

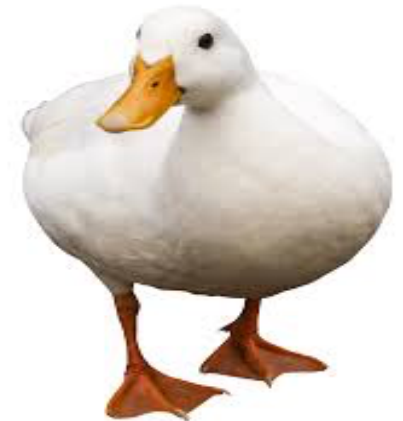


Farm Birds

Presented by: Maryam Al-HadlaQ, Fatima Mohammad,
Sarah Fahad, Fajer Saud, and Shrouq Ali Dashtii

Introduction to genomics (485)

Full 2019



Outline

- Facts about the species
- The genome papers
- Sequencing strategy
- Sequencing method
- Assembly
- Annotation
- Interesting genome facts
- Questions

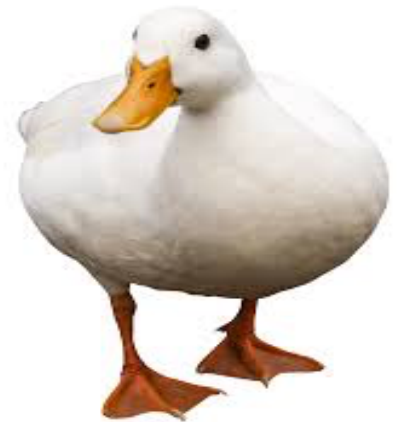
Facts about the species: *Bmabusicola thoracicus*

- Divergent in the Miocene & from francolin
- Differences Phenotypic & behavioral between them
- Documentation for sexual selection
- Demographically different



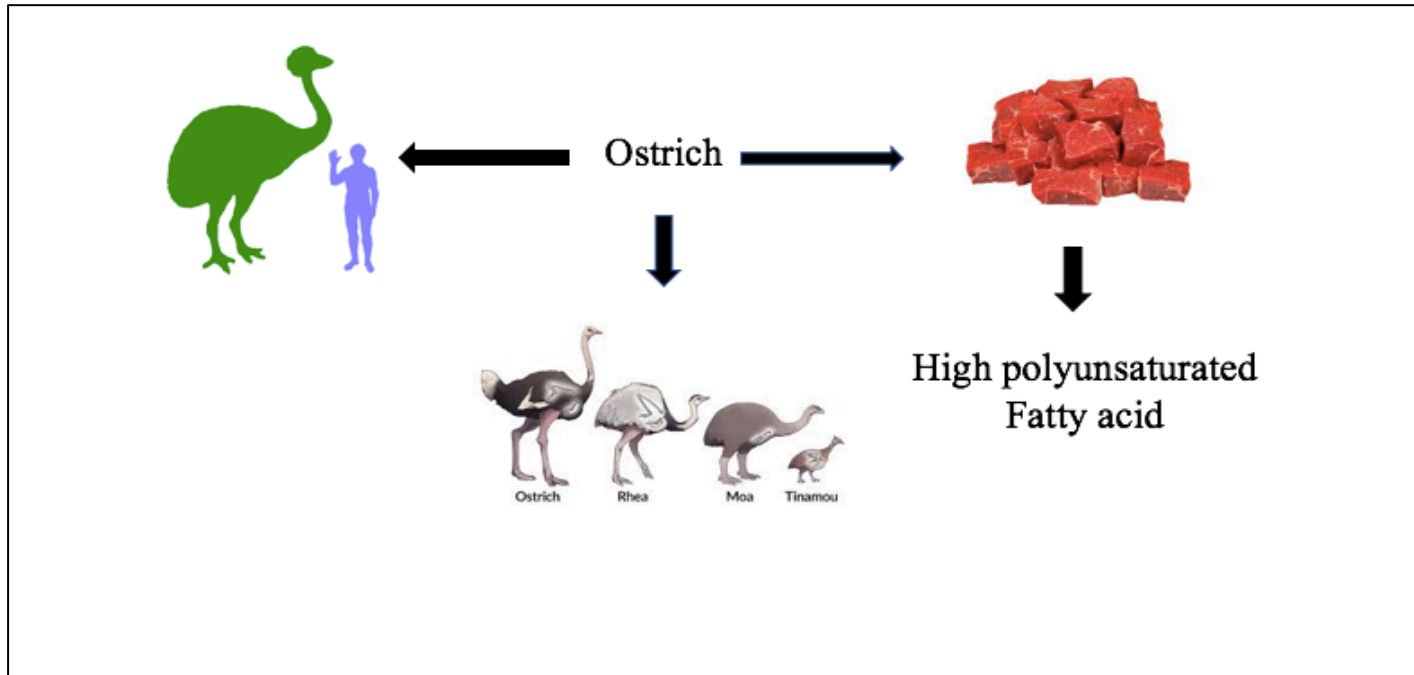
Facts about the species: *Anas Platyrhynchos*

- Most economically important waterfowl
- Body size varies
- Diverged from related chicken and turkey and zebra finch



Facts about the species: Struthio Camelus

- Camelus: A genus comprising the true camels and a number of extinct related animals.



Facts about the species: *Meleagris Gallopavo*

- Member: Phasianidae
- Order: Galloforms
- Microchromosome



Facts about the species: Columba Livia

- Most widely distributed and phenotypically diverse avian species
- Broadly studied
- Model for understanding the molecular basis
- Genetic & genomic studied



The genome papers



G3

Improved Genome Assembly and Annotation for the Rock Pigeon (*Columba livia*)

Carson Holt,^{*,†} Michael Campbell,^{*,†} David A. Keays,[†] Nathaniel Edelman,^{†,‡} Aurélie Kapusta,^{*,†} Emily Maclary,[§] Eric T. Domyan,^{§,**} Alexander Suh,^{††} Wesley C. Warren,^{††} Mark Yandell,^{*,†} M. Thomas P. Gilbert,^{§§,***} and Michael D. Shapiro^{§,‡}

^{*}Department of Human Genetics, [†]USTAR Center for Genetic Discovery, and [‡]Research Institute of Molecular Pathology, Vienna, Austria, [§]Department of Biology, University of Utah, Salt Lake City, UT, ^{**}Department of Biology, Utah Valley University, Orem, UT, ^{††}Department of Evolutionary Biology (EBC), University of Uppsala, Uppsala, Sweden, ^{†††}Genome Institute at Washington University, St. Louis, MO, ^{§§}Natural History Museum of Denmark, University of Copenhagen, Denmark, and ^{***}Norwegian University of Science and Technology, University Museum, Trondheim, Norway
ORCID IDs: 0000-0002-4131-903X (A.K.); 0000-0003-2900-4331 (M.D.S.)



www.sciencemag.org/cgi/content/full/science.1230422/DC1

Supplementary Materials for

Genomic Diversity and Evolution of the Head Crest in the Rock Pigeon

Michael D. Shapiro,^{*} Zev Kronenberg, Cai Li, Eric T. Domyan, Hailin Pan, Michael Campbell, Hao Tan, Chad D. Huff, Haofu Hu, Anna I. Vickrey, Sandra C. A. Nielsen, Sydney A. Stringham, Hao Hu, Eske Willerslev, M. Thomas P. Gilbert, Mark Yandell, Guojie Zhang, Jun Wang^{*}



OPEN

The duck genome and transcriptome provide insight into an avian influenza virus reservoir species

Yinhua Huang^{1,2,20}, Yingrui Li^{3,20}, David W Burt^{2,20}, Hualan Chen⁴, Yong Zhang³, Wubin Qian³, Heebal Kim⁵, Shangquan Gan¹, Yiqiang Zhao¹, Jianwen Li³, Kang Yi³, Huapeng Feng⁴, Pengyang Zhu⁴, Bo Li³, Qiuyue Liu¹, Suan Fairley⁶, Katharine E Magor⁷, Zhenlin Du¹, Xiaoxiang Hu¹, Laurie Goodman³, Hakim Tafer^{8,9}, Alain Vignal¹⁰, Taeheon Lee⁵, Kyu-Won Kim¹¹, Zheya Sheng¹, Yang An¹, Steve Searle⁶, Javier Herrero¹², Martien A M Groenen¹³, Richard P M A Crooijmans¹³, Thomas Faraut¹⁰, Qingle Cai³, Robert G Webster¹⁴, Jerry R Aldridge¹⁴, Wesley C Warren¹⁵, Sebastian Bartschat⁸, Stephanie Kehr⁸, Manja Marz⁸, Peter F Stadler^{8,9}, Jacqueline Smith², Robert H S Kraus^{16,17}, Yaofeng Zhao¹, Liming Ren¹, Jing Fei¹, Mireille Morisson¹⁰, Pete Kaiser², Darren K Griffin¹⁸, Man Rao¹, Frederique Pitel¹⁰, Jun Wang^{3,19} & Ning Li¹



BROWSE PUBLISH ABOUT

FIFTEENTH ANNIVERSARY

OPEN ACCESS PEER-REVIEWED

RESEARCH ARTICLE

Multi-Platform Next-Generation Sequencing of the Domestic Turkey (*Meleagris gallopavo*): Genome Assembly and Analysis

Rami A. Dalloul[Ⓞ], Julie A. Long[Ⓞ], Aleksey V. Zimin[Ⓞ], Luqman Aslam, Kathryn Beal, Le Ann Blomberg, Pascal Bouffard, David W. Burt, Oswald Crasta, Richard P. M. A. Crooijmans, Kristal Cooper, Roger A. Coulombe, Supriyo De, [...]

Kent M. Reed[Ⓞ]

The genome papers

Tiley et al. *BMC Genomics* (2018) 19:336
<https://doi.org/10.1186/s12864-018-4711-0>

BMC Genomics

RESEARCH ARTICLE

Open Access



Comparison of the Chinese bamboo partridge and red Junglefowl genome sequences highlights the importance of demography in genome evolution

G. P. Tiley^{1,2*}, R. T. Kimball¹, E. L. Braun¹ and J. G. Burleigh¹

Zhang et al. *GigaScience* (2015) 4:24
DOI 10.1186/s13742-015-0062-9

(GIGA)¹
SCIENCE

DATA NOTE

Open Access

Improving the ostrich genome assembly using optical mapping data

Jilin Zhang¹, Cai Li^{1,2}, Qi Zhou³ and Guojie Zhang^{1,4*}

Comparative genomics reveals insights into avian genome evolution and adaptation

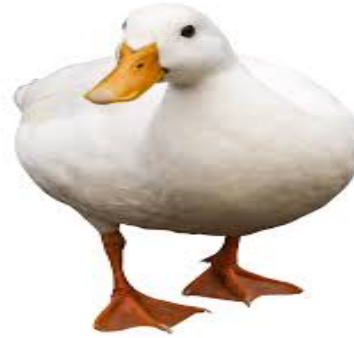
Guojie Zhang,^{1,2,*} Cai Li,^{1,3,*} Qiye Li,^{1,3} Bo Li,¹ Denis M. Larkin,⁴ Chul Lee,^{5,6} Jay F. Storz,⁷ Agostinho Antunes,^{8,9} Matthew J. Greenwold,¹⁰ Robert W. Meredith,¹¹ Anders Ödeen,¹² Jie Cui,^{13,14} Qi Zhou,¹⁵ Luohao Xu,^{1,16} Hailin Pan,¹ Zongji Wang,^{1,17} Lijun Jin,¹ Pei Zhang,¹ Haofu Hu,¹ Wei Yang,¹ Jiang Hu,¹ Jin Xiao,¹ Zhikai Yang,¹ Yang Liu,¹ Qiaolin Xie,¹ Hao Yu,¹ Jinmin Lian,¹ Ping Wen,¹ Fang Zhang,¹ Hui Li,¹ Yongli Zeng,¹ Zijun Xiong,¹ Shiping Liu,^{1,17} Long Zhou,¹ Zhiyong Huang,¹ Na An,¹ Jie Wang,^{1,18} Qiumei Zheng,¹ Yingqi Xiong,¹ Guangbiao Wang,¹ Bo Wang,¹ Jingjing Wang,¹ Yu Fan,¹⁹ Rute R. da Fonseca,³ Alonzo Alfaro-Núñez,³ Mikkel Schubert,³ Ludovic Orlando,³ Tobias Mourier,³ Jason T. Howard,²⁰ Ganeshkumar Ganapathy,²⁰ Andreas Pfenning,²⁰ Osceola Whitney,²⁰ Miriam V. Rivas,²⁰ Erina Hara,²⁰ Julia Smith,²⁰ Marta Farré,⁴ Jitendra Narayan,²¹ Gancho Slavov,²¹ Michael N Romanov,²² Rui Borges,^{8,9} João Paulo Machado,^{8,23} Imran Khan,^{8,9} Mark S. Springer,²⁴ John Gatesy,²⁴ Federico G. Hoffmann,^{25,26} Juan C. Opazo,²⁷ Olle Hästad,²⁸ Roger H. Sawyer,¹⁰ Hee-bal Kim,^{5,6,29} Kyu-Won Kim,⁵ Hyeon Jeong Kim,⁶ Seoae Cho,⁶ Ning Li,³⁰ Yinhua Huang,^{30,31} Michael W. Bruford,³² Xiangjiang Zhan,^{32,33} Andrew Dixon,³⁴ Mads F. Bertelsen,³⁵ Elizabeth Derryberry,^{36,37} Wesley Warren,³⁸ Richard K Wilson,³⁸ Shengbin Li,³⁹ David A. Ray,²⁶ Richard E. Green,⁴⁰ Stephen J. O'Brien,^{41,42} Darren Griffin,²² Warren E. Johnson,⁴³ David Haussler,⁴⁰ Oliver A. Ryder,⁴⁴ Eske Willerslev,³ Gary R. Graves,^{45,46} Per Alström,^{47,48} Jon Fjeldså,⁴⁶ David P. Mindell,⁴⁹ Scott V. Edwards,⁵⁰ Edward L. Braun,⁵¹ Carsten Rahbek,^{46,52} David W. Burt,³³ Peter Houde,⁵⁴ Yong Zhang,¹ Huanming Yang,^{1,53} Jian Wang,¹ Avian Genome Consortium,[§] Erich D. Jarvis,²⁰ M. Thomas P. Gilbert,^{3,56} Jun Wang^{1,53,57,58,59}

Sequencing strategy

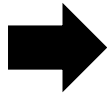
BAC clone library

Whole genome shotgun

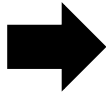
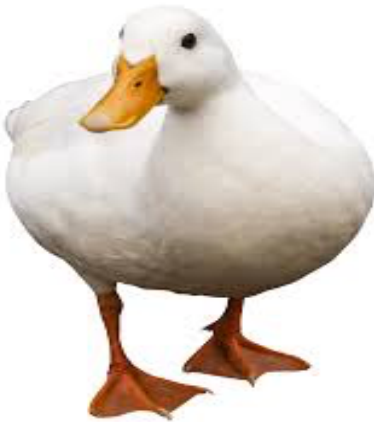
BAC clone library + Whole genome shotgun



Sequencing methods



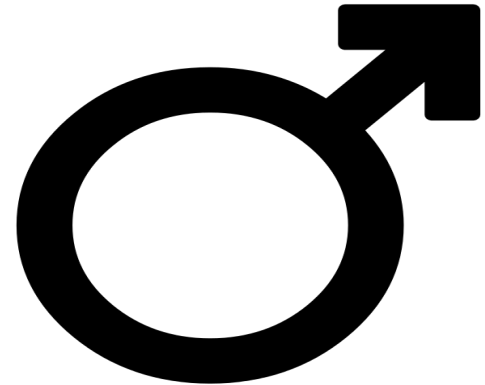
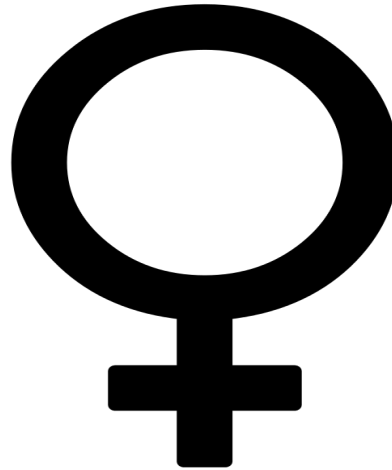
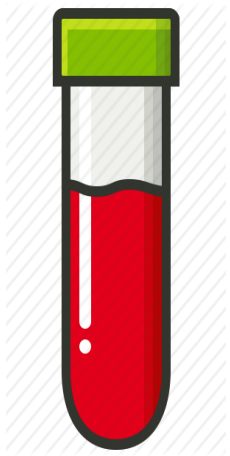
Illumina
Sequencing



Illumina +
Pyrosequencing

Source of DNA

- Genomic Extraction



Genome Assembly

	Genome Size	Coverage	# of contig	# of scaffold	N50 contig	N50 scaffold	GC content
Chicken	1.03 Gb	25x	255,563	163,749	10,589	13,160	20-60%
Duck	1.26 Gb	64x	227,597	78,487	11,206	268	-
Ostrich	1.05 Gb to 1.26 Gb	85x	-	-	HC : 19kb to 55kb LC : 12Kb to 20Kb	29K/3.5 M;1.23G	-
Turkey	1.1Gb	17x	152,641	26,917	12,594	1.5 Mb	-
Rock Pigeon	1.1Gb 1.3Gb	390x 60x	- 143,123	99 38,878	17.45 Mb 22 Kb	- 3.1 Mb	- 41.5%

Genome Annotation

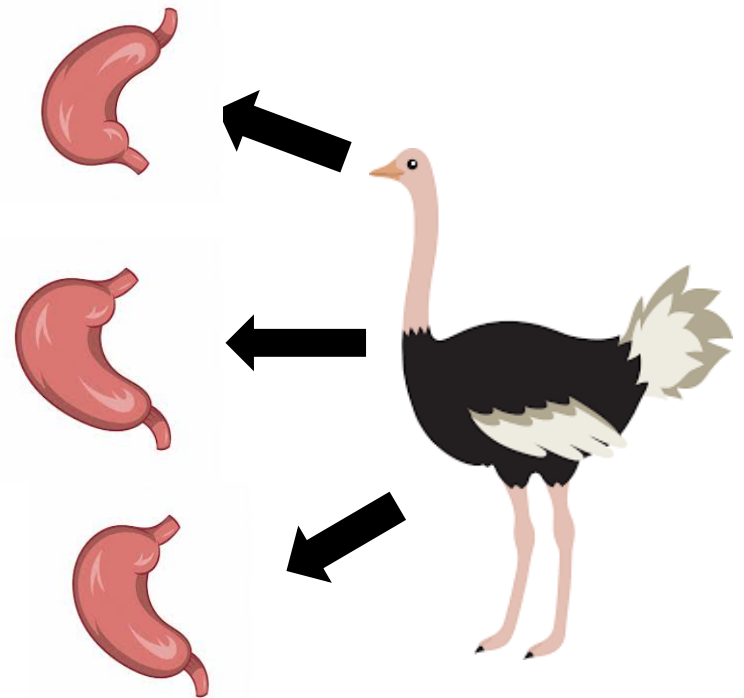
	# of genes	Coding genes	Non-coding genes	SINE's	LINE's	LTR's	# of Reads
Chicken	17,772	-	-	0.08%	6.71%	1.64%	116 Mb
Duck	19,144	-	-	0.12%	4.11%	1.09%	1415 Mb
Ostrich	-	28	-	0.184%	2.87%	0.166%	-
Turkey	15,704	15,093	611	40.34%	50.19%	0.51%	417 Mb
Rock Pigeon	15,392	15,022	705.5	-	-	-	-
	17,300	-	-	-	-	-	75 Mb

Interesting genomics facts

- For *Bamusicola thoracicus*, GC content was generally higher on the microchromosomes.
- The head crest phenotype has evolved just once and spread throughout the species.
- Duck serve as the principle natural reservoir for influenza A viruses.

Interesting genomics facts

- Ostrich have 3 stomachs.
- Ostrich fight with their feet, they kick forward because that's the direction in which their legs bends. “ A solid kick can kill a lion ”



Interesting genomics facts

- High distant species help explain regions conserved during vertebrate evolution. For example, variation in gene content between birds and an egg-laying mammal (platypus) shows functions shared by egg-laying animals in general as well as those unique to egg-laying birds.

Questions

- What are the names of the mentioned journals in this presentation?
- What is the most sequencing method that was used to sequence the DNA for the organisms of farm bird?
- What is the source of DNA mentioned in this presentation?
- Who came up the WGST idea?
- What is the trait that was lost during evolution of avian species? *Hint* it exists in mammals.

Thank you