Cytogenetic Variation in CORE AFRI Oat Lines

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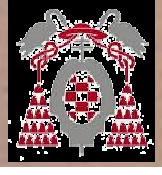


Brigham Young University, Provo, Utah
Y

Oats in Utah, USA!

AKA, *Orphaned Crops R Us…*

Personal genotyping using snps: $200 US

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Jump to a gene: Go a SNP: Go

1 247M Bases 2815 Genes 81k SNPs	2 242M Bases 1860 Genes 81k SNPs	3 199M Bases 1497 Genes 66k SNPs	4 191M Bases 1136 Genes 57k SNPs	5 180M Bases 1276 Genes 58k SNPs	6 170M Bases 1575 Genes 72k SNPs
7 158M Bases 1512 Genes 56k SNPs	8 146M Bases 1013 Genes 51k SNPs	9 140M Bases 1245 Genes 44k SNPs	10 135M Bases 1105 Genes 52k SNPs	11 134M Bases 1850 Genes 51k SNPs	12 132M Bases 1370 Genes 49k SNPs
13 114M Bases 545 Genes 38k SNPs	14 106M Bases 1315 Genes 32k SNPs	15 100M Bases 998 Genes 31k SNPs	16 88M Bases 1098 Genes 31k SNPs	17 78M Bases 1494 Genes 30k SNPs	18 76M Bases 429 Genes 29k SNPs
19 63M Bases 1743 Genes 19k SNPs	20 62M Bases 768 Genes 24k SNPs	21 46M Bases 360 Genes 14k SNPs	22 49M Bases 749 Genes 15k SNPs	X 154M Bases 1376 Genes 30k SNPs	Y 57M Bases 284 Genes 5k SNPs

MT
16k Bases
37 Genes
4k SNPs

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THE ONLY BENCHTOP GENOME CENTER

"a landmark development"

FT FINANCIAL TIMES

"1,000 times more powerful than existing technology."

Give Feedback

Since I have a gypsy y-chromosome and 3% of my genome is neanderthal, I can use the crystal ball…

paternal line

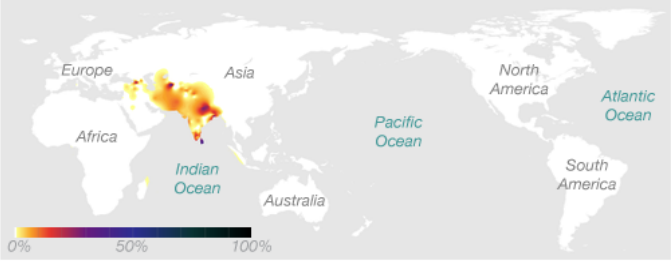
Your Y chromosome DNA determines your paternal haplogroup. What is a haplogroup?

tell a friend

Map | History | Haplogroup Tree

Paternal Haplogroup: R2

Locations of haplogroup R2 circa 500 years ago, before the era of intercontinental travel.



R2 is concentrated in India, Iran and parts of Central Asia. It appears to have arisen somewhere in the Indian subcontinent about 12,000 years ago.

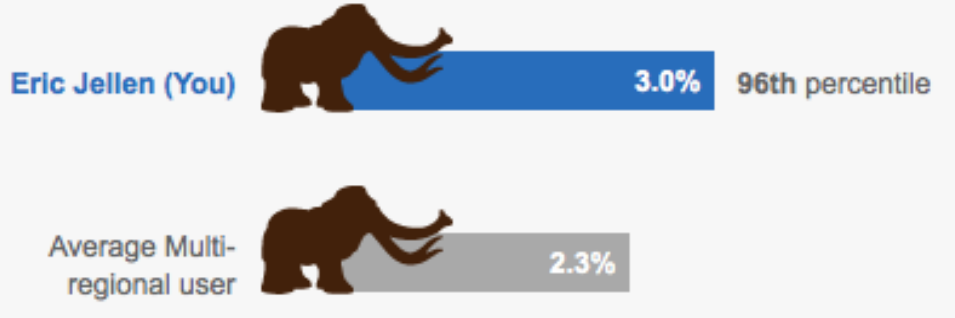
Haplogroup: R2, a subgroup of R
Age: 12,000 years
Region: South Asia, Central Asia
Populations: Indians, Iranians
Highlight: Haplogroup R2 is found across India, central Asia, and the Caucasus.

Your Family and Friends

D2a1b	Japanese Person
E1b1a8a1.	Nigerian Person
E1b1b1a2.	Gerald Lopez, Gerardo Lopez
E1b1b1c	Greg Kirsh

Got Neanderthal DNA?

An estimated 3.0% of your DNA is from Neanderthals.

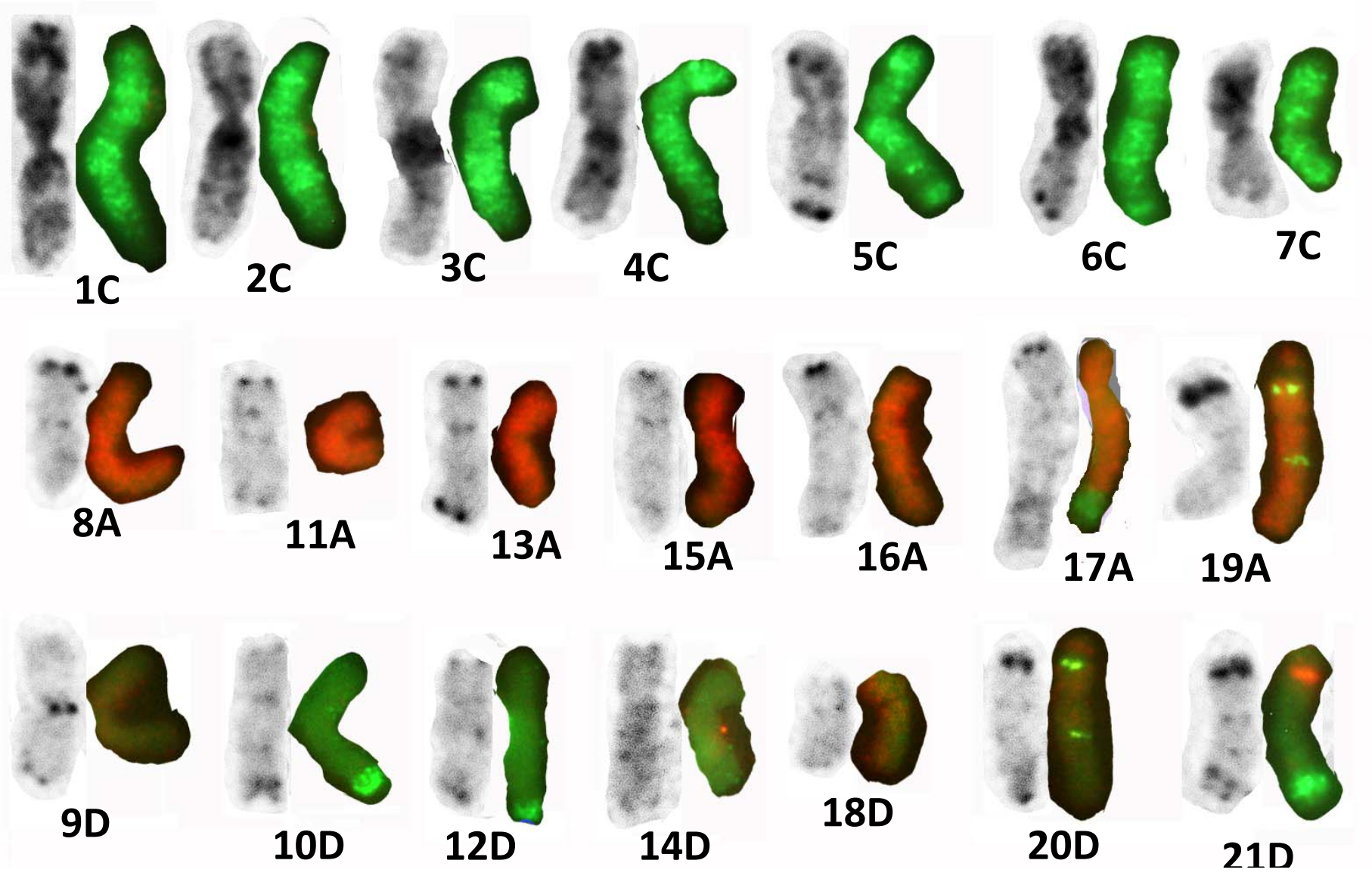


"I see your little, petrified skull … labeled and resting on a shelf somewhere."

Why Care About Oat Chromosome Variation?

- Proper recombination, segregation and assortment depend upon faithful chromosome pairing
- Important genes/QTLs may be linked to chromosome break points
- Recombination failure = reduced breeding efficiency
- Polymorphic C-bands may be useful genetic markers
- Oat chromosomes are big, have nice C-bands, and are therefore FUN to work on!

Uniform Hexaploid Oat Karyotype

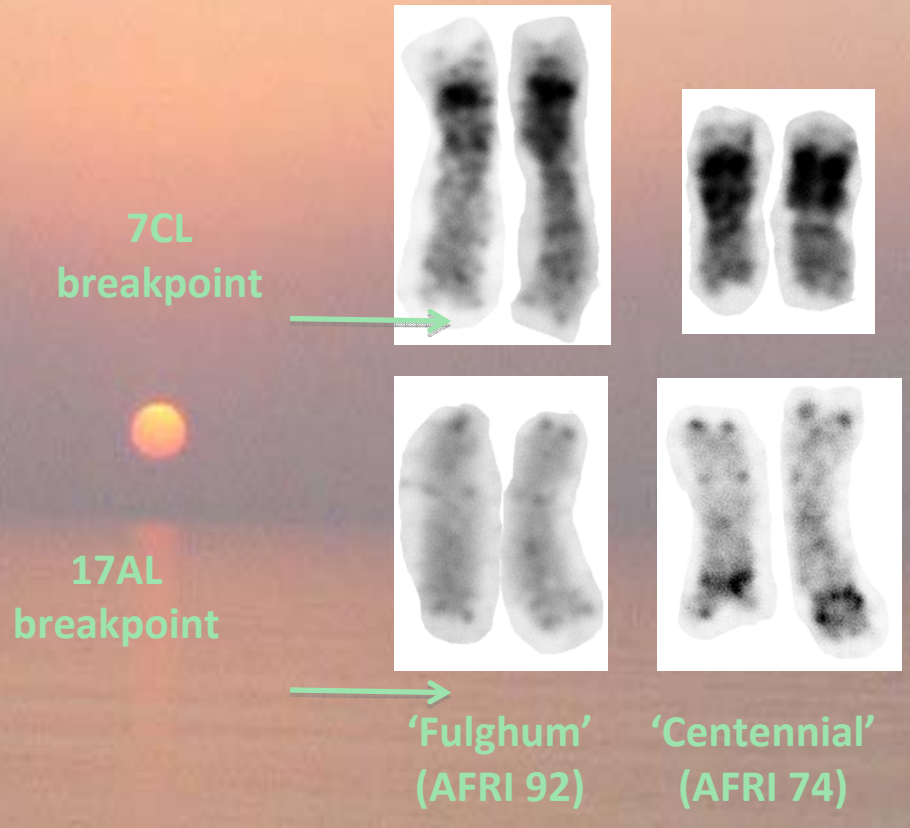


AFRI/NIFA Core Germplasm: 106/~700

Aarre	Coker 227	IL86-5698-3	Noble-2	Salomon	Z615-4
Ajax	Coker 234	Jay	Novojatkovo	Sang	
Ajay	Dal	Jerry	OA1063-8	Sesqui	Other Lines:
Akyutaka	Dancer	Kangaroo	Ogle	Shadow	Binder
Asencao	Dane	Kanota	OT380	SO-1	Borriesa
Assiniboia	Dominik	Kaufman	OT586	Sol-Fi	Fia
Baler	Drummond	Lang	Otana	Stout	Flamingsgold
Belinda	Exeter	Lutz	Pacer	Sun II-1	Gelbhafer
Bia	Flaemingsnova	Maldwyn	Pg11	SW Betania	Pendek
Blaze	Florida 501	MAM 17-5	Pg16	TAM O-301	PI 268616
Boudrias	Ford Early Giant	Marie	Pinnacle	TAM O-397	Seger (Victory)
Bountiful	Freddy	Marion (Canada)	Prescott	Tardis	Stormogul
Boyer	Fulghum	Matilda	ProFi	Triple Crown	Svea
Buckskin	Furlong	Maverick	Provena	Troy	UFRGS 17
Buffalo	Gehl	Melys	Pusa Hybrid G	UFRGS 8	UFRGS 930598
Calibre	Gem	MF9522-523	Ranch	UFRGS 881971	Z595
Centennial	Goslin	MN 811045	Red Rustproof	UFRGS 930605	
Chaps	H927-1-6-1-x-x-24	MN 841801-1	Rigadon	Ukraine reselection	
Cherokee	Hazel	Morgan	Robust	Victoria	
CI 4706-2	HiFi	Mortlock	Ronald	Vista	
Ciav 6209	Hurdal	Morton	Russell	WAOAT2132	

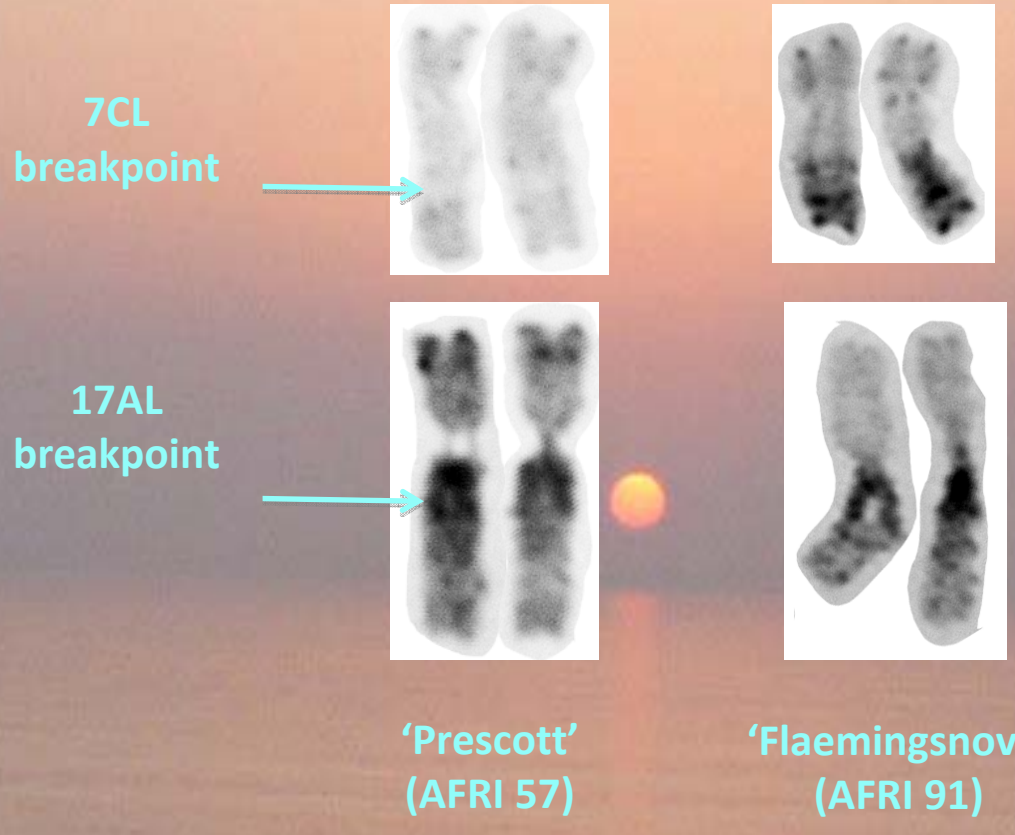
Major Karyotypic Variant #1

- **Translocation 7CS-17AL**
  - **Very common rearrangement in *sativa*- and *fatua*-race oats**
  - **9/105 core AFRI lines are non-translocation or heterogeneous:**
    - HiFi (AFRI 16)
    - La Prevision (AFRI 21)
    - Jerry (AFRI 29)
    - Pusa Hybrid (AFRI 87)
    - Fulghum (AFRI 92)
    - Red Rustproof (AFRI 106)
    - Victoria (AFRI 108)
    - Het Coker 234 (AFRI 54)
    - Het Kanota (AFRI 19)



Major Karyotypic Variant #2

- **Translocation 3CS-14DL**
  - **Discovered in 'OT380' (AFRI 45), 'Flaemingsnova' (AFRI 91), 'Lang' (AFRI 93)**



Major Karyotypic Variant #2

- **Translocation 3CS-14DL**
  - **Originally observed in most 'Sun II' monosomics but not in disomic 'Sun II' by Leggett & Markhand (1995) and Jellen et al. (1997)**

From Jellen et al. 1997, *Theor Appl Genet* 95:1190-1195

aneuploids are presented in Fig. 2. Our results using C-banding are in agreement with those of Leggett and Markhand (1995) who used GISH to identify C-genome monosomes of Sun II. These authors also noted that certain monosomic lines carried a large intergenomic reciprocal translocation. By C-banding, we determined that this interchange involves chromosomes 3C and 14 (Fig. 2). The 3C-14 interchange was present in 15 of the 18 original Sun II monosomics, indicating that the population from which this original set was isolated must have been heterogeneous for the translocation. One of the original Sun II monosomic lines, XI, is monosomic for the $3C^{14}$ translocation chromosome (Table 1). None of the new Sun II mono-

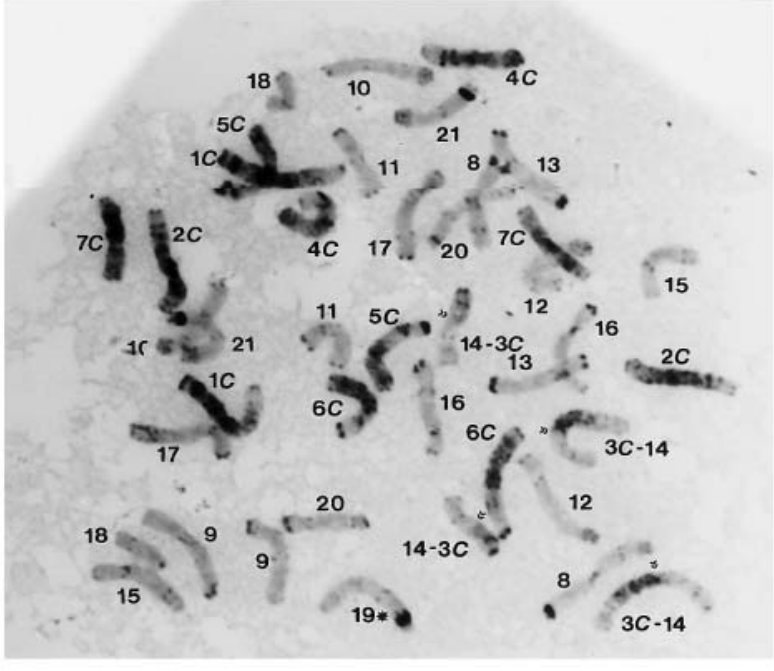


Fig. 2 C-banded root-tip cell from line AVA 91 (Mono XII), monosomic for chromosome 19 (*starred*). An intergenomic translocation involving chromosomes 3C and 14 is indicated with *arrowheads*. This translocation is missing in Sun II lines IV, V, and XVIII, as well as all Sun II aneuploid lines derived from haploids from oat × maize crosses. Magnification is 630

Flaemingsnova

1	2	3
	Flämingsgold	Von Lochow's Gelbhafer
Pendek		Blanche de Siberie
	Binder	Carstens III
		Carstens III
	unnamed_6736	Flämingsgold
Flämingsstahl		unnamed_6737
	Dippes Weiß	Von Lochow's Gelbhafer
		Dippes Überwinder

Sun II

1	2	3
	Victory	Milton (Sweden)
Stjärn		Milton (Sweden)
	Crown (Sweden)	Norsk Propsteier
		Norsk Propsteier
	Seger	Milton (Sweden)
Örn		Milton (Sweden)
	Von Lochow's Gelbhafer	Markische Landsorte
		Markische Landsorte

OT380

1	2	3	4
		OT235	CI964P2-R4
	SO88118		C4963P2-HHAM4
		OT743	unnamed_5324
OT366			Cavell
		unknown	unknown
	J775-1		unknown
		unknown	unknown
			unknown
		OT306	Kelsey
	SO85190		Orbit
		Calibre	Gemini
OT356			Clintford
		S79107	Fraser
	SO85022		unnamed_6974
		Cascade	Random
			Forward (USA)

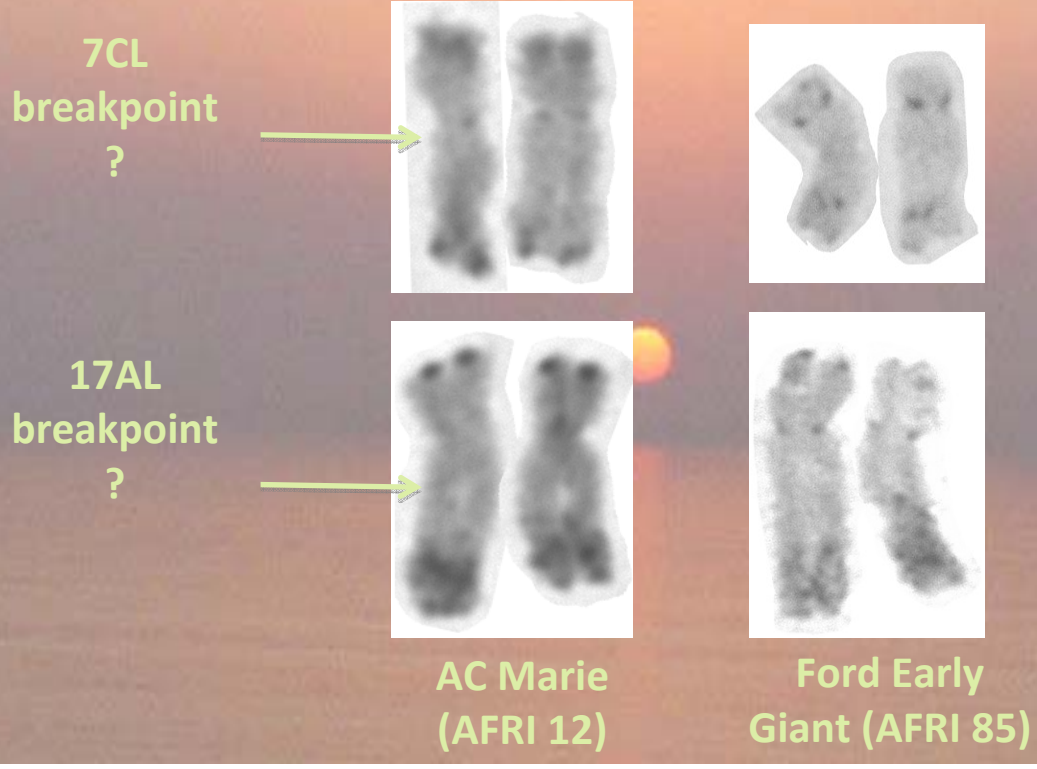
Orn is parent of Fraser

Other Karyotypic Variants

- Rearranged 19A/20D and 17A
- NOR heterochromatin
- 2C arm-ratio
- 9D centromeric heterochromatin
- 5CL telomeric heterochromatin
- HiFi bands: Amagalon chromatin?
- Pg16 tetrasomy

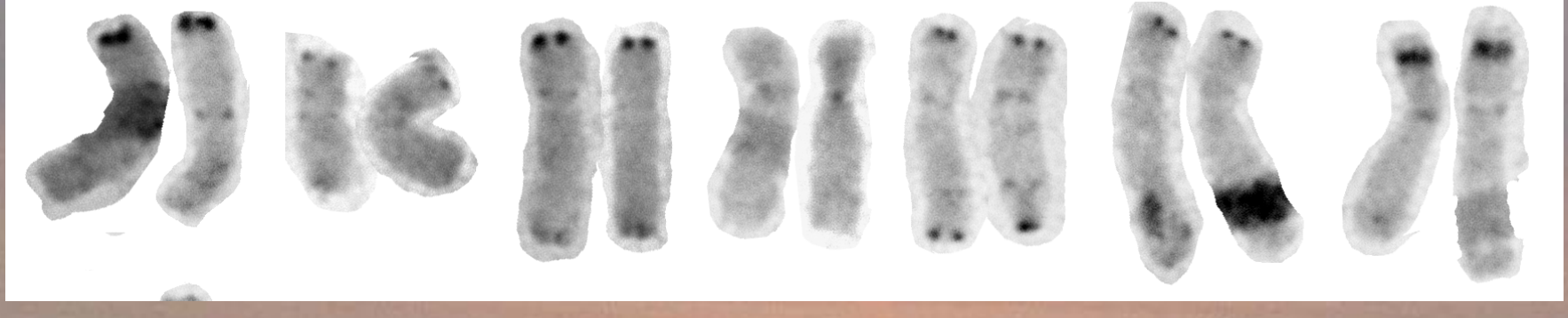
Rearranged 19A/20D

- **Putative translocation 17AS-(19A/20D)S**
  - **Identified in 'Ford Early Giant' (AFRI 85)**
  - **Ergo, the *Green Giant* rearrangement ☺**

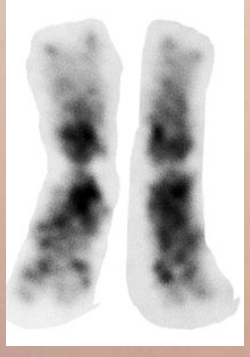


HiFi (top, AFRI 16) vs. Sol-Fi (bottom, AFRI 32)

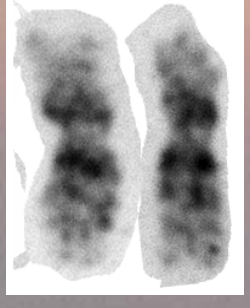
Variation for A-genome chromosome group.



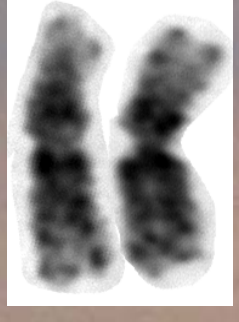
Chromosome 2C Arm-Ratio Variation



Morton (AFRI 11)

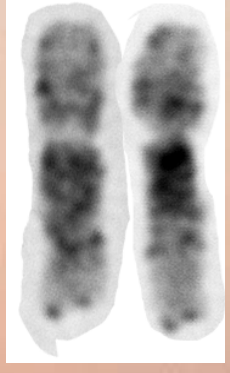


ProFi_CDC (AFRI 46)



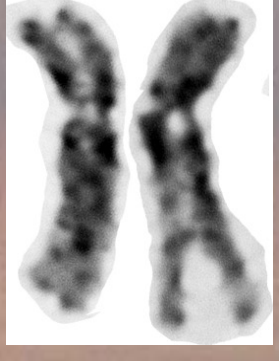
Noble-2 (AFRI 51)

Melys (AFRI 81)



Russell (AFRI 105)

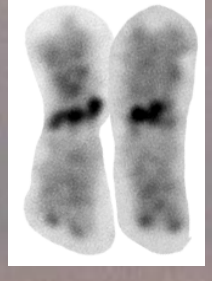
Novojatkovo (AFRI 86)



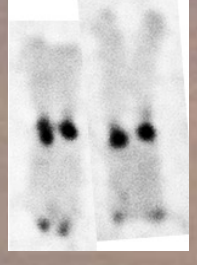
9D Centromeric Heterochromatin

Hurdal (AFRI 2)

Belinda (AFRI 60)

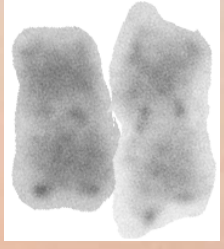


UFRGS 881971 (AFRI 72)



Freddy (AFRI 80)

Gem (AFRI 10)

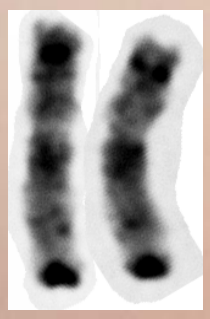


Coker 227 (AFRI 18)

Jay (AFRI 28)

Aarre (AFRI 36)

Variation for Chromosome 5CL Telomere

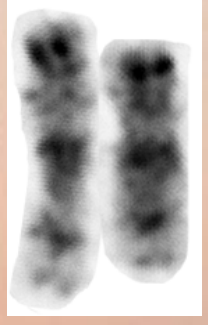


IL86-5698-3 (AFRI 42)

SO-1 (AFRI 47)

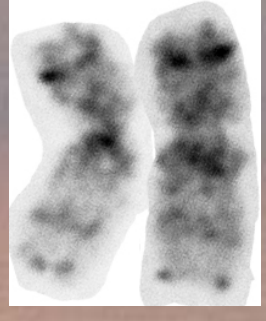
Bountiful (AFRI 83)

OT586 (AFRI 77)

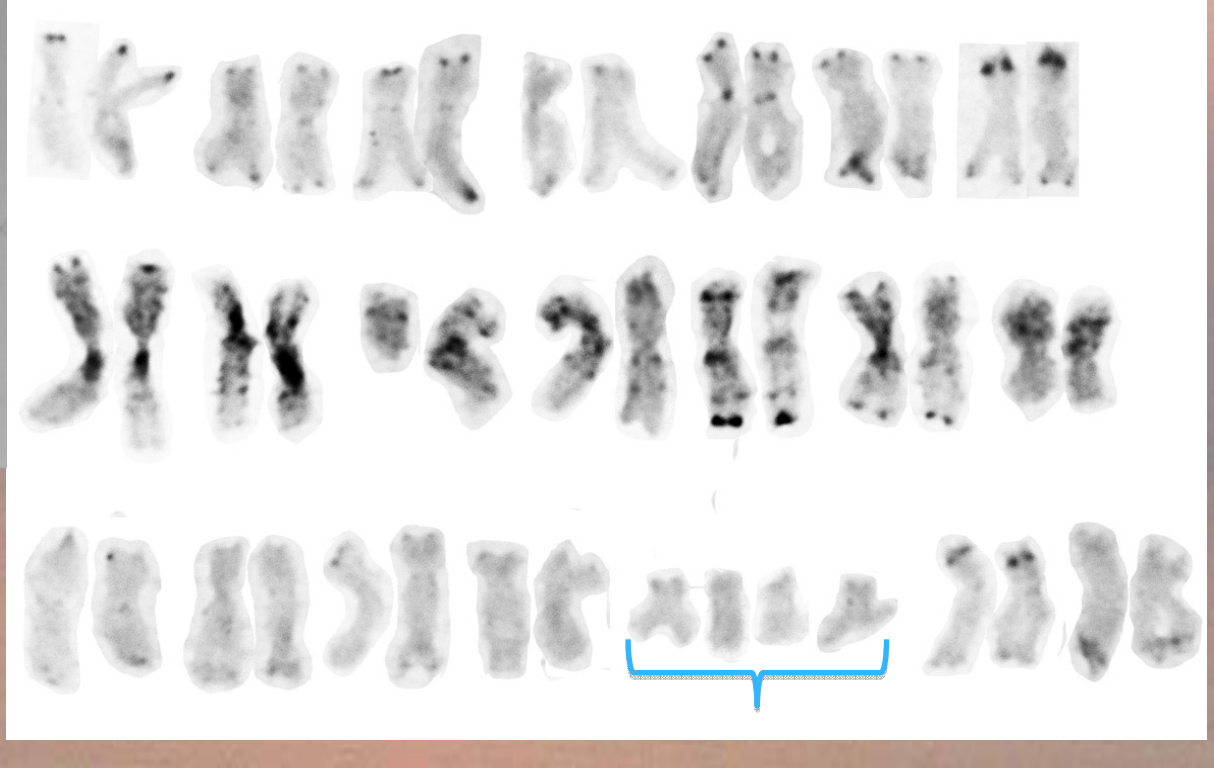


MF9522-523 (AFRI 79)

MN 811045 (AFRI 103)



Line Pg16 (AFRI 66) is an 18D Tetrasomic



Conclusions

- There's a lot of chromosomal variation in the AFRI core oats – *but not nearly as much as might be expected*

- The 3CS-14S reciprocal translocation from Markische Landsorte via Von Lochow's Gelbhafer could be a problem

- *"I'd rather breed macho oat varieties with wimpy names than wimpy oat varieties with macho names*." - Deon 'Big Dog' Stuthman