

Selection and inbreeding

Balancing Selection and Inbreeding

- Higher selection intensities make bigger gain
- Fewer animals are selected, so also more inbreeding
- This trend is more evident with higher rates of fecundity , e.g. with new reproductive technologies
- Genetic evaluation (BLUP) favors selection of related animals

→rationalization of selection make inbreeding restriction methods a necessity

Why restrict inbreeding

- Avoid loss of genetic variation/genetic diversity
- Inbreeding depression
- Increase of homozygotes with deleterious recessives
- Inbreeding is closely associated with risk (and genetic drift)

How to restrict inbreeding?

- Mating policies mostly affect
 - progeny inbreeding (short term)
 - but not *long term* rate of inbreeding ΔF
 - The long term inbreeding rate depends on

effective population size (*N*_e)

• Long term inbreeding is restricted by restricting the average co-ancestry among selected parents

Effective Population Size: Ne

Accounting for unequal sex ratio

 Effective pop'n size (Ne) reduces towards sex with fewer breeding individuals



Males / generation	2	2	2	5	20	1
Females / generation	2	20	200	200	200	99999
Ν	4	22	202	205	220	100,000
Ne	4	7.3	7.9	19.5	72.7	4

With selection, this formula <u>underpredicts</u> inbreeding (2x) But it shows that usually, it is controlled by using enough sires

Inbreeding rate

- Inbreeding occurs due to the mating of relatives
- In a closed population inbreeding is inevitable
- Inbreeding rate (Δ F) describes the increase in F over time

Example of BLUP selection

Terminals - Top 1 Sires	150		Analy	ysis D)ate 1	Friday	, 15 June	2001	Inbreedi	ng 8 Ac	curacies	LAM Transference in Street	BPLAN [•]	
D	Stud of breeding V	Wort	Pwwt	Ywt	Pfat	Pemd	Carcase +	Progeny	Coeff l	Neight (Carcase	Sire	Sire of Dam	
161972 <mark>-1999-</mark> 990196	HILLCROFT FARMS	5.46	14.95	14.94	-1.19	1.62	226.64	38	0.133	83	70	1619721998980093	1630001993930134	
162368 <mark>-1998-</mark> 980211	KURRALEA	6.60	12.39	12.69	-0.89	2.50	215.20	1148		97	96	1623681994940260	8600401992920175	
162204 <mark>-1999-</mark> 990453	BETHELREI	8.52	13.38	15.87	-1.18	1.11	211.75	224		93	89	8601221993930205	1619721995950289	
161972 <mark>-1998-</mark> 980093	HILLCROFT FARMS	5.15	14.40	16.00	-1.08	0.25	207.51	12		80	74	1630001993930134	1603361992920349	
161972 <mark>-1998-</mark> 980527	HILLCROFT FARMS	8.46	13.45	10.97	-1.66	-0.47	204.10	25		85	76	1619721996960091	1630001993930134	
860122 <mark>-1993-</mark> 930205	OHIO	6.95	11.94	13.72	-1.60	0.49	203.76	1522		98	97	8601221992920200	8601221987870073	
161143 <mark>-1999-</mark> 990204	DERRYNOCK	8.39	12.10	12.19	-0.49	2.19	203.60	38		82	76	1623681998980211	240001993930411	
160060 <mark>-1996-</mark> 960004	ANNA VILLA	8.56	14.90	16.18	-0.48	0.24	200.47	151		93	87	1632801992920016	162354199 09005 84	
161143 <mark>-1999-</mark> 990201	DERRYNOCK	5.43	11.83	11.14	-1.19	0.83	199.83	39		83	77 📢	1623681998980211	613151995950042	
230034 <mark>-1997-</mark> 970904	BURWOOD	4.98	11.01	8.82	-2.27	-0.55	198.82	380	0.003	96	92	2300091994940171	2300341994940314	These are sibs so
163677 <mark>-2000-</mark> 000140	FELIX	6.69	13.56	13.36	-0.59	0.61	197.98	56		70	63	1619721995950289	1600341994940020	might not select all
160060 <mark>-1997-</mark> 970115	ANNA VILLA	6.30	14.47	11.69	-0.42	0.24	196.90	118		90	83	1600601996960004	1600601992920057	of them as flock
162204 <mark>-1999-</mark> 990394	BETHELREI	7.42	12.97	14.27	-1.03	0.14	196.85	24		82	74	8601221993930205	1622041996960579	sire
161143 <mark>-1999-</mark> 990064	DERRYNOCK	5.10	11.20	10.10	-0.72	1.60	196.01	18		80	74 🗸	1623681998980211	€40001994940317	
161972-1996-960020	HILLCROFT FARMS	5.32	12.96	10.66	-0.80	0.36	195.20	83		88	75	1630001993930134		
160185-1996-960001	JOLMA	6.19	10.29	10.42	-1.56	0.63	194.57	101		90	83	1630001993930134	1613151991910870	
161235-1997-970830	POLLAMBI	7.10	10.69	10.35	-0.88	1.50	194.54	34		87	79	1700991993930002	1612351991910691	
163677-1999-990307	FELIX	7.09	12.52	11.59	-1.29	-0.47	192.45	54		83	74	8601221993930205	1636771994940008	
162368-1999-990290	KURRALEA	5.53	10.84	10.58	-0.62	1.59	192.11	68		69	62	1623681998980211	1630001993930160	
860074-1995-950044	ADELONG	7.17	14.47	13.22	-0.80	-0.94	191.15	448		96	94	8600741993930189		
163000-1998-980575	RENE	7.59	12.01	13.06	-0.50	0.99	190.92	12		71	60	1623681994940260	8600371992920165	
162368-1997-970443	KURRALEA	6.58	12.13	7.96	-1.00	0.08	190.69	178		88	83	1640001993930411	8600401992920175	
160034-1999-991208	MOSSLEY	5.52	13.45	10.27	-0.53	0.04	190.41	17	0.003	78	70	1621001998980130	1600341994940171	
161437-1999-990006	MARBURN	5 41	10.97	10.93	-1 21	0.37	190 26	14		73	65	1604621994940012	1640001993930411	

Balancing inbreeding and merit



inbreeding or co-ancestry

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Jointly optimizing merit and inbreeding

Wray and Goddard, 1994

 $x'G + \lambda x'Ax$

• merit: x'G

 λ = penalty on inbreeding

- x = vector with each animal's contribution to progeny
- G = the vector with merit (EBV's) for each animal
- Co-ancestry: x'Ax
 - x = vector with each animal's contribution to progeny
 - A = Numerator Relationships Matrix

Remember: $\Delta F = x'Ax/2$ $F_i = 0.5 a_{ii}$

Vector *x* of animal contributions

Source of animals	Animal#	x = Contribution
Male candidates	1 2 3 4 5 6 7 8 	$ \begin{bmatrix} 0 \\ .1 \\ .05 \\ 0 \\ .01 \\ 0 \\ 0 \\ \end{bmatrix} \sum = 0.5 $
Female candidates	101 102 103 104 105 106 107 108	$\sum_{0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\$

Note that this does not only determines number of selected sires and dams, but also allows for unequal contributions

Balancing inbreeding and merit

- Restricting co-ancestry but this slows genetic (short term) progress
- How much inbreeding can we afford?
- Often inbreeding is restricted by limiting ΔF to a certain preset value
- This optimal value may depend on your situation (how open is your nucleus?)

Optimizing genetic contributions

• Maximize objective function

x'G - <u>λ</u>x'Ax

How much inbreeding can we afford?

Question: what is best value for λ ?

Could preset rate of inbreeding (e.g. 1%) and determine λ accordingly (Meuwissen, 1997)

Alternative: look at graph (next slide)



inbreeding or co-ancestry x'Ax

Balancing inbreeding and merit This graph will look different for each population



inbreeding or co-ancestry

_	∑'x	nmales	nfemales	G		Relation	ships M	atrix					
Male 1	0.125	4	4	127	1.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
Male 2	0.125			122	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.00	
Male 3	0.125	Find	l optimal	150	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	
Male 4	0.125	cont	tributions	109	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	
Female 1	0.125			120	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	
Female 2	0.125			123	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.00	
Female 3	0.125			89	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.00	
Female 4	0.125			113	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	
average me	rit of progeny	x'G	119.12										
Inbreeding weight λ -9999999.0								-			13	8.00	
rage co-acestry of progeny x'Ax 0.063											13	6.00 4.00	
			/	(in								2.00	
				0.X) X	ຍ	130.00							
				inde	^						12	8.00	
	/					•					12	6.00	
						[12	4.00	
												2.00	
											12	0.00 8.00	
				0.	000	0.100	0.200		0.300	0.40)0	0.500	

	4				_							
2	/ х	nmale	s nfemales	G		Relation	nships M	latrix				
Male 1	0.127	4	4	127	1.00	0.00	0.25	0.00	0.00	0.00	0.50	0.00
Male 2	0.108			122	0.00	1.00	0.00	0.25	0.00	0.00	0.00	0.50
Male 3	0.129	Fir	nd optimal	150	0.25	0.00	1.00	0.00	0.00	0.00	0.25	0.00
Male 4	0.136	CO	ntributions	109	0.00	0.25	0.00	1.00	0.00	0.00	0.00	0.25
Female 1	0.189			120	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00
Female 2	0.177			123	0.00	0.00	0.00	0.00	0.00	1.00	0.25	0.00
Female 3	0.049			89	0.50	0.00	0.25	0.00	0.00	0.25	1.00	0.00
Female 4	0.085			113	0.00	0.50	0.25	0.25	0.00	0.00	0.00	1.00
average me	rit of progeny	x'G	1 21.91									
Inbreeding	weight									. 00 -7		
rage co-acesti	ry of progeny	x'Ax⁄	0.093			136	136.00					
	, , , , , , , , , , , , , , , , , , , ,										134	.00
				Ø			۴				132	.00
				×	<u>o</u>	/					130	.00
				dex	×	*					128	00
	\checkmark			_ .⊑		•					126	
						+					104	
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											122	.00
					0 000	0.400	0.00	0	0.000		120	1.00
					0.000	0.100	0.20	U	0.300	0.4	00	0.500
co-ancestry (x'Ax)												

Z	Ух `	nmales	nfemales	G		Relation	ships M	atrix				
Male 1	0.000	4	4	127	1.00	0.00	0.25	0.00	0.00	0.00	0.50	0.00
Male 2	0.000			122	0.00	1.00	0.00	0.25	0.00	0.00	0.00	0.50
Male 3	0.500	Find	optimal	150	0.25	0.00	1.00	0.00	0.00	0.00	0.25	0.00
Male 4	0.000	cont	ributions	109	0.00	0.25	0.00	1.00	0.00	0.00	0.00	0.25
Female 1	0.000			120	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00
Female 2	0.500			123	0.00	0.00	0.00	0.00	0.00	1.00	0.25	0.00
Female 3	0.000			89	0.50	0.00	0.25	0.00	0.00	0.25	1.00	0.00
Female 4	0.000			113	0.00	0.50	0.25	0.25	0.00	0.00	0.00	1.00
average me	rit of progeny	x'G	136.50								100	~~
Inbreeding weight λ 0.0								_ _			138.	
rage co-acest	ry of progeny	x'Ax 🌫	0.250				-	_			130.	00
			\sim	6		,					134.	00
				X (X	9 .×	*					132.	00
				inde		+					130.	00
						+					128.	00
						+					120.	00
											124.	00
						•					122.	00
					0.000	0.100	0.200		0.300	0.400)	0.500

	X	nmales	nfemales	G		Relation	ships M	atrix				
Male 1	0.063	4	4	127	1.00	0.00	0.25	0.00	0.00	0.00	0.50	0.00
Male 2	0.076			122	0.00	1.00	0.00	0.25	0.00	0.00	0.00	0.50
Male 3	0.361	Find	optimal	150	0.25	0.00	1.00	0.00	0.00	0.00	0.25	0.00
Male 4	0.000	conti	ibutions	109	0.00	0.25	0.00	1.00	0.00	0.00	0.00	0.25
Female 1	0.208			120	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00
Female 2	0.238			123	0.00	0.00	0.00	0.00	0.00	1.00	0.25	0.00
Female 3	0.000			89	0.50	0.00	0.25	0.00	0.00	0.25	1.00	0.00
Female 4	0.055		_	113	0.00	0.50	0.25	0.25	0.00	0.00	0.00	1.00
average me	rit of progeny	x'G	1 31.75									
Inbreeding weight λ -50.0											138.0	0 -7
rage co-acestry of progeny x'Ax 📩 0.132							-	•			136.0	0-
			\sim	_		*	/					0
				S X							<u>132.0</u>	•
				ex (×	•					130.0	-
	/			ind		•					128.0	-
	\checkmark					•					126.0	0-
											124.0	0-
This is more than simply						•					122.0	0-
	moving ba	ck from B	LUP	0		0 100	0 200		300	0.400	<u>120.0</u>	0 0 500
	to mass se	election		0.	000	0.100	0.200	(0.400	,	0.500
(penalizing family info)							co-ancest	ry (x'Ax)				

Between versus within family selection





<u>Own information</u> (performance or *genotype*):

More variation within families

More within-family selection – *less inbreeding*

Advantage of genomic selection

Ultimately, genetic gain is about utilizing Mendelian sampling Variance

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Conclusion Optimal Contribution Selection

- OCS is the only sensible selection method
 - Optimality subject to some degree of subjectivity
 - Separates best prediction of merit from selection rule
 - Play with number of parents as well as progeny per selected parent → optimizes contributions
 - Different from simply giving more weight to family info
- Hard to deterministically predict response to OCS