

# The Mammalian Genome

Presented by:  
Heba M. Al Sherif  
Bashayer Jamal  
Shaikhah Al Shareefi  
Amna Dawoud  
Hana Hussain



Introduction to genomics (485)  
Fall 2019



# Outline:

- The genome papers
- Introducing mammals
- Facts about the species
- Sequencing strategy
- Sequencing methods
- Assembly
- Annotation
- Interesting genomic fact
- Questions

# The genome papers



## ARTICLE

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OPEN

## Giraffe genome sequence reveals clues to its unique morphology and physiology

Morris Agaba<sup>1,2,3</sup>, Edson Ishengoma<sup>1</sup>, Webb C. Miller<sup>3</sup>, Barbara C. McGrath<sup>3</sup>, Chelsea N. Hudson<sup>3</sup>, Oscar C. Bedoya Reina<sup>3,4</sup>, Aakrosh Ratan<sup>3,5</sup>, Rico Burhans<sup>3</sup>, Rayan Chikhi<sup>6,7</sup>, Paul Medvedev<sup>6,7</sup>, Craig A. Praul<sup>8</sup>, Lan Wu-Cavener<sup>3</sup>, Brendan Wood<sup>3</sup>, Heather Robertson<sup>9</sup>, Linda Penfold<sup>10</sup> & Douglas R. Cavener<sup>1,3</sup>

Vol 453 | 8 May 2016 | doi:10.1038/nature06936

nature

## ARTICLES

## Genome analysis of the platypus reveals unique signatures of evolution

### ARTICLES

https://doi.org/10.1038/s41588-018-0153-5

nature  
genetics

OPEN

## Adaptation and conservation insights from the koala genome

Rebecca N. Johnson<sup>1,2,30,31\*</sup>, Denis O'Meally<sup>2,3,30</sup>, Zhiliang Chen<sup>4,30</sup>, Graham J. Etherington<sup>5</sup>, Simon Y. W. Ho<sup>6,2</sup>, Will J. Nash<sup>5</sup>, Catherine E. Grueber<sup>6,2,6</sup>, Yuanyuan Cheng<sup>2,7</sup>, Camilla M. Whittington<sup>8</sup>, Siobhan Dennison<sup>1</sup>, Emma Peel<sup>2</sup>, Wilfried Haerty<sup>5</sup>, Rachel J. O'Neill<sup>9</sup>, Don Colgan<sup>1</sup>, Tonia L. Russell<sup>10</sup>, David E. Alquezar-Planas<sup>1</sup>, Val Attenbrow<sup>1</sup>, Jason G. Bragg<sup>11,12</sup>, Parice A. Brandies<sup>2</sup>, Amanda Yoon-Yee Chong<sup>5,13</sup>, Janine E. Deakin<sup>14</sup>, Federica Di Palma<sup>5,15</sup>, Zachary Duda<sup>9</sup>, Mark D. B. Eldridge<sup>1</sup>, Kyle M. Ewart<sup>1</sup>, Carolyn J. Hogg<sup>2</sup>, Greta J. Frankham<sup>1</sup>, Arthur Georges<sup>14</sup>, Amber K. Gillett<sup>16</sup>, Merran Govendir<sup>8</sup>, Alex D. Greenwood<sup>17,18</sup>, Takashi Hayakawa<sup>19,20</sup>, Kristofer M. Helgen<sup>1,21</sup>, Matthew Hobbs<sup>6,1</sup>, Clare E. Holleley<sup>22</sup>, Thomas N. Heider<sup>9</sup>, Elizabeth A. Jones<sup>8</sup>, Andrew King<sup>1</sup>, Danielle Madden<sup>3</sup>, Jennifer A. Marshall Graves<sup>11,14,23</sup>, Katrina M. Morris<sup>24</sup>, Linda E. Neaves<sup>1,25</sup>, Hardip R. Patel<sup>26</sup>, Adam Polkinghorne<sup>3</sup>, Marilyn B. Renfree<sup>6,27</sup>, Charles Robin<sup>6,27</sup>, Ryan Salinas<sup>4</sup>, Kyriakos Tsangaras<sup>28</sup>, Paul D. Waters<sup>4</sup>, Shafagh A. Waters<sup>4</sup>, Belinda Wright<sup>1,2</sup>, Marc R. Wilkins<sup>4,10,30</sup>, Peter Timms<sup>29,30</sup> and Katherine Below<sup>2,30,31</sup>

Renfree et al. *Genome Biology* 2011, 12:R81  
http://genomebiology.com/2011/12/8/R81



## RESEARCH

## Open Access

## Genome sequence of an Australian kangaroo, *Macropus eugenii*, provides insight into the evolution of mammalian reproduction and development

Marilyn B Renfree<sup>1,2\*</sup>, Anthony T Papenfuss<sup>1,3,4\*\*</sup>, Janine E Deakin<sup>1,5</sup>, James Lindsay<sup>6</sup>, Thomas Heider<sup>6</sup>, Katherine Below<sup>1,7</sup>, Willem Rens<sup>8</sup>, Paul D Waters<sup>1,5</sup>, Elizabeth A Pharo<sup>2</sup>, Geoff Shaw<sup>1,2</sup>, Emily SW Wong<sup>1,7</sup>, Christophe M Lefèvre<sup>9</sup>, Kevin R Nicholas<sup>9</sup>, Yoko Kuroki<sup>10</sup>, Matthew J Wakefield<sup>1,3</sup>, Kyall R Zenger<sup>1,7,11</sup>, Chenwei Wang<sup>1,7</sup>, Malcolm Ferguson-Smith<sup>8</sup>, Frank W Nicholas<sup>7</sup>, Danielle Hickford<sup>1,2</sup>, Hongshi Yu<sup>1,2</sup>, Kirsty R Short<sup>1,2</sup>, Hannah V Siddle<sup>1,7</sup>, Stephen R Frankenberg<sup>1,2</sup>, Keng Yih Chew<sup>1,2</sup>, Brandon R Menzies<sup>1,2,13</sup>, Jessica M Stringer<sup>1,2</sup>, Shunsuke Suzuki<sup>1,2</sup>, Timothy A Hore<sup>1,14</sup>, Margaret L Delbridge<sup>1,5</sup>, Amir Mohammadi<sup>1,5</sup>, Nanette Y Schneider<sup>1,2,15</sup>, Yanqiu Hu<sup>1,2</sup>, William O'Hara<sup>6</sup>, Shafagh Al Nadaf<sup>1,5</sup>, Chen Wu<sup>7</sup>, Zhi-Ping Feng<sup>3,16</sup>, Benjamin G Cocks<sup>17</sup>, Jianghui Wang<sup>17</sup>, Paul Fliceck<sup>18</sup>, Stephen MJ Searle<sup>19</sup>, Susan Fairley<sup>19</sup>, Kathryn Beal<sup>18</sup>, Javier Herrero<sup>18</sup>, Dawn M Carone<sup>6,20</sup>, Yutaka Suzuki<sup>21</sup>, Sumio Sugano<sup>21</sup>, Atsushi Toyoda<sup>22</sup>, Yoshiyuki Sakaki<sup>10</sup>, Shinji Kondo<sup>10</sup>, Yuichiro Nishida<sup>10</sup>, Shoji Tatsumoto<sup>10</sup>, Ion Mandiou<sup>23</sup>, Arthur Hsu<sup>3,16</sup>, Kaighin A McColl<sup>3</sup>, Benjamin Lansdell<sup>3</sup>, George Weinstock<sup>24</sup>, Elizabeth Kuczek<sup>1,25,26</sup>, Annette McGrath<sup>25</sup>, Peter Wilson<sup>25</sup>, Artem Men<sup>25</sup>, Mehlika Hazar-Rethinam<sup>25</sup>, Allison Hall<sup>25</sup>, John Davis<sup>25</sup>, David Wood<sup>25</sup>, Sarah Williams<sup>25</sup>, Yogi Sundaravadanam<sup>25</sup>, Donna M Muzny<sup>24</sup>, Shalini N Jhangiani<sup>24</sup>, Lora R Lewis<sup>24</sup>, Margaret B Morgan<sup>24</sup>, Geoffrey O Okwuonu<sup>24</sup>, San Juana Ruiz<sup>24</sup>, Jireh Santibanez<sup>24</sup>, Lynne Nazareth<sup>24</sup>, Andrew Cree<sup>24</sup>, Gerald Fowler<sup>24</sup>, Christie L Kovar<sup>24</sup>, Huyen H Dinh<sup>24</sup>, Vandita Joshi<sup>24</sup>, Chyn Jing<sup>24</sup>, Fremiet Lara<sup>24</sup>, Rebecca Thornton<sup>24</sup>, Lei Chen<sup>24</sup>, Jixin Deng<sup>24</sup>, Yue Liu<sup>24</sup>, Joshua Y Shen<sup>24</sup>, Xing-Zhi Song<sup>24</sup>, Janette Edson<sup>25</sup>, Carmen Troon<sup>25</sup>, Daniel Thomas<sup>25</sup>, Amber Stephens<sup>25</sup>, Lankesha Yapa<sup>25</sup>, Tanya Levchenko<sup>25</sup>, Richard A Gibbs<sup>24</sup>, Desmond W Cooper<sup>1,28</sup>, Terence P Speed<sup>1,3</sup>, Asao Fujiyama<sup>22,27</sup>, Jennifer A M Graves<sup>1,5</sup>, Rachel J O'Neill<sup>9</sup>, Andrew J Pask<sup>1,2,6</sup>, Susan M Forrest<sup>1,25</sup> and Kim C Worley<sup>24</sup>

Vol 463 | 21 January 2010 | doi:10.1038/nature08696

nature

## ARTICLES

## The sequence and *de novo* assembly of the giant panda genome

Ruiqiang Li<sup>1,2\*</sup>, Wei Fan<sup>1\*</sup>, Geng Tian<sup>1,3\*</sup>, Hongmei Zhu<sup>1\*</sup>, Lin He<sup>4,5\*</sup>, Jing Cai<sup>3,6\*</sup>, Quanfei Huang<sup>1</sup>, Qingle Cai<sup>1,7</sup>, Bo Li<sup>1</sup>, Yinqi Bai<sup>1</sup>, Zhihe Zhang<sup>8</sup>, Yaping Zhang<sup>6</sup>, Wen Wang<sup>6</sup>, Jun Li<sup>1</sup>, Fuwen Wei<sup>9</sup>, Heng Li<sup>10</sup>, Min Jian<sup>1</sup>, Jianwen Li<sup>1</sup>, Zhaolei Zhang<sup>11</sup>, Rasmus Nielsen<sup>12</sup>, Dawei Li<sup>1</sup>, Wanjun Gu<sup>13</sup>, Zhentao Yang<sup>1</sup>, Zhaoling Xuan<sup>1</sup>, Oliver A. Ryder<sup>14</sup>, Frederick Chi-Ching Leung<sup>15</sup>, Yan Zhou<sup>1</sup>, Jianjun Cao<sup>1</sup>, Xiao Sun<sup>16</sup>, Yonggui Fu<sup>17</sup>, Xiaodong Fang<sup>1</sup>, Xiaosen Guo<sup>1</sup>, Bo Wang<sup>1</sup>, Rong Hou<sup>8</sup>, Fujun Shen<sup>8</sup>, Bo Mu<sup>1</sup>, Peixiang Ni<sup>1</sup>, Runmao Lin<sup>1</sup>, Wubin Qian<sup>1</sup>, Guodong Wang<sup>3,6</sup>, Chang Yu<sup>1</sup>, Wenhui Nie<sup>6</sup>, Jinhuan Wang<sup>6</sup>, Zhigang Wu<sup>1</sup>, Huiqing Liang<sup>1</sup>, Jiumeng Min<sup>1,7</sup>, Qi Wu<sup>9</sup>, Shifeng Cheng<sup>1,7</sup>, Jue Ruan<sup>1,3</sup>, Mingwei Wang<sup>1</sup>, Zhongbin Shi<sup>1</sup>, Ming Wen<sup>1</sup>, Binghang Liu<sup>1</sup>, Xiaoli Ren<sup>1</sup>, Huisong Zheng<sup>1</sup>, Dong Dong<sup>11</sup>, Kathleen Cook<sup>11</sup>, Gao Shan<sup>1</sup>, Hao Zhang<sup>1</sup>, Carolin Kosiol<sup>18</sup>, Xueying Xie<sup>13</sup>, Zuhong Lu<sup>13</sup>, Hancheng Zheng<sup>1</sup>, Yingrui Li<sup>1,3</sup>, Cynthia C. Steiner<sup>14</sup>, Tommy Tsan-Yuk Lam<sup>15</sup>, Siyuan Lin<sup>1</sup>, Qinghui Zhang<sup>1</sup>, Guoqing Li<sup>1</sup>, Jing Tian<sup>1</sup>, Timing Gong<sup>1</sup>, Hongde Liu<sup>16</sup>, Dejin Zhang<sup>16</sup>, Lin Fang<sup>1</sup>, Chen Ye<sup>1</sup>, Juanbin Zhang<sup>1</sup>, Wenbo Hu<sup>17</sup>, Anlong Xu<sup>17</sup>, Yuanyuan Ren<sup>1</sup>, Guojie Zhang<sup>1,3,6</sup>, Michael W. Bruford<sup>19</sup>, Qibin Li<sup>1,3</sup>, Lijia Ma<sup>1,3</sup>, Yiran Guo<sup>1,3</sup>, Na An<sup>1</sup>, Yujie Hu<sup>1,3</sup>, Yang Zheng<sup>1,3</sup>, Yongyong Shi<sup>5</sup>, Zhiqiang Li<sup>5</sup>, Qing Liu<sup>1</sup>, Yanling Chen<sup>1</sup>, Jing Zhao<sup>1</sup>, Ning Qu<sup>1,7</sup>, Shancen Zhao<sup>1</sup>, Feng Tian<sup>1</sup>, Xiaoling Wang<sup>1</sup>, Haiyin Wang<sup>1</sup>, Lizhi Xu<sup>1</sup>, Xiao Liu<sup>1</sup>, Tomas Vinar<sup>20</sup>, Yajun Wang<sup>21</sup>, Tak-Wah Lam<sup>22</sup>, Siu-Ming Yiu<sup>22</sup>, Shiping Liu<sup>23</sup>, Hemin Zhang<sup>24</sup>, Desheng Li<sup>24</sup>, Yan Huang<sup>24</sup>, Xia Wang<sup>24</sup>, Guohua Yang<sup>1</sup>, Zhi Jiang<sup>1</sup>, Junyi Wang<sup>1</sup>, Nan Qin<sup>1</sup>, Li Li<sup>1</sup>, Jingxiang Li<sup>1</sup>, Lars Bolund<sup>1</sup>, Karsten Kristiansen<sup>1,2</sup>, Gane Ka-Shu Wong<sup>1,25</sup>, Maynard Olson<sup>26</sup>, Xiuqing Zhang<sup>1</sup>, Songgang Li<sup>1</sup>, Huanming Yang<sup>1</sup>, Jian Wang<sup>1</sup> & Jun Wang<sup>1,2</sup>

# Introducing Mammals

- Mammals are endothermic animals.
- Special Features: Hair or fur and mammary glands.
- Most mammals give birth to live young.
- Have the most genetic similarity to human.



*Giraffa camelopardalis tippelskirchi*

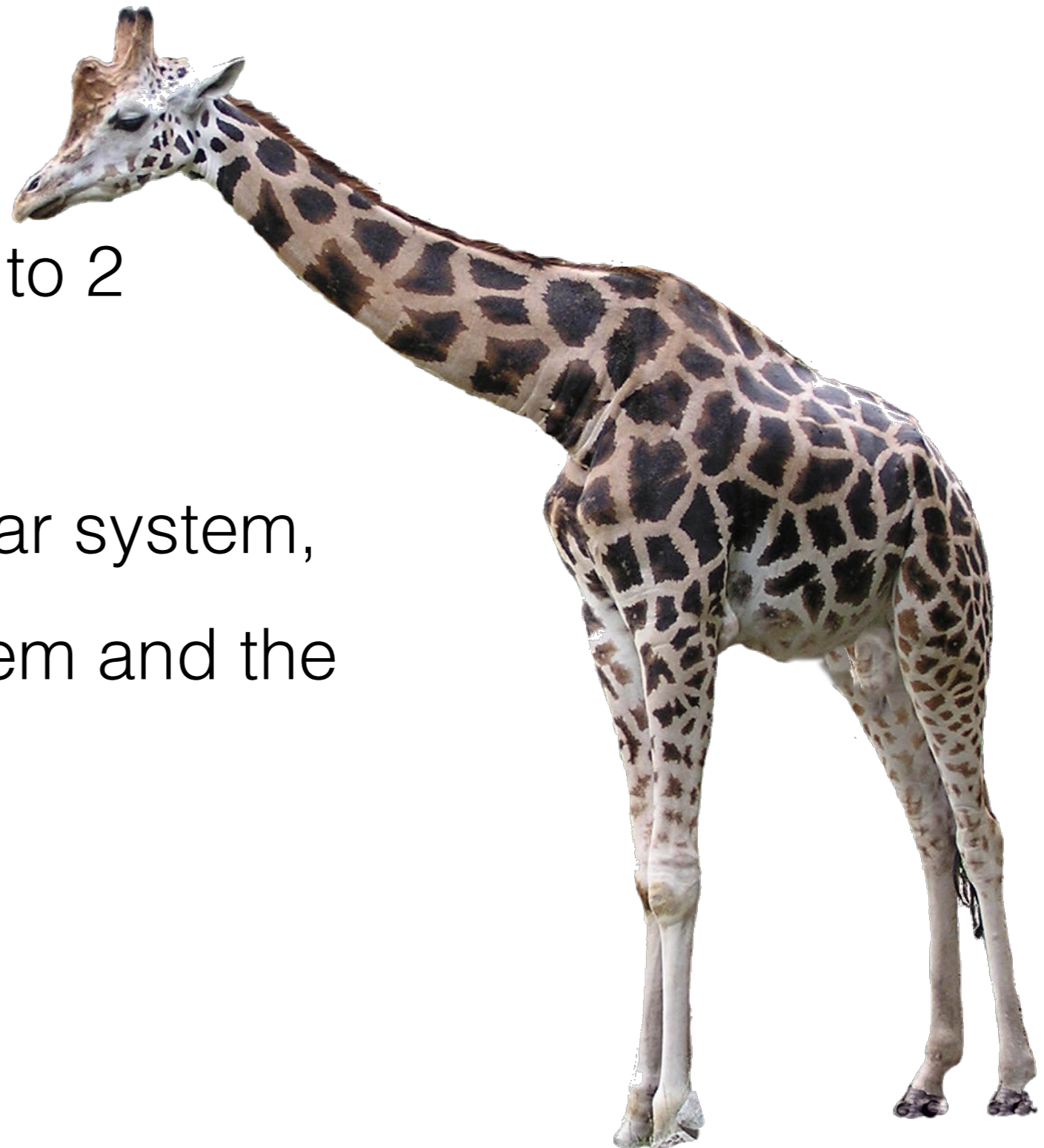
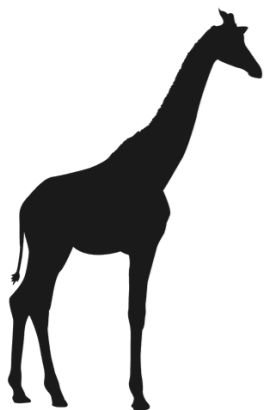
Masai Giraffe

By: Heba M. Al Sherif



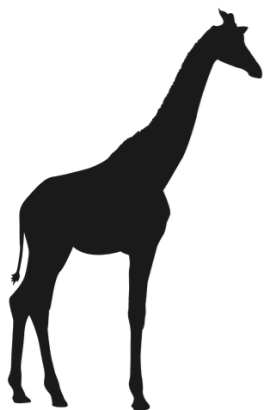
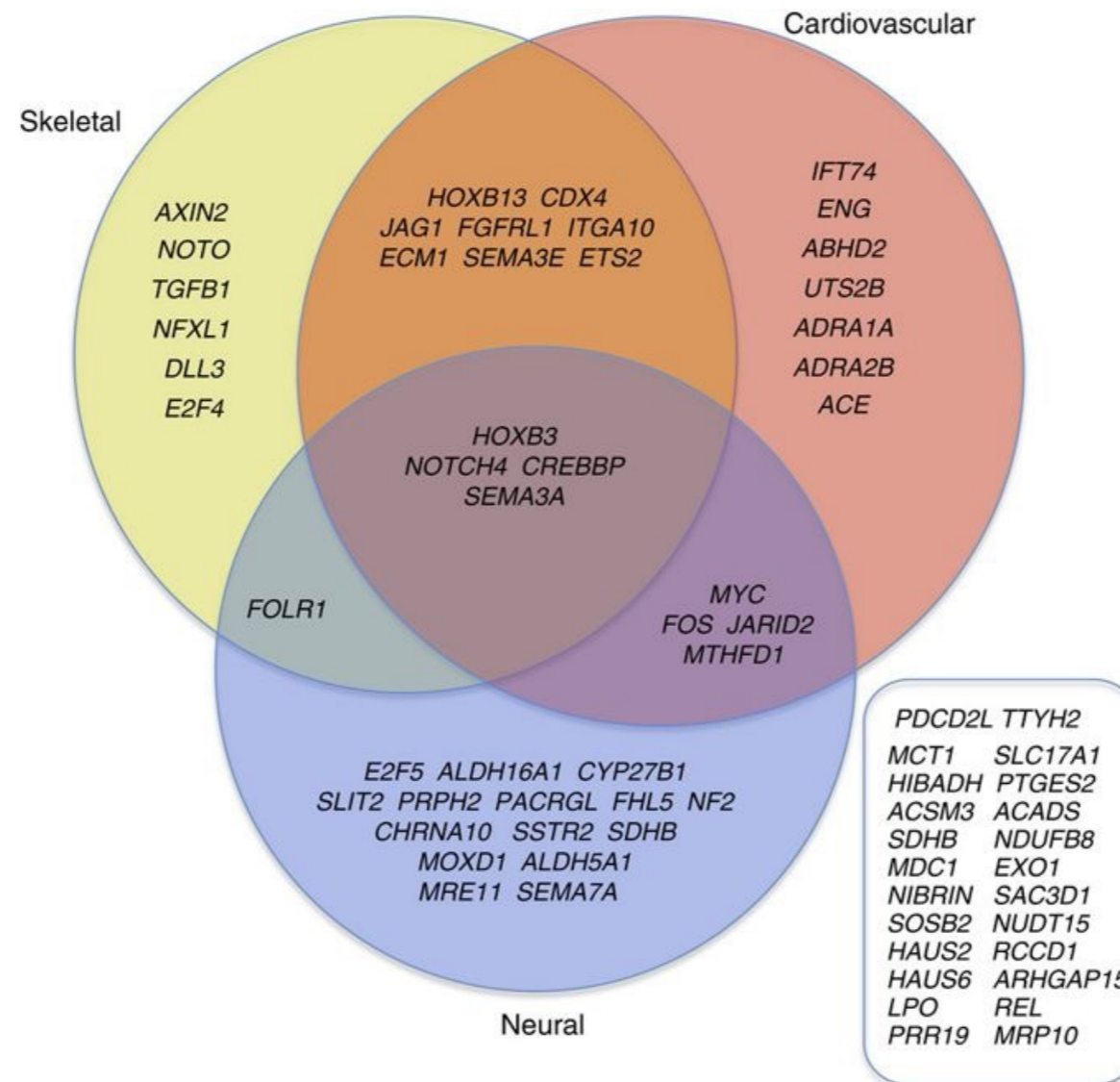
# Giraffe

- *Giraffa camelopardalis tippelskirchi*.
- *Okapia johnstoni*.
- Tallest living animal.
- Neck length reaches up to 2 meters.
- Affects the cardiovascular system, the musculoskeletal system and the nervous system.



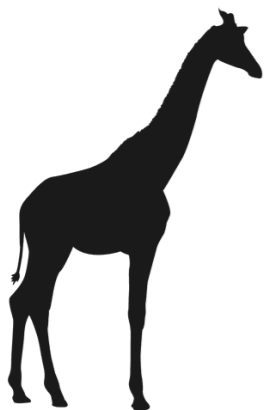
# Giraffe

- 70 genes exhibit multiple signs of adaptation.
- HOX, NOTCH and FGF signaling pathways
- FGFR1 is the strongest candidate for unique growth.



# Giraffe

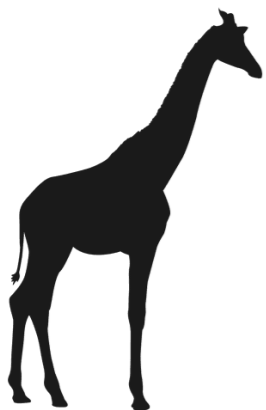
- *Liver samples for two female giraffes and one male okapi.*
- *Sequencing strategy: WGS*
- *Sequencing method: Illumina*
- *Assembly: SOAPdenovo2 and GapCloser*
- *Chromosomes: Giraffe 30 and Okapi 44-46*
- *Predicted genes: 17K*





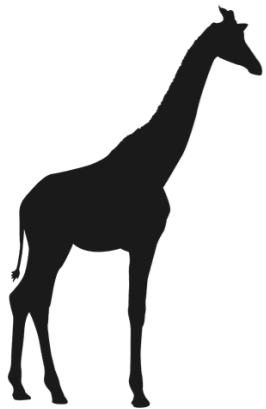
# Giraffe

	Genome size	Coverage	GC%	# Contigs	N50 contig	# Scaffolds	N50 Scaffold
Giraffe	2.9 Gb	30x	41.5%	2 M	47 Kb	2 M	339.6 Kb
Okapi	3.3 Gb	30x	42.3%	3.8 M	33.7 Kb	3.7 M	104.6 Kb



# Interesting Facts

- Giraffe has to spread it's front legs to be able to reach the ground.
- Giraffe spots are like human fingerprints.



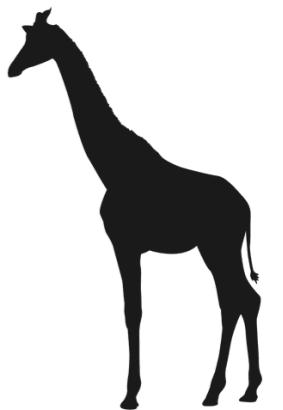
# Questions

**What are the most distinctive features of mammals?**

1. Covered in hair or fur
2. Mammary glands

**What are the systems most effected by the giraffe height?**

1. Cardiovascular system
2. Musculoskeletal system
3. Nervous system





*Ailuropoda melanoleura.*

**“Giant panda”**

By: Hana Hussain



# Fact about the species:

- The *Ailuropoda melanoleura* simply known as pandas; is a species of bear that have a distinctive black and white fur.
- Commonly found in the mountains of central and western China.
- They are good at climbing trees; swimming and they spend 14 hours eating per day.
- They are one of the rarest animal and is under immense threat from habitat loss.
- The panda genome contains 20 pairs of autosomes and one pair of sex chromosomes ( $2n=42$ ).



# Genome facts:

- Taste is an important factor in the development of dietary habits.
- The five components of basic taste one of them is umami, which can be tasted in foods like meats, cheese, broth, stock which contain a high level of the amino acid and glutamate.
- Lack of *T1R1* gene prevent the panda from expressing a functional umami taste receptor, which may partly explain why the panda diet is primarily herbivorous despite its taxonomic classification as a carnivore.
- The panda appears to have all the genes needed for a carnivorous digestive system but lacks digestive cellulase genes, therefore they depend on its gut microbiome to digest the bamboo.



➤ **Sources of DNA:**

- Peripheral venous blood was collected 3-year-old female giant panda.

➤ **The Sequence stargates:**

- Whole-genome shotgun sequencing strategy was used.

➤ **The Sequence methods:**

- Illumina Genome Analyser sequencing technology was used.

➤ **The Assembly:**

- The genome sequence was assembled with short reads using SOAP de-novo software.

➤ **The Annotation:**

- Genome size = 2.4 Gb
- % of the genome that contains genes = 3.2%
- GC content= Between 20% and 80%.



Contig N50	Scaffold N50	Genome size	GC%	% of the genome that contains genes	T.E.	LTR	LINE	SINE	# SNP
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40 kb	1.3 Mb	2.4 Gb	Between 20% and 80%.	3.2 %	36.2%	5.6%	18.2%	7.9%	2.7 million heterozygous SNPs.
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## Question:

**Why the panda diet is primarily herbivorous despite its taxonomic classification as a carnivore?**

- ✓ The panda lack *T1R1* gene that prevent them from expressing a functional umami taste receptor.





**“Platypus”**  
*Ornithorhynchus anatinus*

**By : Bashayer Jamal.**





# Platypus

**Order:** Monotremata

**Common name:** Platypus  
(*Platy*: flat, *Pus*: foot)



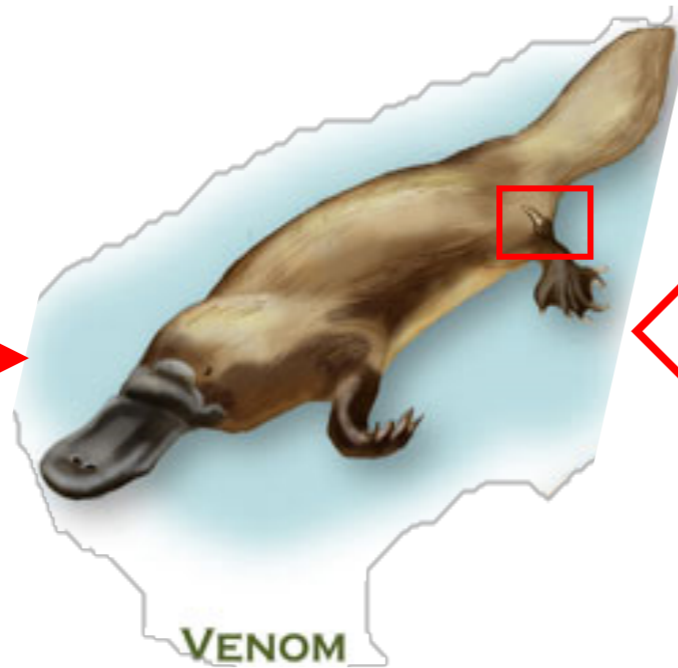
**Scientific name:**  
*Ornithorhyncus anatinus*.  
(*Ornitho*: **bird**, *rhyncus*: **snout**. *Anatinus*:  
**duck-like**).

**Habitat:** Fresh water (Australia).



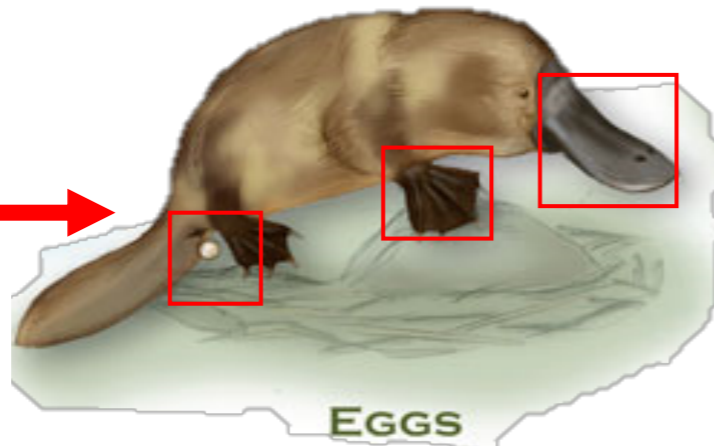
# Biology of Platypus

REPTILES



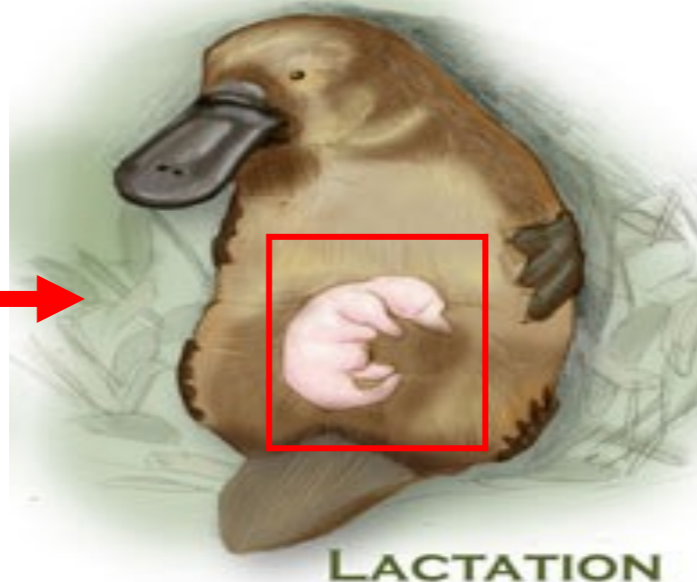
Venomous spurs in **males**, on their hind legs.

BIRDS



They have webbed feet, duck-like bill and the **females** are oviparous (lay eggs).

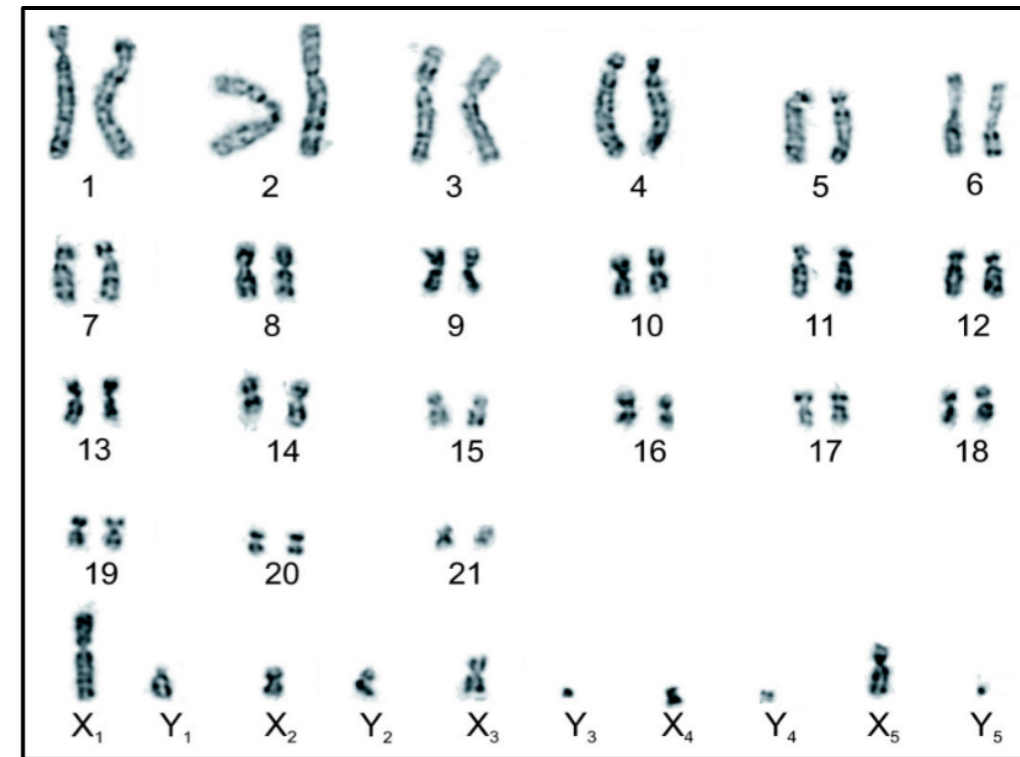
MAMMALS



Their skin **covered** with **dense fur**, they feed their young with a **pouches** of the **skin in their abdomen**.

# Platypus Genome

- They are **2n=52** chromosomes (**26 pairs**).
- They have an **XY system**.
- The **males** are a **heterozygous** (**5 pairs of XY**).
- The **females** are a **homozygous** (**5 pairs of XX**).



Karyotype of **male** platypus

Female

XX XX XX XX XX

Egg

X X X X X

Zygote

XX XX XX XX XX

Male

XY XY XY XY XY

Sperm

X X X X X

or

Y Y Y Y Y

Sperm

or

XY XY XY XY XY



# Interesting Fact








## Hunting

- **Under the water**, platypus's **eyes & ears** are **closed**. They locate their food using the **electroreceptors** ( in the bill).
- **Platypus** and **Cormorant** feeding together, the cormorant **pecks** the platypus to make it **dive for food**.



- The **X-chromosome** is very similar to the **Z-chromosome** in the **chicken**, but **not similar** to human **X**.

	Human	Kangaroo	Platypus	Chicken
Sex chromosomes	♀ XX ♂ XY	♀ XX ♂ XY	♀ X <sub>1</sub> X <sub>1</sub> X <sub>2</sub> X <sub>2</sub> X <sub>3</sub> X <sub>3</sub> X <sub>4</sub> X <sub>4</sub> X <sub>5</sub> X <sub>5</sub> ♂ X <sub>1</sub> Y <sub>1</sub> X <sub>2</sub> Y <sub>2</sub> X <sub>3</sub> Y <sub>3</sub> X <sub>4</sub> Y <sub>4</sub> X <sub>5</sub> Y <sub>5</sub>	♀ ZW ♂ ZZ
X and Z chromosome similarity	 X	 X	  X <sub>1</sub> X <sub>5</sub>	 Z
Sex determination	SRY	SRY	?	DMRT1?

# Assembly & Annotation

Assembly	Annotation
Genome size: 2.7 Gb	LTR: 13,723
GC content: 45.5%	LINE: 2,491,710
Sequencing strategy: BAC & WGS	SINE: 2,529,582
Assembly method: PCAP & FISH	Low complexity: 52,125
Sequencing coverage: 6X	
Contig N50: 39.589 kb	
Scaffold N50: 298 kb	
Number of contigs: 177.028	
Number of scaffold: 61.239	



# Questions

- 1) Why it is a semi-aquatic (neither terrestrial nor aquatic)?
  - Olfactory receptors & the males venomous.
  - Webbed feet.
  
- 2) Can you eat platypus?
  - No, the platypus is **poisonous** so it's **not edible**.
  
- 3) What about their egg?
  - You can, but they are only 11mm in diameter, it would take a **lot of them to make a meal**.





**“Australian kangaroo”**  
***Macropus eugenii.***

**by: Amna Dawoud**



# Facts about the specie:



**Common name:** Tammar wallaby

**Order:** Diprotodontia

**Scientific name:** macropus eugenii

- “Ile Eugene island” South Australia

## **Distribution:**

- Humans : kangaroos
- National symbol of Australia

## **Characteristics:**

- Food Habits: herbivore
- Use hopping as their primary method of locomotion.
- Can jump 3m high and 7.6m long.
- $2n = 16$



# Sequencing:

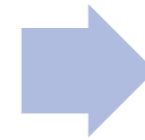
DNA source

- Lung tissue



Strategy

- WGS



Methods

- Sanger
- ABI SOLID
- illumina



# Genome Assembly:

## Meug\_1.0

- Sanger sequencing
- 2x

## Meug\_1.1

- ABI SOLID
- additional 5.9x

## Meug\_2

- Illumina
- 5x



# Genome Assembly:

- Genome size  $\approx$  2.9 Gb

version	Contigs no.	Scaffolds no.	N50/contig	N50/ scaffold
Meug_1	1.211 million	616,418	2.5 kb	-
Meug_1.1	1.174 million	277,711	2.6 kb	41.8 kb
Meug_2	1.111 million	379,858	2.91 kb	34.3 kb



# Genome Annotation:



- RepeatMasker & RepeatModeler programs.
- Repbase database

<b>total Interspersed repeats</b>	<b>Transposons</b>	<b>LTR</b>	<b>LINE</b>	<b>SINEs</b>
52.8%	2.9%	3.91%	28.6%	11.7%
	(3)	(25)	(4)	(1)

<b>Identified genes</b>	<b>Protein coding</b>	<b>Pseudo-genes</b>	<b>GC %</b>	<b>CpG</b>
18,258	15,290	1,496	38.8%	3.55

# Genomic Facts :

## life cycle:

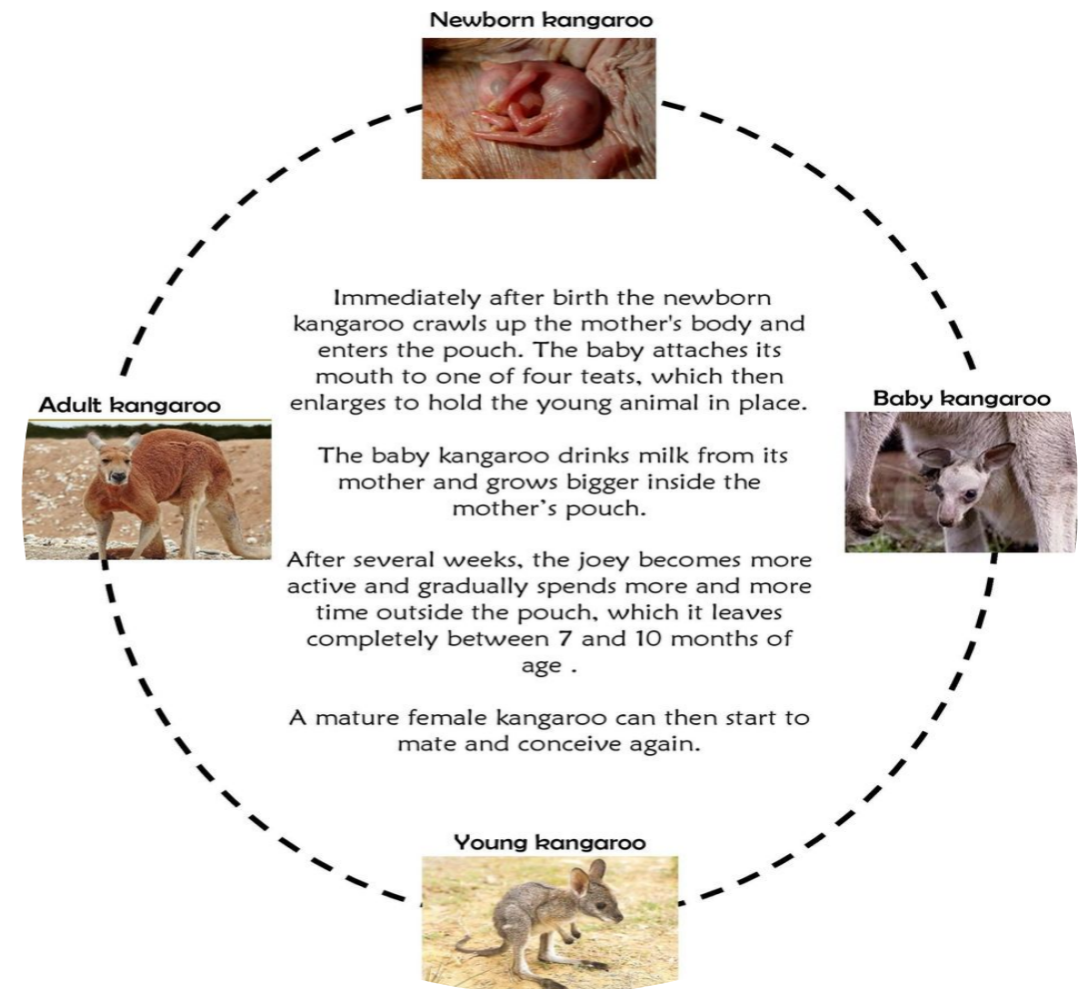
- Short gestation & long lactation

## Immunity:

- Immune factors (antimicrobial peptides)

## Concurrent asynchronous lactation:

- lactation genes:
  - Milk production: (CSN1,CSN2,CSN3,LALBA &LGB)
  - Marsupial Phase- specific: (LLPA, LLPB & WAP)



# Questions:

- 1. Which one do you think is the best version of -Meug assemblies & why?**

(Meug\_2); smallest number of contigs covers 50% of the assembled genome

- 2. What is the unique feature in marsupials life cycle:**

Complete their development inside the pouch





**“Koala”**  
*Phascolarctos cinereus.*

By: Shaikhah Al-Shareefi.



# Facts about the species :

- The koala is a marsupial mammal (pouched mammals).
- The word 'koala' is thought to mean 'no drink' or 'no water' in the Aboriginal language.
- It sleeps 22h, They live and sleep in the eucalyptus trees.
- Koalas do not build nests.
- Pear-shaped body provides stability while the koala sits in trees.





# Facts about the species :

- The koala's young are born while still at the embryonic stage, It crawls into the mother's posteriorly opening pouch and attaches to a teat, where it remains for 6–7 months. It continues to suck after it has left the pouch until about a year old.
- The species was heavily exploited by a pelt trade (1870s to late 1920s), which harvested millions of animals.
- threats are primarily due to loss and fragmentation of habitat, climate change and disease.



# Interesting Facts:

## Ability to tolerate a highly toxic diet :

- koala's diet of *eucalyptus* leaves contains high levels of plant secondary metabolites that would be lethal to most other mammals.
- Koalas experience little competition for food resources.
- Adaptive expansion of CYP2C and maintenance of duplicates appear to have worked in concert, resulting in higher enzyme levels for detoxification.
- Due to the low caloric content of this diet, the koala rests and sleeps up to 22 h a day.
- meloxicam, a nonsteroidal anti-inflammatory drug (NSAID) known to be metabolized by the protein product of *CYP2C* in humans . Is so rapidly metabolized in the koala and a handful of other eucalypt-eating marsupials.
- Anti-chlamydia antibiotics such as chloramphenicol are degraded rapidly by koalas.





# Interesting Facts:

## Taste, smell and food choice :

- expansion of one lineage of vomeronasal receptor type 1 (*V1R*) genes associated with the detection of nonvolatile odorants. There are six such genes in koala, and none found in, human, mouse, dog, platypus or chicken.
- The expansion of one lineage of *V1R* genes is consistent with the koala's ability to discriminate among diverse plant secondary metabolites.
- genomic evidence of expansions within the taste receptor families that would enable the koala to optimize ingestion of leaves with a higher moisture and nutrient content in concert with the concentration of toxic plant secondary metabolites in their food plants.
- functional duplication of the aquaporin 5 gene, which plays a role in the generation of saliva, tears and pulmonary secretions.
- The *TAS2R* family has a role in 'bitter' taste, enabling recognition of structural toxins such as terpenes, phenols and glycosides.

- DNA source: tissue biopsy.
- Sequencing strategy: hierarchical
- Sequencing method : illumina.
- Assembly: *de novo*
- Annotation: structural annotation (automated genome annotation).



# Questions:

1. How does the koala genome force the organism on just one type of food?
2. koala is born with no immunity, how do they gain it?



	Genome size	Coverage	GC%	# Contigs	N50 contig	# Scaffolds	N50 Scaffold
koala	3.42Gbb	57.3 ×	39%	1906	11.6Mb	-	11,589 (contig)



	Genome size	Coverage	GC%	# Contigs	N50 contig	# Scaffolds	N50 Scaffold	chromosomes
Giraffe	2.9 Gb	30x	41.5%	2 M	47 Kb	2 M	339.6 Kb	30
platyus	2.7 Gb	6X	45.5%	177.028	39.589 kb	61.239	298 kb	52 (26 pairs).
Giant panda	2.4 Gb	56x	Between 20% and 80%.		40 kb		1.3 Mb	
koala	3.42 Gb	57.3 x	39%	1906	11.6Mb	-	-	16
kangaroo	≈ 2.9 Gb	2x		1.211 M	2.5 kb	616,418	-	
		5.9x	38.8%	1.174 M	2.6 kb	277,711	41.8 kb	16
		5x		1.111 M	2.91 kb	379,858	34.3 kb	