Linkage in the Merino central test sire evaluation schemes.

D Cottle[*] J James[†]

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Linkage in the Merino Central Test Sire Evaluation Schemes

David Cottle and J. James
Department of Wool and Animal Science
The University of New South Wales.
Sydney NSW 2052.

Summary

The proposed running of an elite link Merino sire evaluation scheme in 1996 using link sires from previous programs was estimated to have a relatively minor influence on the linkage between schemes with or without bloodline groups being fitted. If a substantial section of the industry decides to fine up their flocks by introducing semen from finer bloodlines it would be in the industry's interests to have the fine and medium schemes well linked, which is not the case at the present. Running an elite sire program at a central test site would provide a valuable extension tool that could help overcome resistance to the adoption of sire evaluation in industry.

It is proposed that 6 medium and 6 fine wool link sires, preferably from bloodline groups 2, 6, 9, 10 and 11, should each be inseminated to 30 medium wool and 30 fine wool ewes at a Central test site in future. The progeny should be followed through to 22 months of age. The progeny could be used to demonstrate the consistency of linked sire evaluation results, the size of sire by environment interactions and the effects of crossing sire and ewe strains. The results will improve the linkage (decrease PEVs) between medium and fine bloodline groups by more than 10% in most cases and by smaller amounts between medium groups and between the two fine groups.
Keywords: Merino sire evaluation, linkage, central test

Introduction

Medium wool Merino central test sire evaluation (CTSE) has been conducted since 1987 in the Riverina. Additional medium wool sites have since been initiated in NSW (Macquarie), WA and SA. Fine wool CTSE have been conducted in the New England area since 1990. CTSE have been developed to allow breeders to increase genetic progress by improved across flock selection of sires. A wide range of both measured and visually assessed traits are recorded to allow breeders with a wide range of objectives to benefit. The information allows participating breeders to bench mark their home-tested sires to elite sires from throughout Australia. The CTSE program provides the only objective comparisons of genetic merit of rams from different studs which are independently conducted and publicly available to the industry.

Both CTSE and 6 on-farm sire evaluation program results have been entered into a centralised database (Swan et. al 1992, Swan and Woolaston 1994). The database is being used to study two main areas of concern in BLUP analysis of sire evaluation results -the maintenance of adequate links among CTSE and on-farm tests and sire by environment interaction (SEI). Ashtiani and James (1992) showed that when tested sires come from different genetic groups, the best accuracy (in terms of average prediction error variances (PEV) of EBVs of tested sires) is obtained when about one third of all progeny in CTSE come from reference or link sires.

From 1989-1994, of the 5,564 progeny born in the Riverina and Macquarie medium wool schemes, 1,560 or 28% have been from link sires. Thus the accuracy of EBVs is expected to be near optimum. From 1990-1994, of the 2,248 progeny born in the New England scheme, 391 or 17% have been from link sires, thus linkage is suboptimal. From 1989-1994, of the 8,202 progeny born in the Riverina, Macquarie, WA and New England schemes only 129 (from 2 rams only) or 1.6% have been from sires with progeny in both the fine and the medium wool schemes. The linkage between the fine and medium schemes is well below optimum.

Two of studbreeders' major concerns with linked CTSE results are the unknown SEI and the adequacy of linkage or connectedness. If 10-16 rams nominated by the CTSE committees as elite link sires (Cottle et al. 1994) from a number of sites and years were all progeny tested together in the same program it would be provide a strong extension message if the progeny were shown to perform in the manner predicted from linked analysis (I. Rogan pers. comm.). Apart from the important extension benefit, running such an elite program may have other advantages, ie. the connectedness between programs will be increased resulting in an improvement in PEV and the amount and quality of SEI data would be improved.

This paper considers the theoretical consequences on linkage between medium wool schemes if an elite link sire program had been run in 1996 and/or was run in 2000. The improvement in linkage (assessed as the change in prediction error variances between bloodline groups) between fine and medium schemes is also studied using two different sets of link sires in 1996. The effect of running a link program on the accuracy of SEI estimates from the combined CTSE/on-farm database is reported in James and Cottle (1997).

Methods

Linkage

The average prediction error variances of differences between EBVs of sires were calculated as suggested by Kennedy and Trus (1993). For each design and model a matrix of the coefficients of the mixed model equations incorporating fixed effects of tests and genetic groups, and random effects of sires within genetic groups was

constructed, using heritabilities of either 0.3 or 0.5 for the random effects. These values
of heritability cover the range for most traits of interest. These matrices were then
inverted, diagonal elements of the inverse giving error variances of the fixed effects and
prediction error variances of random effects, while off-diagonal elements gave
corresponding covariances. These were used to calculate the average prediction error
variances of sire EBVs, taking into account differences between genetic groups where
appropriate as well as differences between random genetic effects. Variances of
differences between individual group means were also calculated in a similar manner.
These are also referred to as prediction error variances (PEV) though they are actually
sampling error variances, because in the present context the distinction is not important.
Since genetic and environmental variances are assumed known, the actual records are
not required for these calculations, only the numbers of progeny per sire in each trial.

Two types of genetic groups were used. In the first, each sire was regarded as coming
from a genetic group defined by the site/year in which the ram was first progeny tested.
This corresponds to the system used by Ashtiani and James (1992) and will lead to
groupings which are entirely pragmatic, and may not correspond to real genetic groups,
but can be formed without exercise of arbitrary judgements. For the second type of
genetic group, 10 groups (for the medium scheme analysis) or 11 groups (for the
combined fine and medium wool analysis) were defined as a compromise between number
of groups and differentiation between groups. Groups have to be defined more broadly
than by birth year within flock origin or by bloodline until the volume of data increases.
Sires were allocated to one of the following mutually exclusive groups: 1) Merryville,
2) Egelabra, 3) Hazeldean 4) Haddon Rig, 5) Riverina Peppin, 6) Boonoke, 7)
Wanganella, 8) Ashrose/Collinsville, 9) Rambouillet, 10) Mixed, 11) Winton/Sierra
Park.

Three analyses were conducted.

Analysis 1 (Medium common links)

Data from the Hay, Deniliquin, Dubbo and WA CTSE from 1989-1994 were used.
The data for 1995-2000 were simulated (30 progeny/sire) with and without an elite link
program in 1996 and/or 2000. The sires chosen for the 1996 program were Sire codes
1106, 1709, 2001, 2005, 2007, 2206, 2208, 2307, 2901, 3001, 3104, 3206. The first
and second digit in the sire code represent the site and year respectively, thus these sires
came from 3 sites and 4 years. The 2000 link sires were 2005, 2208, 2307, 2401, 2501,
2601, 3401, 3501, 3601, 5303, 5401, 5501. There were 333 rams in the analysis.
Average PEVs were calculated with and without groups.

Analysis 2 (Medium/Fine common links)

Data from the Hay, Deniliquin, Dubbo, WA and New England CTSE were used
from 1989-1995. The data for 1995-2000 were simulated (30 progeny/sire) with and
without an elite link program in 1996 and/or 2000. The sires chosen for the 1996
program were Sire codes 1106, 1709, 2005, 2010, 2206, 2208, 3006, 3104, 4001,

4003, 4007, 4015, 4109 and 4306. The first and second digit in the sire code represent the site and year respectively, thus these sires came from 4 sites and 5 years. The 2000 link sires were 2005, 2208, 2401, 2501, 2601, 3401, 3501, 4015, 4401, 4501, 5303, 5401, 5501. There were 478 rams in the analysis. The PEVs of individual group comparisons were estimated.

Analysis 3 (Medium/Fine targeted group links)

Data from the Hay, Deniliquin, Dubbo, WA and New England CTSE were used from 1989-1995. From analysis 2 it was found that groups 9, 6, 2, 10 and 11 had the weakest linkage (highest PEVs). Therefore the sires chosen for the 1996 link program came from these groups (in brackets) and were Sire Codes 1904 (10), 2105 (10), 2202 (10), 2303 (10), 2306 (6), 2403 (6), 3202 (2), 3509 (9), 4001 (1), 4003 (11), 4306 (11) and 5309 (6). There were 242 rams in the analysis. The PEVs of individual group comparisons were estimated. The analysis was also conducted without groups.

Results and Discussion

Analysis 1

The average PEV of EBV differences for the medium wool schemes (1989-2000) with and without elite link schemes in 1996 and 2000 for no genetic groups, site x year groups and bloodline groups are given in Table 1.

Table 1 The average PEV of EBV differences between sires (in genetic variance units) for the medium wool schemes (1989-2000) with and without elite link schemes in 1996 and 2000 for no genetic groups, site x year groups and bloodline groups. The average PEV of bloodline mean differences is also given. The variance proportion compared with no elite link schemes is given in brackets

Heritability		Link	schemes	
	-	1996+2000	1996	2000
No genetic groups				
0.3	.1605	.1583 (.986)	.1593 (.993)	.1596 (.994)
0.5	.1106	.1086 (.982)	.1095 (.991)	.1097 (.992)
Site/year groups				
0.3	.2986	.2835 (.949)	.2847 (.954)	.2964 (.993)
0.5	.2217	.2132 (.962)	.2139 (.965)	.2205 (.994)
Bloodline groups				
0.3	.1655	.1628(.983)	.1641(.991)	.1642(.992)
0.5	.1133	.1109(.979)	.1121(.989)	.1121(.990)
Bloodline Means				
0.3	.0251	.0250 (.994)	.0250 (.997)	.0250 (.996)
0.5	.0380	.0377 (.994)	.0379 (.997)	.0378 (.996)

If no genetic groups were assumed to exist and heritability equals 0.5, then the improvement in PEV by the addition of both link programs was 1.8%, each scheme improving PEV by about 0.9%. If each site x year was regarded as a genetic group and heritability equals 0.5, then the improvement in PEV when either both linkage schemes or the 1996 scheme were included was about 4%. The 2000 program only improved PEV by 0.6%. When bloodline grouping was assumed and heritability equals 0.5, then the PEV was improved by both programs by only 0.7%, each scheme contributing about 0.3% improvement.

The maximum improvement in PEV of EBV differences when an elite sire linkage scheme was run was 5.1% for 1996 plus 2000 (4.7% for the 1996 program and 0.7% for the 2000 program) when heritability was assumed to be 0.3 and site x year grouping was used. This improvement is relatively small and suggests the schemes are already satisfactorily linked. Thus running the proposed 1996 link scheme would have mainly served an extension and public relations purpose, in terms of improving connectedness.

The PEV was much lower when sires were grouped by bloodline rather than site/year of first use and was similar to that with no groups. This is to be expected for two reasons. First, with a smaller number of groups, a larger fraction of comparisons between sires will be within groups, so that errors in estimating genetic groups means will not affect the PEV. Second, the group means will be more accurately estimated, both because of a larger number of observations per group, and because connections between groups are better. Thus, where genetic groups can be reasonably defined, by bloodline, this approach is to be preferred.

The percentage improvement by including link schemes when bloodline groupings were analysed was little different from that when no groups were assumed. The percentage improvement was lower with higher heritability when site x year groups were analaysed, but greater in the other two cases, though the effect was not large. The effect of link schemes on the accuracy of medium wool bloodline comparisons is slight because these bloodlines are already satisfactorily linked.

Analysis 2

The PEVs for differences between individual groups for results from 1989-2000 for no link schemes (Case 1), link schemes in 1996 and 2000 (Case 2), link scheme in 1996 only (Case 3) and link scheme in 2000 only (Case 4) are shown in Appendix 1 and the percentage improvements in PEVs by the addition of link schemes in Figures 1-5. The inclusion of link schemes in 1996 and/or 2000 on average made only small improvements in the PEVs of group comparisons. The groups with the largest PEVs (and lowest linkage) were Groups 9, 6, 2, 10 and 11. For the link sires chosen the percentage improvement in PEVs was greatest for the comparison of groups 4 (13%) and 8 (15%) with the fine groups (1 and 11). This level of improvement could be worthwhile for rambreeders considering changing their semen source between these groups, eg. Haddon Rig or Collinsville to Merryville.

Fig. 1   Percentage improvement due to additional link schemes in PEVs of group 1 and 11 sires (fine) compared to all groups - Case 2: 1996+2000, Case 3: 1996, Case 4 2000. Heritability = 0.3 (see Appendix 1)
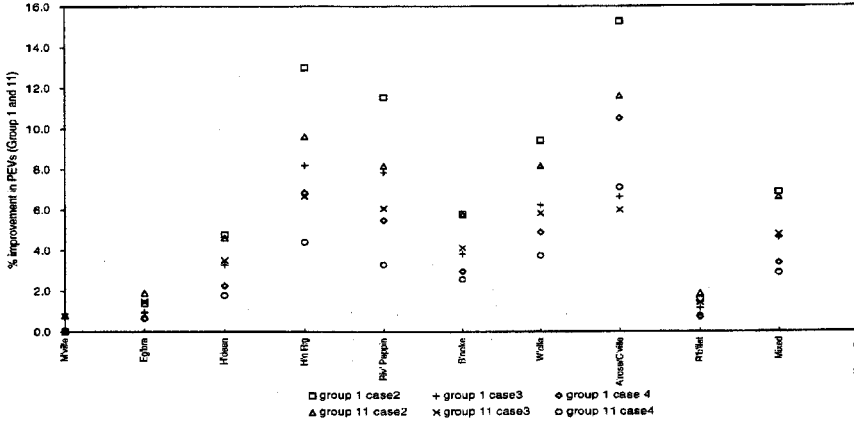
Fig. 2   Percentage improvement due to additional link schemes in PEVs of group 2 and 3 sires compared to all groups - Case 2: 1996+2000, Case 3: 1996, Case 4 2000. Heritability = 0.3 (see Appendix 1)
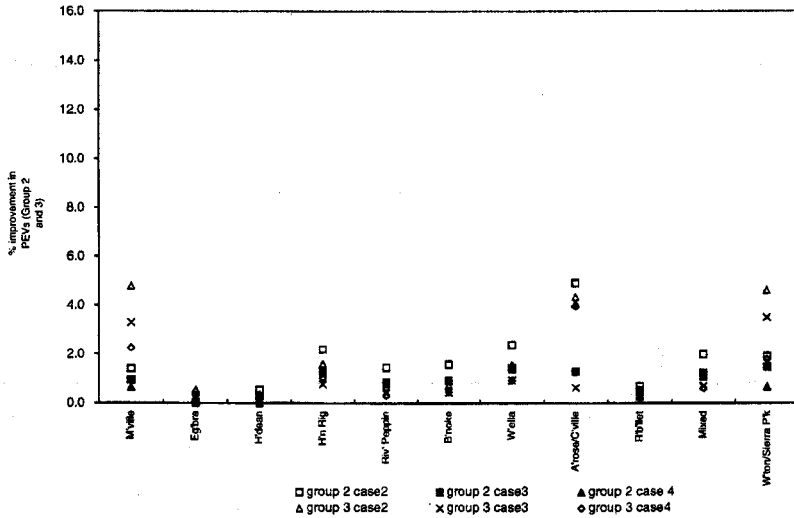
Fig. 3   Percentage improvement due to additional link schemes in PEVs of group 4 and 5 sires compared to all groups - Case 2: 1996+2000, Case 3: 1996, Case 4 2000. Heritability = 0.3 (see Appendix 1)

□ group 4 case2	◇ group 4 case 4	▵ group 5 case2
× group 5 case3	○ group 5 case4	+ group 4 case3

Fig. 4   Percentage improvement due to additional link schemes in PEVs of group 6 and 7 sires compared to all groups - Case 2: 1996+2000, Case 3: 1996, Case 4 2000. Heritability = 0.3 (see Appendix 1)

| □ group 6 case2	+ group 6 case3	◇ group 6 case 4
▵ group 7 case2	× group 7 case3	○ group 7 case4

Fig.5   Percentage improvement due to additional link schemes in PEVs of group 8 and 9 sires compared to all groups - Case 2: 1996+2000, Case 3: 1996, Case 4 2000. Heritability = 0.3 (see Appendix 1)
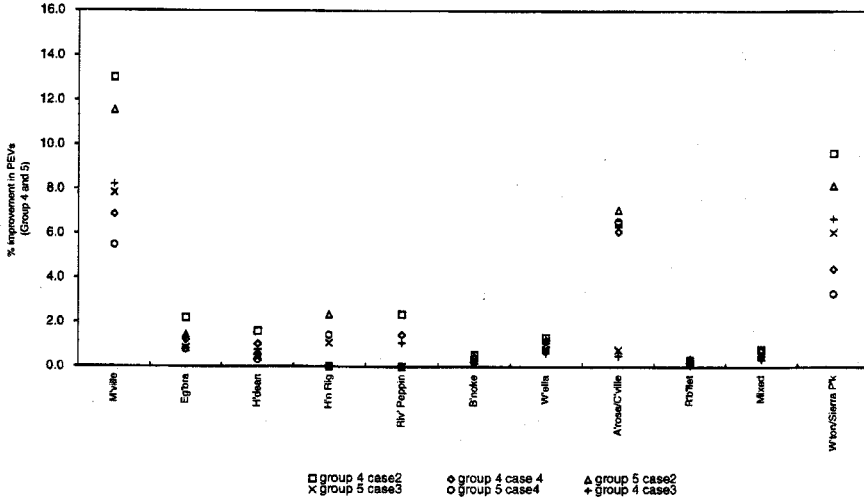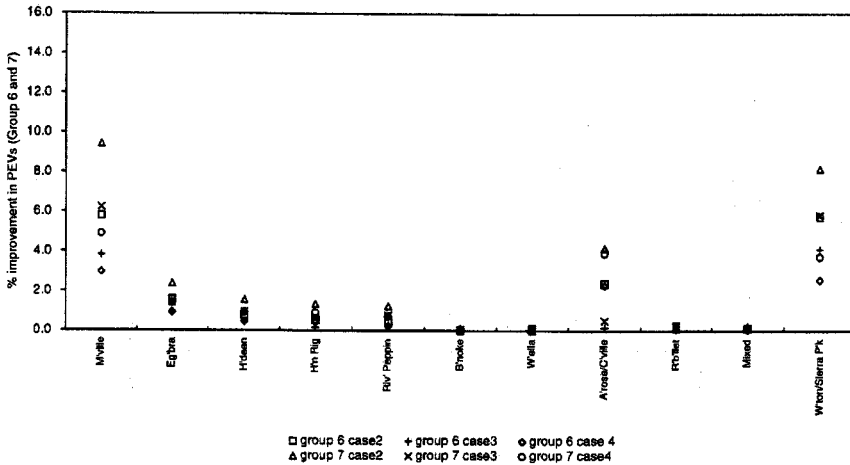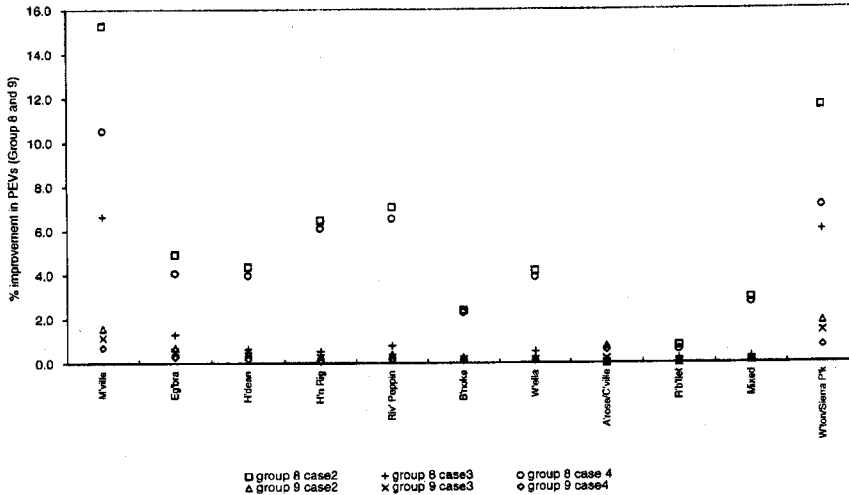

Analysis 3

This is concerned with the possible improvement to be achieved by a 1996 link scheme using link sires from the poorest linked groups, rather than the hypothetical group of trials up to 2000 considered in analysis 2. The average PEVs of EBV differences with and without groups are given in Table 2. The PEVs between individual groups for results between 1989-1996 for no link scheme or a 1996 link scheme are given in Appendix 2. The results are similar to Analysis 2, in that generally the chosen link sires on average had only small effects on PEVs and the percentage improvements in PEVs (Appendix 3, Graphs 6-7) were greatest for the comparison of the fine groups (1 and 11) with all other groups, in particular groups 10, 6, 8 and 4.

Table 2   The average PEV of EBV differences (in genetic variance units) for the fine and medium wool schemes (1989-1996) with and without an elite link scheme in 1996 for no genetic groups (between sires) and bloodline groups (between groups). The variance proportion compared with no elite link schemes is given in brackets

Heritability	Link schemes	
	-	1996
No genetic groups		
0.3	.1612	.1580 (.980)
0.5	.1114	.1086 (.975)
Bloodline groups		
0.3	.0269	.0250 (.929)
0.5	.0406	.0383 (.944)

Fig. 6 Percentage Improvement in PEVs from 1996 link schemes with sires from the poorest linked groups compared to no link scheme. Group comparisons (1-6), Heritability = 0.3

    ■ Group 1 + Group 2 ○ Group 3 □ Group 4 × Group 5 ▲ Group 6
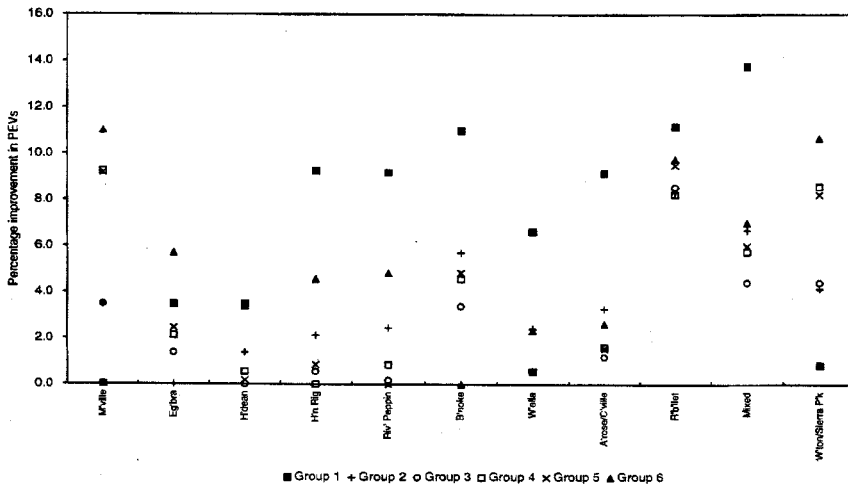
The use of the link sires chosen from groups 9, 6, 2, 10 and 11 has resulted in a small improvement in PEVs compared to the link sires chosen in Analysis 2. If group 9 (Rambouillet) is disregarded, the average PEVs of differences between bloodlines with or without the additional link scheme are reasonably low (0.02-0.03 genetic variance units). The linkage of groups between the fine and medium wool schemes is reasonable as rams from groups 1 and 11 have been used in both fine and medium schemes. The addition of the 1996 link scheme does not improve the average PEVs of differences between sires very markedly as most sire comparisons in the analysis are between medium sires and the results are largely determined by these comparisons.

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Appendix 1 Analysis 2: Prediction error variances for EBV comparisons between groups. Heritability = 0.3

a) No link tests

Group1	2	3	4	5	6	7	8	9	10	11
1	0	0.009869	0.006636	0.005239	0.004060	0.012279	0.008271	0.006925	0.064803	0.011847	0.006190
2	0.009869	0	0.012773	0.010426	0.010054	0.018035	0.013937	0.012674	0.069757	0.017466	0.013789
3	0.006636	0.012773	0	0.006485	0.005742	0.013258	0.009250	0.007711	0.066027	0.012939	0.010796
4	0.005239	0.010426	0.006485	0	0.003278	0.010695	0.006529	0.005013	0.062456	0.010011	0.009625
5	0.004060	0.010054	0.005742	0.003278	0	0.009506	0.005669	0.004555	0.062421	0.009249	0.008260
6	0.012279	0.018035	0.013258	0.010695	0.009506	0	0.012436	0.011750	0.069918	0.016286	0.016602
7	0.008271	0.013937	0.00925	0.006529	0.005669	0.012436	0	0.007706	0.065526	0.012437	0.012615
8	0.006925	0.012674	0.007711	0.005013	0.004555	0.01175	0.007706	0	0.064581	0.011305	0.011289
9	0.064803	0.069757	0.066027	0.062456	0.062421	0.069918	0.065526	0.064581	0	0.067894	0.069141
10	0.011847	0.017466	0.012939	0.010011	0.009249	0.016286	0.012437	0.011305	0.067894	0	0.016193
11	0.006190	0.013789	0.010796	0.009625	0.00826	0.016602	0.012615	0.011289	0.069141	0.016193	0
Mean	0.012375	0.017162	0.013783	0.011796	0.011163	0.017342	0.014034	0.013046	0.060229	0.016875	0.015864

Overall Mean 0.018515

b) 1996 and 2000 link tests

Group1	2	3	4	5	6	7	8	9	10	11
1	0	0.009731	0.006319	0.004557	0.003591	0.011567	0.007491	0.005868	0.063782	0.011034	0.006140
2	0.009731	0	0.012704	0.010197	0.009909	0.017752	0.013605	0.012051	0.069275	0.017118	0.013527
3	0.006319	0.012704	0	0.006382	0.005704	0.013158	0.009106	0.007375	0.065717	0.012792	0.010297
4	0.004557	0.010197	0.006382	0	0.003201	0.010637	0.006442	0.004688	0.062265	0.009931	0.008698
5	0.003591	0.009909	0.005704	0.003201	0	0.009464	0.005599	0.004233	0.062188	0.009175	0.007585
6	0.011567	0.017752	0.013158	0.010637	0.009464	0	0.012422	0.011469	0.069737	0.016267	0.015644
7	0.007491	0.013605	0.009106	0.006442	0.005599	0.012422	0	0.007383	0.065374	0.012409	0.011583
8	0.005868	0.012051	0.007375	0.004688	0.004233	0.011469	0.007383	0	0.064076	0.010972	0.009977
9	0.063782	0.069275	0.065717	0.062265	0.062188	0.069737	0.065374	0.064076	0	0.067759	0.067845
10	0.011034	0.017118	0.012792	0.009931	0.009175	0.016267	0.012409	0.010972	0.067759	0	0.015121
11	0.006140	0.013527	0.010297	0.008698	0.007585	0.015644	0.011583	0.009977	0.067845	0.015121	0
Mean	0.011825	0.016897	0.013596	0.011545	0.010968	0.017102	0.013765	0.012554	0.05982	0.016598	0.015129

Overall Mean 0.018164

c) 1996 link test only

Group1	2	3	4	5	6	7	8	9	10	11
1	0	0.009776	0.006418	0.004809	0.003742	0.011811	0.007756	0.006465	0.064062	0.011301	0.006142
2	0.009776	0	0.012736	0.010287	0.009969	0.017871	0.013738	0.01251	0.069393	0.017251	0.013586
3	0.006418	0.012736	0	0.006435	0.005719	0.013201	0.009164	0.007662	0.065803	0.012849	0.010417
4	0.004809	0.010287	0.006435	0	0.003243	0.010678	0.006488	0.004987	0.062301	0.009977	0.008983
5	0.003742	0.009969	0.005719	0.003243	0	0.009479	0.005625	0.00452	0.062266	0.009206	0.00776
6	0.011811	0.017871	0.013201	0.010678	0.009479	0	0.012427	0.011731	0.069806	0.016274	0.015917
7	0.007756	0.013738	0.009164	0.006488	0.005625	0.012427	0	0.007667	0.065437	0.01242	0.011879
8	0.006465	0.01251	0.007662	0.004987	0.00452	0.011731	0.007667	0	0.064451	0.011274	0.010611
9	0.064062	0.069393	0.065803	0.062301	0.062266	0.069806	0.065437	0.064451	0	0.067829	0.068157
10	0.011301	0.017251	0.012849	0.009977	0.009206	0.016274	0.01242	0.011274	0.067829	0	0.01542
11	0.006142	0.013586	0.010417	0.008983	0.00776	0.015917	0.011879	0.010611	0.068157	0.01542	0
Mean0.012026	0.017011	0.013673	0.011654	0.011048	0.0172	0.013873	0.012898	0.059955	0.016709	0.015352

Overall Mean   0.018309

d) 2000 link test only

Group1	2	3	4	5	6	7	8	9	10	11
1	0	0.009805	0.006487	0.00488	0.003838	0.011916	0.007866	0.006196	0.064352	0.011448	0.006186
2	0.009805	0	0.012731	0.010299	0.009975	0.017869	0.013741	0.012158	0.069558	0.017277	0.013698
3	0.006487	0.012731	0	0.006419	0.005724	0.013198	0.009164	0.007405	0.065902	0.012861	0.010603
4	0.004880	0.010299	0.006419	0	0.003231	0.010649	0.00647	0.004707	0.062405	0.00996	0.009201
5	0.003838	0.009975	0.005724	0.003231	0	0.009484	0.005628	0.004257	0.062317	0.009209	0.007988
6	0.011916	0.017869	0.013198	0.010649	0.009484	0	0.012428	0.011481	0.069843	0.016279	0.016175
7	0.007866	0.013741	0.009164	0.00647	0.005628	0.012428	0	0.007405	0.06546	0.012423	0.012144
8	0.006196	0.012158	0.007405	0.004707	0.004257	0.011481	0.007405	0	0.064192	0.010997	0.010487
9	0.064352	0.069558	0.065902	0.062405	0.062317	0.069843	0.06546	0.064192	0	0.067818	0.068621
10	0.011448	0.017277	0.012861	0.00996	0.009209	0.016279	0.012423	0.010997	0.067818	0	0.015727
11	0.006186	0.013698	0.010603	0.009201	0.007988	0.016175	0.012144	0.010487	0.068621	0.015727	0
Mean0.012089	0.01701	0.013681	0.011656	0.011059	0.017211	0.013885	0.012662	0.060042	0.016727	0.01553

Overall Mean   0.018323

Appendix 2   Analysis 3: Prediction error variances for EBV comparisons between groups. Link sires selected from groups with poor linkage. Heritability = 0.3

a) No link tests

Group1	2	3	4	5	6	7	8	9	10	11
1	0	0.017792	0.014925	0.009544	0.007641	0.019938	0.016643	0.012749	0.068163	0.016672	0.010263
2	0.017792	0.000000	0.024229	0.017393	0.017167	0.028979	0.025478	0.021744	0.075722	0.025450	0.023901
3	0.014925	0.024229	0.000000	0.013461	0.012595	0.023638	0.020182	0.016434	0.072085	0.020450	0.021312
4	0.009544	0.017393	0.013461	0.000000	0.005759	0.016759	0.013248	0.009087	0.063507	0.013114	0.016247
5	0.007641	0.017167	0.012595	0.005759	0.000000	0.014807	0.011699	0.007883	0.063519	0.011778	0.014139
6	0.019938	0.028979	0.023638	0.016759	0.014807	0.000000	0.021357	0.018312	0.074651	0.022109	0.026644
7	0.016643	0.025478	0.020182	0.013248	0.011699	0.021357	0.000000	0.015270	0.070337	0.018695	0.023357
8	0.012749	0.021744	0.016434	0.009087	0.007883	0.018312	0.015270	0.000000	0.067569	0.015352	0.019437
9	0.068163	0.075722	0.072085	0.063507	0.063519	0.074651	0.070337	0.067569	0.000000	0.069462	0.074841
10	0.016672	0.025450	0.020450	0.013114	0.011778	0.022109	0.018695	0.015352	0.069462	0.000000	0.023399
11	0.010263	0.023901	0.021312	0.016247	0.014139	0.026644	0.023357	0.019437	0.074841	0.023399	0.000000

b) 1996 link test

Group1	2	3	4	5	6	7	8	9	10	11
1	0	0.017175	0.014406	0.008662	0.00694	0.017744	0.015541	0.011581	0.060536	0.014376	0.010177
2	0.017175	0.000000	0.023895	0.017023	0.016747	0.027329	0.024863	0.021032	0.069412	0.023746	0.022912
3	0.014406	0.023895	0.000000	0.013386	0.012574	0.022839	0.020064	0.016238	0.065918	0.019547	0.020373
4	0.008662	0.017023	0.013386	0.000000	0.005710	0.015996	0.013174	0.008940	0.058263	0.012359	0.014854
5	0.006940	0.016747	0.012574	0.005710	0.000000	0.014094	0.011630	0.007759	0.057474	0.011071	0.012975
6	0.017744	0.027329	0.022839	0.015996	0.014094	0.000000	0.020858	0.017830	0.067354	0.020560	0.023800
7	0.015541	0.024863	0.020064	0.013174	0.011630	0.020858	0.000000	0.015152	0.064444	0.018103	0.021701
8	0.011581	0.021032	0.016238	0.008940	0.007759	0.017830	0.015152	0.000000	0.061366	0.014616	0.017713
9	0.060536	0.069412	0.065918	0.058263	0.057474	0.067354	0.064444	0.061366	0.000000	0.062767	0.066479
10	0.014376	0.023746	0.019547	0.012359	0.011071	0.020560	0.018103	0.014616	0.062767	0.000000	0.020412
11	0.010177	0.022912	0.020373	0.014854	0.012975	0.023800	0.021701	0.017713	0.066479	0.020412	0.000000

Appendix 3   Analysis 3: Percentage improvement from link program on PEVs of group comparisons. Heritability = 0.3

Group	1	2	3	4	5	6	7	8	9	10	11
1	0.0	3.5	3.5	9.2	9.2	11.0	6.6	9.2	11.2	13.8	0.8
2	3.5	0.0	1.4	2.1	2.4	5.7	2.4	3.3	8.3	6.7	4.1
3	3.5	1.4	0.0	0.6	0.2	3.4	0.6	1.2	8.6	4.4	4.4
4	9.2	2.1	0.6	0.0	0.9	4.6	0.6	1.6	8.3	5.8	8.6
5	9.2	2.4	0.2	0.9	0.0	4.8	0.6	1.6	9.5	6.0	8.2
6	11.0	5.7	3.4	4.6	4.8	0.0	2.3	2.6	9.8	7.0	10.7
7	6.6	2.4	0.6	0.6	0.6	2.3	0.0	0.8	8.4	3.2	7.1
8	9.2	3.3	1.2	1.6	1.6	2.6	0.8	0.0	9.2	4.8	8.9
9	11.2	8.3	8.6	8.3	9.5	9.8	8.4	9.2	0.0	9.6	11.2
10	13.8	6.7	4.4	5.8	6.0	7.0	3.2	4.8	9.6	0.0	12.8
11	0.8	4.1	4.4	8.6	8.2	10.7	7.1	8.9	11.2	12.8	0.0