#### Стая птичьих геномов















# Questions

What is the most likely phylogeny of sequenced avian species?

What features of avian genomes made them unique and different from other clades?

What lineage- and clade-specific adaptations could be linked to changes in avian genomes?

What are the patterns of avian chromosome evolution?



## **Avian Genome Size Reduction: Why?**

#### Birds have the lowest genome size among amniotes

0.91 Gbp in hummingbird





#### Why?

#### Faster gene regulation (Hughes and Hughes, 1995)



#### **Avian Genome Size Reduction: How?**

Smaller intron sizes, intergenic regions and fewer no. transposable elements (4-10% most birds)





### **Avian Genome Size Reduction: How?**

#### Ancestral microdeletions in avian genomes absent from other Reptilia genomes



### **Conserved Sequence Elements in Avian Genomes**

#### Avian genomes have more constrain elements (7.5%) than mammalian ones (2.2%)



~12.5% are associated with protein-coding genes



#### **Transcription Factor Binding Sites in Conserved Elements**

**Avian CNEs:** 

✓ Metabolism

**Amniote CNEs:** 

✓ Signal regulation
✓ Stimulus responses
✓ Development



# **Adaptive Phenotypes: Flight**



**Reduced number of bones** 

#### Bones must be light & strong

#### **Pneumatisation**

Out of 89 genes related to ossification 49 show signatures of positive selection

Highest dN/dS: *AHSG* – bone mineral density *P2RX7* – bone homeostasis



# **Adaptive Phenotypes: Flight**



**Effective gas exchange** 

**Constant volume lungs** 

Five genes related to lung development in mammals were lost in birds

Feather development (α- and β-keratins)





# **Adaptive Phenotypes: Edentulism**

#### Fossil records indicate that several extinct birds had teeth...



#### Edentulism could have evolved multiple times in avian evolution



## **Adaptive Phenotypes: Edentulism**

#### Avian genomes:

- ✓ Multiple pseudogene fossils of enamel and dentin genes
- ✓ Different mutations in different avian lineages
- All genomes have same deletions in four enamel genes: ENAM, AMELX, AMTN, and MMP20
  and one dentin gene: DSPP

✓ Common ancestor or all birds likely had no mineralized teeth



### **Adaptive Phenotypes: Visual System**

- ✓ Birds maintained tetrapod ancestral set of cones
- ✓ Birds have higher number of opsin genes than mammals
- ✓ Four classes of opsin genes found in birds suggest a tetrochromatic vision in birds
- Penguins only 3 classes of opsins consistent with aquatic mammals who also lost (1-2) cone pigments



## **Features of Bird Karyotypes**

✓ Stable no. of chromosomes (2n = ~80) in the majority of species

✓ Presence of many micro-chromosomes





Griffin's laboratory

# Long-Range Sequence Assembly in Whole-Genome Shotgun Sequencing



Green, Nature Reviews Genetics, 2001

#### **Reference Assisted Chromosome Assembly**



Kim, et al., 2012 (PNAS)



University of London

# **Automatic Identification and Classification of EBRs**

#### Hypotheses:

*Chicken EBR* = Opossum, Lizard, Ostrich, Finch, Duck, Turkey *Galliformes EBR* = Opossum, Lizard, Ostrich, Finch, Duck *Galloanserae EBR* = Opossum, Lizard, Ostrich, Finch *Neoavian EBR* = Opossum, Lizard, Ostrich *Avian EBR* = Opossum, Lizard Sauropsida= Opossum

#### Likelihood of a hypothesis:



		EBR expected under $H_i$ ?		
		Yes	No	
EBR detected?	Yes	1 - β <sub>j</sub>	$R_{jk}$	
	No	$eta_j$	1	





### **Recovery Rate of Reference-Specific EBRs**







Classification	Detected	Expected	Rearrangement
Classification	no. EBRs	no. EBRs	rate (EBRs/MY)
Lineage-specific			
Pekin duck	130	113	1.77
Emperor penguin	43	38	2.23
Anna's hummingbird	99	92	2.38
Chimney swift	56	45	1.36
Killdeer	27	25	0.38
Chicken	16	16	0.68
Domestic pigeon	114	102	1.55
American crow	40	37	1.96
Common cuckoo	110	106	1.61
Little egret	47	40	0.78
Peregrine falcon	99	86	1.59
Medium ground finch	40	35	3.95
Golden collared manakin	44	35	3.90
Turkey	255	255	10.86
Budgerigar	199	181	3.51
Crested ibis	42	39	0.71
Hoatzin	50	39	0.70
Downy woodpecker	184	147	2.78
Adelie penguin	55	47	2.82
Ostrich	137	124	1.39
Zebra finch	53	47	5.20
Clade-specific			
Galliformes	42	42	0.84
Galloanserae	15	23	1.02
Trochiliformes + Apodiformes	2	2	0.08
Ciconiiformes	3	3	0.74
Passeroidea	14	14	1.37
Passeroidea + Corvoidea	19	21	1.73
Passeriformes	16	17	0.72
Sphenisciformes	4	4	0.09
Passeriformes + Psittaciformes + Falconiformes +	2	4	4.41
Piciformes + Ciconiiformes + Sphenisciformes +			
Charadriiformes + Opisthocomiformes			
Non-galloanserae	11	13	0.58
Non-galloanserae + non-columbiformes	1	1	0.86
Neognathae	9	14	5.73
Avian	9	14	0.10
Total/average EBRs	1,796*	1,821	1.53**





Are transposable elements associated with chromosome rearrangements in birds?

Could stability of bird karyotypes be associated with lower fraction of TEs in bird genomes?

Are evolutionary breakpoint regions (EBRs) in birds related to lineage-specific phenotypes?

Could evolutionary stable chromosome intervals (msHSBs) in reptiles be related to class-/group-specific phenotypes?



#### **Rates of Chromosome Rearrangements in Birds**



Royal Veterinary College University of London

# **Rates of Chromosome Rearrangements in Birds**



EBRs:



Significantly enriched in TEs (p<0.05)

Elevated no. TEs

Negatively associated with TEs



# No. of TEs Correlates with the Rearrangement Rates in Passeriformes



Royal Veterinary College University of London

# msHSBs are Enriched for Genes Related to Ancestral Phenotypes

TERM	AVIAN	ARCHOSAURIAN	ARCHOSAURIAN/ TESTUDINES	SAUROPSID
Reproductive developmental process	*	*	*	
Development of primary sexual characteristics	×	*	×	*
Positive regulation of biosynthetic process	*		*	
Positive regulation of macromolecule biosynthetic process	*		*	
Cytoskeletal protein binding	*	*		
Positive regulation of gene expression	*	*	*	
Transcription factor complex	×	×		
Positive regulation of transcription	×		×	
Positive regulation of transcription, DNA-dependent	*	*	×	
Regulation of transcription from RNA polymerase II promoter	×	*	×	
Positive regulation of nitrogen compound metabolic process	*		*	
Pattern specification process	*			
Embryonic morphogenesis	*	×		
Regionalization	*	*		
Appendage/Limb development	×			
Nuclear lumen	×			
Lipid binding	*			
Retina development in camera-type eye	*	*		
Nucleotide binding	×			



# Archosaurian msHSBs Contain Genes Related to Retina Development







Repérant et al., 2006



Nesbitt, 2011

Genes in archosaurian msHSBs:

SOX2, RBP4, PROX1, PRPH2, VSX2, IKZF1, TGIF1, CHD7

# Avian-msHSBs are Enriched for Genes Related to Limb Development

#### Alligators and crocodiles have 5 digit limbs

Archaeopteryx had feathers and was able to fly, but it still had the digit I in limbs





ARCHOSAURIA



**DLX5:** responsible for feathered phenotypes

#### BMPR1B:

expressed in chicken wings

No expression in the area of digit I leading to the lack of digit I in birds

Welten et al., 2005



*DLX5/6, BMPR1B, SHOX, HOXA11* Farré et al., submitted

# Possible Changes in Regulation in Birds Due to New Conserved Non-coding Elements (CNEs) in msHSBs

#### DLX5



#### BMPR1B



CNEs present in birds but not in other vertebrates



## **GO Enrichment in Avian Lineage-Specific EBRs**

EBR classification	GO term	No. genes	Fold- enrichment	FDR (%)	No. EBRs
Budgerigar	Forebrain development	12	2.74	5.47	11
	Neuron differentiation	15	2.33	6.83	13
	Neuron development	12	2.62	8.19	11
	Response to wounding	11	2.77	8.35	11
Common	Mitotic cell cycle	11	3.57	1.14	11
cuckoo	Condensed chromosome	7	4.88	2.67	5
	M phase	10	3.25	4.5	9
Little egret	Passive transmembrane transport	10	4.15	0.59	5
	Cation channel activity	7	4.32	5.61	4
Anna's hummingbird	Hexose metabolic process	10	2.9	9.7	8
Peregrine falcon	RNA degradation	6	6.13	2.29	6
	Soluble fraction	5	6.23	8.35	4
Downy woodpecker	Histidine metabolism	6	10.3	0.16	5



# Forebrain Development Pathways in Avian HSBs and Parrot EBRs





#### **Summary**

Avian genomes contain traces of adaptations related to avianspecific phenotypes

Chromosome rearrangements in animals are likely to be caused by TEs and other repetitive sequences

Rates of rearrangements are not equal in evolution and correlate with increased diversification rates

msHSBs are enriched in genes related to ancestral- or clade-specific phenotypes

EBRs tend to rearrange genes related to species-specific and adaptive features



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