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Selection method of a performance test considering carcass data in Japanese Black cattle

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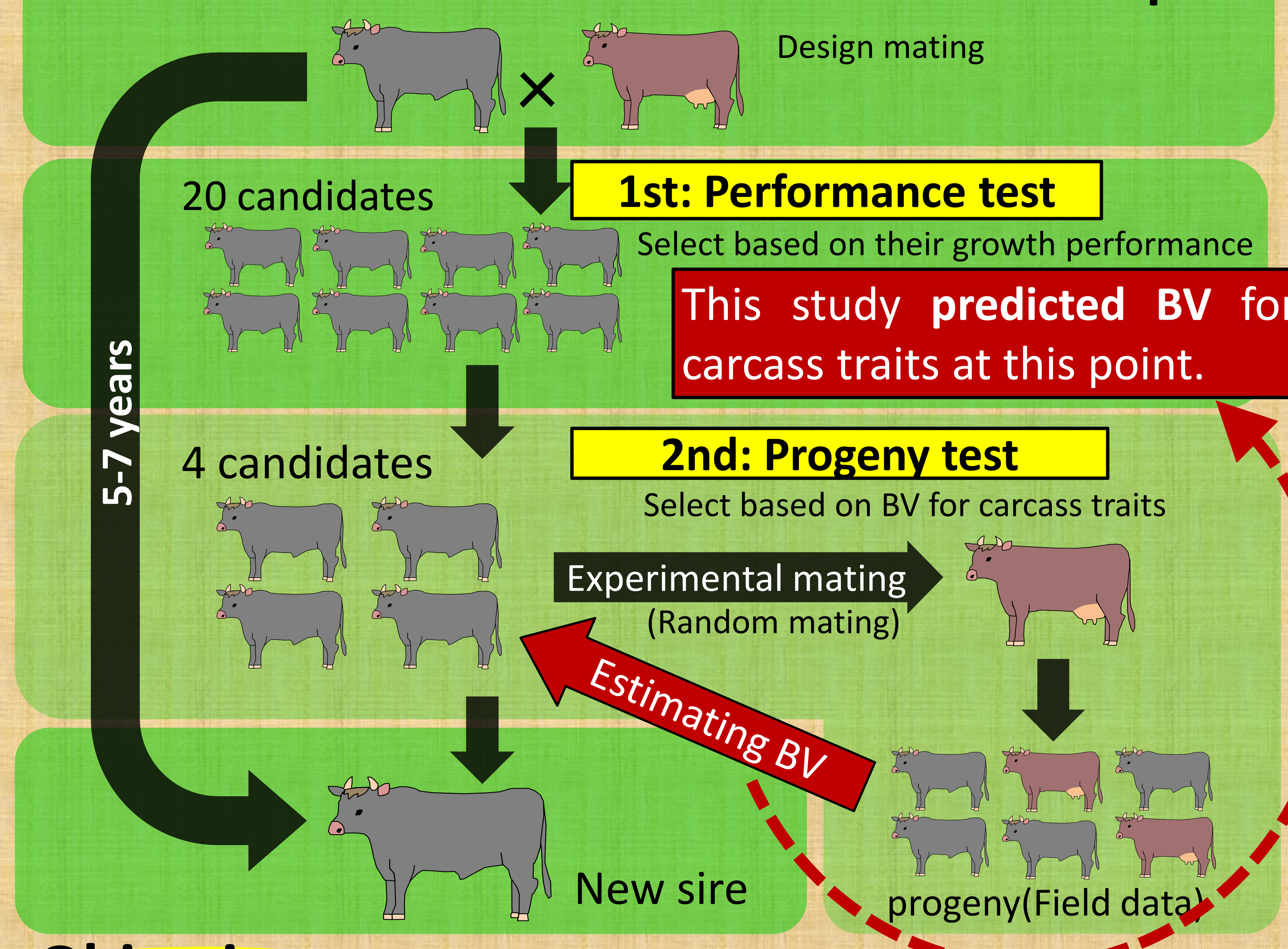
Introduction

In Japan, improvement of sire of beef cattle (Japanese black cattle; Wagyu) is conducted by **two step selections**. In first selection (performance test), candidate bulls are selected based on their **growth performance**, such as daily gain and weight. And in second selection (progeny test), they are selected based on their **breeding values for carcass traits** estimated with their progeny carcass data. Therefore it takes **5 or 7 years** to provide new bulls, and it needs **a significant cost**.

Outline of the current selection of sire in Japan



Objectives

In our study, in order to shorten the period of the two-step selection, we investigated the effectiveness to **predict breeding values** for meat productivity of candidate bulls without their progeny carcass data at the performance test by using previously slaughtered carcass records.

Materials and Methods

▷Animals

Data analyzed were records of 512 Japanese black bulls at Miyagi Prefecture Animal Industry Experiment Station form 1978 to 2004 and records of 30,746 carcass data from carcass markets in Miyagi prefecture form 1988 to 2004.

▷Traits

Performance traits were body weight at start of the test (**BWS**), body weight at finish of the test (**BWF**), final grade (**FG**), concentrate intake (**CONI**), total digestible nutrient intake (**TDNI**) and average daily gain during the test period (**DG**); carcass traits were carcass weight (**CWT**), beef marbling score (**BMS**), rib eye area (**REA**), rib thickness (**RT**), subcutaneous fat thickness (**SFT**) and yield estimate (**YE**).

▷Genetic parameters

Genetic parameters were estimated with **514** Performance-tested Japanese Black bulls (from 1978 to 2004) and **30,746** filed carcass data (from 1988 to 2004) using 2-trait animal model (1 from performance traits and the other form carcass traits).

▷Predicted Breeding Values at the performance test (PBV)

As for performance-tested bulls from 1990 to 1994, breeding value were **predicted per year** binding **previously slaughtered fattening cattle** by multiple-trait model (6 traits from performance test traits and 1 trait from carcass traits) using the genetic parameters described above. Number of carcass data used are showed in **Table 1**.

▷Estimated Breeding Values with siblings and progeny (EBV)

Breeding values with siblings and progeny were also estimated per year. In addition to the data sets for PBV, EBV were estimated with siblings and progeny of the bulls including animals **slaughtered after endpoint of the performance test**. Number of carcass data used are showed in **Table 1**.

▷Correlations between PBV and EBV

<u>In order to investigate the **effectiveness of PBV**, correlations between PBV and EBV were calculated for each carcass traits.</u>

▷Table1. Number of carcass records used for PBV and EBV per year of the performance test

Year of performance test	PBV	Sibling and progeny slaughtered after the test	EBV
1990	**897**	10,702	**11,599**
1991	**1,492**	26,587	**28,079**
1992	**2,171**	18,617	**20,788**
1993	**2,675**	20,788	**23,463**
1994	**3,544**	19,430	**22,974**

(Number of performance-tested bulls were **20** per year)

▷Statistical models

Genetic parameters and breeding values (PBV and EBV) were estimated using REML by VCE-5 and PEST, respectively. Statistical models were;

$$y_i = Xb_i + Za_i + e_i$$

where $\mathbf{y}_i$ is a vector of observations for then *i*th trait; $\mathbf{b}_i$ for performance traits is a vector of fixed effects including a contemporary tested-group and covariate including age at the end of the test, and for carcass traits is a vector of fixed effects including slaughter year, slaughter season, sex, parity, slaughter place and feeding place and covariate including slaughter age; $\mathbf{a}_i$ is a vector of random animal effects; $\mathbf{e}_i$ is a vector of random errors; **X** and **Z** are incidence matrices relating records of the trait to the fixed effects and the random effects, respectively.

Results

▷Table 2. Genetic correlations (r_G±S.E.) between performance traits and carcass traits

Traits		Carcass traits					
		CWT	BMS	REA	RT	SFT	YE
Performance traits	BWS	**0.38**±0.13	**-0.26**±0.10	**0.02**±0.03	**0.01**±0.12	**0.12**±0.12	**-0.24**±0.10
	BWF	**0.36**±0.12	**-0.15**±0.07	**-0.03**±0.05	**0.05**±0.01	**0.13**±0.13	**-0.24**±0.09
	DG	**0.18**±0.04	**0.12**±0.02	**-0.21**±0.31	**0.26**±0.27	**0.56**±0.27	**-0.48**±0.34
	FG	**0.53**±0.17	**-0.10**±0.23	**0.33**±0.25	**0.08**±0.01	**-0.01**±0.04	**-0.03**±0.18
	CONI	**0.16**±0.17	**0.22**±0.14	**0.08**±0.01	**0.42**±0.18	**0.17**±0.17	**0.02**±0.19
	TDNI	**0.16**±0.06	**0.06**±0.01	**-0.21**±0.27	**0.30**±0.16	**0.27**±0.13	**0.31**±0.22

◆Genetic correlations of **BWS** and **BWF** with **CWT** were significantly positive, but significantly negative with **BMS** and **YE.**

◆Genetic correlations of **DG** with **CWT** and **BMS** were significantly positive, but also significantly positive with **SFT** (positive is undesirable).

▷Table 3. Correlations between PBV and EBV

CWT	BMS	REA	RT	SFT	YE
0.85	0.81	0.65	0.77	0.00	0.74

◆Correlation coefficients between PBV and EBV for carcass traits were very high to slightly high(0.65-0.89), except in **SFT**.

Conclusion

Correlations between PBV and EBV were very high. The results indicate that the selection based on PBV for carcass traits at performance test is effective.

Therefore the results in this study suggest that the selection at the earlier stage is available.