

Diethard Tautz

Publication list grouped according to research topics

Each topic is introduced with a few sentences and the most important publications in the context are labeled with *. The order of the topics follows roughly a temporal sequence, the newest publications are listed first under each topic. Note that several publications could be listed under more than one topic, but they are restricted to single ones.

Simple sequences and genetic fingerprinting

This work started with my PhD thesis which dealt with a first generic description of simple sequences as repetitive components of eukaryotic genomes. At the time, I could only speculate that these sequences would be variable due to their generation by slippage processes. During my postdoc time in Cambridge, I developed a computer algorithm to generally trace the effects of slippage in sequences derived from public databases (which were still rather rare at the time) and to show that they were associated with fast evolutionary divergence. The proof for their usefulness in DNA fingerprinting was only possible after the development of PCR amplification. But given that I knew what to expect, I could quickly generate a proof of principle, which led also to a general patent application. This happened at the time during my move to Munich, where I conducted the further experiments. Since I had only very limited possibilities to work with human material at that time, I focused the further work on collaborations with partners from the behavioral ecology and population genetic fields, which resulted in a series of papers on different model systems (listed also under the topic "Behavioral ecology" and "Speciation").

Wolf, J.B.W., Tautz, D., Caccone, A., Steinfartz, S. (2005). Development of new microsatellite loci and evaluation of loci from other pinniped species for the Galapagos sea lion (*Zalophus californianus wollebaeki*). *Conservation Genetics* 7, 461-465.

Steinfartz, S., Küsters, D., Tautz, D. (2004). Isolation and characterization of polymorphic tetranucleotide microsatellite loci in the fire salamander *Salamandra salamandra* (Amphibia: Caudata). *Molecular Ecology Notes*, 4, 626-628.

Wilhelm, K., Dawson, D.A., Gentle, L.K., Horsfield, G.F., Schlötterer, C., Greig, C., East, M., Hofer, H., Tautz, D., Burke, T. (2003). Characterization of spotted hyena, *Crocuta crocuta* microsatellite loci. *Molecular Ecology Notes*, 3, 360-362.

Mayer, F., Schlötterer, C., Tautz, D. (2000). Polymorphic microsatellite loci in vespertilionid bats isolated from the noctule bat *Nyctalus noctula*. *Molecular Ecology*, 9, 2208-2209.

Haberl, M., Tautz, D. (1999). Tri- and tetranucleotide microsatellite loci in honey bees (*Apis mellifera*) - A step towards quantitative genotyping. *Molecular Ecology*, 8, 1358-1359.

Engbrecht, C.C., Largiader, C.R., Hänfling, B., Tautz, D. (1999). Isolation and characterization of polymorphic microsatellite loci in the European bullhead *Cottus gobio* L. (Osteichthyes) and their applicability to related taxa. *Molecular Ecology*, 8, 1966-1969.

Gockel, J., Harr, B., Schlötterer, C., Arnold, W., Gerlach, G., Tautz, D. (1997). Isolation and characterization of microsatellite loci from *Apodemus flavicollis* (Rodentia, Muridae) and *Clethrionomys glareolus* (rodentia, cricetidae). *Molecular Ecology*, 6, 597-599.

* Gerloff, U., Schlötterer, C., Rassmann, K., Rambold, I., Hohmann, G., Fruth, B., Tautz, D. (1995). Amplification of hypervariable simple sequence repeats (microsatellites) from excremental DNA of wild living bonobos (*Pan paniscus*). *Molecular Ecology*, 4, 515-518.

Tautz, D., Schlötterer, C. (1994). Simple sequences. *Current Opinion in Genetics and Development*, 4, 832-837.

Tautz, D. (1993). Notes on the definition and nomenclature of tandemly repetitive DNA sequences. pp 21-28. In *DNA Fingerprinting: State of the Science*, eds. S.D.J. Pena, R. Chakraborty, J.T. Epplen & A.J. Jeffreys, Birkhäuser Verlag, Basel.

Rassmann, K., Schlötterer, C., Tautz, D. (1991). Isolation of simple-sequence loci for use in polymerase chain reaction-based DNA fingerprinting. *Electrophoresis*, 12, 113-118.

Tautz, D. (1990). Genomic finger printing goes simple. *BioEssays*, 12, 44-46.

*Tautz, D. (1989). Hypervariability of simple sequences as a general source for polymorphic DNA markers. *Nucleic Acids Research*, 17, 6463-6471.

*Tautz, D., Trick, M., Dover, G.A. (1986). Cryptic simplicity in DNA is a major source of genetic variation. *Nature*, 322, 652-656.

- *Tautz, D., Renz, M. (1984). Simple sequences are ubiquitous repetitive components of eukaryotic genomes. *Nucleic Acids Research*, 12, 4127-4138.
- Tautz, D., Renz, M. (1984). Simple DNA sequences of *Drosophila virilis* isolated by screening with RNA. *Journal of Molecular Biology*, 172, 229-235.

Patterns of molecular evolution

My interests in the patterns of molecular evolution started with my PhD thesis and continues up to today. The papers listed here reflect this in various ways. Of particular importance are the papers that present evidence for episodic evolution, which is in contrast to the often-assumed clock-like evolution. They form the background for the concept of phylostratigraphy that is listed under "Evolution of new genes".

- * Prabh, N., Tautz, D. (2021). Frequent lineage-specific substitution rate changes support an episodic model for protein evolution. *G3 (Bethesda)* 11 (12): jkab333.
- Chebib, J., Jackson, B. C., Lopez-Cortegano, E., Tautz, D., Keightley, P. D. (2021). Inbred lab mice are not isogenic: genetic variation within inbred strains used to infer the mutation rate per nucleotide site. *Heredity* 126:107-116.
- Bekpen C, Tautz D. (2019). Human core duplicon gene families: game changers or game players? *Brief Funct Genomics elz016*: doi: 10.1093/bfgp/elz016
- Bekpen C, Xie C, Nebel A, Tautz D. (2018). Involvement of SPATA31 copy number variable genes in human lifespan. *Aging* 10: 674-688.
- Bekpen C, Künzel S, Xie C, Eaaswarkhanth M, Lin Y-L, Gokcumen O, Akdis CA, Tautz D. (2017). Segmental duplications and evolutionary acquisition of UV damage response in the SPATA31 gene family of primates and humans. *BMC Genomics* 18: 222
- * Savard, J., Tautz, D., Lercher, M.J. (2006). Genome-wide acceleration of protein evolution in flies (Diptera). *BMC Evol Biol.* 6: 7
- Tautz, D., Lässig, M. (2004). Of statistics and genomes. *Trends in Genetics*, 20, 344-346.
- Marais, G., Domazet-Lošo, T., Tautz, D., Charlesworth, B. (2004). Correlated evolution of synonymous and nonsynonymous sites in *Drosophila*. *Journal of Molecular Evolution*, 59, 771-779.
- Schmid, K.J., Tautz, D. (1999). A comparison of homologous developmental genes from *Drosophila* and *Tribolium* reveals major differences in length and trinucleotide repeat content. *Journal of Molecular Evolution*, 49, 558-566.
- Schmid, K.J., Nigro, L., Aquadro, C.F., Tautz, D. (1999). Large number of replacement polymorphisms in rapidly evolving genes of *Drosophila*: Implications for genome-wide surveys of DNA polymorphism. *Genetics*, 153 4, 1717-1729.
- Tautz, D., Nigro, L. (1998). Microevolutionary divergence pattern of the segmentation gene *hunchback* in *Drosophila*. *Molecular Biology and Evolution*, 15, 1403-1411.
- * Friedrich, M., Tautz, D. (1997). An episodic change of rDNA nucleotide substitution rate has occurred during the emergence of the insect order diptera. *Molecular Biology and Evolution*, 14, 644-653.
- Schlötterer, C., Vogl, C., Tautz, D. (1997). Polymorphism and locus-specific effects on polymorphism at microsatellite loci in natural *Drosophila melanogaster* populations. *Genetics*, 146, 309-320.
- Lukowitz, W., Schröder, C., Glaser, G., Hülskamp, M., Tautz, D. (1994). Regulatory and coding regions of the segmentation gene *hunchback* are functionally conserved between *Drosophila virilis* and *Drosophila melanogaster*. *Mechanisms of Development*, 45, 105-115.
- * Schlötterer, C., Tautz, D. (1994). Chromosomal homogeneity of *Drosophila ribosomal* DNA arrays suggests intrachromosomal exchanges drive concerted evolution. *Current Biology*, 4, 777-783.
- Schlötterer, C., Hauser, M.-T., Von Haeseler, A., Tautz, D. (1994). Comparative evolutionary analysis of rDNA ITS regions in *Drosophila*. *Molecular Biology and Evolution*, 11, 513-522.
- Sommer, R.J., Retzlaff, M., Goerlich, K., Sander, K., Tautz, D. (1992). Evolutionary conservation pattern of zinc-finger domains of *Drosophila* segmentation genes. *Proceedings of the National Academy of Sciences of the United States of America*, 89, 10782-10786.
- Schlötterer, C., Tautz, D. (1992). Slippage synthesis of simple sequence DNA. *Nucleic Acids Research*, 20, 211-215.
- * Schlötterer, C., Amos, B., Tautz, D. (1991). Conservation of polymorphic simple sequence loci in cetacean species. *Nature*, 353, 63-65.

- Treier, M., Pfeifle, C., Tautz, D. (1989). Comparison of the gap segmentation gene *hunchback* between *Drosophila melanogaster* and *Drosophila virilis* reveals novel modes of evolutionary change. *EMBO Journal*, 8, 1517-1525.
- Hancock, J.M., Tautz, D., Dover, G.A. (1988). Evolution of the secondary structures and compensatory mutations of the ribosomal RNAs of *Drosophila melanogaster*. *Molecular Biology and Evolution*, 5, 393-414.
- Tautz, D., Hancock, J.M., Webb, D.A., Tautz, C., Dover, G.A. (1988). Complete sequences of the rRNA genes of *Drosophila melanogaster*. *Molecular Biology and Evolution*, 5, 366-376.
- Tautz, D., Tautz, C., Webb, D., Dover, G.A. (1987). Evolutionary divergence of promoters and spacers in the rDNA family of four *Drosophila* species. Implications for molecular coevolution in multigene families. *Journal of Molecular Biology*, 195, 525-542.
- Dover, G.A., Tautz, D. (1986). Conservation and divergence in multigene families: alternatives to selection and drift. *Philosophical transactions of the Royal Society of London. Series B: Biological sciences*, 312, 275-289.
- Tautz, D., Dover, G.A. (1986). Transcription of the tandem array of ribosomal DNA in *Drosophila melanogaster* does not terminate at any fixed point. *EMBO Journal*, 5, 1267-1273.
- Franz, G., Tautz, D., Dover, G.A. (1985). Conservation of major nuclease S1-sensitive sites in the non-conserved spacer region of ribosomal DNA in *Drosophila* species. *Journal of Molecular Biology*, 183, 519-527.

Behavioural ecology

This topic lists papers that resulted from collaborations with partners (including two PhD students with their own systems) interested in applying simple sequence-based fingerprinting to population samples that were of particular relevance to questions of behavioral ecology, mate selection and fitness.

- Steinfartz, S., Stemshorn, K., Kuesters, D., Tautz, D. (2006). Patterns of multiple paternity within and between annual reproduction cycles of the fire salamander (*Salamandra salamandra*) under natural conditions *Journal of Zoology*, 268, 1-8.
- * Kappeler, P.M., Wimmer, B., Zinner, D., Tautz, D. (2002). The hidden matrilineal structure of a solitary lemur: Implications for primate social evolution. *Proceedings of the Royal Society - Biological Sciences (Series B)*, 269, 1755-1763.
- Haberl, M., Tautz, D. (1999). Paternity and maternity frequencies in *Apis mellifera sicula*. *Insectes Sociaux*, 46, 137-145.
- Hohmann, G., Gerloff, U., Tautz, D., Fruth, B. (1999). Social bonds and genetic ties: Kinship, association and affiliation in a community of bonobos (*Pan paniscus*). *Behaviour*, 136, 1219-1235.
- *Gerloff, U., Hartung, B., Fruth, B., Hohmann, G., Tautz, D. (1999). Intracommunity relationships, dispersal pattern and paternity success in a wild living community of Bonobos (*Pan paniscus*) determined from DNA analysis of faecal samples. *Proceedings of the Royal Society - Biological Sciences (Series B)*, 266, 1189-1195.
- Haberl, M., Tautz, D. (1998). Sperm usage in honey bees. *Behavioral Ecology and Sociobiology*, 42, 247-255.
- Petri, B., Pääbo, S., von Haeseler, A., Tautz, D. (1997). Paternity assessment and population subdivision in a natural population of the larger mouse-eared bat *Myotis myotis*. *Molecular Ecology*, 6, 235-242.
- *Amos, B., Schlötterer, C., Tautz, D. (1993). Social structure of pilot whales revealed by analytical DNA profiling. *Science*, 260, 670-672.

Drosophila segmentation

The work on *Drosophila* segmentation genes started with my move back from Cambridge to the group of Herbert Jäckle in Tübingen. It started with the cloning of the gap gene *hunchback* and continued with a general analysis of regulatory interactions of maternal genes and gap genes in the early segmentation gene cascade. The work showed that the maternal and zygotic *hunchback* gradient is crucially involved in setting up the anterior posterior segmentation pattern in *Drosophila*.

- * Schulz, C., Tautz, D. (1994). Autonomous concentration-dependent activation and repression of *Krüppel* by *hunchback* in the *Drosophila* embryo. *Development*, 120, 3043-3049.

- Hülskamp, M., Lukowitz, W., Beermann, A., Glaser, G., Tautz, D. (1994). Differential regulation of target genes by different alleles of the segmentation gene *hunchback* in *Drosophila*. *Genetics*, 138, 125-134.
- Tautz, D. (1992). Genetic and molecular analysis of early pattern formation in *Drosophila*. pp 308-327. In *Development: The molecular genetic Approach*, eds. V.E.A. Russo, S. Brody, D. Cove, S. Ottolenghi & G.B. Ruvkun, Springer Verlag, Heidelberg.
- Hülskamp, M., Tautz, D. (1991). Gap genes and gradients - The logic behind the gaps. *BioEssays*, 13, 261-268.
- Tautz, D. (1991). Genetic and molecular analysis of pattern formation processes in *Drosophila*. pp 273-282. In *Constructional morphology and evolution*, eds. N. Schmidt-Kittler and K. Vogel, Springer Verlag, Heidelberg.
- *Hülskamp, M., Pfeifle, C., Tautz, D. (1990). A morphogenetic gradient of *hunchback* protein organizes the expression of the gap genes *Krüppel* and *knirps* in the early *Drosophila* embryo. *Nature*, 346, 577-580.
- *Hülskamp, M., Schröder, C., Pfeifle, C., Jäckle, H., Tautz, D. (1989). Posterior segmentation of the *Drosophila* embryo in the absence of a maternal posterior organizer gene. *Nature*, 338, 629-632.
- Schröder, C., Tautz, D., Seifert, E., Jäckle, H. (1988). Differential regulation of the two transcripts from the *Drosophila* gap segmentation gene *hunchback*. *EMBO Journal*, 7, 2881-2887.
- *Tautz, D. (1988). Regulation of the *Drosophila* segmentation gene *hunchback* by two maternal morphogenetic centres. *Nature*, 332, 281-284.
- *Tautz, D., Lehmann, R., Schnürch, H., Schuh, R., Seifert, E., Kienlin, A., Jones, K., Jäckle, H. (1987). Finger protein of novel structure encoded by *hunchback*, a second member of the gap class of *Drosophila* segmentation genes. *Nature*, 327, 383-389.
- Tautz, D., Jäckle, H. (1987). Molecular analysis of regulatory genes in *Drosophila* segmentation. pp 125-136. In *Hormones and Cell Regulation XI*, eds J. E. Dumont & J. Nunez, John Libbey & Co, Montrouge (France), Vol. 153.
- Jäckle, H., Tautz, D., Schuh, R., Seifert, E., Lehmann, R. (1986). Cross-regulatory interactions among the gap genes of *Drosophila*. *Nature*, 324, 668-670.

Evolution of developmental processes

This research topic developed out of my combined interests in evolutionary patterns and genetic mechanisms of developmental processes. It started with a comparative analysis of segmentation genes in other insects, but broadened quickly into other arthropods and eventually also zebrafish. Most of the work was done in Munich (Department of Zoology) and in Cologne. In Cologne it broadened also into comparative analyses of neuronal development and appendage development. Central to much of the work was the development of the beetle *Tribolium*, which resulted also in a large collaboration for a genome project. Among the key discoveries were a re-writing of the text books on head segment homologies in arthropods and a segmentation gene that coded for polycistronic microproteins.

- Tautz D. (2019). The continued mystery of the phylotypic stage. In *Perspectives on Evolutionary and Developmental Biology*, edit. Fusco, G., pp. 141-149, Padova University Press
- Aranda, M., Marques-Souza, H., Bayer, T., Tautz, D. (2008). The role of the segmentation gene *hairy* in *Tribolium*. *Development Genes and Evolution* 218: 465-477.
- Tribolium Sequencing Consortium (2008). The genome of the model beetle and pest *Tribolium castaneum* *Nature* 452, 949-955.
- Marques-Souza H., Aranda M., Tautz D. (2008). Delimiting the conserved features of *hunchback* function for the trunk organization of insects. *Development* 135, 881-888.
- * Savard, J., Marques-Souza, H., Aranda, M., Tautz, D. (2006). A segmentation gene in *Tribolium* produces a polycistronic mRNA that codes for multiple conserved peptides. *Cell* 126, 559 - 569.
- Sieger, D., Ackermann, B., Tautz, D. Gajewski, M. (2006). *her1* and *her13.2* homologues are jointly required for somitic border specification along the entire axis of the fish embryo *Developmental Biology* 293, 242-251.
- Prpic, N.-M., Janssen, R., Damen, W.G.M., Tautz, D. (2005). Evolution of dorsal-ventral axis formation in arthropod appendages: *H15* and *optomotor-blind/bifid*-type T-box genes in the millipede *Glomeris marginata* (Myriapoda: Diplopoda). *Evolution and Development*, 7, 51-57.
- Hartenstein, V., Tautz, D. (2004). Development genes and evolution – Founded as Roux's archives of development biology *Development Genes and Evolution* 214, 579-581.
- Sieger, D., Tautz, D., Gajewski, M. (2004). *her11* is involved in the somitogenesis clock in zebrafish. *Development Genes and Evolution*, 214, 393-406.

- Eckert, C., Aranda, M., Wolff, C., Tautz, D. (2004). Separable stripe enhancer elements for the pair-rule gene *hairy* in the beetle *Tribolium*. *EMBO Reports*, 5, 638-642.
- Tautz, D. (2004). Segmentation. *Developmental Cell*, 7, 301-312.
- Tautz, D. (2003). Chordate evolution in a new light. *Cell*, 113, 812-813.
- Weller, M., Tautz, D. (2003). *Prospero* and *snail* expression during spider neurogenesis. *Development Genes and Evolution*, 213, 554-566.
- Stollewerk, A., Tautz, D., Weller, M. (2003). Neurogenesis in the spider: New insights from comparative analysis of morphological processes and gene expression patterns. *Arthropod Structure and Development*, 32, 5-16.
- Sieger, D., Tautz, D., Gajewski, M. (2003). The role of Suppressor of Hairless in Notch mediated signalling during zebrafish somitogenesis. *Mechanisms of Development*, 120, 1083-1094.
- Prpic, N.-M., Tautz, D. (2003). The expression of the proximodistal axis patterning genes *Distal-less* and *dachshund* in the appendages of *Glomeris marginata* (Myriapoda: Diplopoda) suggests a special role of these genes in patterning the head appendages. *Developmental Biology*, 260, 97-112.
- Gajewski, M., Sieger, D., Alt, B., Leve, C., Hans, S., Wolff, C., Rohr, K.B., Tautz, D. (2003). Anterior and posterior waves of cyclic *her1* gene expression are differentially regulated in the presomitic mesoderm of zebrafish. *Development*, 130, 4269-4278.
- Tautz, D. (2002). entry "Regulatory Genes" in *Encyclopedia of Evolution*, ed. Pagel, M., Oxford University Press
- Tautz, D. (2002). entry "Segmentation" in *Encyclopedia of Evolution*, ed. Pagel, M., Oxford University Press
- Beermann, A., Jay, D.G., Beeman, R.W., Hülkamp, M., Tautz, D., Jürgens, G. (2001). The *Short antennae* gene of *Tribolium* is required for limb development and encodes the orthologue of the *Drosophila* distal-less protein. *Development*, 128, 287-297.
- Leve, C., Gajewski, M., Rohr, K.B., Tautz, D. (2001). Homologues of *c-hairy1* (*her9*) and *lunatic fringe* in zebrafish are expressed in the developing central nervous system, but not in the presomitic mesoderm. *Development Genes and Evolution*, 211, 493-500.
- * Stollewerk, A., Weller, M., Tautz, D. (2001). Neurogenesis in the spider *Cupiennius salei*. *Development*, 128(14), 2673-2688.
- Schröder, R., Eckert, C., Wolff, C., Tautz, D. (2000). Conserved and divergent aspects of terminal patterning in the beetle *Tribolium castaneum*. *Proceedings of the National Academy of Sciences of the United States of America*, 97, 6591-6596.
- * Damen, W.G.M., Weller, M., Tautz, D. (2000). Expression patterns of *hairy*, *even-skipped*, and *runt* in the spider *Cupiennius salei* imply that these genes were segmentation genes in a basal arthropod. *Proceedings of the National Academy of Sciences of the United States of America*, 97, 4515-4519.
- Tautz, D. (2000). Evolution of transcriptional regulation. *Current Opinion in Genetics and Development*, 10, 575-579.
- Damen, W.G.M., Tautz, D. (1999). Comparative molecular embryology of arthropods: The expression of Hox genes in the spider *Cupiennius salei*. *Invertebrate Reproduction and Development*, 36, 203-209.
- Rohr, K.B., Schulte-Merker, S., Tautz, D. (1999). Zebrafish *zic1* expression in brain and somites is affected by BMP and hedgehog signalling. *Mechanisms of Development*, 85, 147-159.
- Schröder, R., Jay, D.G., Tautz, D. (1999). Elimination of *EVE* protein by CALI in the short germ band insect *Tribolium* suggests a conserved pair-rule function for *even skipped*. *Mechanisms of Development*, 80, 191-195.
- Damen, W.G.M., Tautz, D. (1999). *Abdominal-B* expression in a spider suggests a general role for *Abdominal-B* in specifying the genital structure. *Journal of Experimental Zoology –Part B – Molecular and developmental evolution*, 285, 85-91.
- Rohr, K.B., Tautz, D., Sander, K. (1999). Segmentation gene expression in the mothmidge *Clogmia albipunctata* (Diptera, Psychodidae) and other primitive dipterans. *Development Genes and Evolution*, 209, 145-154.
- Tautz, D. (1998). Debatable homologies. *Nature*, 395, 17-19.
- Schulz, C., Schröder, R., Hausdorf, B., Wolff, C., Tautz, D. (1998). A *caudal* homologue in the short germ band beetle *Tribolium* shows similarities to both, the *Drosophila* and the vertebrate *caudal* expression patterns. *Development Genes and Evolution*, 208, 283-289.
- Wolff, C., Schröder, R., Schulz, C., Tautz, D., Klingler, M. (1998). Regulation of the *Tribolium* homologues of *caudal* and *hunchback* in *Drosophila*: evidence for maternal gradient systems in a short germ embryo. *Development*, 125, 3645-3654.
- Damen, W.G.M., Tautz, D. (1998). A Hox class 3 orthologue from the spider *Cupiennius salei* is expressed in a Hox-gene-like fashion. *Development Genes and Evolution*, 208, 586-590.

- * Damen, W.G.M., Hausdorf, M., Seyfarth, E.-A., Tautz, D. (1998). A conserved mode of head segmentation in arthropods revealed by the expression pattern of Hox genes in a spider. *Proceedings of the National Academy of Sciences of the United States of America*, 95, 10665-10670.
- Tautz, D. (1996). Selector genes, polymorphisms, and evolution. *Science*, 271, 160-161.
- Li, Y., Brown, S.J., Hausdorf, B., Tautz, D., Denell, R.E., Finkelstein, R. (1996). Two *orthodenticle*-related genes in the short-germ beetle *Tribolium castaneum*. *Development Genes and Evolution*, 206, 35-45.
- Falciani, F., Hausdorf, B., Schröder, R., Akam, M., Tautz, D., Denell, R., Brown, S. (1996). Class 3 Hox genes in insects and the origin of *zen*. *Proceedings of the National Academy of Sciences of the United States of America*, 93, 8479-8484.
- Schulz, C., Tautz, D. (1995). Zygotic *caudal* regulation by *hunchback* and its role in abdominal segment formation of the *Drosophila* embryo. *Development*, 121, 1023-1028.
- Tautz, D., Sommer, R.J. (1995). Evolution of segmentation genes in insects. *Trends in Genetics*, 11, 23-27.
- Wolff, C., Sommer, R., Schröder, R., Glasert, G., Tautz, D. (1995). Conserved and divergent expression aspects of the *Drosophila* segmentation gene *hunchback* in the short germ band embryo of the flour beetle *Tribolium*. *Development*, 121, 4227-4236.
- Sommer, R.J., Tautz, D. (1994). Expression patterns of *twist* and *snail* in *Tribolium* (Coleoptera) suggest a homologous formation of mesoderm in long and short germ band insects. *Developmental Genetics*, 15, 32-37.
- Tautz, D., Friedrich, M., Schroder, R. (1994). Insect embryogenesis - What is ancestral and what is derived? *Development*, 120 SUPPL., 193-199.
- Tautz, D. (1994). Evolutionary analysis of genes involved in early pattern formation in *Drosophila*. pp 525-536. In *Molecular Ecology and Evolution: Approaches and Applications*, eds. B. Schierwater, B. Streit, G.P. Wagner and R. DeSalle, Birkhäuser Verlag, Basel.
- * Sommer, R.J., Tautz, D. (1993). Involvement of an orthologue of the *Drosophila* pair-rule gene *hairy* in segment formation of the short germ-band embryo of *Tribolium* (Coleoptera). *Nature*, 361, 448-450.
- Tautz, D. (1992). Redundancies, development and the flow of information. *BioEssays*, 14, 263-266.
- Sommer, R., Tautz, D. (1991). Asynchronous mitotic domains during blastoderm formation in *Musca domestica* L. (Diptera). *Roux's Archives of Developmental Biology*, 199, 373-376.
- Sommer, R., Tautz, D. (1991). Segmentation gene expression in the housefly *Musca domestica*. *Development*, 113, 419-430.

Molecular phylogeny

The work on molecular phylogeny reconstruction was triggered by the need to re-evaluate homology relationships among the organisms that we used for the evo-devo work. The work started directly with a major discovery on the phylogenetic relationship among the major arthropod lineages, which went against seemingly well-established text-book knowledge. Another major finding was a revised relationship among insect lineages, based on the data that we generated for the *Tribolium* genome project.

- Schwarzer, J., Misof, B., Tautz, D., Schliewen, U.K. (2009). The root of the East African cichlid radiations. *BMC Evolutionary Biology* 9, 186.
- Tautz, D. (2007). Morphologie versus DNA-Sequenzen in der Phylogenie-Rekonstruktion *Species, Phylogeny and Evolution* 1, 9-16.
- * Savard, J., Tautz, D., Richards, S., Weinstock, G.M., Gibbs, R.A., Werren, J.H., Tettelin, H., Lercher, M.J. (2006). Phylogenomic Analysis Reveals Bees and Wasps (Hymenoptera) at the Base of the Radiation of Holometabolous Insects. *Genome Research* 16, 1334-1338.
- Steinfartz, S., Hwang, U.W., Tautz, D., Oz, M., Veith, M. (2002). Molecular phylogeny of the salamandrid genus *Neuregus*: Evidence for an intrageneric switch of reproductive biology. *Amphibia Reptilia*, 23, 419-431.
- Friedrich, M., Tautz, D. (2001). Arthropod rDNA phylogeny revisited: A consistency analysis using Monte Carlo simulation. *Annales de la Societe Entomologique de France*, 37, 21-40.
- * Hwang, U.W., Friedrich, M., Tautz, D., Park, C.J., Kim, W. (2001). Mitochondrial protein phylogeny joins myriapods with chelicerates. *Nature*, 413, 154-157.
- Gagneux, P., Wills, C., Gerloff, U., Tautz, D., Morin, P.A., Boesch, C., Fruth, B., Hohmann, G., Ryder, O.A., Woodruff, D.S. (1999). Mitochondrial sequences show diverse evolutionary histories of African hominoids. *Proceedings of the National Academy of Sciences of the United States of America*, 96, 5077-5082.

- Hwang, U.W., Kim, W., Tautz, D., Friedrich, M. (1998). Molecular Phylogenetics at the Felsenstein Zone: Approaching the Strepsiptera Problem Using 5.8S and 28S rDNA Sequences. *Molecular Phylogenetics and Evolution*, 9, 470-480.
- Friedrich, M., Tautz, D. (1997). Evolution and phylogeny of the Diptera: A molecular phylogenetic analysis using 28S rDNA sequences. *Systematic Biology*, 46, 674-694.
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Population genetic patterns

My lab attracted several times highly gifted PhD students who were interested to use molecular markers to unravel population genetic patterns. They came with specific expertise on their model system and made use of the molecular typing infrastructure in my lab. Some of these projects developed also into explicit speciation mechanism studies that are separately listed.

- Krehenwinkel, H., Tautz, D. (2015). Eco-genomic analysis of the poleward range expansion of the wasp spider *Argiope bruennichi* shows rapid adaptation and genomic admixture. *Global Change Biology* 21: 4320-4332.
- * Krehenwinkel, H., Tautz, D. (2013). Northern range expansion of European populations of the wasp spider *Argiope bruennichi* is associated with global warming-correlated genetic admixture and population-specific temperature adaptations. *Molecular Ecology* 22, 2232-2248.
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- * Steinfartz, S., Veith, M., Tautz, D. (2000). Mitochondrial sequence analysis of *Salamandra* taxa suggests old splits of major lineages and postglacial recolonizations of Central Europe from distinct source populations of *Salamandra salamandra*. *Molecular Ecology*, 9, 397-410.
- * Engbrecht, C.C., Freyhof, J., Nolte, A., Rassmann, K., Schliewen, U., Tautz, D. (2000). Phylogeography of the bullhead *Cottus gobio* (Pisces: Teleostei: Cottidae) suggests a pre-Pleistocene origin of the major central European populations. *Molecular Ecology*, 9, 709-722.
- Rassmann, K., Trillmich, F., Tautz, D. (1997). Hybridization between the Galapagos land and marine iguana (*Conolophus subcristatus* and *Amblyrhynchus cristatus*) on Plaza Sur. *Journal of Zoology*, 242, 729-739.
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- Rassmann, K., Arnold, W., Tautz, D. (1994). Low genetic variability in a natural alpine marmot population (*Marmota marmota*, Sciuridae) revealed by DNA fingerprinting. *Molecular Ecology*, 3, 347-353.

Speciation

Thinking about mechanisms of speciation were triggered by my discussions with students and postdocs in Cambridge. But the first real project in this field started with Uli Schliewen in Munich, who was interested in demonstrating a case of sympatric speciation of Cichlids in a crater lake in Cameroon. We went on an expedition to collect the samples and Uli used the expertise for mitochondrial sequence analysis in Svante Pääbo's lab at that time to show a monophyletic origin of the lineages in the lake. This turned out to be the first demonstration for unequivocal sympatric speciation that was even accepted by Ernst Meyer. This was the start of several further projects on patterns of speciation, including the first discovery of very rapid hybrid speciation. Papers on mouse speciation questions are listed under "Wildmouse as a model system".

- Ornelas-García, C.P., Elena G. Gonzalez, E.G., Tautz, D., Doadrio, I. (2023). Lack of genetic differentiation between two sympatric lacustrine morpho-species within the *Astyanax* (Characidae: Teleostei) genus, Mexico. *Ichthyological Research*, <https://doi.org/10.1007/s10228-023-00917-1>

- Stemshorn, K.C., Reed, F.A., Nolte, A.W., Tautz, D. (2011). Rapid formation of distinct hybrid lineages after secondary contact of two fish species (*Cottus* sp.). *Molecular Ecology* 20, 1475-1491.
- * Nolte, A.W., Tautz, D. (2010). Understanding the onset of hybrid speciation. *Trends in Genetics* 26, 54-58.
- * Wolf, J.B.W., Bayer, T., Haubold, B., Schilhabel, M., Rosenstiel, P., Tautz, D. (2010). Nucleotide divergence versus gene expression differentiation: 454 transcriptome sequencing in natural isolates from the carrion crow and its hybrid zone with the hooded crow. *Molecular Ecology Suppl.* 1, 162 - 175.
- Wolf, J.B., Harrod, C., Brunner, S., Salazar, S., Trillmich, F., Tautz, D. (2008). Tracing early stages of species differentiation: ecological, morphological and genetic divergence of Galápagos sea lion populations. *BMC Evol Biology* 8,150.
- * Steinfartz, S., Weitere, M., Tautz, D. (2007). Tracing the first step to speciation: ecological and genetic differentiation of a salamander population in a small forest. *Molecular Ecology* 16, 4550 - 4561.
- Wolf, J.B.W., Tautz, D., Trillmich, F. (2007). Galapagos and Californian sea lions are separate species: genetic analysis of the genus *Zalophus* and its implications for conservation management. *Frontiers in Zoology* 4, 20.
- Schliewen, U.K., Kocher, T.D., McKaye, K.R., Seehausen, O., Tautz, D. (2006). Evolutionary biology: evidence for sympatric speciation? *Nature* 444, E12-13.
- Nolte, A.W., Freyhof, J., Tautz, D. (2006). When invaders meet locally adapted types: rapid moulding of hybrid zones between two species of sculpins (*Cottus*, Pisces) in the Rhine system *Molecular Ecology* 15, 1983-1993.
- * Nolte, A.W., Freyhof, J., Stemshorn, K.C., Tautz, D. (2005). An invasive lineage of sculpins, *Cottus* sp. (Pisces, Teleostei) in the Rhine with new habitat adaptations has originated from hybridization between old phylogeographic groups. *Proceedings of the Royal Society - Biological Sciences (Series B)*, 272, 2379-2387.
- Doebeli, M., Dieckmann, U., Metz, J.A.J., Tautz, D. (2005). What we have also learned: Adaptive speciation is theoretically plausible. *Evolution*, 59, 691-695.
- Tautz, D. (2004). Phylogeography and patterns of incipient speciation. In *Adaptive speciation*, eds. U. Dieckmann, M. Doebeli, H. Metz and D. Tautz, Cambridge University Press.
- Tautz, D. (2003). Evolutionary biology: Splitting in space. *Nature*, 421, 225-226.
- * Schliewen, U., Rassmann, K., Markmann, M., Markert, J., Kocher, T., Tautz, D. (2001). Genetic and ecological divergence of a monophyletic cichlid species pair under fully sympatric conditions in Lake Ejagham, Cameroon. *Molecular Ecology*, 10, 1471-1488.
- * Schliewen, U.K., Tautz, D., Pääbo, S. (1994). Sympatric speciation suggested by monophyly of crater lake cichlids. *Nature*, 368, 629-632.

Evolution of new genes

This is my longest standing project line, which started in Munich and continues until now. The focus was initially on genes that could contribute to adaptations through fast evolution. This resulted in the discovery of *de novo* gene formation and included eventually also experimental evolution approaches on the fitness effects of random peptides. Particularly important in this context was also the development of phylostratigraphy by my collaborator Tomislav Domazet-Lošo, as a method to detect patterns of gene evolution connected to major evolutionary innovations. The work on *de novo* gene evolution was mostly funded by an ERC advanced grant. Overall, this line of work has substantially changed our understanding of the evolution of genes.

- Heinen, T., Xie, C., Keshavarz, M., Stappert, D., Künzel, S., Tautz, D. (2022). Evolution of a new testis-specific functional promoter within the highly conserved Map2k7 gene of the mouse. *Front. Genet.* 12: 812139.
- Bhave, D., Tautz, D. (2021). Effects of the expression of random sequence clones on growth and transcriptome regulation in *Escherichia coli*. *Genes (Basel)* 13(1): 53.
- Castro, J.F., Tautz, D. (2021). The Effects of Sequence Length and Composition of Random Sequence Peptides on the Growth of *E. coli* Cells. *Genes (Basel)* 12(12): 1913
- * Xie, C., Bekpen, C., Künzel, S., Keshavarz, M., Krebs-Wheaton, R., Skrabar, N., Ullrich, K., Tautz, D. (2019). A *de novo* evolved gene in the house mouse regulates female pregnancy cycles. *eLife* 8: e44392.
- Bekpen C, Xie C, Tautz D. (2018). Dealing with the adaptive immune system during *de novo* evolution of genes from intergenic sequences. *BMC Evol Biol.* 18: 121.
- Tautz D, Neme R, (2018). Reply to 'No beneficial fitness effects of random peptides'. *Nat Ecol Evol.* 2: 1048.
- * Neme R, Amador C, Yildirim B, McConnell E, Tautz D. (2017). Random sequences are an abundant source of bioactive RNAs or peptides. *Nature Ecology and Evolution* 1, 0127.

- Domazet-Lošo T, Carvunis A-R, Albà M, Šestak MS, Bakarić R, Neme R, Tautz D. (2017). No evidence for phylostratigraphic bias impacting inferences on patterns of gene emergence and evolution. *Molecular Biology and Evolution* 34: 843-856.
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- Tautz D, Neme R, Domazet-Lošo T. (2013). Evolutionary Origin of Orphan Genes. In: *eLS*. John Wiley & Sons, Ltd: Chichester. DOI: 10.1002/9780470015902.a0024601
- Neme, R., Tautz, D. (2013). Phylogenetic patterns of emergence of new genes support a model of frequent de novo evolution. *BMC Genomics* 14, 117.
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- Domazet-Lošo, T., Tautz, D. (2010). Phylostratigraphic tracking of cancer genes suggests a link to the emergence of multicellularity in metazoa. *BMC Biology* 8, 66.
- * Heinen, T.J., Staubach, F., Häming, D., Tautz, D. (2009). Emergence of a new gene from an intergenic region. *Curr Biology* 19, 1527-1531.
- Domazet-Lošo, T., Tautz, D. (2008). An ancient evolutionary origin of genes associated with human genetic diseases. *Molecular Biology and Evolution* 25, 2699-2707.
- * Domazet-Lošo T., Brajković J., Tautz D. (2007). A phylostratigraphy approach to uncover the genomic history of major adaptations in metazoan lineages. *Trends in Genetics* 23, 533-539.
- Domazet-Lošo, T., Tautz, D. (2003). An evolutionary analysis of orphan genes in *Drosophila*. *Genome Research*, 13, 2213-2219.
- * Schmid, K.J., Tautz, D. (1997). A screen for fast evolving genes from *Drosophila*. *Proceedings of the National Academy of Sciences of the United States of America*, 94, 9746-9750.

Wild mouse as model system

My interest to develop the house mouse into a model system for tracing the genetic mechanisms of adaptation started in Cologne. The classic model system for such work was *Drosophila* at that time, but I was looking for a model system where the ecology and adaptation history was better understood and which would also allow to make more direct inferences on adaptations in mammals. Our initial work, including the first collections, rested substantially on the work of the Montpellier group of scientists who had developed the framework for house mouse phylogeography and genetics. With the move to Plön, it was possible to expand the work substantially in many different directions. It led to many exciting new insights and we have collected a huge amount of data which will be further analyzed in the coming years.

- Zhang, W. Y., Tautz, D. (2022). Tracing the origin and evolutionary fate of recent gene retrocopies in natural populations of the house mouse. *Mol Biol Evol.* 39(2): msab360.
- Keshavarz, M., Savriama, Y., Refki, P., Savriama, Y., Reeves, R.G., Tautz, D. (2021). Natural copy number variation of tandemly repeated regulatory SNORD RNAs leads to individual phenotypic differences. *Molecular Ecology* 30: 4708-4722.
- * Zhang, W. Y., Xie, C., Ullrich, K. K., Zhang, Y. E., Tautz, D. (2021). The mutational load in natural populations is significantly affected by high primary rates of retroposition. *Proc. Nat. Acad. Sci. USA* 118: e2013043118.
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- Ullrich, K., Tautz, D. (2020). Population Genomics of the House Mouse and the Brown Rat. *Methods Mol Biol.* 2090: 435-452.
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- * Linnenbrink M, Teschke M, Montero I, Vallier M, Tautz D. (2018). Meta-populational demes constitute a reservoir for large MHC allele diversity in wild house mice (*Mus musculus*). *Front Zoology* 15: 15.
- Hirose M, Schilf P, Gupta Y, Zarse K, Künstner A, Fähnrich A, Busch H, Yin J, Wright MN, Ziegler A, Vallier M,

- Belheouane M, Baines JF, Tautz D, Johann K, Oelkrug R, Mittag J, Lehnert H, Othman A, Jöhren O, Schwaninger M, Prehn C, Adamski J, Shima K, Rupp J, Häsler R, Fuellen G, Köhling R, Ristow M, Ibrahim SM. (2018). Low-level mitochondrial heteroplasmy modulates DNA replication, glucose metabolism and lifespan in mice. *Scientific Reports* 8: 5872.
- Gertler C, Schlegel M, Linnenbrink M, Hutterer R, König P, Ehlers B, Fischer K, Ryll R, Lewitzki J, Sauer S, Baumann K, Breithaupt A, Faulde M, Teifke JP, Tautz D, Ulrich RG. (2017). Indigenous house mice dominate small mammal communities in Northern Afghan military bases. *BMC Zoology* 2:15
- * Harr B, Karakoc E, Neme R, Teschke M, Pfeifle C, Pezer Ž, Babiker H, Linnenbrink M, Montero I, Scavetta R, Abai MR, Molins MP, Schlegel M, Ulrich RG, Altmüller J, Franitza M, Büntge A, Künzel S, Tautz D. (2016). Genomic resources for wild populations of the house mouse, *Mus musculus* and its close relative *Mus spretus*. *Scientific Data* 3: 160075. doi: 10.1038/sdata.2016.75.
- Babiker, H., Tautz, D. (2015). Molecular and phenotypic distinction of the very recently evolved insular subspecies *Mus musculus helgolandicus* ZIMMERMANN, 1953. *BMC Evol Biol* 15: 160.
- Hasenkamp, N., Solomon, T., Tautz D. (2015). Selective sweeps versus introgression - population genetic dynamics of the murine leukemia virus receptor *Xpr1* in wild populations of the house mouse (*Mus musculus*). *BMC Evol Biol* 15: 248.
- * Pezer Z, Harr B, Teschke M, Babiker H, Tautz D. (2015). Divergence patterns of genic copy number variation in natural populations of the house mouse (*Mus musculus domesticus*) reveal three conserved genes with major population-specific expansions. *Genome Research* 25: 1114-1124.
- Hardouin EA, Orth A, Teschke M, Darvish J, Tautz D, Bonhomme F. (2015). Eurasian house mouse (*Mus musculus* L.) differentiation at microsatellite loci identifies the Iranian plateau as a phylogeographic hotspot. *BMC Evol Biol* 15: 26.
- Lorenc A, Linnenbrink M, Montero I, Schilhabel MB, Tautz D. (2014). Genetic differentiation of hypothalamus parentally biased transcripts in populations of the house mouse implicate the Prader-Willi syndrome imprinted region as a possible source of behavioral divergence. *Mol Biol Evol.* 31: 3240-3249.
- * von Merten S, Hoier S, Pfeifle C, Tautz D. (2014). A role for ultrasonic vocalisation in social communication and divergence of natural populations of the house mouse (*Mus musculus domesticus*). *PLoS ONE* 9:e97244.
- Bryk J, Tautz D. (2014). Copy number variants and selective sweeps in natural populations of the house mouse (*Mus musculus domesticus*). *Front Genetics* 5:153.
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- Boell L, Tautz D. (2011). Micro-evolutionary divergence patterns of mandible shapes in wild house mouse (*Mus musculus*) populations. *BMC Evolutionary Biology* 11, 306.
- * Hardouin, E.A., Chapuis, J.L., Stevens, M.I., van Vuuren, J.B., Quillfeldt, P., Scavetta, R.J., Teschke, M., Tautz, D. (2010). House mouse colonization patterns on the sub-Antarctic Kerguelen Archipelago suggest singular primary invasions and resilience against re-invasion. *BMC Evol Biol* 10, 325.
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- Teschke, M., Mukabayire, O., Wiehe, T., Tautz, D. (2008). Identification of selective sweeps in closely related populations of the house mouse based on microsatellite scans. *Genetics* 180, 1537–1545.
- Voolstra, C., Tautz, D., Farbrother, P., Eichinger, L., Harr, B. (2007). Contrasting evolution of expression differences in the testis between species and subspecies of the house mouse. *Genome Research* 17, 42-49.

- Harr, B., Voolstra, C., Heinen, T., Baines, J., Rottscheidt, R., Ihle, S., Müller, W., Bonhomme, F., Tautz, D. (2006). A change of expression in the conserved signaling gene *MKK7* is associated with a selective sweep in the western house mouse *Mus musculus domesticus*. *Journal of Evolutionary Biology* 19, 1486 - 1496.
- * Ihle, S., Ravaoarimanana, I., Thomas, M., Tautz, D. (2006). An Analysis of Signatures of Selective Sweeps in Natural Populations of the House Mouse. *Molecular Biology and Evolution* 23, 790-797.
- Thomas, M., Ihle, S., Ravaoarimanana, I., Kraechter, S., Wiehe, T., Tautz, D. (2005). Microsatellite variability in wild populations of the house mouse is not influenced by differences in chromosomal recombination rates. *Biological Journal of the Linnean Society*, 84, 629-635.

Technology development

My very first published paper was on technology development and this was always an important part of the lab to aid the different scientific projects. The most important technology development was the procedure for whole-mount in situ hybridization that has changed the whole field of developmental genetics and is one of the key technologies that is still much applied.

- Savriama, Y., Tautz, D. (2022). Testing the accuracy of 3D automatic landmarking via genome-wide association studies. *G3 (Bethesda)* 12(2): jkab443.
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- * Reeves RG, Tautz D. (2017). Automated phenotyping indicates pupal size in *Drosophila* is a highly heritable trait with a polygenic basis. *Genes, Genomes, Genetics* 7: 1277-1286.
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- Pozhitkov, A.E., Tautz, D., Noble, P.A. (2007). Oligonucleotide microarrays: widely applied--poorly understood. *Briefings in Functional Genomics and Proteomics* 6: 141-148.
- Thomas, M., Möller, F., Wiehe, T., Tautz, D. (2007). A pooling approach to detect signatures of selective sweeps in genome scans using microsatellites. *Molecular Ecology Notes* 7(3), 400-403.
- Nolte, A.W., Stemshorn, K.C., Tautz, D. (2005). Direct cloning of microsatellite loci from *Cottus gobio* through a simplified enrichment procedure. *Molecular Ecology Notes*, 5, 628-636.
- Pozhitkov, A., Stemshorn, K., Tautz, D. (2005). An algorithm for the determination and quantification of components of nucleic acid mixtures based on single sequencing reactions. *BMC Bioinformatics* 6, 281.
- Haberl, M., Tautz, D. (1999). Comparative allele sizing can produce inaccurate allele size differences for microsatellites. *Molecular Ecology*, 8, 1347-1349.
- Karp, A., Edwards, K.J., Bruford, M., Funk, S., Vosman, B., Morgante, M., Seberg, O., Kremer, A., Boursot, P., Arctander, P., Tautz, D., Hewitt, G.M. (1997). Molecular technologies for biodiversity evaluation: Opportunities and challenges. *Nature Biotechnology*, 15, 625-628.
- Schröder, R., Tautz, D., Jay, D.G. (1996). Chromophore-assisted laser inactivation of *even skipped* in *Drosophila* precisely phenocopies genetic loss of function. *Development Genes and Evolution*, 206, 86-88.
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- Lehmann, R., Tautz, D. (1994). In situ hybridization to RNA. *Methods in Cell Biology*, 44, 575-598.

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Quantitative genetics

My interest in quantitative genetics started in 1998 with a conceptual talk that I gave at a Royal Society meeting and its corresponding paper. The question was how much the Evo-Devo work with its focus on genes regulating the early developmental processes allows us to understand the formation and evolution of the phenotype of the individuals. It took a while until we got the first experimental approaches going in this direction. But the technical means with respect to high-throughput genomic analysis and phenotyping have only recently become available. It is the topic with the most promising prospects for major discoveries in the future.

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- * Zhang, W. Y., Reeves, G. R., Tautz, D. (2021). Testing implications of the omnigenic model for the genetic analysis of loci identified through genome-wide association. Current Biology 31:1092-1098.
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DNA taxonomy

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