

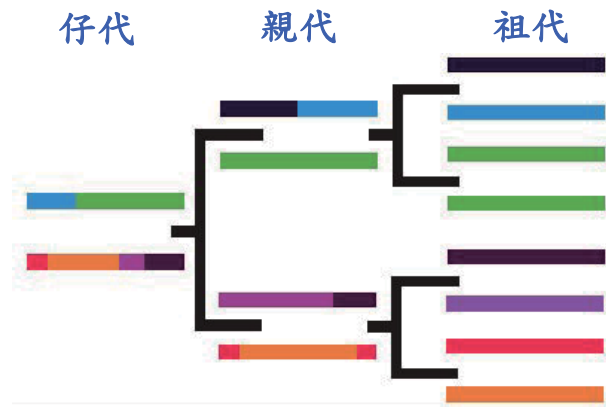
乳牛基因體檢測服務



鉸肽朊生物科技有限公司

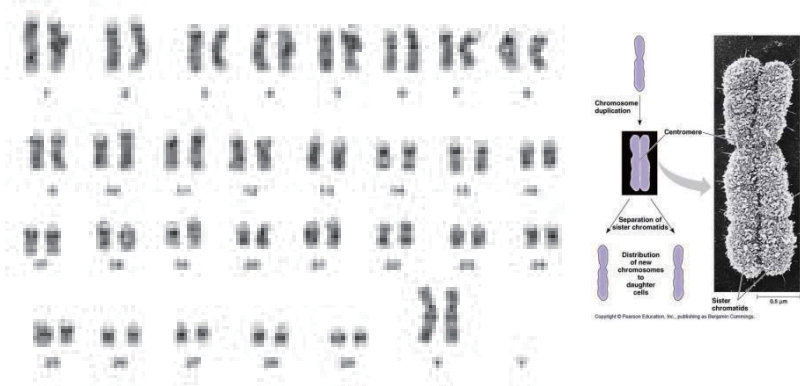
報告人：蘇少儀

乳牛選拔 龍生九子個個不同



• Bob Weaber, Ph.D.

乳牛表現潛力都建檔在染色體上的 基因組之中



畜群遺傳改進基本觀念

遺傳改進速度 = (選拔強度 × 選拔信度 × 族群變異度) / (世代間距)

Rate of genetic gain ΔG

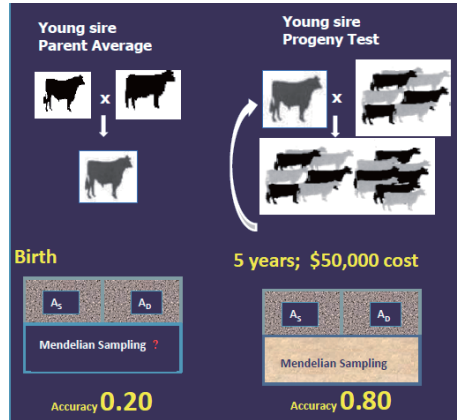
$$\begin{aligned} \Delta G &= (i_m r_m + i_f r_f) / (L_m + L_f) \text{ genetic standard deviation/year} \\ &= (2 \times 0.8 + 0) / (6 + 2) = 0.2 \text{ s.d./year (progeny test)} \\ &= (2 \times 0.6 + 0.8 \times 0.6) / (2 + 2) = 0.42 \text{ (genomic selection)} \end{aligned}$$

i = intensity of selection
 r = accuracy of selection
 L = generation interval

Modified from Goddard. (2009) BIF Meeting

Animal Biotechnology and Genomics Education

現行乳用種公牛選拔模式



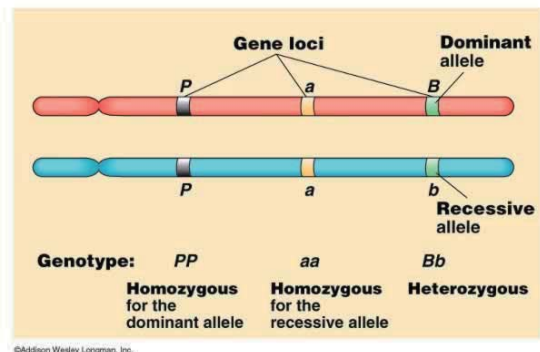
2009年牛基因體序列完全解碼



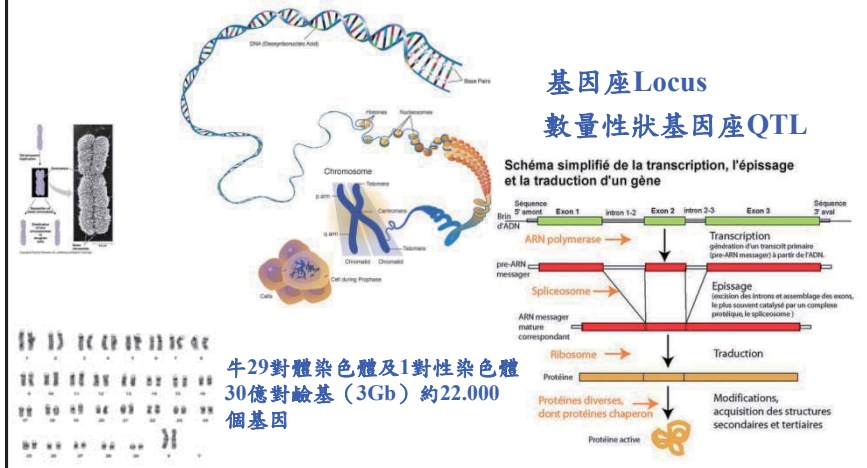
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分子育種科技演進

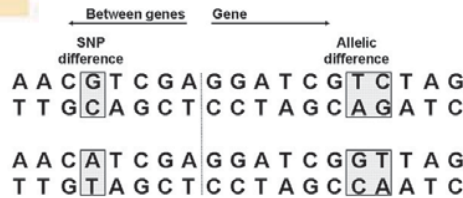
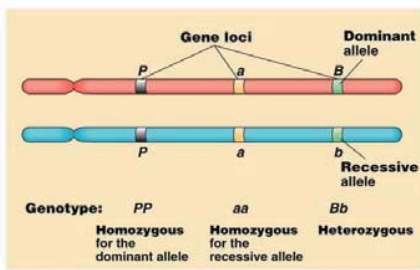
QTL Mapping → MAS → Genomic Selection
 數量性狀基因座定位 基因標記輔助選種 基因體選種



四個鹼基譜出每一頭牛獨特的生命篇章



單核苷酸多型性 (Single Nucleotide Polymorphism)



牛第十四對染色體上上乳脂百分率具顯著關聯的單核苷酸多型性 (SNP) 基因標記分佈

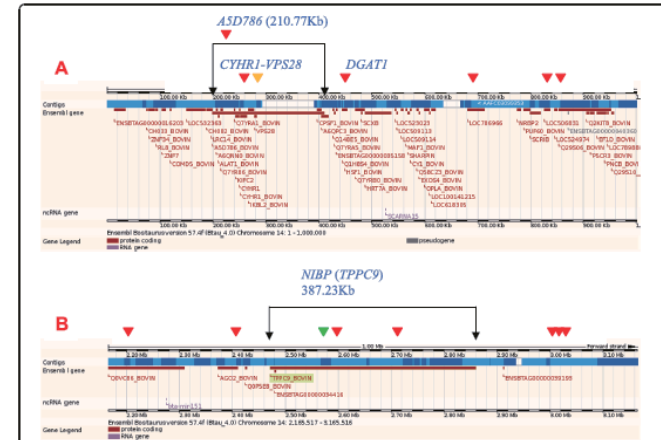
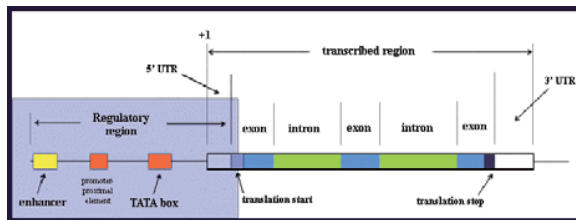


Figure 3 A 2.81 Mb gene cluster on *Bos taurus* chromosome 14 that was associated with significant effects of single nucleotide polymorphisms for fat percentage. Red arrow, fat percentage effect; gold arrow, milk yield effect; green arrow, fat yield effect A) 1 Mb region with ASD786, CYHR1, VPS28, and DGAT1 genes; ASD786 was second largest gene in the cluster and contained CHYR1 and VPS28. B) 1 Mb region with NIBP, the largest gene in the cluster.

Cole et al. BMC Genomics 2011, 12:408

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單核苷酸多型性 (Single Nucleotide Polymorphism)



SNP WWWIEBIOE.COM

Individual 1	A C G T G T C	G	G T C T T A A A	Maternal chromosome
	A C G T G T C	C	G T C T T A A A	Paternal chromosome
Individual 2	A C G T G T C	G	G T C T T A A A	Maternal chromosome
	A C G T G T C	G	G T C T T A A A	Paternal chromosome
Individual 3	A C G T G T C	C	G T C T T A A A	Maternal chromosome
	A C G T G T C	C	T A C T T A A A	Paternal chromosome

The position of the SNP is indicated by the box. Individual 1 is heterozygous, while Individuals 2 and 3 are homozygous.

對偶基因 Allele

Normal	TCTAAGTCCGTATAA AGATTCAAGCATATT AGATTCAAGCATATT TCTAAGTCCGTATAA	Green
Carrier	TCTAAGTCCGTATAA AGATTCAAGCATATT AGATTCAAGCATATT TCTAAGTCCGTATAA	Yellow
Disease	TCTAAGTCCGTATAA AGATTCAAGCATATT AGATTCAAGCATATT TCTAAGTCCGTATAA	Red

美系荷蘭種乳牛各染色體上與13個預期傳遞能力 (PTA) 的生產、健康及生殖性狀存有最顯著關聯效應之100個單核苷酸多

Table 1 Distribution of the top 100 most significant SNP effects for predicted transmitting abilities for 13 production, health, and reproduction traits of contemporary U.S. Holsteins by chromosome

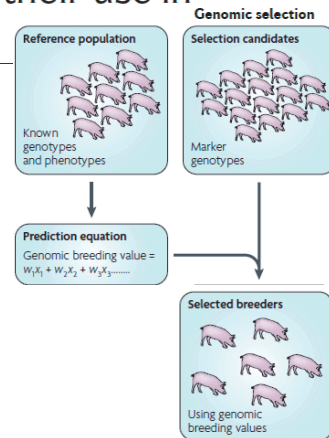
Chr	MT	FY	PC	PPC	FL	SCS	SCE	DCE	SSB	DSB	NM	All traits
1	2	4	4	4	5	15	4	17	7	6	7	3
2	3	0	0	0	1	11	2	0	0	0	2	0
3	10	4	1	4	1	9	7	17	4	0	4	6
4	3	2	2	0	0	4	0	0	2	0	3	0
5	2	2	2	7	13	0	4	0	7	3	10	0
6	2	2	5	1	6	2	9	0	0	6	0	1
7	0	6	1	1	2	11	13	15	4	11	0	6
8	2	1	0	0	0	4	1	3	0	2	0	3
9	7	6	1	1	2	0	0	0	4	3	1	6
10	5	0	0	0	3	0	2	6	1	0	4	0
11	3	3	3	1	3	0	1	0	1	0	0	5
12	2	1	1	2	3	0	6	0	8	2	6	1
13	13	12	8	1	1	0	1	2	1	0	0	7
14	2	1	1	24	2	0	0	0	2	0	6	4
15	1	0	0	0	1	2	0	0	1	1	4	5
16	1	0	0	0	0	2	11	1	0	0	3	0
17	4	7	6	11	14	9	1	5	20	21	7	2
18	8	4	6	5	4	8	2	5	9	12	6	4
19	2	3	2	0	0	0	0	0	0	0	3	0
20	0	2	11	0	2	0	2	0	1	1	1	5
21	4	1	5	0	5	0	0	0	2	1	6	5
22	1	0	0	0	0	3	0	0	0	1	0	3
23	5	5	9	2	3	0	1	0	2	1	1	16
24	2	1	2	2	2	1	1	0	1	1	3	0
25	0	2	0	3	0	0	5	1	0	0	1	0
26	0	7	6	6	10	9	3	4	6	10	9	1
27	5	6	7	0	1	1	1	0	3	1	0	1
28	0	0	5	0	1	2	0	3	3	1	1	3
29	0	0	0	0	0	1	2	1	0	2	1	1
X	11	16	11	19	16	15	9	12	12	16	15	12
U	0	0	0	1	0	2	1	1	1	0	1	2
P ^a	10 ¹⁰	10 ¹⁴	10 ¹⁰	10 ¹⁷	10 ¹⁰	10 ¹⁰	10 ¹⁵	10 ¹⁰	10 ¹⁰	10 ¹⁴	10 ¹⁴	10 ¹⁴
R ²	0.42	0.43	0.42	0.46	0.40	0.54	0.54	0.53	0.52	0.42	0.56	0.55

SNP, single nucleotide polymorphism; Chr, chromosome; MT, milk yield; FY, fat yield; PC, protein yield; PPC, fat percentage; FL, productive life; SCS, somatic cell score; DPR, daughter pregnancy rate; SCE, service sire calving ease; DCE, daughter calving ease; SSB, service sire stillborn; DSB, daughter stillborn; NM, net merit; U, unknown; Boldface indicates a 10 significant SNP effects. ^aRoundover for P value for top 100 most significant SNPs for trait. R², variation accounted for by the top 100 SNPs for the trait.

Cole et al. BMC Genomics 2011, 12:408

Mapping genes for complex traits in domestic animals and their use in breeding programmes

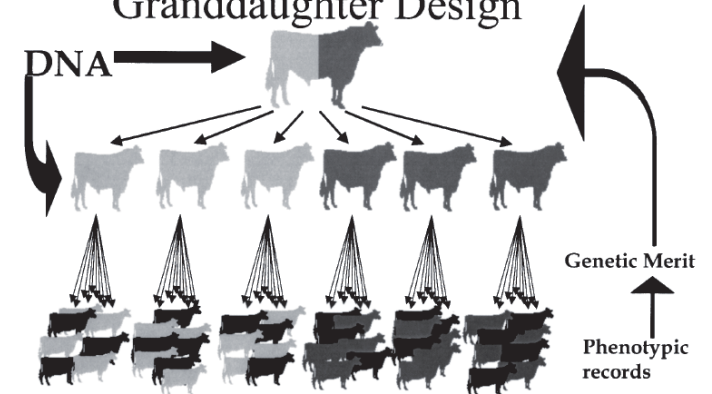
Michael E. Goddard** and Ben J. Hayes†



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乳牛基因體選拔性狀評比資訊庫 數據建立與維護

Granddaughter Design



J. Anim. Sci. 79(E. Suppl.):E307-E315

Mapping genes for complex traits in domestic animals and their use in breeding programmes

Michael E. Goddard** and Ben J. Hayes†

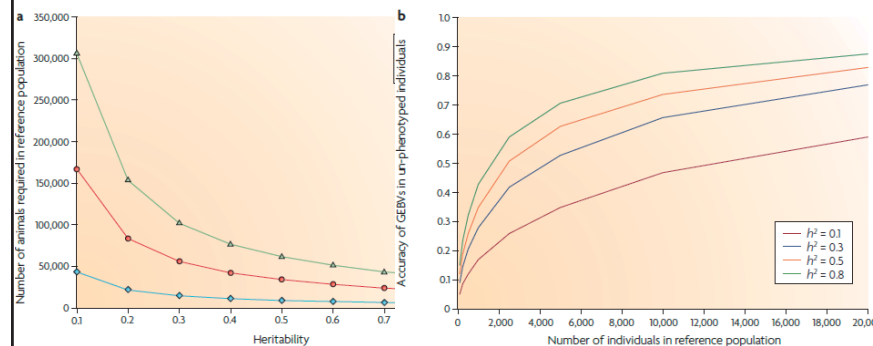


Figure 3 | Calculation of number of animals in a reference population and accuracy of breeding values. **a** | Number of animals needed in a reference population. To achieve an accuracy of 0.7 for estimated genomic breeding values (GEBVs) calculated from SNPs requires an increasing number of animals in the reference population as the heritability declines or the N_r of the population increases. **b** | Accuracy of GEBVs of un-phenotyped individuals with increasing number of phenotype records in the reference population used to estimated SNP effects, for different heritabilities (h^2). N was 100.

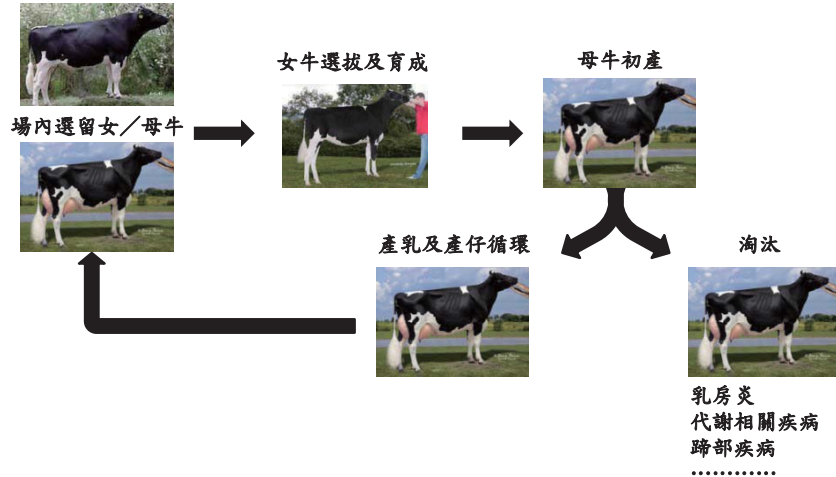
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大量準確基因型及表現型數據源自 公牛檢定、供精公牛、DHI紀錄

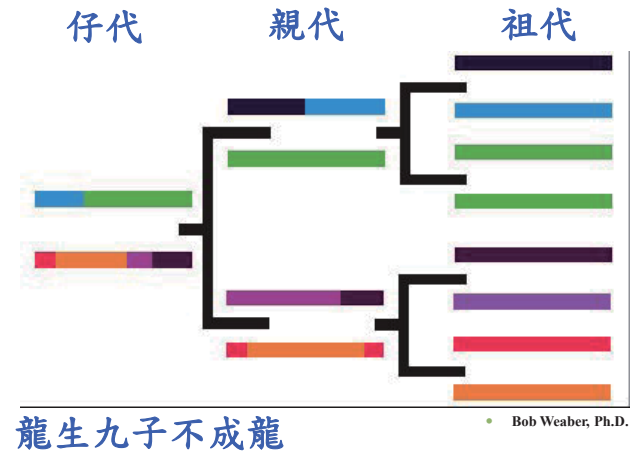
- 公牛檢定：基因型及表現型
- 供精公牛：表現型及（基因型）
- DHI：表現型

臺灣酪農乳牛選種模式

選用優良種牛精液



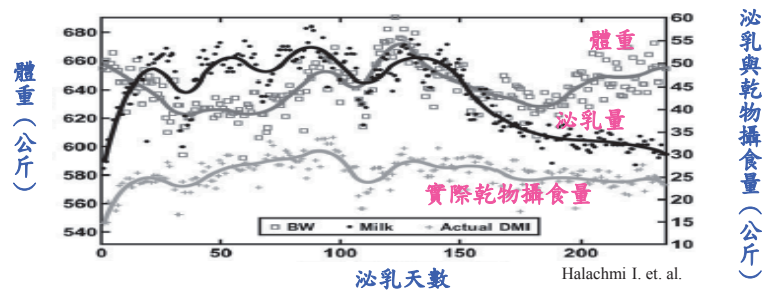
應用SNPs標記辨識特定染色體位置及溯源特定性狀基因



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適者生存的乳牛選種模式有陷阱喔!!!

臺灣的氣候與飼養模式可能造就場內產乳性狀不優母牛的后裔愈多
 高產母牛常見瘤胃過酸症、酮病、第四胃異位、胎衣滯留、難產、亞臨床型乳房炎、...等都影響泌乳量
 泌乳量低，失重少，產仔牛後愈早發情及受孕.....



乳牛選種新法

基因體檢測已經可以做為乳牛選種的依據了!!!
 乳牛高產乳是多基因所控制的數量遺傳性狀!!!

借力使力，不費力！
 喝牛奶不必養乳牛！
 臺灣乳牛基因體選拔借用
 美國農部建立及維護的
 基因體比對資料庫

