplexing dynamics of *Wolbachia* proteins for cytoplasmic incompatibility. *PLOS Biol.*, 20, e3001644.
2. Moriyama, M., Hayashi, T., and Fukatsu, T. (2022) A mucin protein predominantly expressed in the female-specific symbiotic organ of the stinkbug *Plautia stali*. *Sci. Rep.* 12, 7782.
3. Fukumori, K., Oguchi, K., Ikeda, H., Shinohara, T., Tanahashi, M., Moriyama, M., Koga, R., and Fukatsu, T. (2022) Evolutionary dynamics of host organs for microbial symbiosis in tortoise leaf beetles (Coleoptera: Chrysomelidae: Cassidinae). *mBio* 13, e03691-21.
4. Shibao, H., Kutsukake, M., Matsuyama, S., and Fukatsu, T. (2022) Linoleic acid as corpse recognition signal in a social aphid. *Zool. Lett.* 8, 2.
5. Nishino, T., Hosokawa, T., Meng, X.Y., Koga, R., Moriyama, M., and Fukatsu, T. (2021) Environmental acquisition of gut symbiotic bacteria in the saw-toothed stinkbug *Megymenum gracilicorne* (Hemiptera: Pentatomidae: Dinidoridae). *Zoological Science* 38, 213-222.
6. Reis, F., Kirsch, R., Pauchet, Y., Bauer, E., Bilz, L. C., Fukumori, K., Fukatsu, T., Kolsch, G., and Kaltenpoth, M. (2020) Bacterial symbionts support larval sap feeding and adult folivory in (semi-)aquatic reed beetles. *Nat. Commun.* 11, 2964.
7. Mondal, S.I., Akter, A., Koga, R., Hosokawa, T., Dayi, M., Murase, K., Tanaka, R., Shigenobu, S., Fukatsu, T., and Kikuchi, T. (2020) Reduced genome of the gut symbiotic bacterium “*Candidatus Benitsuchiphilus tojoi*” provides insight into its possible roles in ecology and adaptation of the host insect. *Front. Microbiol.* 11, 840.
8. Hirota, B., Meng, X.Y., and Fukatsu, T. (2020) Bacteriome-associated endosymbiotic bacteria of *Nosodendron* tree sap beetles. *Front. Microbiol.* 11, 588841.
9. Nikoh N., Tsuchida T., Koga R., Oshima K., Hattori M., Fukatsu T. (2020) Genome analysis of "Candidatus Regiella insecticola" strain TUt, facultative bacterial symbiont of the pea aphid *Acyrtosiphon pisum*. *Microbiol. Resour. Announc.* 9, e00598-20.
10. Noda, T., Okude, G., Meng, X.Y., Koga, R., Moriyama, M., and Fukatsu, T. (2020) Bacteriocytes and *Blattabacterium* endosymbionts of the German cockroach *Blattella germanica*, the forest cockroach *B. nipponica*, and other cockroach species. *Zool. Sci.* 37, 399-410.
11. Kubota, K., Watanabe, K., Zhu, X.J., Kawakami, K., Tanahashi, M., and Fukatsu, T. (2020) Evolutionary relationship between *Platycerus* stag beetles and their mycangium-associated yeast symbionts. *Front. Microbiol.* 11, 1436.
12. Egan, S., Fukatsu, T., and Francino, M.P. (2020) Opportunities and challenges to microbial symbiosis research in the microbiome era. *Front. Microbiol.* 11, 1150.
13. Hosokawa, T., and Fukatsu, T. (2020) Relevance of microbial symbiosis to insect behavior. *Curr. Opin. Insect Sci.* 39, 91-100.
14. Nishide, Y., Kageyama, D., Hatakeyama, M., Yokoi, K., Jouraku, A., Tanaka, H., Koga R., Futahashi, R., and Fukatsu, T. (2020) Diversity and function of multicopper oxidase genes in the stinkbug *Plautia stali*. *Sci. Rep.* 10, 3464.
15. Fukatsu, T. (2019) Grand challenges to launching an ideal platform for publishing microbe-insect symbiosis studies. *Front. Microbiol.* 10, 2542.
16. Kuechler, S.M., Fukatsu, T., and Matsuura, Y. (2019) Repeated evolution of bacteriocytes in lygaeoid stinkbugs. *Environ. Microbiol.* 21, 4378-4394.
17. Hosokawa, T., Imanishi, M., Koga, R., and Fukatsu, T. (2019) Diversity and evolution of bacterial symbionts in the gut symbiotic organ of jewel stinkbugs (Hemiptera: Scutelleridae). *Appl. Entomol. Zool.* 54, 359-367.
18. Kutsukake, M., Uematsu, K., and Fukatsu, T. (2019) Plant manipulation by gall-forming social aphids for waste management. *Front. Plant Sci.* 10, 933.
19. Oishi, S., Moriyama, M., Koga, R., and Fukatsu, T. (2019) Morphogenesis and development of midgut symbiotic organ of the stinkbug *Plautia stali* (Hemiptera: Pentatomidae). *Zool. Lett.* 5, 16.
20. Ohbayashi, T., Futahashi, R., Terashima, M., Barriere, Q., Lamouche, F., Takeshita, K., Meng, X.Y., Mitani, Y., Sone, T., Shigenobu, S., Fukatsu, T., Mergaert, P., and Kikuchi, Y. (2019) Comparative cytology, physiology and transcriptomics of *Burkholderia insecticola* in symbiosis with the bean bug *Riptortus pedestris* and in culture. *ISME J.* 13, 1469-1483.
21. Nikoh, N., Koga, R., Oshima, K., Hattori, M., and Fukatsu, T. (2019) Genome sequence of “*Candidatus Serratia symbiotica*” strain IS, a facultative bacterial symbiont of the pea aphid *Acyrtosiphon pisum*. *Microbiol. Resour.*

- Announc.* 8, e00272-19.
22. Nishide, Y., Kageyama, D., Yokoi, K., Tanaka, H., Futahashi, R., and Fukatsu T. (2019) Functional crosstalk across IMD and Toll pathways: insight into the evolution of incomplete immune cascades. *Proc. Biol. Sci* 286, 20182207.
 23. Matsuura, Y., Moriyama, M., Lukasik, P., Vanderpool, D., Tanahashi, M., Meng, X.Y., McCutcheon, J.P., and Fukatsu, T.* (2018) Recurrent symbiont recruitment from fungal parasites in cicadas. *Proc. Natl. Acad. Sci. U. S. A.* 115, E5970-E5979.
 24. Nikoh, N., Tsuchida, T., Maeda, T., Yamaguchi, K., Shigenobu, S., Koga, R., and Fukatsu T. (2018) Genomic insight into symbiosis-induced insect color change by a facultative endosymbiont “*Candidatus Rickettsiella viridis*”. *mBio* 9, e00890-18.
 25. Tanahashi, M., and Fukatsu, T. (2018) *Natsumushi*: Image measuring software for entomological studies. *Entomol. Sci.* 21, 347-360.
 26. Nishide, Y., Onodera-Tanifuji, N., Tanahashi, M., Moriyama, M., Fukatsu, T. and Koga, R. (2017) Aseptic rearing procedure for the stinkbug *Plautia stali* (Hemiptera: Pentatomidae) by sterilizing food-derived bacterial contaminants. *Appl. Entomol. Zool.* 53, 407-415.
 27. Anbutsu, H., Moriyama, M., Nikoh, N., Hosokawa, T., Futahashi, R., Tanahashi, M., Meng, X.Y., Kuriwada, T., Mori, N., Oshima, K., Hattori, M., Fujie, M., Satoh, N., Maeda, T., Shigenobu, S., Koga, R., and Fukatsu, T. (2017) Small genome symbiont underlies cuticle hardness in beetles. *Proc. Natl. Acad. Sci. U. S. A.* 114, E8382-E8391.
 28. alem, H., Bauer, E., Kirsch, R., Berasategui, A., Cripps, M., Weiss, B., Koga, R., Fukumori, K., Vogel, H., Fukatsu, T., Kaltenpoth, M. (2017) Drastic genome reduction in an herbivore's pectinolytic symbiont. *Cell* 171, 1520-1531.
 29. Fukumori, K., Koga, R., Nikoh, N., and Fukatsu, T. (2017) Symbiotic bacteria associated with gut symbiotic organ and female genital accessory organ of the leaf beetle *Bromius obscurus* (Coleoptera: Chrysomelidae). *Appl. Entomol. Zool.* 52, 589-598.
 30. Hirota, B., Okude, G., Anbutsu, H., Futahashi, R., Moriyama, M., Meng, X.Y., Nikoh, N., Koga, R., and Fukatsu, T.* (2017) A novel, extremely elongated, and endocellular bacterial symbiont supports cuticle formation of a grain pest beetle. *mBio* 8, e01482-17.
 31. Okude, G., Koga, R., Hayashi, T., Nishide, Y., Meng, X.Y., Nikoh, N., Miyanoshita, A., and Fukatsu, T. (2017) Novel bacteriocyte-associated pleomorphic symbiont of the grain pest beetle *Rhyzopertha dominica* (Coleoptera: Bostrichidae). *Zool. Lett.* 3, 13.

計画・古澤力

1. Koganezawa, Y., Umetani, M., Sato, M., Wakamoto, Y. (2022) History-Dependent Physiological Adaptation to Lethal Genetic Modification under Antibiotic Exposure. *eLife*. 11, e74486.
2. Uchida, Y., Shigenobu, S., Takeda, H., Furusawa, C., and Irie, N. (2022). Potential contribution of intrinsic developmental stability toward body plan conservation. *BMC Biol.* 20, 82.
3. Kanai, Y., Tsuru, S., and Furusawa, C. (2022). Experimental demonstration of operon formation catalyzed by insertion sequence. *Nucleic Acids Res.* 50, 1673-1686.
4. Furusawa, C., Tanabe, K., Ishii, C., Kagata, N., Tomita, M., and Fukuda, S. (2021). Decoding gut microbiota by imaging analysis of fecal samples. *iScience* 24, 103481.
5. Maeda, T., Kawada, M., Sakata, N., Kotani, H., and Furusawa, C. (2021). Laboratory evolution of Mycobacterium on agar plates for analysis of resistance acquisition and drug sensitivity profiles. *Sci Rep* 11, 15136.
6. Shimaya, T., Okura, R., Wakamoto, Y., Takeuchi, K. A. (2021) Scale invariance of cell size fluctuations in starving bacteria. *Commun. Phys.* 4, 238.
7. Seike, T., Sakata, N., Matsuda, F., and Furusawa, C. (2021). Elevated Sporulation Efficiency in Fission Yeast *Schizosaccharomyces japonicus* Strains Isolated from *Drosophila*. *J. Fungi*. 7, 350.
8. Seike, T., Sakata, N., Shimoda, C., Niki, H., and Furusawa, C. (2021). The sixth transmembrane region of a pheromone G-protein coupled receptor, Map3, is implicated in discrimination of closely related pheromones in *Schizosaccharomyces pombe*. *Genetics* 219, iyab150.
9. Maeda, T., Kotani, H., and Furusawa, C. (2021). Morphological change of coiled bacterium *Spirosoma linguale* with acquisition of β-lactam resistance. *Sci. Rep.* 11, 13278.
10. Seita, A., Nakaoka, H., Okura, R., Wakamoto, Y. (2021) Intrinsic growth heterogeneity of mouse leukemia cells underlies differential susceptibility to a growth-inhibiting anticancer drug. *PLoS ONE*. 16, e0236534.
11. Maeda, T., Shibai, A., Yokoi, N., Tarusawa, Y., Kawada, M., Kotani, H., and Furusawa, C. (2021). Mutational property of newly identified mutagen l-glutamic acid γ-hydrazide in *Escherichia coli*. *Mutat. Res.* 823, 111759.
12. Maeda, T., Iwasawa, J., Kotani, H., Sakata, N., Kawada, M., Horinouchi, T., Sakai, A., Tanabe, K., and Furusawa, C. (2020). High-throughput laboratory evolution reveals evolutionary constraints in *Escherichia coli*. *Nat. Commun* 11, 5970.
13. Horinouchi, T., Maeda, T., Kotani, H., and Furusawa, C. (2020). Suppression of antibiotic resistance evolution by single-gene deletion. *Sci. Rep* 10, 4178.
14. Horinouchi, T., and Furusawa, C. (2020). Understanding metabolic adaptation by using bacterial laboratory

- evolution and trans-omics analysis. *Biophys. Rev.* 12, 677-682.
15. Furusawa, C., and Irie, N. (2020). Toward understanding of evolutionary constraints: experimental and theoretical approaches. *Biophys. Rev.* 12, 1155-1161.
 16. Maeda, T., Horinouchi, T., Sakata, N., Sakai, A., and Furusawa, C. (2019). High-throughput identification of the sensitivities of an Escherichia coli ΔrecA mutant strain to various chemical compounds. *J. Antibiot.* 72, 566-573.
 17. Kobayashi-Kirschvink, K. J., Nakaoka, H., Oda, A., Kamei, K. F., Noshio, K., Fukushima, H., Kanesaki, Y., Yajima, S., Masaki, H., Ohta, K., and Wakamoto, Y. (2018) Linear Regression Links Transcriptomic Data and Cellular Raman Spectra. *Cell Systems* 7, 104-117.E4.
 18. Furusawa, C., Horinouchi, T., and Maeda, T. (2018). Toward prediction and control of antibiotic-resistance evolution. *Curr. Opin. Biotechnol.* 54, 45-49.
 19. Horinouchi, T., Maeda, T., and Furusawa, C. (2018). Understanding and engineering alcohol-tolerant bacteria using OMICS technology. *World J. Microbiol. Biotechnol.* 34, 157.
 20. Kaneko, K., and Furusawa, C. (2018). Macroscopic Theory for Evolving Biological Systems Akin to Thermodynamics. *Annu. Rev. Biophys.* 47, 273-290.
 21. Shibai, A., Maeda, T., Kawada, M., Kotani, H., Sakata, N., and Furusawa, C. (2019). Complete Genome Sequences of Three Star-Shaped Bacteria, Stella humosa, Stella vacuolata, and Stella Species ATCC 35155. *Microbiol. Resour. Announc.* 8(32), e00719.
 22. Shibai, A., Satoh, K., Kawada, M., Kotani, H., Narumi, I., and Furusawa, C. (2019). Complete Genome Sequence of a Radioresistant Bacterial Strain, Deinococcus grandis ATCC 43672. *Microbiol. Resour. Announc.* 8(45), e01226.
 23. Furusawa, C., and Kaneko, K. (2018). Formation of dominant mode by evolution in biological systems. *Phys. Rev E.* 97, 042410.
 24. Hatakeyama, T.S., and Furusawa, C. (2017). Metabolic dynamics restricted by conserved carriers: Jamming and feedback. *PLoS Comput. Biol.* 13, e1005847.
 25. Horinouchi, T., Sakai, A., Kotani, H., Tanabe, K., and Furusawa, C. (2017). Improvement of isopropanol tolerance of Escherichia coli using adaptive laboratory evolution and omics technologies. *J. Biotechnol.* 255, 47-56.
 26. Horinouchi, T., Suzuki, S., Kotani, H., Tanabe, K., Sakata, N., Shimizu, H., and Furusawa, C. (2017). Prediction of Cross-resistance and Collateral Sensitivity by Gene Expression profiles and Genomic Mutations. *Sci. Rep.* 7, 14009.

計画・長谷部光泰

1. Fukushima, K., Narukawa, H., Palfalvi, G., and Hasebe, M. (2021). A discordance of seasonally covarying cues uncovers misregulated phenotypes in the heterophylloous pitcher plant *Cephalotus follicularis*. *Proc. Royal Soc. B: Biol. Sci.* 288, 20202568.
2. Mano, H., and Hasebe, M. (2021). Rapid movements in plants. *J. Plant Res.* 134, 3–17.
3. Suda, H., Mano, H., Toyota, M., Fukushima, K., Mimura, T., Tsutsui, I., Hedrich, R., Tamada, Y., and Hasebe, M. (2020). Calcium dynamics during trap closure visualized in transgenic Venus flytrap. *Nature Plants* 6, 1219–1224. .
4. Palfalvi, G., Hackl, T., Terhoeven, N., Shibata, T.F., Nishiyama, T., Ankenbrand, M., Becker, D., Förster, F., Freund, M., Iosip, A., Kreuzer, I., Saul, F., Kamida, C., Fukushima, K., Shigenobu, S., Tamada, Y., Adamec, L., Hoshi, Y., Ueda, K., Winkelmann, T., Fuchs, J., Schubert, I., Schwacke, R., Al-Rasheid, K., Schultz, J., Hasebe, M., and Hedrich, R. (2020). Genomes of the Venus flytrap and close relatives unveil the roots of plant carnivory. *Curr. Biol.* 30, 2312-2320.
5. Renner, T., Lan, T., Farr, K.M., Ibarra-Laclette, E., Herrera-Estrella, L., Schuster, S.C., Hasebe, M., Fukushima, K., and Albert, V.A. (2018). Carnivorous plant genomes. In Carnivorous Plants, A.M. Ellison, and L. Adamec, eds. (Oxford: Oxford Univ. Press), pp. 135–153.
6. Yilamujiang, A., Zhu, A., Ligabue-Braun, R., Bartram, S., Witte, C.P., Hedrich, R., Hasabe, M., Schöner, C.R., Schöner, M.G., Kerth, G., Carlini, C.R., and Mithöfer, A. (2017). Coprophagous features in carnivorous Nepenthes plants: A task for ureases. *Sci. Rep.* 7, 11647.

公募・田村宏治

7. Miyamoto, K., Kawakami, K., Tamura, K. and Abe, G.(2022) Developmental independence of median fins from the larval fin fold revises their evolutionary origin. *Sci. Rep.* 12, 7521.
8. Yamanaka, S., Murai, H., Saito, D., Abe, G., Tokunaga, E., Iwasaki, T., Takahashi, H., Takeda, H., Suzuki, T., Shibata, N., Tamura, K. and Sawasaki T (2021) Thalidomide and its metabolite 5-hydroxythalidomide induce teratogenicity via the cereblon neosubstrate PLZF. *EMBO J.* e105375.
9. Tanaka, Y., Kudoh, H., Abe, G., Yonei-Tamura., S. and T., Tamura, K. (2020) Evolutionary cell biology on the fin-to-limb transition". *Evolutionary Developmental Biology - A Reference Guide*. Nuno de la Rosa, L., Müller, G. eds. Springer, Cham.
10. Yoshida, K., Kawakami, K., Abe, G. and T., Tamura, K. (2020) Zebrafish can regenerate endoskeleton in larval pectoral fin but the regenerative ability declines. *Dev. Biol.* 463, 110-123.

11. Uemoto T., Abe, G. and T., Tamura, K. (2020) Regrowth of zebrafish caudal fin regeneration is determined by the amputated length. *Sci. Rep.* 10, 649.
12. Abe, G., Hayashi, T., Yoshida, K., Yoshida, T., Kudoh, H., Sakamoto, J., Konishi, A., Kamei, Y., Takeuchi, T., Tamura, K. and Yokoyama, H. (2020) Insights regarding skin regeneration in non-amniote vertebrates: skin regeneration without scar formation and potential step-up to a higher level of regeneration. *Semin. Cell Dev. Biol.* 100, 109-121.
13. Hamada, H., Uemoto, T., Tanaka, Y., Honda, Y., Kitajima, K., Umeda, T., Kawakami, A., Shinya, M., Kawakami, K., Tamura, K. and Abe, G. (2019) Pattern of fin rays along the antero-posterior axis based on their connection to distal radials. *Zool. Lett.* 5:30.
14. Wakamatsu, Y., Egawa, S., Terashita, Y., Kawasaki, H., Tamura, K., and Suzuki, K. (2019) ox code model of heterodont tooth in mammals revised. *Sci. Rep.* 9, 12865.
15. Hayashi, S., Tamura K., and Yokoyama, H. (2019). Chromatin dynamics underlying the precise regeneration of a vertebrate limb – Epigenetic regulation and cellular memory. *Semin. Cell Dev. Biol.* S1084-9521, 30196-4.
16. Egawa, S., Saito, D., Abe, G., and Tamura, K. (2018). Morphogenetic mechanism of the acquisition of the dinosaur-type acetabulum. *Roy. Soc. Open Sci.* 5, 180604.
17. Yokoyama, H., Kudo, N., Todate, M., Shimada, Y., Suzuki, M., and Tamura, K. (2018). Skin regeneration of amphibians - A novel model for skin regeneration as adults. *Dev. Growth Diff.* 60, 316-325.

公募・守野孔明

1. Morino, Y (2022). Dynamic evolutionary history of spiralian-specific TALE homeobox genes in mollusks *Dev. Growth Differ.*, 1-12
2. Phuangphong, S., Tsunoda, J., Wada, H., Morino, Y (2021) Duplication of spiralian-specific TALE genes and evolution of the blastomere specification mechanism in the bivalve lineage *EvoDevo* 12:1, 1-16

公募・土松隆志

1. Tsuchimatsu, T., and Fujii, S. (2022). The selfing syndrome and beyond: diverse evolutionary consequences of mating system transitions in plants. *Phil. Trans. R. Soc. B*, 377, 20200510.
2. Bamba, M., Aoki, S., Kajita, T., Setoguchi H., Watano, Y., Sato, S., and Tsuchimatsu, T., (2020). Massive rhizobial genomic variation associated with partner quality in *Lotus–Mesorhizobium* symbiosis. *FEMS Microbiol. Ecol.* 96, fiaa202.
3. Tsuchimatsu, T., Kakui, H., Yamazaki, M., Marona, C., Tsutsui, H., Hedhly, A., Meng, D., Sato, Y., Städler, T., Grossniklaus, U., Kanaoka, M.M., Lenhard, M., Nordborg, M., and Shimizu, K.K., (2020). Adaptive reduction of male gamete number in the selfing plant *Arabidopsis thaliana*. *Nat. Commun.* 11, 2885.
4. Fujii, S., Tsuchimatsu, T., Kimura, Y., Ishida, S., Tangpranomkorn, S., Shimosato-Asano, H., Iwano, M., Furukawa, S., Itoyama, W., Wada, Y., Shimizu, K.K., and Takayama, S., (2019). Identification of a stigmatic gene functions in inter-species incompatibility in the Brassicaceae. *Nat. Plants* 5, 731-741.
5. Bamba, M., Aoki, S., Kajita, T., Setoguchi H., Watano, Y., Sato, S., and Tsuchimatsu, T., (2019). Exploring genetic diversity and signatures of horizontal gene transfer in nodule bacteria associated with *Lotus japonicus* in natural environments. *Mol. Plant-Microbe Interact.* 32, 1110-1120.
6. Bamba, M., Kawaguchi, Y.W., and Tsuchimatsu, T., (2019). Plant adaptation and speciation using population genomic approaches. *Dev. Growth Diff.* 61, 12-24.
7. 土松隆志, 安田晋輔, 高田美信, 北柴大泰, 新倉聰, 藤本龍, 柿崎智博 (2019)「アブラナ科植物における自家不和合性研究の最前線と育種現場での利用」『育種学研究』 doi:10.1270/jsbbr.21.W03
8. 土松隆志 (2018)「集団ゲノミクスが解き明かす植物進化のダイナミクス：適応をゲノムから探る」『化学と生物』 社団法人 日本農芸化学会 56: 317-323.

公募・小林徹也

1. Kato, T., and Kobayashi, T.J. (2021). Understanding adaptive immune system as reinforcement learning. *Phys. Rev. Res.* 3, 013222.
2. Nakashima, S., Kobayashi, T.J. (2022). Acceleration of evolutionary processes by learning and extended Fisher's fundamental theorem. *Phys. Rev. Res.* 4, 013069.

公募・岡田泰和

1. Okada K, Katsuki M, Sharma MD, Kiyose K, Seko T, Okada Y, Wilson AJ, and Hosken DJ.(2021). Natural selection increases female fitness by reversing the exaggeration of a male sexually selected trait. *Nat. Commun.*12,3420.
2. Kiyose, K., Katsuki, M., Suzuki, Y., Okada K and Okada Y. (2021). Octopaminergic system orchestrates combat and mating behaviors: a potential regulator of alternative male mating tactics in an armed beetle. *J Insect Physiol.* 131,104211.
3. Kiyose, K., Okada, Y., Katsuki, M., Suzuki, Y.,and Okada K. Sexually selected traits and life history traits of larger and smaller males of the horned flour beetle *Gnatocerus cornutus*.(2021). *Ecol. Entomol.* 46, 807-815.

4. Kiyose, K., Katsuki, M., Suzaki Y., Okada, K., and Okada, Y. (2020) Older males are more competitive in male fights and more aggressive towards females in the broad-horned flour beetle *Gnatocerus cornutus*. *Behav. Ecol. Sociobiol.* 74,36.
5. Okada, K., Katsuki, M., Kiyose, K., and Okada Y. (2020). Older males are more competitive in male fights and more aggressive towards females in the broad-horned flour beetle *Gnatocerus cornutus* *Behav. Ecol. Sociobiol.* 74,36.
6. Okada, Y., Katsuki, M., Okamoto, N., Fujioka, H., and Okada, K.(2019). A specific type of insulin-like peptide regulates the conditional growth of a beetle weapon. *PloS Biol.*17, e3000541.
7. Fujioka, H., and Okada, Y. (2019). Liquid exchange via stomodeal trophallaxis in the ponerine ants Diacamma sp. from Japan. *J. Ethol.* 37, 371-375.
8. Okada, K., Okada, Y., Dall, S., and Hosken, D. (2019). Loser-effect duration evolves independently of fighting ability. *Proc. Royal Soc. B* 286,20190582
9. Fujioka, H., Abe, M.S., and Okada, Y. (2019). Observation of plugging behaviour reveals entrance-guarding schedule of morphologically specialised caste in *Colobopsis nipponicus*. *Ethology* 125,526-534.
10. Fujioka, H., Abe, M.S., and Okada, Y. (2019). Ant activity-rest rhythms vary with age and interaction frequencies of workers. *Behav. Ecol. Sociobiol.* 73, 30.
11. Ohbayashi, K., Ishikawa, N., Hodoki, Y., Okada, Y., Nakano, S., Ito, M., and Shimada, M. (2019). Rapid development and characterization of EST-SSR markers for the honey locust seed beetle, *Megabruchidius dorsalis* (Coleoptera: Bruchidae), using *de novo* transcriptome analysis based on next-generation sequencing. *Appl. Entomol. Zool.* 54, 141-145.

公募・小敷大輔

1. Rui, C., Li, J., Koyabu, D. (2022). A bibliometric analysis of research trends in bat echolocation studies between 1970 and 2021. *Ecol. Inform.*, in press.
2. Abel, P., Pommery, Y. Ford, D.P., Koyabu, D., Werneburg, I.(2022) Skull sutures and cranial mechanics in the Permian reptile *Captorhinus aguti* and the evolution of the temporal region in early amniotes. *Front. Ecol. Evol.*, in press.
3. Zhang, Z., Koyabu, D., Yaryhin, and O. Werneburg, I. (2022) Morphological association between muscle attachment and ossification sites in the late cartilaginous skull of tuatara embryos. *J. Morphol.*, 283,908-931.
4. Nojiri, T., Tu, V.T., Sohn, J.H., and Koyabu, D (2022). On the sequence heterochrony of cranial ossification of bats in the light of Haeckel's recapitulation theory. *J. Exp. Zool. B.* 338, 137-148.
5. Higashiyama, H., Koyabu, D., Hirasawa, T., Werneburg, I., Kuratani, S., and Kurihara, H. Mammalian muzzle as an evolutionary novelty (2021). *Proc. Natl. Acad. Sci. U.S.A.* .118, e2111876118.
6. López-Aguirre, C., Hand, S.J., Koyabu, D., Tu, V.T., Wilson, L.A.B. Prenatal developmental trajectories of fluctuating asymmetry in bat humeri (2021). *Front. Cell Dev. Biol.* 9, 639522.
7. Nojiri, T., Wilson, L.A.B., López-Aguirre, C., Tu, V.T., Kuratani, S., Ito, K., Higashiyama, H., Son, N.T., Fukui, D., Sadier, A., Sears, K.E., Endo, H., Kamihori, S., Koyabu, D.* Embryonic evidence uncovers convergent origins of laryngeal echolocation in bats (2021). *Curr. Biol.* 31, 1353-1365.e3.
8. Nojiri, T., Fukui, D., Werneburg, I., Saitoh, T., Endo, H., Koyabu, D. Embryonic staging of bats with special reference to *Vespertilio sinensis* and its cochlear development (2021). *Dev. Dyn.* 250, 1140-1159.
9. López-Aguirre, C.*, Wilson, L.A.B., Koyabu, D., Tu, V.T., Hand, S.J. Variation in cross-sectional shape and biomechanical properties of the bat humerus under Wolff's law (2021). *Anat. Rec.* 340, 1937-1952.
10. Ito, K., Tu, V. T., Eiting, T. P., Nojiri, T., Koyabu, D. On the embryonic development of the nasal turbinals and their homology in bats (2021). *Front. Cell Dev. Biol.* 23, 613545.
11. Tu, V.T., Görföl, T., Csorba, G., Arai, S., Kikuchi, F., Fukui, D., Koyabu, D., Furey, N.M., Bawm, S., Lin, K.S., Alviola, P., Hang, C.T., Son, N.T., Tuan, T.A., Hassanin, A. Integrative taxonomy and biogeography of Asian yellow house bats (Vespertilionidae: *Scotophilus*) in the Indomalayan Region (2021). *J. Zool. Syst. Evol.* 59, 772-795.
12. López-Aguirre, C., Hand, S.J., Koyabu, D., Tu, V.T., and Wilson, L.A.B. (2021) Phylogeny and foraging behaviour shape modular morphological variation in bat humeri. *J. Anat.* 238, 1312-1329.
13. Sohn, J.H., Fukui, D., Nojiri, T., Minowa, K., Kimura, J.,and Koyabu, D. (2021) Three-dimensional and histological observations on male genital organs of greater horseshoe bat, *Rhinolophus ferrumequinum* *J. Mammal. Evol.* 28, 559-571.
14. Sano, K., Beyene, Y., Katoh, S., Koyabu, D., Endo, H., Asfaw, B., and Suwa, G (2020). A 1.4-million-year-old used bone handaxe from Konso, Ethiopia, shows advanced tool technology in the early Acheulean. *Proc. Natl. Acad. Sci. U.S.A.* 117, 18393-18400.
15. Sohn, J., Kimura, J., Koyabu, D. (2020). 3D model related to the publication: three-dimensional and histological observations on male genital organs of greater horseshoe bat, *Rhinolophus ferrumequinum*. *Morphomuseum* <https://doi.org/10.18563/journal.m3.113>
16. López-Aguirre, C., Hand, S.J., Koyabu, D., Son, N.T. and Wilson, L.A.B. (2019). Postcranial heterochrony, modularity, integration and disparity in the prenatal ossification in bats (Chiroptera). *BMC Evol. Biol.* 19, 75
17. López-Aguirre, C., Hand, S.J., Koyabu, D., Son, N.T. and Wilson, L.A.B. (2019). Prenatal allometric trajectories and the developmental basis of postcranial phenotypic diversity in bats (Chiroptera). *J. Exp. Zool. B.* 332, 36-

49.

18. Ledevin, R., and Koyabu, D. (2019). Patterns and constraints of craniofacial variation in colobine monkeys: disentangling the effects of phylogeny, allometry and diet. *Evol. Biol.* 46, 14–34.
19. Oh, J.W., Minami, M., Ikeda, S., Takatsuki, S., Oonishi, N., Higuchi, N., Okada, A., Kimura, J., and Koyabu, D. (2019). Non-invasive age estimation by cranial suture closure in Japanese sika deer (*Cervus nippon*). *Mammal Study* 44, 147-155.
20. Ito, T., and Koyabu, D. (2018). Biogeographic variation in skull morphology across the Kra Isthmus in dusky leaf monkeys. *J. Zool. Syst. Evol.* 56, 599-610. Nojiri, T., Werneburg, I., Son, N.T., Tu, V.T., Sasaki, T., Maekawa, Y., and Koyabu, D. (2018). Prenatal cranial bone development of Thomas's horseshoe bat (*Rhinolophus thomasi*): with special reference to petrosal morphology. *J. Morphol.* 279, 809-827.

公募・上野博史

1. Ueno, H., Sawada, H., Soga, N., Sano, M., Nara, S., Tabata, KV., Su'etsugu, M., and Noji, H (2021). Amplification of over 100 kbp DNA from Single Template Molecules in Femtoliter Droplets. *ACS Synth. Biol.* 10, 2179-2186.
2. Ueno, H., Kato, M., Minagawa, Y., Hirose, Y., and Noji, H (2021). Elucidation and control of low and high active populations of alkaline phosphatase molecules for quantitative digital bioassay. *Protein Sci.* 30, 1628-1639.
3. Soga, N., Ota, A., Nakajima, K., Watanabe, R., Ueno, H., and Noji, H (2020). Monodisperse Liposomes with Femtoliter Volume Enable Quantitative Digital Bioassays of Membrane Transporters and Cell-Free Gene Expression. *ACS Nano* 14, 11700-11711.
4. Akama, K., Iwanaga, N., Yamawaki, K., Okuda, M., Krupali, J., Ueno, H., Soga, N., Minagawa, Y., and Noji, H (2019). Wash- and amplification-free digital immunoassay based on single particle motion analysis. *ACS Nano* 13, 13116-13126.
5. Minagawa, Y., Ueno, H., Tabata, KV., and Noji, H (2019). Mobile imaging platform for digital influenza virus counting. *Lab on a Chip* 19, 2678-2687

公募・田中幹子

1. Cordeiro, IR., Yu, R., and Tanaka, M. (2020). Regulation of the limb shape in the Chinese softshell turtle: insights into the evolution of interdigital cell death. *Evol. Dev.* e12352.
2. Cordeiro, IR., and Tanaka, M. (2020). Environmental oxygen is a key modulator of the development across species: from molecules to ecology. *BioEssays* 42, 202000025.
3. Cordeiro, IR., Kabashima, K., Ochi, H., Munakata, K., Nishimori, C., Laslo, M., Hanken J., and Tanaka, M. (2019). Environmental oxygen exposure allows for the evolution of interdigital cell death in limb patterning. *Dev. Cell* 50, 155-166.
4. Kawahata, K., Cordeiro, IR., Ueda, S., Sheng, G., Moriyama, Y., Yu, R., Koizumi, M., Okabe, M., and Tanaka, M. (2019). Evolution of the avian digital pattern. *Sci. Rep.* 9, article number 8560.
5. Ueda, S., Cordeiro, IR., Moriyama, Y., Nishimori, C., Kai, K., Yu, R., Nakato, R., Shirahige, K., and Tanaka, M. (2019). Cux2 refines the forelimb field by controlling expression of *Raldh2* and *Hox* genes. *Biol. Open* 8, bio040584.
6. Tanaka, M. (2019). Preface: Ecology, Evolution and Development. *Dev. Growth Dev.* Special Issue “Ecology, Evolution and Development”. 61, 3-4.
7. Ueda, S., Suzuki, S., and Tanaka M. (2017). Transgene introduction into the chick limb bud by electroporation. *Methods Mol. Biol.*: Avian and Reptilian Developmental Biology. Vol. 1650, 203-208.
8. Tanaka, M. (2017) Evolution of vertebrate limb development (version 2.0). *Essential for Life Sciences*

公募・石川由希

1. Ishikawa, Y., Kimura, MT., and Toda, MJ. (2022). Biology and ecology of the Oriental flower-breeding *Drosophila elegans* and related species. *Fly*. 16, 207-220.
2. Kim H, Horigome M, Ishikawa Y, Li F, Lauritzen JS, Card G, Bock DD, and Kamikouchi A.(2020). Wiring patterns from auditory sensory neurons to the escape and song-relay pathways in fruit flies. *J. Comp. Neurol.* 528, 2068-2098.
3. Sato, K., Tanaka, R., Ishikawa, Y., and Yamamoto, D. (2020). Behavioral Evolution of *Drosophila*: Unraveling the Circuit Basis. *Genes*. 11, 157.
4. Ishikawa, Y., Fujiwara, M., Wong, J., Ura, A., and Kamikouchi A. (2020). Stereotyped Combination of Hearing and Wind/Gravity-Sensing Neurons in the Johnston's Organ of *Drosophila*. *Front. Physiol.* 10, 1552.
5. Yamazaki SJ, Ohara K, Ito K, Kokubun N, Kitanishi T, Takaichi D, Yamada Y, Ikejiri Y, Hiramatsu F, Fujita K, Tanimoto Y, Yamazoe-Umemoto A, Hashimoto K, Sato K, Yoda K, Takahashi A, Ishikawa Y, Kamikouchi A, Hiryu S, Maekawa T, and Kimura KD. (2019) STEFTR: A Hybrid Versatile Method for State Estimation and Feature Extraction From the Trajectory of Animal Behavior. *Front. Neurosci.* 13, 626
6. Ishikawa, Y., Okamoto, N., Yoneyama, Y., Maeda, N., and Kamikouchi, A. (2019). A single male auditory response test to quantify auditory behavioral responses in *Drosophila melanogaster*. *J. Neurogenet.* in press.
7. Yamada, D., Ishimoto, H., Li, X., Kohashi, T., Ishikawa, Y., and Kamikouchi, A. (2018). GABAergic local interneurons shape female fruit fly response to mating songs. *J. Neurosci.* 38, 4329-4347.

公募・市橋伯一

1. Mizuuchi, R., Furubayashi, T., and Ichihashi, N. (2022) Evolutionary transition from a single RNA replicator to a multiple replicator network. *Nat. Commun.* 13, 1460
2. Yukawa, K., Mizuuchi, R., and Ichihashi, N. (2021). Relaxed Substrate Specificity in Q β Replicase through Long-Term In Vitro Evolution. *Life*, 12, 32
3. Mizuuchi, R., and Ichihashi, N. (2020). Translation-coupled RNA replication and parasitic replicators in membrane-free compartments. *Chem. Commun.*, 56, 13453-13456.
4. Furubayashi, T., Ueda, K., Bansho, Y., Motooka, D., Nakamura, S., Mizuuchi, R., and Ichihashi, N. (2020). Emergence and diversification of a host-parasite RNA ecosystem through Darwinian evolution. *eLIFE* 9, e56038
5. Mizuuchi, R., Usui, K., Ichihashi, N. (2020). Structural transition of replicable RNAs during in vitro evolution with Q β replicase. *RNA* 26, 83-90.

公募・細田一史

1. Hosoda, K., Seno, S., Murakami, N., Matsuda, H., Osada, Y., and Kondoh, M. (2020) A model ecosystem of twelve cryopreservable microbial species allowing for a non-invasive approach. *bioRxiv*. 2020.10.23.351742.

公募・塙間敬

1. Hiruma, K., Kobae, Y., and Toju, H. (2018). Beneficial associations between Brassicaceae plants and fungal endophytes under nutrient-limiting conditions: evolutionary origins and host–symbiont molecular mechanisms. *Curr. Opin. Plant Biol.* 44, 145-154.

公募・守屋央朗

1. Namba, S., Kato, H., Shigenobu, S., Makino, T., and Moriya, H. (2022). Massive expression of cysteine-containing proteins causes abnormal elongation of yeast cells by perturbing the proteasome. *G3.(Bethesda)* 30, jkac106.
2. Horiuchi, S., Namba, S., Saeki, N., Satoh, A., and Moriya, H. (2022). Identification of uncharacterized proteins potentially localized to mitochondria (UPMs) in *Saccharomyces cerevisiae* using a fluorescent protein unstable in the cytoplasm. *Yeast*. 39, 303-311.
3. Ishikawa, K., Ishihara, A., and Moriya, H. (2020). Exploring the Complexity of Protein-Level Dosage Compensation that Fine-Tunes Stoichiometry of Multiprotein Complexes. *PLoS Genet.* 16, e1009091.
4. Mori, Y., Yoshida, Y., Satoh, A., and Moriya, H. (2020). Development of an experimental method of systematically estimating protein expression limits in HEK293 cells. *Sci. Rep.* 10, 4798.
5. Moriya, H. (2020). The expression level and cytotoxicity of green fluorescent protein are modulated by an additional N-terminal sequence. *AIMS Biophys.* 7, 121-132.
6. Kintaka, R., Makanae, K., Namba, S., Kato, H., Kito, K., Ohnuki, S., Ohya, Y., Andrews, B.J., Boone, C., and Moriya, H. (2020). Genetic profiling of protein burden and nuclear export overload. *Elife* 9.
7. Saeki, N., Eguchi, Y., Kintaka, R., Makanae, K., Shichino, Y., Iwasaki, S., Kanno, M., Kimura, N., and Moriya, H. (2020). N-terminal deletion of Swi3 created by the deletion of a dubious ORF YJL175W mitigates protein burden effect in *S. cerevisiae*. *Sci. Rep.* 10, 9500.
8. Abe-Kanoh, N., Kunisue, N., Myojin, T., Chino, A., Munemasa, S., Murata, Y., Satoh, A., Moriya, H., and Nakamura, Y. (2019). Yeast screening system reveals the inhibitory mechanism of cancer cell proliferation by benzyl isothiocyanate through down-regulation of Mis12. *Sci. Rep.* 9, 8866.
9. Eguchi, Y., Makanae, K., Hasunuma, T., Ishibashi, Y., Kito, K., and Moriya, H. (2018). Estimating the protein burden limit of yeast cells by measuring the expression limits of glycolytic proteins. *Elife* 7.

公募・安岡有理

1. Jansen, C., Paraiso, K.D., Zhou, J.J., Blitz, I.L., Fish, M.B., Charney, R.M., Cho, J.S., Yasuoka, Y., Sudou, N., Bright, A.R., Wlizla, M., Veenstra, G.J.C., Taira, M., Zorn, A.M., Mortazavi, A., and Cho, K.W.Y (2022). Uncovering the mesendoderm gene regulatory network through multi-omic data integration. *Cell Reports* 38, 110364.
2. Yasuoka, Y. and Taira, M. (2021). LIM homeodomain proteins and associated partners: Then and now. *Curr. Top. Dev. Biol.* 145, 113-166.
3. Yasuoka, Y (2020). Morphogenetic Mechanisms Forming the Notochord Rod: the Turgor Pressure-Sheath Strength Model. *Deve, Growth Differ.* 62, 379-390.
4. Yasuoka Y (2020). Enhancer Evolution in Chordates: Lessons from Functional Analyses of Cephalochordate Cis-Regulatory Modules. *Dev. Growth Differ.* 62, 279-300.
5. Yasuoka, Y., Matsumoto, M., Yagi, K., and Okazaki, Y (2020). Evolutionary History of GLIS Genes Illuminates their Roles in Cell Reprogramming and Ciliogenesis. *Mol. Biol. Evol.* 37, 100-109.
6. Yasuoka, Y., Tando, Y., Kubokawa, K., and Taira, M (2019). Evolution of cis-regulatory modules for the head organizer gene goosecoid in chordates: comparisons between *Branchiostoma* and *Xenopus*. *Zool. Lett.* 5, 27.

公募・大林龍胆

1. Fujiwara. T., Hirooka. S., Ohbayashi. R., Onuma. R., and Miyagishima. SY (2020). Relationship between cell cycle and diel transcriptomic changes in metabolism in a unicellular red alga. *Plant Physiol.* 184, 1484-1501.
2. Ohbayashi. R., Hirooka. S., Onuma. R., Kanesaki. Y., Hirose. Y., Kobayashi. Y., Fujiwara. T., Furusawa. C., and Miyagishima. SY (2020). Evolutionary changes in DnaA-independent chromosomal replication in cyanobacteria. *Front. Microbiol.* 11,786.
3. Watanabe. S., Saito. S., Suezaki. Y., Seguchi. T., and Ohbayashi. R.(2019). Specific binding of DnaA box motif in the cyanobacterium *Synechococcus elongatus* PCC 7942. *J. Gen. Appl. Microbiol.* 66, 80-84.
4. Ohbayashi. R., Nakamachi. A., Hatakeyama. TS., Kanesaki. Y., Watanabe. S., Chibazakura. T., Yoshikawa. H., and Miyagishima. SY (2019) Coordination of polyploid chromosome replication with cell size and growth in a cyanobacterium. *mBio*, 10, e00510-19.
5. 大林龍胆 (2021)「細胞増殖に伴うラン藻の複数コピーゲノムの維持機構」、生物工学会誌、99(8):p425-428

公募・新美輝幸

1. Ando, T., and Niimi, T. (2019). Development and evolution of color patterns in ladybird beetles: A case study in *Harmonia axyridis*. *Dev. Growth Differ.* 61, 73-84.
2. 新美輝幸, 安藤俊哉, 森田慎一 (2019). RNAi 法で探る非モデル昆虫の形作りの仕組み. 日本農薬学会誌, 44, 219-225.
3. Ando, T., Matsuda, T., Goto, K., Hara, K., Ito, A., Hirata, J., Yatomi, J., Kajitani, R., Okuno, M., Yamaguchi, K., Kobayashi, M., Takano, T., Minakuchi, Y., Seki, M., Suzuki, Y., Yano, K., Itoh, T., Shigenobu, S., Toyoda, A., and Niimi, T. (2018). Repeated inversions within a *pannier* intron drive diversification of intraspecific colour patterns of ladybird beetles. *Nat. Commun.* 9, 3843.

公募・阿部玄武

1. Miyamoto, K., Kawakami, K., Tamura, K. and Abe, G.(2022) Developmental independence of median fins from the larval fin fold revises their evolutionary origin. *Sci. Rep.* 12, 7521.
2. Yamanaka, S., Murai, H., Saito, D., Abe, G., Tokunaga, E., Iwasaki, T., Takahashi, H., Takeda, H., Suzuki, T., Shibata, N., Tamura, K. and Sawasaki T.(2021) Thalidomide and its metabolite 5-hydroxythalidomide induce teratogenicity via the cereblon neosubstrate PLZF. *EMBO J.* e105375.
3. Tanaka, Y., Kudoh, H., Abe, G., Yonei-Tamura., S. and T., Tamura, K. (2020) Evolutionary cell biology on the "fin-to-limb transition". *Evolutionary Developmental Biology - A Reference Guide*. Nuno de la Rosa, L., Müller, G. eds. Springer, Cham.
3. Yoshida, K., Kawakami, K., Abe, G. and T., Tamura, K (2020) Zebrafish can regenerate endoskeleton in larval pectoral fin but the regenerative ability declines. *Dev. Biol.*, 463, 110-123.
4. Uemoto T., Abe, G. and T., Tamura, K. (2020) Regrowth of zebrafish caudal fin regeneration is determined by the amputated length. *Sci. Rep.* 10, 649.
5. Abe, G., Hayashi, T., Yoshida, K., Yoshida, T., Kudoh, H., Sakamoto, J., Konishi, A., Kamei, Y., Takeuchi, T., Tamura, K. and Yokoyama, H. (2020) Insights regarding skin regeneration in non-amniote vertebrates: skin regeneration without scar formation and potential step-up to a higher level of regeneration. *Semin Cell Dev. Biol.*,100, 109-121.

公募・東山大毅

1. Higashiyama, H. Koyabu, D., Hirasawa, T., Werneburg, I., Kuratani, S., Kurihara, H. (2021). Mammalian face as an evolutionary novelty. *Proc. Nat. Acad. Sci. U.S.A*118, e2111876118.
2. Nojiri, T., Wilson, L.A.B., Lopez-Aguirre, C., Tu, V.T., Kuratani, S., Ito, K., Higashiyama, H., Son, N.T., Fukui, D., Sadier, A., Sears, K.E., Endo, H., Kamihori, S., Koyabu, D. (2021). Embryonic evidence uncovers convergent origins of laryngeal echolocation in bats. *Curr. Biol.* 31, 1353-1365.

公募・鈴木郁夫

1. Amunts K, Andersson M, Armstrong NJ, Bernard M, Blackburn NB, Blangero J, Boomsma DI, Brodaty H, Brouwer RM, Bülow R, Bøen R, Cahn W, Calhoun VD, Caspers S, Ching CRK, Cichon S, Ciufolini S, Crespo-Facorro B, Curran JE, Dale AM, Dalvie S, Dazzan P, de Geus EJC, de Zubicaray GI, de Zwartje SMC, Desrivieres S, Doherty JL, Donohoe G, Draganski B, Ehrlich S, Eising E, Espeseth T, Feigin K, Fisher SE, Fladby T, Frei O, Frouin V, Fukunaga M, Gareau T, Ge T, Glahn DC, Grabe HJ, Groenewold NA, Gústafsson Ó, Haavik J, Haberg AK, Hall J, Hashimoto R, Hehir-Kwa JY, Hibar DP, Hillegers MHJ, Hoffmann P, Holleran L, Holmes AJ, Homuth G, Hottenga JJ, Hulshoff Pol HE, Ikeda M, Jahanshad N, Jockwitz C, Johansson S, Jönsson EG, Jørgensen NR, Kikuchi M, Knowles EEM, Kumar K, Le Hellard S, Leu C, Linden DEJ, Liu J, Lundervold A, Lundervold AJ, Maillard AM, Martin NG, Martin-Brevet S, Mather KA, Mathias SR, McMahon KL, McRae AF, Medland SE, Meyer-Lindenberg A, Moberget T, Modenato C, Sánchez JM, Morris DW, Mühlleisen TW, Murray RM, Nielsen J, Nordvik JE, Nyberg L, Loohuis LMO, Ophoff RA, Owen MJ, Paus T, Pausova Z, Peralta JM, Pike GB, Prieto C, Quinlan EB, Reinbold CS, Marques TR, Rucker JJH, Sachdev PS, Sando SB, Schofield PR, Schork AJ, Schumann G, Shin J, Shumskaya E, Silva AI, Sisodiya SM, Steen VM, Stein DJ, Strike LT, Suzuki IK, Tamnes

- CK, Teumer A, Thalamuthu A, Tordesillas-Gutiérrez D, Uhlmann A, Ulfarsson MO, van 't Ent D, van den Bree MBM, Vanderhaeghen P, Vassos E, Wen W, Wittfeld K, Wright MJ, Agartz I, Djurovic S, Westlye LT, Stefansson H, Stefansson K, Jacquemont S, Thompson PM, and Andreassen OA; (2021). 1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. *Transl. Psychiatry* 11, 182.
2. Bergoglio E, Suzuki IK, Togashi K, Tsuji M, Takeuchi S, Koizumi H, and Emoto K. (2021) Spatial and temporal diversity of DCLK1 isoforms in developing mouse brain. *Neuro. Res.* 170 154-165.
 3. De Franco E, Lytrivi M, Ibrahim H, Montaser H, Wakeling MN, Fantuzzi F, Patel K, Demarez C, Cai Y, Igoillo-Esteve M, Cosentino C, Lithovius V, Viñinen H, Jokitalo E, Laver TW, Johnson MB, Sawatani T, Shakeri H, Pachera N, Haliloglu B, Ozbek MN, Unal E, Yıldırım R, Godbole T, Yıldız M, Aydin B, Bilheu A, Suzuki I, Flanagan SE, Vanderhaeghen P, Senée V, Julier C, Marchetti P, Eizirik DL, Ellard S, Saarimäki-Vire J, Otonkoski T, Cnop M, Hattersley AT. (2020). YIPF5 mutations cause neonatal diabetes and microcephaly through endoplasmic reticulum stress. *J.Clin. Invest.* 130, 6338-6353.

公募・寺島浩行

1. Terashima, H., Hori, K., Ihara, K., Homma, M., and Kojima, S. (2022) Mutations in the stator protein PomA affect switching of rotational direction in bacterial flagellar motor. *Sci. Rep.* 12, 2979.

公募・大澤志津江

1. Wada, Y., Ohsawa, S., and Igaki, T. (2021). Yorkie ensures robust tissue growth in Drosophila ribosomal protein mutants. *Development*, 148, dev198705.
2. Akai, N., Ohsawa, S., Sando Y., and Igaki, T. (2021). Epithelial cell-turnover ensures robust coordination of tissue growth in Drosophila ribosomal protein mutants. *PLoS Genet.* 17, e1009300.

公募・鈴木孝幸

1. Ishishita S, Kitahara S, Takahashi M, Iwasaki S, Tatsumoto S, Hara I, Kaneko Y, Kinoshita K, Yamaguchi K, Harada A, Ohmori Y, Ohkawa Y, Go Y, Shigenobu S, Matsuda Y, and Suzuki T(2022) Uterus-specific transcriptional regulation underlies eggshell pigment production in Japanese quail. *PLoS One*, 17, e0265008

公募・石川麻乃

1. Ishikawa, A., Yamanouchi, S., Iwasaki, W., and Kitano, J. (2022). Convergent copy number increase of genes associated with freshwater colonisation in fishes. *Phil. Trans. Roy. Soc. B.* 377, 20200509.
2. Yoshitake, K., Ishikawa, A., Yonezawa, R., Kinoshita, S., Kitano, J., and Asakawa, S. (2022). Construction of a chromosome-level Japanese stickleback species genome using ultra-dense linkage analysis with single-cell sperm sequencing. *NAR genom. bioinform.* 4, lqac026.
3. Ishikawa, A., Stuart, Y.E., Bolnick, D.I., Kitano, J. (2021). Copy number variation of a fatty acid desaturase gene *Fads2* associated with ecological divergence in freshwater stickleback populations. *Biol. Lett.* 17, 20210204.
4. Twining, C., Bernhardt, J., Derry, A., Cameron, H., Ishikawa, A., Kabeya, N., Kainz, M., Kitano, J., Kowarik, C., Ladd, S.N., Leal, M., Schärnweber, K., Shipley, J., and Matthews, B. (2021). The evolutionary ecology of fatty-acid variation: implications for consumer adaptation and diversification. *Ecol. Lett.* 24, 1709-1731.
5. Kakioka, R., Kume, M., Ishikawa, A., Ansai, S., Hosoki, T.K., Yamasaki, Y.Y., Nagano, A.J., Toyoda, A., and*Kitano, J. (2021). Genetic basis for variation in the number of cephalic pores in a hybrid zone between closely related species of gobies, *Gymnogobius breunigii* and *Gymnogobius castaneus*. *Biol. J. Linn. Soc.* 133, 143-154.
6. Ravinet, M., Kume, M., Ishikawa, A., and Kitano, J. (2020). Patterns of genomic divergence and introgression between Japanese stickleback species with overlapping breeding habitats. *J. Evol. Biol.* 34, 114-127.
7. Kakioka, R., Mori, S., Kokita, T., Hosoki, T.K., Nagano, A.J., Ishikawa, A., Kume, M., Toyoda, A., and Kitano, J. (2020). Multiple waves of freshwater colonisation of the three-spined stickleback in the Japanese Archipelago. *BMC Evol. Biol.* 20, 143.
8. Kitano, J., Kakioka, R., Ishikawa, A., Toyoda, A., and Kusakabe, M.. (2020) Differences in the contributions of sex-linkage and androgen regulation to sex-biased gene expression in juvenile and adult sticklebacks. *J Evol. Biol.* 33, 1129-1138.
9. Ishikawa, A. and Kitano, J. (2020) Diversity in reproductive seasonality in the three-spined stickleback, *Gasterosteus aculeatus*. *J. Exp. Biol.* 223, jeb208975.

【学会発表】計画班の国際学会のみ

計画・倉谷滋

1. Kuratani, S. “Developmental bases for the acquisition of the turtle shell”1st AsiaEvo Conference、April18-20,2021, Sheraton Daimesha Resort Hotel, Shenzhen, China
2. Kuratani, S. “Development of cyclostomes and early evolution of vertebrates”A Symposium to Celebrate the

Award of the Japan Prize to Dr. Max D. Cooper April 23th 2018 RIKEN, Center for Integrative Medical Sciences, Yokohama, Japan

3. Kuratani, S "Development and evolution of the turtle shell" 6th Turtle Evolution Symposium May25-28, 2018, Waseda campus of Waseda University, Tokyo Japan
4. Kuratani, S. "Development and evolution of a novel musculoskeletal pattern in the turtle" Tokyo2018 Cell and Developmental Biology Meeting June 6-8, 2018, Tower Hall Funabori, Tokyo, Japan.
5. Kuratani S. "Evolution and development of the cranium in early vertebrates" The 46th Naito conference on Mechanisms of Evolution and Biodiversity, October 2-5, 2018 Chaterase Gateaux Kingdom, Sapporo, Japan
6. Pascual Anaya, J. "Hagfish genome provides insights into cyclostome biology and early vertebrate evolution" QMUL New Horizons in Genomics: Non-model Organism Genomics, July 3rd. 2019, School of Biological and Chemical Sciences, London, U.K
7. Kuratani, S "Origin and Early Evolution of the Vertebrate Body Plan: Defining the Head in the Embryo" The 12th International Congress of Vertebrate Morphology, July 21-25, 2019, Grandior, Prague, Czech Republic
8. Hirasawa, T., and Kuratani, S. "The Evolutionary Reconstructions of Skeletal Muscles in Tetrapods" The 12th International Congress of Vertebrate Morphology, July 21-25, 2019, Grandior, Prague, Czech Republic
9. Pascual Anaya, J." Origin of vertebrates at the light of the hagfish genome" SMBE Meeting 2019 July 21-25, 2019 Manchester Central, Manchester, United Kingdom
10. Kuratani, S. "Craniofacial Diversity in Early Evolution of Vertebrates" Constraints and Plasticity in Development and Evolution, June 3-4, 2021.Online.
11. Hirasawa T. "Early evolution of the vertebrate morphology: a view from evolutionary developmental biology" 2nd AsiaEvo Conference Aug. 17, 2021 -Online
12. Kuratani, S. "Development of the hagfish and early evolution of vertebrates" 2nd Fipar webinar IFAA (International Federation of Association of Anatomists) WEBINAR SERIES 2021 Oct 13th, 2021 Online.
13. Hirasawa, T. "The mammalian diaphragm as an evolutionary novelty. "3rd Palaeontological Virtual Congress Dec. 1—15, 2021 Online

計画・金子邦彦

1. Koichi Fujimoto. "Quantitative modeling of multicellular mechanics promoting pathogenesis and organogenesis", Taiwan Society of Evolution and Computational Biology. International Symposium on Evolutionary Genomics and Bioinformatics 2022, March 12-13 2022, Taipei, Taiwan/Online.
2. Kunihiko Kaneko、Relevance of Noise to Adaption and Evolution、Stochastic Resonance 40、2021/09/13、Perugia, Online Talk
3. Kunihiko Kaneko、Universal Biology in Adaptation and Evolution: Dimensional Reduction, and Fluctuation-Response Relationship、Statistical Physics of Complex Systems、2021/09/10、(Trieste, Online Talk)
4. Kunihiko Kaneko、Macroscopic Theory for Adaptation and Evolution: Multilevel Consistency, Dimensional Reduction, and Fluctuation-Response Relationship、Solvay Workshop on 'Nonlinear Phenomena and Complex Systems'、2021/06/15、Brussels,online
5. Kunihiko Kaneko、Universal Biology in Adaptation and Evolution: Multilevel Consistency, Dimension Reduction, and Fluctuation-Response Relationship、Statistical Biological Physics: From Single Molecule to Cell、2020/12/09、online
6. K. Horibe, K. Hironaka, K. Matsushita, K. Fujimoto、The surface geometry of living things induces a topological change of a chemical traveling wave during morphogenesis、EMBL-IBEC Winter Conference、2020/02/10-12、バルセロナ、スペイン
7. K. Horibe, K. Hironaka, K. Matsushita, K. Fujimoto、The surface geometry of cerebral cortex induces topological changes of cortical traveling waves、4th HBP Student Conference on Interdisciplinary Brain Research、2020/01/21-22、Pisa, イタリア
8. Naoya Kamamoto, Katsuyoshi Matsushita, Mitsuyasu Hasebe, Koichi Fujimoto、How does cell division generate phyllotactic pattern in bryophytes?、日本植物学会第 83 回大会 国際シンポジウム Beyond Fibonacci patterns and the golden angle: phyllotactic variations and their cellular origin、2019/9/15-17、仙台
9. Kunihiko Kaneko、Dimension-Reduction Theory for Direction and Constraint in Phenotypic Evolution、From Molecular Basis to Predictability and Control of Evolution、2019/7/、Sweden
10. Koichi Fujimoto, Alice Tsuboi、Cell competition for space is controlled by apoptosis-induced change of local epithelial topology. 、2018 ICTS Workshop on Cellular Dynamics and Microbiome Studies、2018/11/29-30、Hong Kong, China
11. Kunihiko Kaneko、Dimension Reduction and Relevance of Slow Modes in Biological Dynamical Systems、Dynamics Days Asia Pacific、2018/11/2、China
12. Kunihiko Kaneko、Multilevel consistency, dimension reduction, and slow dynamics in biology、Quantitative Life Science Workshop2018、2018/10/16、Korea
13. Koichi Fujimoto, Alice Tsuboi 、Competition for space is controlled by apoptosis-induced change of local epithelial topology、Quantitative Life Science Workshop、2018/10/15-18、Seoul, Korea
14. Kuhihiko Kaneko、Complex-Systems Approach to an Ecosystem of Interacting Cells: Differentiation, Symbiosis, and Diversification、Research meeting: Principles of Microbial Ecosystems 2018、2018/9/4、Tokyo
15. Koichi Fujimoto, Miho S. Kitazawa、Constrained variation of floral organ arrangement in basal eudicots: a

- correlation with species diversity of the organ number. Euro Evo Devo, 2018/6/26-29, Galway, Ireland
16. Kuhihiko Kaneko, Phenotypic robustness, fluctuations and plasticity, 7th Euro Evo Devo, 2018/6/27, Galway, Ireland
 17. Kenji Okubo, Kunihiko Kaneko, Evolution and Genetics of Gene Regulatory Network in Diploid Recombination, 25th International Congress on Sexual Plant Reproduction, 2018/6/12, Gifu, Japan
 18. Kunihiko Kaneko, Reproduction of a Set of Diverse Molecules, Minority Control, and Arrival of Evolvability, Workshop "Puzzles and Solutions in Astrobiology", 2018/5/14, Tokyo, Japan
 19. Kuhihiko Kaneko, Is a macroscopic description of biological systems possible? , Physics of Living Matter, 2018/4/25, USA
 20. Miho S. Kitawaza, Koichi Fujimoto , Constrained variation in organ arrangements of basal eudicot flowers , The 1st AsiaEvo Conference, 2018/4/18-20, Shenzhen, China
 21. S Aoki, K Kaneko , Evolution of intracellular symbiosis: Theoretical approach , 1st AsiaEvo Conference, 2018/4/19, China
 22. T Sato, K Kaneko, Emergence of Low-dimensional Structure in Evolution of Highdimensional Cell Model, 1st AsiaEvo Conference, 2018/4/19, China uhihiko Kaneko, Phenotypic evolvability, 1st Asia Evo Conference, 2018/4/18, China
 23. Kunihiko Kaneko, Macroscopic Theory of Phenotypic Adaptation and Evolution: Fluctuation-Response, Genetic Assimilation, and Dimension Reduction, Evolution of Diversity, 2018/2/27, France
 24. Kenji Okubo, Robustness and Genetic Load of Gene Regulatory Network in Recombining Diploids, Evolution of Diversity, 2018/2/25, France
 25. Kunihiko Kaneko , Universality in Phenotypic Adaptation and Evolution: Fluctuationresponse, Genetic Assimilation, and Dimension Reduction, Non-equilibrium dynamics and information processing in biology, 2018/2/7, Okinawa, Japan
 26. Motohiro Fujiwara, Shunsuke Miyashima, Keiji Nakajima, Koichi Fujimoto, Localized cell proliferation and growth regulate root vascular bundle cell patterning, Taiwan-Japan Plant Biology 2017, 2017/11/3-5, Taipei, Taiwan
 27. Kunihiko Kaneko, Universality in Biology? Fluctuation-response relationship and Deep Linearity in Adaptation and Evolution, ENS-UTokyo symposium, 2017/11/, Tokyo, Japan
 28. Kunihiko Kaneko, Universality in Biology?: (I) Consistency Principle for Complex Systems-Biology (II) Robustness, Plasticity in Adaptation and Evolution, EON Workshop on Universal Biology, 2017/8/25, Tokyo, Japan
 29. Takeuchi N., Hogeweg P., Kaneko K., The Origin of a Genome Through Spontaneous Symmetry Breaking: A Computational Modeling Study, 18th International Conference on the Origin of Life, 2017/7/20, USA
 30. Kunihiko Kaneko, Macroscopic Theory of Phenotypic Adaptation and Evolution: Fluctuation-response, Genetic Assimilation, and Deep Linearity, 117th Statistical Mechanics Conference, 2017/5/, USA
 31. Kunihiko Kaneko, From a set of catalytic reactions to reproduction of cells: Perspective from Universal Biology, The Origin of Life Workshop, 2017/5/, Tokyo, Japan

計画・入江直樹

1. Irie, N. Can we predict evolutionary outcome of animal body plan? International Congress of Zoology (2021.Nov.24) Cape Town (online)
2. Irie, N. Internal factors of biological system that biases evolutionary outcome. ICG-16 (2021.Oct.28) Qindao(online)
3. Irie, N. Possible constraints by developmental robustness. AsiaEvo (2021.Aug.16) Tokyo (online)
4. Irie, N. Developmental robustness may bias macroevolutionary outcome. 17th Spanish Society for Developmental Biology Meeting (2020.Nov.19) Spain (online)
5. Irie, N. Potential double-edged sword effect of gene re-usage toward evolutionary diversification. Molecular Biology Society of Japan, Workshop: Phenotypic evolvability (2019.Dec.4) Hakata, Japan
6. Irie, N. Possible bias toward micro- and macro-evolutionary conservation by developmental systems Workshop reconciling micro-macro evolution (2019.Oct.28) Oslo, Norway
7. Irie, N. Do echinoderm embryos follow hourglass-like divergence? ICG-Ocean 2019 (2019.Sep.22) Qindao, China
8. Irie, N. Haeckel's recapitulation theory refuted by the hourglass model? 112th Annual Meeting of the German Zoological Society, Jena, Germany (2019.)
9. Irie, N. Development and Evolution. SERB School in Evolutionary Biology (2019.Mar.14) Bengaluru, India
10. Irie, N. The developmental hourglass model in animal embryogenesis. Developmental Biology of Sea Urchin and other Marine Invertebrates 2018, (2018.Oct.19) Woods Hole, USA
11. Irie, N. "Cost of complexity" contributed to the vertebrate bodyplan conservation? Euro EvoDevo 2018, (2018.Jun.26) Galway, Ireland
12. Irie, N. Gene re-usages constrained the evolvability of animal bodyplan? EvoDevo Seminar series, Cambridge University, Dept. of Zoology (2018.May.16) Cambridge, UK
13. Irie, N. "Cost of complexity" hypothesis supported in animal embryonic evolution? The 1st AsiaEvo conference (2018.Apr.18) ShenZhen, China

14. Irie, N. In search for a general law of animal embryonic evolution? The 12th International Workshop on Advanced Genomics [12AGW] (2017.Jun.29) Hitotsubashi Hall, Tokyo, Japan
15. Irie, N. What are the potential mechanisms that made vertebrates' bodyplan conserved? Symposium 03 - 50th Anniversary Meeting of Japanese Society of Developmental Biologists (2017.May.10) Tokyo, Japan
16. The developmental hourglass model: the law of embryonic evolution? From Genetic Networks to a Cellular Wiring Diagram (2017.Apr.26) Tokyo, Japan

計画・深津武馬

1. Fukatsu, T.* "Toward understanding the general principle of animal-microbe symbiosis", World Microbe Forum 2021, 21 June 2021, Online
2. Fukatsu, T.* "Symbiosis, Evolution, and Biodiversity" International Union of Microbiological Societies Congress 2020, 16-20 November 2020, Online.
3. Fukatsu T.* "Symbiosis, evolution, and biodiversity" International Symposium on Advanced Ecology and Evolution 2019, 16 July 2019, Tsukuba, Japan.
4. Oishi, S., Moriyama, M., Koga, R., and Fukatsu, T.* "Morphogenesis and development of midgut symbiotic organ of stinkbug" Gordon Research Conference on Animal-Microbe Symbioses, 17-20 June 2019, West Dover, VT, USA.
5. Kuechler, S.M., Tokuda, G., Fukatsu, T., and Matsuura, Y.* "Embryonic dynamics and symbiotic organ formation in lygaeoid bugs (Heteroptera: Lygaeoidea)" Gordon Research Conference on Animal-Microbe Symbioses, 19-20 June 2019, West Dover, VT, USA.
6. Fukatsu, T.* "Symbiosis for beetle's hardness" The 1st AsiaEvo Conference, 20 April 2018, Shenzhen, China.
7. Fukatsu, T.* "Recurrent replacement of eroding ancient endosymbiont by domesticated fungal pathogens" The 10th International Wolbachia Conference, 20 June 2018, Salem, MT, USA.
8. Fukatsu, T.* "Fate of extreme genome reduction in ancient bacterial endosymbionts" SMBE 2018, 9 July 2018, Yokohama, Japan.
9. Fukatsu, T.* "Symbiosis, evolution and biodiversity" The 46th Naito Conference on Mechanisms of Evolution and Biodiversity, 3 October 2018, Sapporo, Japan.
10. Koga, R.* "An experimental approach for deciphering the first steps in the evolution of essential insect symbiosis" The 46th Naito Conference on Mechanisms of Evolution and Biodiversity, 3 October 2018, Sapporo, Japan.
11. Moriyama, M.* "Gut symbiotic bacteria confer insect body pigmentation" The 46th Naito Conference on Mechanisms of Evolution and Biodiversity, 3 October 2018, Sapporo, Japan.
12. Fukatsu, T.* "Symbiosis for cuticle hardness of beetles" The 29th CDB Meeting "Mavericks, New Models in Developmental Biology", 19 October 2017, Kobe, Japan.

計画・古澤力

1. Furusawa, C. "Toward prediction and control of microbial evolution: Analysis of phenotypic constraints in laboratory evolution", BDR Symposium 2022, Mar. 5 2022, Online
2. Wakamoto, Y. "Inferring multi-omics states from cellular Raman spectra" 2022 AIST-KU Joint Workshop – Recent Trends in Biosensing and Bioimaging, Feb. 2 2022, Online
3. Furusawa, C. "Toward prediction and control of microbial evolution: Analysis of phenotypic constraints", 2nd AsiaEvo Conference, Aug. 16 2021, Online
4. Furusawa, C. "Toward prediction and control of microbial evolution: Analysis of phenotypic constraints", Quantitative evolution, phylogeny and ecology: from models to data and back, Feb 2 2021, Online
5. Furusawa, C. "High-dimensional data acquisition for analysis of microbial evolution and ecology", The 29th Hot Spring Harbor International Symposium, Feb. 7 2020, Hakata, Japan.
6. Furusawa, C. "Analysis of Evolutionary Constraints and Plasticity by Microbial Laboratory Evolution and Computational Models", 2nd Joint Symposium between MBI and UBI, Sep. 19 2019, Hongo, Tokyo.
7. Nakaoka, H., Wakamoto, Y. "Slow adaptation to low-glucose environments", 10th International Fission Yeast Meeting POMBE, July 17 2019, Barcelona, Spain.
8. Furusawa, C. "High-dimensional data acquisition for analysis of microbial evolution and ecology", The 1st Symposium of China-Japan Joint Laboratory for Natural Products and Chemical Biology--Trends in Gut Microbiome Research, Dec. 3 2019, Hangzhou, China.
9. Furusawa, C. "Analysis of Evolutionary Constraints and Plasticity by Microbial Laboratory Evolution and Computational Models", From Molecular Basis to Predictability and Control of Evolution, July 12 2019, Stockholm, Sweden.
10. Furusawa, C. "Analysis of Phenotypic Constraints and Plasticity by Microbial Laboratory Evolution", The 20th International Conference on Systems Biology, Nov 4 2019, Okinawa, Japan.
11. Furusawa, C. "High-throughput Laboratory Evolution of E. coli to Unveil Phenotypic Plasticity and Constraint", The 46th Naito Conference Mechanisms of Evolution and Biodiversity, Oct. 2 2018, Sapporo, Japan.
12. Furusawa, C. "High-throughput laboratory evolution of E. coli: toward understanding of phenotypic plasticity and constraint", Euro EvoDevo 2018, Jun. 26 2018, Galway, Ireland.
13. Furusawa, C. "High-throughput Laboratory Evolution of E. coli to Unveil Phenotypic Plasticity and Constraint", 1st AsiaEvo, Apr. 18 2018, Shenzhen, China.

14. Furusawa, C. "Phenotypic diversity and constraints in microbial adaptive evolution", Les Houches Winter School "Evolution of Diversity", Feb. 25 2017, Les Houches, France.

15.

計画・長谷部光泰

1. Hasebe, M. "Evolution of movement and carnivory in flowering plants" The 29th Center of Developmental Biology Meeting "Mavericks, New Models in Developmental Biology", October 23 2017, RIKEN CDB, Kobe, Japan.
2. Hasebe, M. "Genome biology to understand the evolution of carnivory and movement in plants" The 2017 International Symposium on Evolutionary Genomics and Bioinformatics, November 6 2017, Tzu Chi University, HuaRen, Taiwan.
3. Hasebe, M. "Effects of cellular changes to the evolution of land plant development and life cycle" The 65th NIBB Conference and Marchantia Workshop 2017, December 16-18 2017, NIBB, Okazaki, Japan.
4. Hasebe, M. "Evolution of plant carnivory and movement" Naito Conference, October 3 2018, Sapporo, Japan.
5. Hasebe, M. "Evolution of plant carnivory and movement", The international symposium in the Annual Meeting of the Society of Molecular Biology, November 28 2018, Yokohama, Japan.
6. Hasebe, M. "Evolution of Carnivory and movement in Plants", Japan Taiwan Plant Biology 2019, March 15 2019, Nagoya, Japan.
7. Hasebe, M. "Plastic responses to environmental stimuli in carnivorous plants", International Webinar on Plant Developmental Plasticity: A Molecular Perspective, September 28 2021, Acharya Nagarjuna Univ., India.

【図書】

1. 村上安則、倉谷 滋（コーディネーター）(2021) 「脳進化絵巻 -脊椎動物の進化神経学-」共立出版 234P
2. 倉谷滋 (2019). 進化する形 進化発生学入門（講談社現代新書）
3. 金子邦彦、澤井哲、高木拓明、古澤力. (2020) 細胞の理論生物学、東京大学出版会、345P
4. 金子邦彦. (2019) 普遍生物学：物理に宿る生命、生命の紡ぐ物理(東大出版会)、305P
5. 長谷部光泰 (2020) 「陸上植物の形態と進化」裳華房、248 pp
6. 市橋伯一 (2019) 協力と裏切りの生命進化史 (光文社新書)
7. 小林 徹也 編 (2018), 「定量生物学：生命現象を定量的に理解するために」, 化学同人, 278p.
8. 小林 徹也, 杉村, 薫, 舟橋, 啓 共編著者 (2020) 「機械学習を生命科学に使う！：シーケンスや画像データをどう解析し、新たな生物学的発見につなげるか？」, 羊土社, 238p

【研究成果による産業財産権の出願・取得状況】

1. 取得済み トランスクリプトーム推定装置およびトランスクリプトーム推定方法、特許、特許第 6993682 号 発明者：若本祐一、小林鉱石 出願年：2017 権利者：国立大学法人 東京大学 取得年：2021 国内
2. 取得済み TRANSCRIPTOME ESTIMATION DEVICE AND TRANSCRIPTOME ESTIMATION METHOD、特許、US 10,379,052 B2 発明者：Yuichi Wakamoto, Koseki Kobayashi 出願年：2018 権利者：The University of Tokyo 取得年：2019 海外

研究成果

本領域では、個体間差や環境変化による表現型変化、発生上の揺らぎなど、短期的時間スケールで観察される表現型揺らぎを定量し、長期的な時間スケールで起こる表現型進化の制約や方向性との関係を実験的に解析、それに基づき、揺らぎ応答進化理論の検証と修正を行い、制約進化理論を構築する。その目的に向けて、[研究項目1] 表現型の揺らぎ・環境応答の定量解析、[研究項目2] 進化的制約・方向性の定量解析、[研究項目3] 制約進化理論の構築、の3項目のもとに研究を行うこととした。進化学全体における普遍的な原理を探求するため、分子から生態系レベルにわたる多様な生物材料と、多様な進化現象（遺伝子発現プロファイル進化、環境耐性進化、発生進化、共生進化等）を対象とした。

【研究項目1】 表現型揺らぎと環境応答・進化応答を定量するため、各班が異なった生物材料を用いて研究を進めた結果、領域発足前は大腸菌を用いた実験（下記古澤班）のみにより妥当性が示されていた揺らぎ応答進化理論が、分子進化（下記市橋班）、個体発生（下記入江班）など様々な階層において成り立つことが示され、当初目的を達成した。

【研究項目2】 進化の時間スケールの異なる大腸菌、出芽酵母、脊椎動物を用いて、表現型進化がどのように制約をされているかを定量的に解析し、その背後にあるメカニズムを推察できるデータ取得を実現、その進化的制約からの逸脱がどのように生じるかに関して新たな知見を得ることに成功した。例えば、大腸菌ではどの薬剤に耐性になるかに制約がかかっていたが、それは、転写因子による制御のバランスに由来していることがわかった。さらに、脊椎動物の発生過程では、器官形成期に環境変動や突然変異による変化表現型変化が小さいという制約がかかっていたが、これは、異なる発生ステージ間の制御遺伝子の使いまわしに由来していることがわかった。以上から、さまざまな生物における異なった時間スケールの進化において生じる制約は、どれも遺伝子制御ネットワークにおけるバランスによって引き起こされている可能性が高いことがわかり、当初目標を達成した。

【研究項目3】 金子班を中心として行われた理論的研究に加え、金子班・古澤班・倉谷班・大林班の共同研究により、揺らぎ応答進化理論の適用範囲が進化過程を経ることによって拡大することがわかった。そして、従来の揺らぎ応答進化理論に、異なる階層間の相互作用を加えることで、細胞内の分子集団やホスト-ペラサイト系などの生態系において、表現型進化の制約や進化のしやすい方向性を定量的に推定できるようになった。

以上のように、表現型の揺らぎと進化の制約・方向性について、分子レベルから生態系レベルまで様々な階層での定量解析が進み、揺らぎ応答進化理論が広い範囲で成り立つことが示された。さらに、表現型の少数自由度への制約や階層進化理論など、従来の揺らぎ応答進化理論を超える枠組みの構築に成功した。本領域の申請時には、計画班により細胞レベルから動植物などの多細胞レベルの解析が計画されていたが、公募班の参入により、分子レベル（市橋班・上野班）や微生物生態系（細田班）など、当初の予定を超えた多様な階層において、表現型揺らぎと進化的制約の関係が明らかとなった。これらの結果は、設定目標を予定通り達成するとともに、今後の進化学に大きな影響を与える包括的な進化理論の構築をもたらしたことから、目標を達成できたと判断している。