

Genetische verschillen tussen pluimveerassen

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Themadag Fokkerij en behoud van vitale kippenrassen



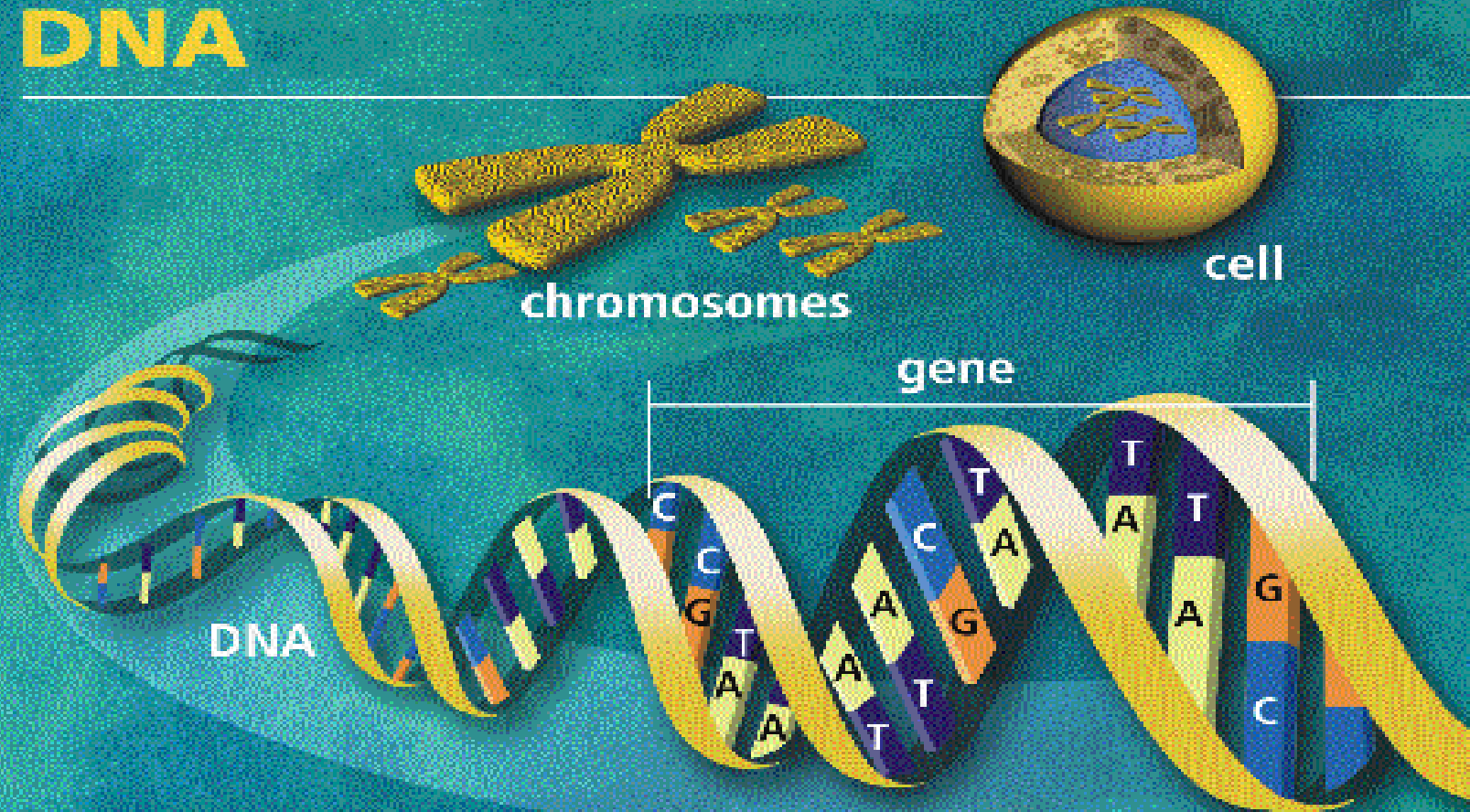
Introductie

- Het kippen genoom
- Wat zijn genetische verschillen
 - Uitleg enkele termen
- Genetische verschillen vroeger en nu
 - Microsatelliet merkers
 - Single nucleotide polymorphism (SNP)
- Resultaten



Het erfelijk materiaal (DNA)

DNA



7-5-2014



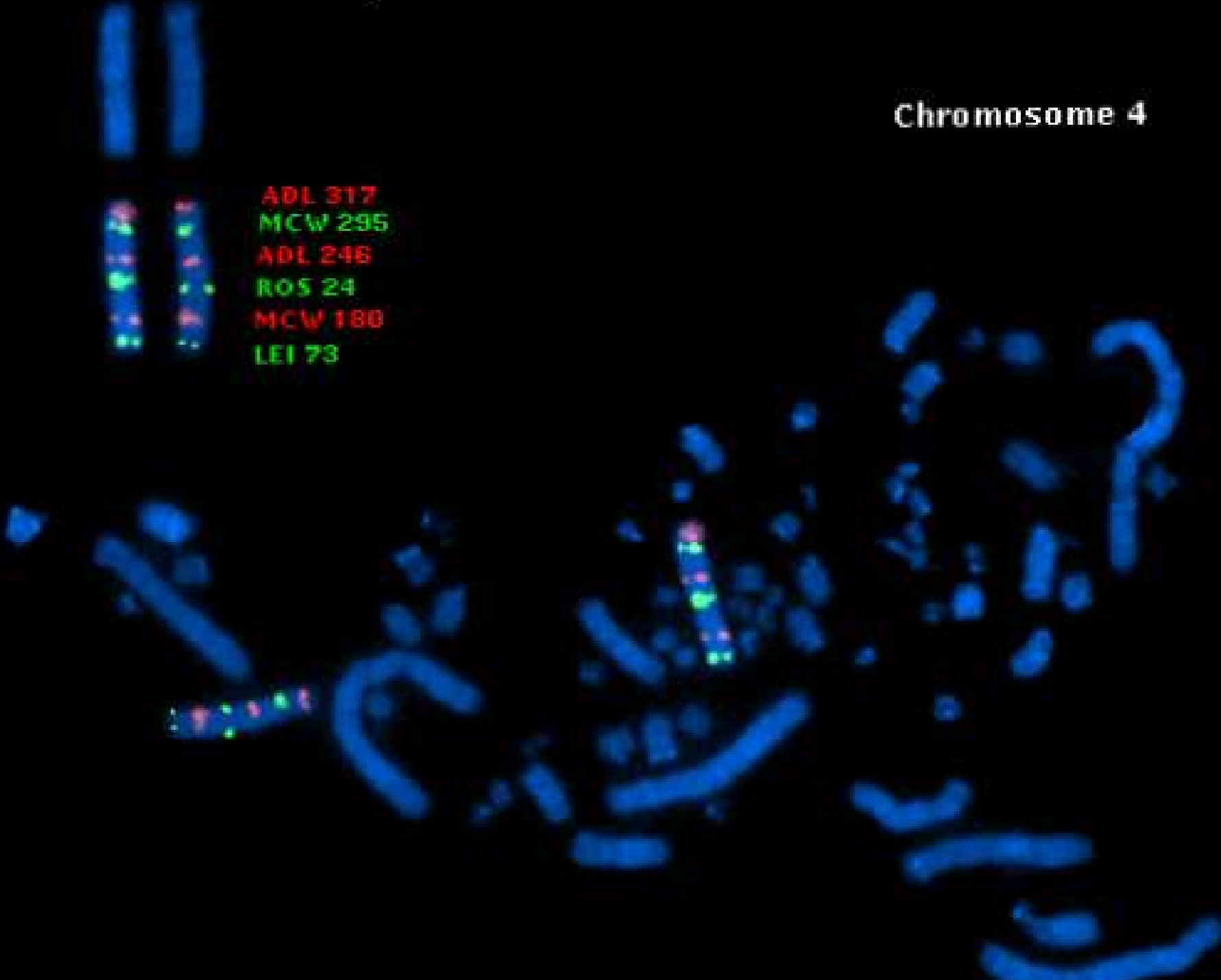
Het kippen genoom: een aantal feiten

- 38 paar autosomen en 1 paar sex chromosomen (ZZ = Male, ZW = Female)
- Twee chromosomale subtypes: macrochromosomen en microchromosomen - waarbij microchromosomen gendichter zijn
- Genetische ~ 3800 cM
- Fysisch ~ 1.2×10^9 bp



Chromosome 4

- ADL 317
- MCW 295
- ADL 246
- ROS 24
- MCW 180
- LEI 73



Genetische markers kunnen worden verdeeld in twee groepen:

■ punt mutaties

- gatctgatgcgtgggatgaggcg
- gatctgatgcgtgagatgaggcg

SNP
RFLP
AFLP

■ Indels (insertion/deletions)

- gatctgatgcgtgatgctgatcgtgatgaggcg
- gatctgatgcgtg gatgaggcg

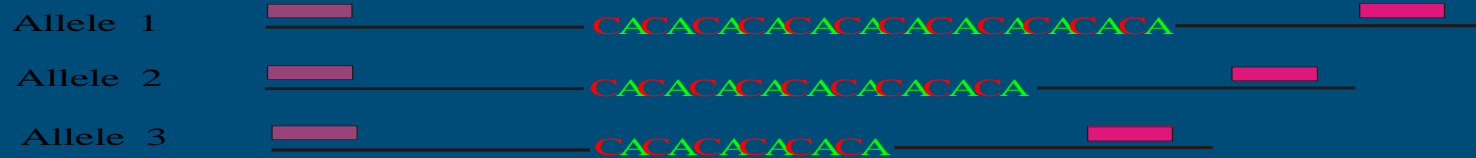
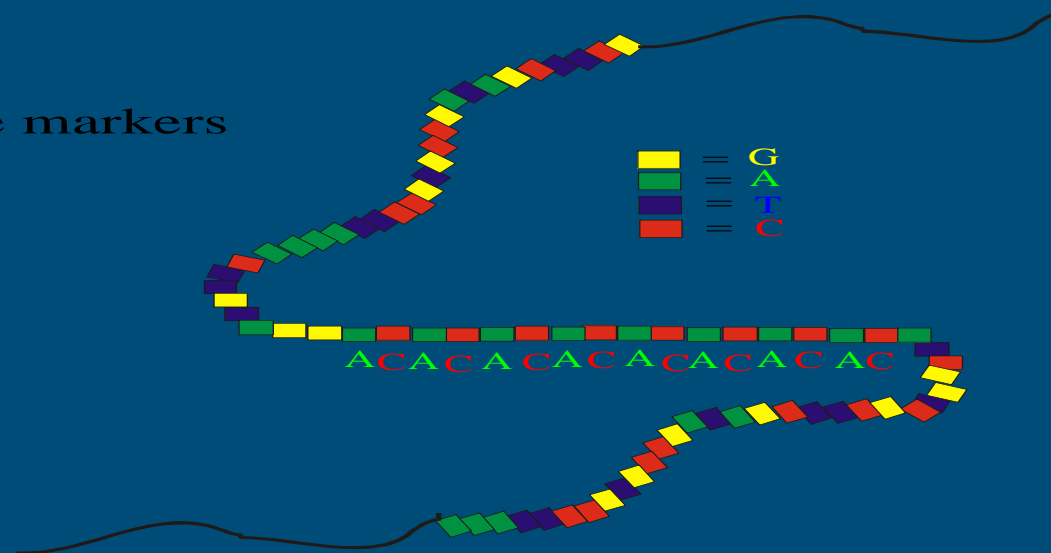
RFLP
AFLP

Microsatellites
Minisatellites



Genotypering m.b.v. een microsatelliet merker

Microsatellite markers



Termen

Homozygoot = een dier heeft dezelfde vorm van een gen op een locus op beide homologe chromosomen

Heterozygoot = een dier heeft verschillende vormen van een gen op een locus op beide homologe chromosomen

Haplotype = Twee of meer allelen op een chromosoom welke samen overerven



Microsatelliet markers: genotype

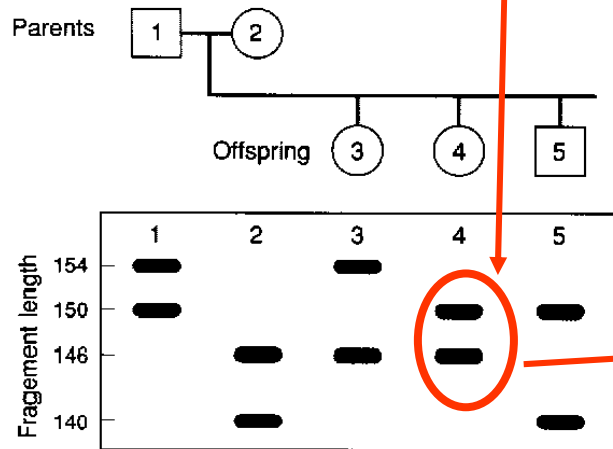
- After PCR, an animal with two bands/peaks detected is heterozygote.

-After PCR, an animal with only one band/peak detected is homozygote.

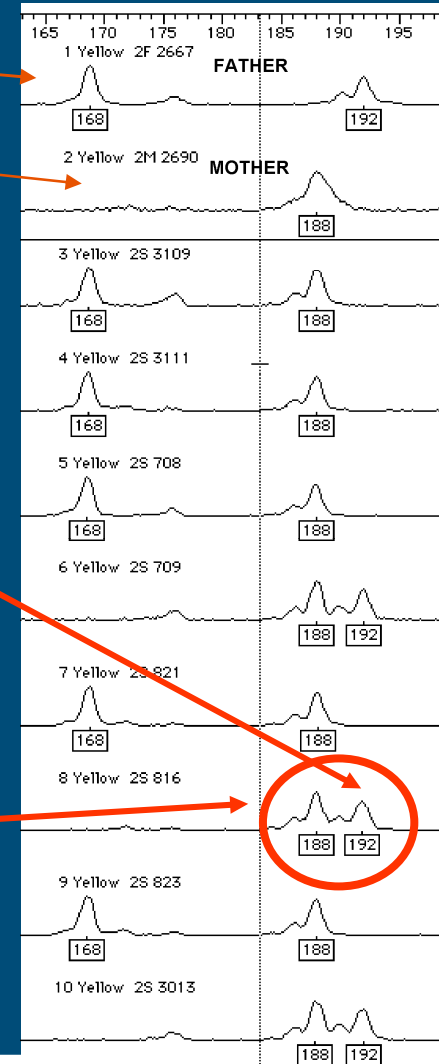
-The **genotype** for an animal are the bands/peaks shown in one lane of a gel

with a minimal of one and a maximum of two.

(b) Inheritance of the Polymorphic STS shown in (a)



Genotype:
Een dier; twee allelen



Oud hollandse Hoenderrassen

Landhoenders

Groninger Meeuw
Lakenvelder
Drents Hoen
Assendelfter Hoen
Fries Hoen
Hollands Hoen

kuif en baardhoenders

Baardkuif Hoen
Ned. Uilenbaard
Hollands Kuifhoen
Kraaikop
Brabanter
Hollands Kriel
Ned. Sabelpootkriel

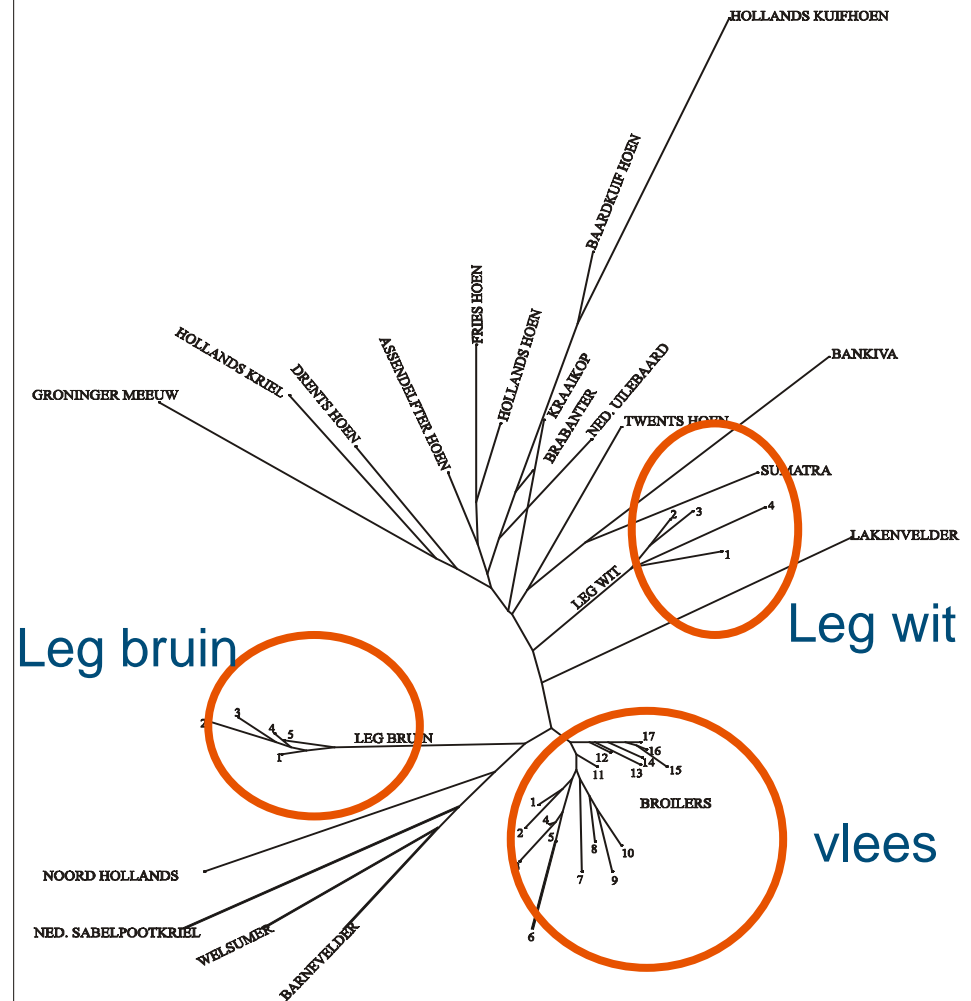
Nieuw Nederlandse hoenderrassen

Barnevelder
Welsumer
Noord Hollands Hoen
Twents Hoen



Fylogenetische boom

microsatelliet merkers



Het kippen genoom



Mircosatelliet merkers:
- 12.000

SNP:
- 3,4 miljoen



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Genetische markers kunnen worden verdeeld in twee groepen:

■ Point mutations

- gatctgatgcgtg^ggatgaggcg
- gatctgatgcgtg^agatgaggcg

SNP
RFLP
AFLP

■ Indels (insertion/deletions)

- gatctgatgcgtggatgctgatcgtgatgaggcg
- gatctgatgcgtg gatgaggcg

RFLP
AFLP

Microsatellites
Minisatellites



SNP = Single Nucleotide Polymorphism

Sequence 1 CTGCGTCTGAGGGGTGGTATGCAGATCTTCGTGAAGACC

Sequence 2 CTGCGTTTGAGGGGTGATATGCAGATCCTTCGTGAAGACC

Sequence 3 CTGCGTTTGAGGGGTGGTATGCAGATCCTTCGTGAAGACC



- SNP frequentie :
 - Mens: 1 SNP elke 1300 bp
 - varken: 1 SNP elke 350 bp
 - Kip 1 SNP elke 200 bp

Veel SNPs zijn bekend bij verschillende soorten

mens: 13.1 million SNPs

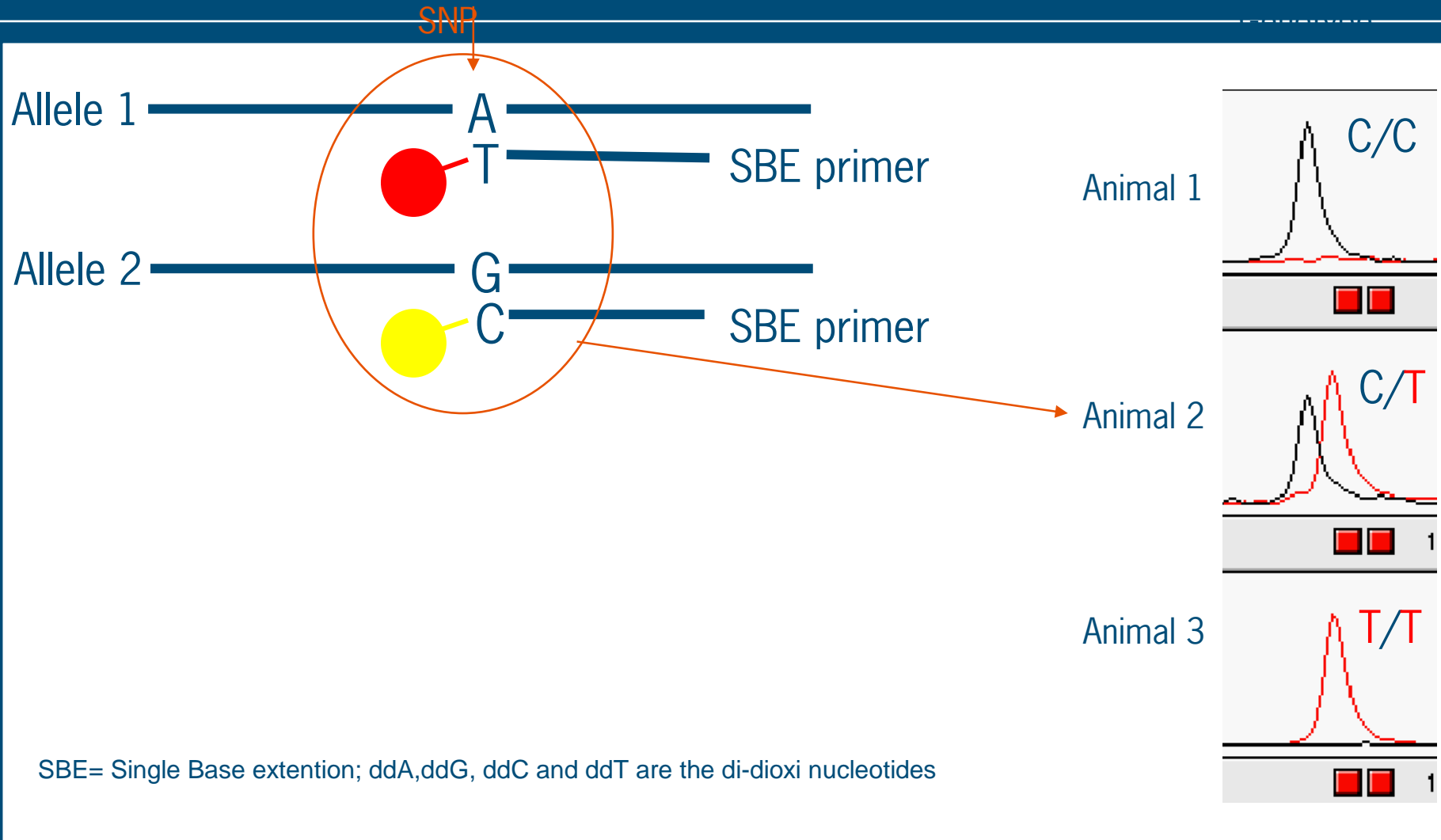
Kip: 3.3 million

Hond: 3 million

Muis: 14.8 million



SNP typing

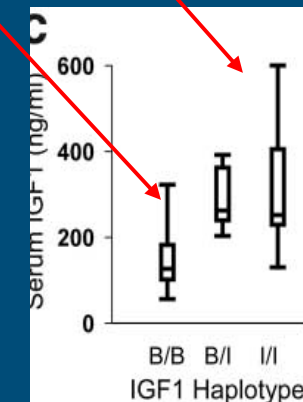
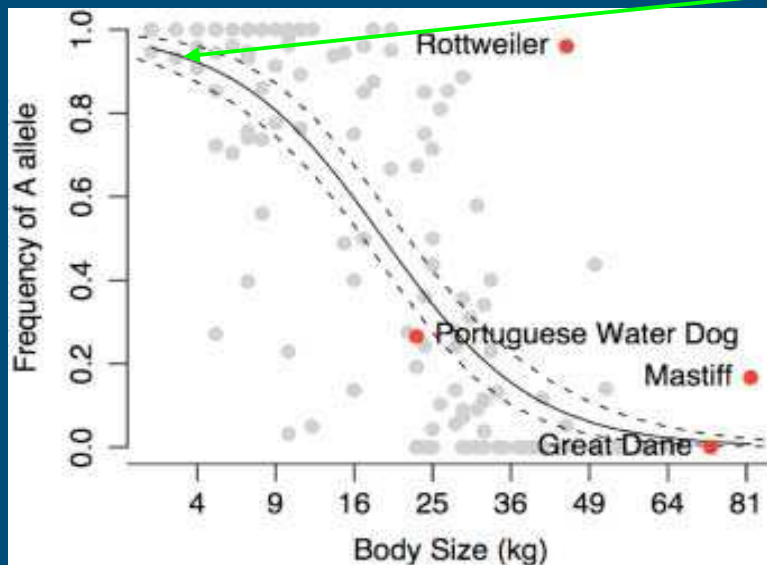


Mutaties in regelende elementen hebben een drastisch effect op het fenotype

A Single *IGF1* Allele Is a Major Determinant of Small Size in Dogs

Nathan B. Sutter,¹ Carlos D. Bustamante,² Kevin Chase,³ Melissa M. Gray,⁴ Keyan Zhao,⁵ Lan Zhu,² Badri Padhukasahasram,² Eric Karlins,¹ Sean Davis,¹ Paul G. Jones,⁶ Pascale Quignon,¹ Gary S. Johnson,⁷ Heidi G. Parker,¹ Neale Fretwell,⁶ Dana S. Mosher,¹ Dennis F. Lawler,⁸ Ebenezer Satyaraj,⁸ Magnus Nordborg,⁵ K. Gordon Lark,³ Robert K. Wayne,⁴ Elaine A. Ostrander^{1*}

The domestic dog exhibits greater diversity in body size than any other terrestrial vertebrate. We used a strategy that exploits the breed structure of dogs to investigate the genetic basis of size. First, through a genome-wide scan, we identified a major quantitative trait locus (QTL) on chromosome 15 influencing size variation within a single breed. Second, we examined genetic variation in the 15-megabase interval surrounding the QTL in small and giant breeds and found marked evidence for a selective sweep spanning a single gene (*IGF1*), encoding insulin-like growth factor 1. A single *IGF1* single-nucleotide polymorphism haplotype is common to all small breeds and nearly absent from giant breeds, suggesting that the same causal sequence variant is a major contributor to body size in all small dogs.

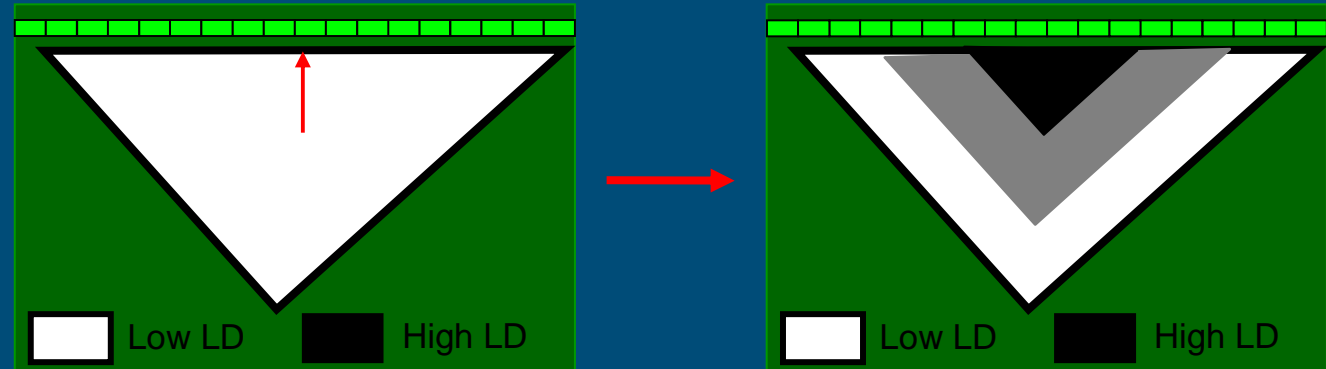


Haplotype blokken

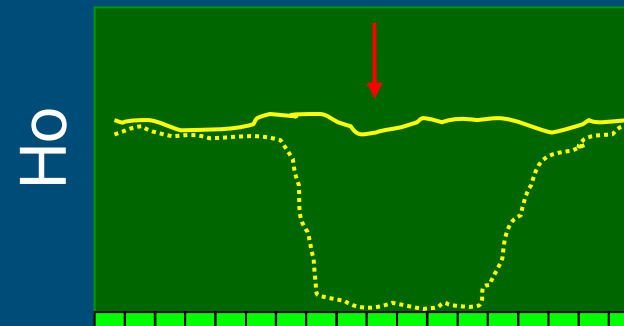


Signatures of selective sweep

1: Increased LD



2: Decreased Heterozygosity



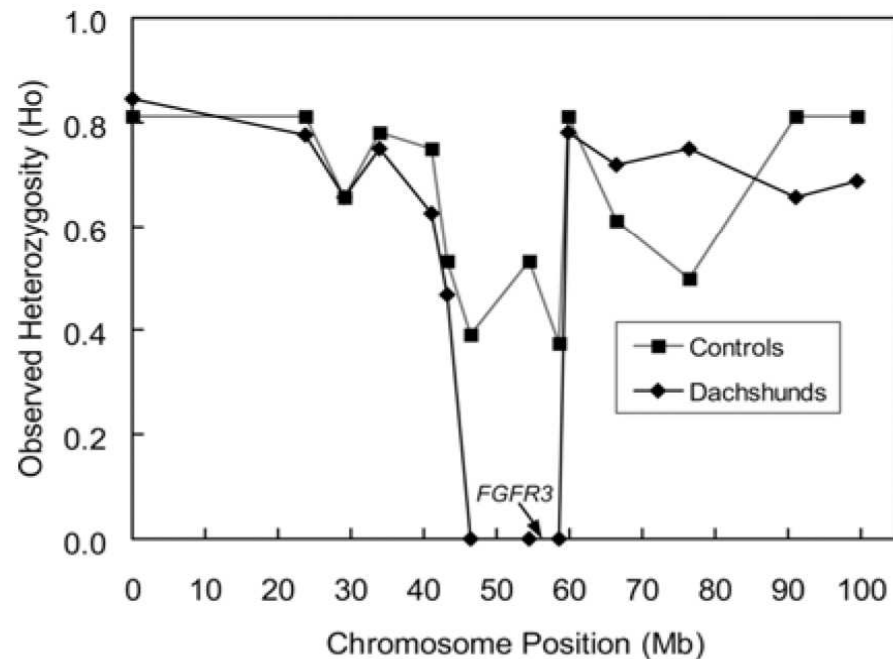
3: Deviation of expected ancestral/derived state frequency



Selection detectable in the genome because of 'hitchhiking' effects

Complete sweep on the FGFR3 region in Dachshund

FIBROBLAST GROWTH FACTOR RECEPTOR 3 (FGFR3) is a leading cause of achondroplasia in humans



Pollinger et al., 2006
Selective sweep mapping of
genes with large phenotypic effects.
Genome Res. 15:1809-1819



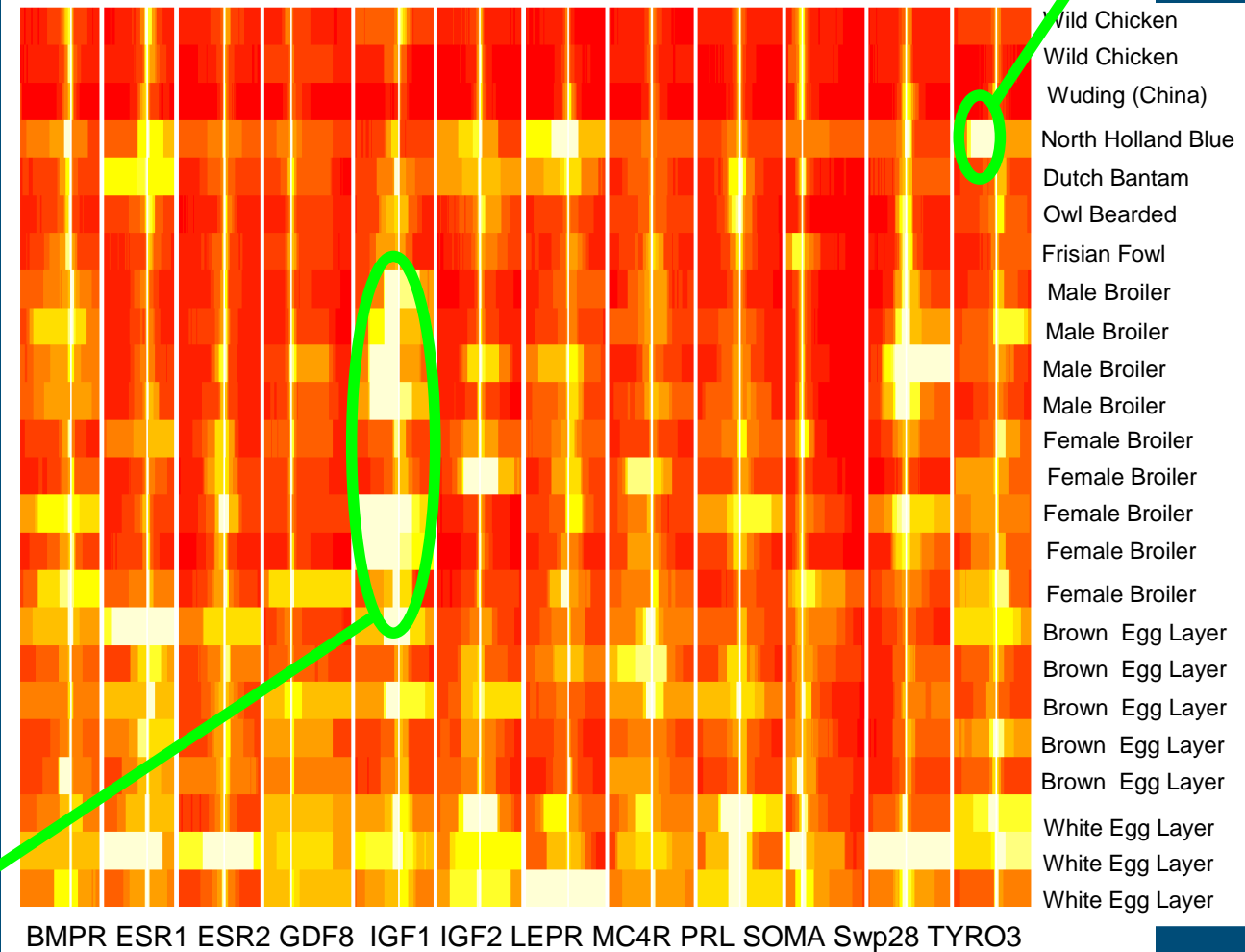
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Finding signatures of selection in the chicken genome

Color gene for Noordhollandse Blauwe

■ Low HH
■ high HH

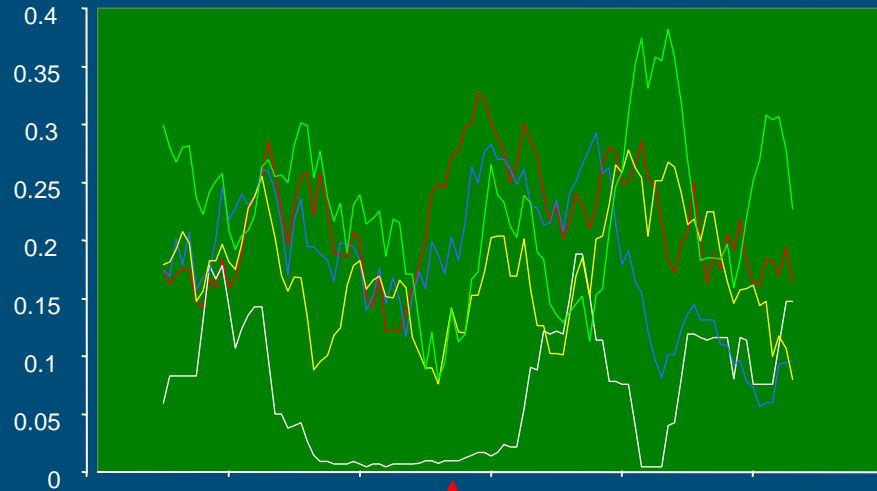


(almost) universal in broilers at IGF1

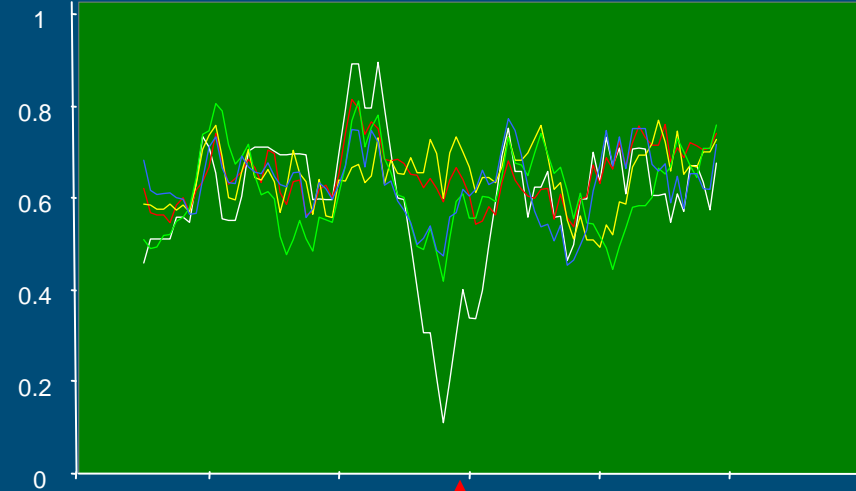
Decay of Haplotype Homozygosity (HH) relative to target gene

TYRO3 (een van de genen betrokken bij kleur)

Heterozygosity



Frequency of ancestral state



- Male Broiler (open)
- Red Jungle Fowl (wild)
- Female Broiler (open)
- Uilenbaard
- Noorhollandse Blauwe

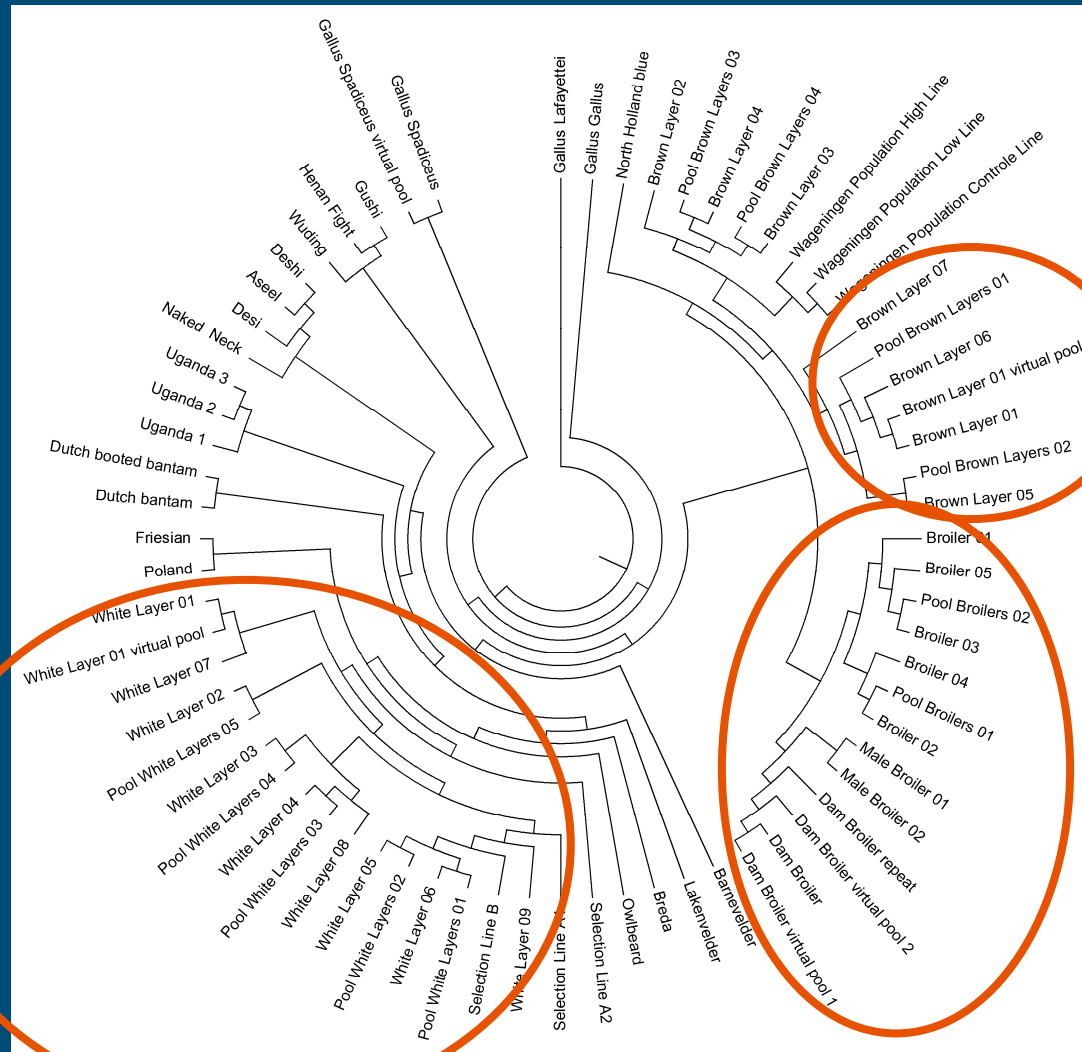


20.000 SNPs in kip

	# SNPs	Gallus gallus			Asian	European	Commercial	Selection	
		Lafayettei	Spadiceus	gallus	Aseel	Friesian	White layer	Male broiler line A1	
Macro Chromosomes									
chr1	2728	6.34	66.43	69.06	73.40	59.87	45.36	75.11	25.92
chr2	2101	6.93	66.90	71.82	71.78	59.59	37.08	72.44	27.51
chr3	1556	7.35	68.12	72.69	76.61	66.11	41.90	78.66	24.94
chr4	1281	5.17	67.27	70.65	71.43	61.12	45.16	72.83	29.51
chr5	810	7.23	66.30	71.11	71.98	61.48	43.21	74.94	32.35
chr6	647	7.19	67.75	72.53	74.54	62.44	43.89	77.01	26.23
chr7	715	7.67	69.09	70.77	72.59	62.38	44.54	78.74	30.49
chr8	578	6.26	67.76	70.42	69.72	60.90	45.16	75.61	20.93
Micro Chromosomes									
chr9	476	6.74	68.21	70.80	76.26	55.67	39.58	74.16	14.92
chr10	395	9.07	67.09	70.63	75.70	65.57	43.04	75.70	22.53
chr11	520	7.09	65.77	66.54	74.57	60.77	35.07	69.81	24.42
chr12	519	9.13	68.21	72.83	75.92	59.27	42.58	73.03	26.78
chr13	449	6.68	61.02	68.15	70.60	65.26	43.30	73.05	25.84
chr14	378	6.54	67.46	71.16	75.40	65.08	54.38	76.98	40.48
chr15	322	6.69	61.49	70.19	67.39	63.04	40.06	77.02	26.71
chr17	272	10.49	65.44	68.01	73.16	56.99	36.40	76.84	23.16
chr18	271	7.84	65.44	77.57	79.78	62.87	36.53	73.16	21.69
chr19	246	5.79	70.73	73.58	75.20	66.67	37.40	79.67	25.61
chr20	361	9.22	62.88	64.27	71.47	55.40	30.47	71.47	22.16
chr21	245	11.86	64.49	71.84	71.43	59.59	49.39	77.14	37.55
chr22	138	10.85	44.20	52.90	58.70	53.62	31.16	61.59	23.91
chr23	187	13.11	65.24	73.26	75.94	70.05	52.41	79.14	27.27
chr24	236	10.34	67.80	63.98	66.10	59.75	45.76	71.19	30.08
chr26	147	4.23	64.63	68.03	74.15	72.11	46.26	76.87	32.65
chr27	146	10.56	63.70	73.29	75.34	69.18	50.00	79.45	23.97
chr28	151	12.00	64.90	66.89	75.50	62.91	48.34	72.19	21.85
Sex Chromosomes									
W	13	23.08	46.15	46.15	50.00	61.54	38.46	69.23	38.46
Z	893	2.67	58.79	63.27	58.90	43.11	22.65	60.13	7.39
Unassigned SNPs									
chr0	536	9.13	64.67	67.10	64.76	52.52	33.96	68.28	25.93
Total % informative SNPs per population		6.95	64.41	68.60	71.32	61.20	41.50	73.84	26.25



Fylogenetische boom (mbv 20.000 SNPs)



Witte Leg

Bruine leg

vlees



Waarom oud Hollandse hoenderrassen

- Biodiversiteit
 - Bijdrage aan de totale genetische variatie
- Andere selectie
 - Kunnen bijdrage aan het verkleinen van haplotype (bv bij het opsporen naar genetische defecten)



Verzoek

- Nieuw genetisch materiaal van de oud hollandse hoenderrassen (andere rassen zijn welkom)
 - Bloed
 - Bevruchte eieren (bv 18 dagen oude embryo's inde vriezer)
- Aantal dieren per ras: 30
- Zo min mogelijk verwante dieren welke het gehele vertegenwoordigen.



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