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Genetic similarity and relationships of DNA fingerprints with performance and with heterosis in Japanese quail lines from two origins and under reciprocal recurrent or within-line selection for early egg production

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Abstract – DNA fingerprints of Japanese quail male and female pure line breeders were obtained with probes 33.6, 33.15, and R18 1 and they yielded a total of 59 scoreable bands. Bandsharing ($0 < BS < 1$) was calculated within and between six quail lines of two origins, and under reciprocal recurrent (AA and BB), within-line (DD and EE) or no (PP and FF) selection Twenty one pair types were compared. BS was 0.30 higher within line than between lines. BS with the control line was smaller for reciprocal recurrent selection lines than for lines under individual selection. Bandsharing between the two reciprocal recurrent selection lines was 0.19 lower than between lines under individual selection. These results indicate that the two selection methods had different effects on the genetic constitution of the lines, in agreement with previous observations made from the analysis of biochemical polymorphisms with the same set of birds. Egg production and weight traits of pure and crossbred progeny from fingerprinted quail were obtained and compared, and a linear relationship with the measure of bandsharing was estimated. No significant regression coefficient of performance on BS was found over all progeny genetic types. Heterosis from individual matings could also be estimated under the two selection methods since the same birds were parents of both pure and crossbred performance-tested quail. The association of heterosis with the difference between BS of parents of the purebreds and BS of parents of their half-sib crossbreds was favourable and significant for early production traits in lines DD and EE, but no relationship was found in lines

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AA and BB. These results indicate that the high level of heterosis obtained through reciprocal recurrent selection, and the heterosis observed under within-line selection may have, partly at least, a different genetic determinism. Therefore, the relationship of heterosis with BS may also depend on the past history of selection in the lines.

Japanese quail / bandsharing / DNA fingerprint / heterosis / production

Résumé – Ressemblance des empreintes génétiques et liaisons avec les performances et l'hétérosis chez des cailles japonaises de deux origines et sous sélection directe ou réciproque récurrente pour la ponte précoce. Les sondes 33.6, 33.15 et R18.1 ont été utilisées pour obtenir les empreintes génétiques à partir de l'ADN de cailles japonaises reproductrices mâles et femelles de six lignées en sélection récurrente réciproque (AA et BB), en sélection individuelle (DD et EE) ou maintenues sans sélection (PP et FF), et provenant de deux origines. Les 21 types de paires possibles ont été comparés à l'aide du coefficient de partage de bande BS ($0 < BS < 1$). BS était plus élevé de 0,30 intra-lignée qu'inter-lignée. La ressemblance génétique avec la lignée contrôle non sélectionnée, mesurée par BS, était moindre pour les lignées AA et BB que pour DD et EE. De plus, BS entre les deux lignées sous sélection réciproque récurrente était inférieur de 0,19 à la valeur obtenue entre celles sous sélection individuelle. Ces résultats indiquent que les deux méthodes de sélection ont bien eu chacune un effet différent sur la constitution génétique des lignées. Ils confirment ainsi des observations antérieures issues de l'analyse des polymorphismes biochimiques du même échantillon d'animaux. La descendance femelle pure et croisée des cailles aux empreintes génétiques connues a été mise en épreuve de ponte de façon à étudier la relation linéaire entre les performances de chaque caille et le BS de ses parents mais aucun lien significatif n'a été mis en évidence. L'hétérosis des croisements individuels a pu être estimé car les mêmes parents ont eu une descendance pure et croisée. L'association de l'hétérosis avec la différence de BS entre les paires de cailles parentes de la descendance pure et celles parentes de la descendance de leurs demi-sœurs croisées était significative et favorable pour les caractères mesurés en début d'épreuve de ponte chez les lignées DD et EE, mais aucune relation n'a été trouvée chez les lignées AA et BB. Ces résultats indiquent que le fort hétérosis obtenu par la sélection réciproque récurrente et l'hétérosis observé dans les lignées sous sélection individuelle pourraient avoir, au moins en partie, un déterminisme génétique différent Plus généralement, il semble que la relation de l'hétérosis avec BS puisse dépendre aussi de la sélection pratiquée dans les lignées.

caille japonaise / partage de bande / empreinte génétique / hétérosis / production

1. INTRODUCTION

The study of the genetic diversity of farm animals can be approached by using molecular markers. Counting and comparing bands of DNA fingerprints (DFP) has already been tried in order to evaluate the genetic relationship among poultry populations [2,4,7,16], on the grounds that BS, a commonly used measure of band sharing [10], is correlated to genetic similarity [11]. Complex association between some DFP bands and production traits has also been reported in chickens [3]. In the same species, limited observations on purebreds and crossbreds even indicated that heterosis might be inversely related to BS [5,

8] at the population level, but the absence of a consistent relationship of DFP bandsharing with heterosis was also reported [1] at the level of the individual, so the link between BS and purebred or crossbred performance has not yet been unequivocally established in poultry, and more generally in farm animals. The present uncertainty may be due to several causes like the number of probes and the sample size used for DFP [16] or the amount of genetic variation in the population [1], not to mention the unknown underlying biological relations between molecular markers like DFP and zootechnical traits. Also, DFP has been little studied in other poultry species [15,24,25].

In a recent selection experiment on early egg production in Japanese quail, we set up experimental lines from two different origins to evaluate and compare the evolution of heterosis under within-line and reciprocal recurrent selection [19]. We also studied long-term egg production and heterosis [20]. At the same time, a population study of biochemical polymorphisms was conducted in these lines [13,14] in an effort to globally evaluate to what extent 13 generations of artificial selection had modified the underlying genome. Therefore, these populations constituted a well described and original set of lines to contribute new information on DFP, on its association with egg production and related traits, and to experimentally evaluate the merit of BS as an indicator variable to help plan matings for better purebred or crossbred progeny performance.

The objective of the present work was three-fold. First, BS from DFP was used to describe the overall genetic similarity between six quail lines in relation to the selection method and the original stock. Second, relationships between BS of parents and progeny performance were evaluated. Finally, associations between BS of individual pairs of parents and heterosis of their progeny were estimated and discussed.

2. MATERIALS AND METHODS

2.1. Lines and selection

Lines and selection procedures have been described previously [19]. Briefly, the six selection lines were set up from two quail stocks (Tab. I). Three lines (Jouy origin) AA, DD and PP were started with sets of sibs from a medium-size line selected for shell porosity [17], and the other three lines (Tours origin) BB, EE and FF were made up in the same way from a large-size line kept as a control in a selection experiment on behaviour traits [18]. Selection was for a high number of normal eggs laid between 34 and 98 days of age. In lines DD and EE, females were under individual selection (IND), and the males kept as breeders were sibs of the selected females. In lines AA and BB under reciprocal recurrent selection (REC), males and females were ranked according to the mean egg production of their reciprocal crossbred half sisters AB and BA. Lines PP and FF were control lines. Reproduction was by single pair mating with no full-sibbing in lines under selection, and by pool mating in control lines. All birds from the selection lines were identified individually. Breeders selected at generation 12 produced purebred (AA, BB, DD, EE) and

Table I. Description of the experimental population (breeders and generation 13 pure and crossbred performance-tested progeny).

Breeders										
Line	AA	BB	DD	EE	PP	FF				
Selection method	Recurrent selection		Within-line selection		No selection					
Origin	Jouy	Tours	Jouy	Tours	Jouy	Tours				
Total number	44	44	40	40	Pool mating	Pool mating				
Number sampled for FP	42	42	35	38	All (19)	All (25)				
Number of bands ($\mu \pm$ SD)										
Probe 33.6	4.0 ± 1.8	8.0 ± 1.6	7.3 ± 1.7	7.4 ± 1.9	4.5 ± 1.7	8.4 ± 1.8				
Probe 33.15	0.7 ± 0.9	2.7 ± 1.0	2.6 ± 0.9	2.8 ± 1.2	2.6 ± 1.1	2.7 ± 1.0				
Probe R18.1	2.6 ± 1.1	4.4 ± 1.5	3.7 ± 0.9	2.8 ± 1.2	1.7 ± 1.3	3.8 ± 1.1				
All probes	7.3 ± 2.4	15.1 ± 2.4	13.6 ± 2.2	13.0 ± 2.8	8.8 ± 2.8	14.8 ± 2.5				
Performance-tested progeny										
Genetic type	AA	AB	BA	BB	DD	DE	ED	EE	No pedigreed progeny	
Number obtained from sampled breeders	51	56	72	59	46	57	60	64	–	–
Number used to estimate the relation between BS and heterosis	42	42	51	50	36	38	31	38	–	–

crossbred (AB, BA, DE, ED) generation 13 progeny which were tested for long-term production [20]. However, only progeny from breeders with DFP (Tab. I) were used in the present work to evaluate the relationship between BS and performance. Among them, only those offspring from the 88 breeders with the four genetic (two purebred and two crossbred) classes of progeny were used to study the association between BS and heterosis (Tab. I). Therefore, data for the last analysis were made of 22 complete sets (14 for REC and 8 for IND) of four parents (two per pure line) with their four progeny types.

2.2. Husbandry and traits

At 34 days of age, generation 13 females were put into separate cages of two four-tier egg-laying batteries. The unit was under a 14 h photoperiod of artificial light, and temperature was set at 20 °C. Quail had free access to drinking water and to a custom-made "low protein" diet (2 500 kCal · kg^{-1} ME, 10% moisture, 12% ash, 19% crude protein, 4% fat and 3% crude fiber) to try and enhance expression of heterosis by limiting feed quality. Traits recorded individually and studied in the present work were body weight at 34 days of age (BW), age at first egg (AFE), total egg numbers at 98 and 431 days of age (EN1 and EN2) and egg weight after six months in the test (EW).

2.3. DNA fingerprinting

Blood was obtained from all parents of generation 13 quail which were alive at the time of sampling, after the reproduction period (Tab. I). DNA was extracted from 80 μL of blood after hemolysis at 4 °C in lysis buffer (10 mM Tris pH 8, 1 mM $MgCl_2$, 150 mM NaCl and 1% NP-40). Next, it was incubated in an extraction buffer (50 mM Tris pH 9.5, 100 mM EDTA, 1% SDS and 200 $\mu g \cdot \mu L^{-1}$ proteinase K), then it was precipitated with 4.5 mL dimethyl-formamide/acetone (5:95) and put back into suspension in TE buffer. Finally, DNA was precipitated again with pure ethanol, resuspended in 2 mL TE buffer, and DNA concentration was determined by spectrophotometry. Pooled samples were also prepared with DNA from 10 males and 10 females for each selected line and from all quail for each control line. They were used as controls on each blot. From each individual sample and each pool, 8 μg DNA aliquots were digested with 6 units · μg^{-1} DNA of *Hinf*I restriction endonuclease. Digested DNA was electrophoresed in 0.8% agarose gel at 2 V · cm^{-1} for 42 h, and Southern-blotted onto a charged membrane in 0.4 N NaOH. Three probes, R18.1 [6], 33.6 and 33.15 [9], were used to reveal variable number tandem repeat (VNTR) loci as bands (Tab. I). Blots were hybridised overnight at 42 °C for R18.1 and at 63 °C for 33.6 and 33.15, and then they were washed twice (at 65 °C) or three times (at 63 °C) respectively. Fragments hybridised with the labelled R18.1 probe were revealed (in up to one day) by chemiluminescent detection. Those obtained successively with labelled 33.6 and 33.15 probes were detected with an X-ray cassette (after up to one week exposure). The number of scoreable bands was 28, 12 and 19, for probes 33.6, 33.15 and R18.1 respectively.

2.4. Statistical analyses

First, between all possible pairs (for a total number of 20 100 pairs from 21 combinations of lines) of birds sampled for DFP, BS was calculated as the ratio of the number of bands common to two individuals over the mean total number of bands counted for the same two birds [10]. Then, in order to evaluate and compare genetic similarity among all genetic types, each set of within- and between-line individual BS values was constituted from the maximum number of nonoverlapping pairs of quail that could be extracted from all possible pairs. Therefore, all 21 BS sets were made up of independent BS values: for two lines with n and m fingerprinted quail, the maximum possible size of each BS data set (Tabs. I and II) was $n/2$, $m/2$ and $\min(n, m)$, within line and between lines respectively [12]. A one-way analysis of variance of BS was carried out, with the combination of two lines as the main effect (21 levels). Differences due to line, stock origin and selection method were estimated by the appropriate linear combinations of least-squares means from the analysis of variance. Next, separately for each production trait, performances of all progeny were compared by an analysis of covariance, with BS of the parents as the covariable and with the genetic type of the progeny as the main effect. Finally, for the 22 complete sets of purebred and crossbred data from progeny of four parents from two lines, heterosis for each production variable was estimated as the difference between purebred and crossbred least-squares means in each set. A relationship between heterosis of progeny and BS of parents was obtained by linear regression of heterosis (expressed as % of purebred average least-squares mean) from the average BS difference between the corresponding two parental pairs of purebreds and two parental pairs of crossbreds (expressed as % of purebred average least-squares mean). Multiple comparison of means was done with the Duncan test, and all analyses were carried out with the GLM procedure from the SAS library [23].

3. RESULTS

3.1. Genetic relationship between all lines

Within- and between-line means BS are given in Table II. Within-line, average BS was between 0.51 and 0.67, and it varied from 0.17 to 0.44 between lines. The lowest values were obtained for bandsharing between lines AA and BB (BS_{AB}) and between control lines PP and FF (BS_{PF}). Table II also gives the ranking of the means. There was little overlap of within- and between-line BS. Line AA had intermediate BS with line DD from the same origin and low similarity with all other lines. On the contrary, line DD had similar and intermediate (from 0.28 to 0.36) levels of bandsharing with all other lines. The range of BS values between lines BB or EE and the others was large (from 0.17 or 0.20 to 0.44). Specific comparisons between BS values are in Table III. BS within lines under selection was higher than within the corresponding control line for both REC ($P < 0.01$) and IND ($P < 0.001$) lines. Both lines BB and EE from the Tours origin have maintained higher levels of BS ($P < 0.05$) with

Table II. Bandsharing (mean ± SD) within (on the diagonal) and between Japanese quail lines selected for early egg production, and comparison (a–j) of all line pairs.

Line	AA		BB		DD		EE		PP		FF	
AA	0.57 ± 0.12	b, c[2]	0.17 ± 0.10	j	0.31 ± 0.15	e, f, g	0.20 ± 0.11	i, j	0.22 ± 0.11	h, i, j	0.20 ± 0.11	i, j
	n[1] $= 21$		$n = 42$		$n = 35$		$n = 38$		$n = 19$		$n = 25$	
BB			0.62 ± 0.10	a, b	0.36 ± 0.08	e	0.44 ± 0.12	d	0.25 ± 0.12	g, h, i	0.29 ± 0.09	e, f, g, h
			$n = 21$		$n = 35$		$n = 38$		$n = 19$		$n = 25$	
DD					$0\ 67 \pm 0.13$	a	0.36 ± 0.11	e, f	0.28 ± 0.12	f, g, h	0.33 ± 0.10	e, f
					$n = 17$		$n = 35$		$n = 19$		$n = 25$	
EE							0.57 ± 0.13	b, c	0.25 ± 0.14	g, h, i	0.32 ± 0.12	e, f, g
							$n = 19$		$n = 19$		$n = 25$	
PP									0.51 ± 0.19	c, d	0.19 ± 0.11	i, j
									$n = 9$		$n = 19$	
FF											0.52 ± 0.16	c
											$n = 12$	

[1] total number of independent values of bandsharing (BS) from individual quail pairs.
[2] mean BS from line pairs with no common letter are significantly different ($P < 0.05$).

Table III. Genetic similarity measured by bandsharing (BS) among lines of Japanese quail from two origins and under recurrent, within-line, or no selection for early egg production.

Comparison	Contrast	Significance
Overall line pairs	See Table II	***
Origin[1] of line pair (single line-two lines)	0.30	***
Within-line BS		
$0.5(BS_{AA} - BS_{PP}) + 0.5(BS_{BB} - BS_{FF})$	0.08	**
$0.5(BS_{DD} - BS_{PP}) + 0\ 5(BS_{EE} - BS_{FF})$	0.11	***
$0\ 5(BS_{AA} - BS_{DD}) + 0.5(BS_{BB} - BS_{EE})$	−0.03	NS
Relatedness to control line, within selection method		
$0.5(BS_{AP} - BS_{BF}) + 0.5(BS_{DP} - BS_{EF})$	−0.06	*
Relatedness to control line, within stock origin		
$0\ 5(BS_{AP} - BS_{DP}) + 0.5(BS_{BF} - BS_{EF})$	−0.05	†
Relatedness of homologous selection lines		
$BS_{AB} - BS_{DE}$	−0.19	***
$BS_{AB} - BS_{PF}$	−0.02	NS
$BS_{DE} - BS_{PF}$	0.17	***
Combination of pair type (one or two lines) and selection (within-line or recurrent) $(0.25BS_{DD} + 0.25BS_{EE} - 0.5BS_{DE}) - (0.25BS_{AA} + 0.25BS_{BB} - 0.5BS_{AB})$	−0.08	***

[1] BS from 6 single-line pairs (AA,BB...PP) and 15 two-line pairs (AB,AD,...EP, PF) are written as BS_{AA}, ., BS_{PF}.
*** $P < 0.001$; ** $P < 0\ 01$; * $P < 0\ 05$; † $P < 0\ 10$; NS . not significant.

their control line FF than their respective REC and IND counterparts, lines AA and DD, have with line PP. BS_{AB} was smaller than BS_{DE} ($P < 0.001$) and it was similar to BS_{PF}. The difference between average within-line BS and corresponding between-line BS was larger ($P < 0.001$) for REC lines than for IND lines.

3.2. Production traits and bandsharing in lines under selection

The results of the performance test and relationship between each trait and BS are in Table IV. For all five traits, the line accounted for a significant proportion of the total variance ($P < 0.001$). Crossbred quail started laying eggs earlier than all pure lines ($P < 0.05$), but line BB. Early egg production EN1 was higher for crossbreds and for line EE ($P < 0.05$). After 13 months of testing, EN2 was also higher in crossbred birds ($P < 0.05$), but it was as high for line DD and intermediate for line EE. Egg weight was higher in the lines from the Tours origin ($P < 0.05$), and it was intermediate in crosses. Body weight was higher in REC crosses and in line EE ($P < 0.05$), closely followed

Table IV. Average performance (with SD) of Japanese quail purebred and crossbred types and coefficient (b) of linear regression on bandsharing (BS) of parents.

	Average performance						Analysis of covariance		
Trait	AA	AB/BA	BB	DD	DE/ED	EE	R^2	Line	b
Age at first egg (AFE),	44.2^{a}	37.8^{d}	39.8^{c}	41.5^{b}	$38.9^{c,d}$	38.0^{d}	0.26	***	−2.3†
days	(4.9)	(2.9)	(3.1)	(5.4)	(2.8)	(2.9)			
Egg number after 65 days	44.2^{c}	56.1^{a}	49.3^{b}	51.5^{b}	56.9^{a}	55.1^{a}	0.21	***	0.34 NS
in laying test (EN1)	(12.9)	(5.3)	(9.8)	(7.5)	(4.8)	(11.4)			
Egg number after	247^{d}	$314^{a,b}$	$255^{c,d}$	$301^{a,b}$	327^{a}	$282^{b,c}$	0.09	***	−16.4 NS
13 months in	(113)	(86)	(92)	(101)	(86)	(90)			
laying test (EN2)									
Egg weight (EW), g	9.6^{e}	11.5^{c}	11.8^{b}	10.2^{d}	$11.5^{b,c}$	12.1^{a}	0.44	***	−0.3 NS
	(0.7)	(0.9)	(1.0)	(0.8)	(0.8)	(0.9)			
Body weight	162^{d}	201^{a}	194^{b}	170^{c}	191^{b}	199^{a}	0.42	***	−5.7 NS
at 34 days (BW), g	(15.6)	(16.6)	(18.7)	(14.4)	(13.6)	(15.1)			

$^{a-e}$ values with no common superscript are significantly different ($P < 0.05$).
*** $P < 0.001$; † $P < 0.10$; NS: not significant.

by the IND crosses and line BB. The coefficient of regression on BS was not significant for any of the five traits.

3.3. Heterosis and bandsharing in lines under selection

Results on heterosis and BS are in Table V. Heterosis from REC lines was significant for all traits ($P < 0.001$), but it was only significant for EN1 ($P < 0.01$) and EN2 ($P < 0.05$) in the IND lines. Heterosis from REC lines was at least twice higher ($P < 0.01$ to $P < 0.001$) than that from IND lines for all traits but for EN2. No significant linear relationship between heterosis and BS difference was obtained for the REC lines. On the contrary, favorable associations were found for the IND lines: the regression coefficient was significant ($P < 0.05$) for EN1 and BW.

4. DISCUSSION

4.1. Genetic similarity between lines

Compared to the results obtained with chickens [5] and quail [24], a total of only 59 bands were scored but 19 to 42 birds from each line were fingerprinted, so the size of the data set should be satisfactory enough to evaluate genetic variability using DFP [16]. On the contrary, for each line under selection the sample was not chosen at random from all generation 12 birds but it was made of the breeders only, that is the top 30% ranked birds. The impact of this sampling on the comparison of BS between lines is difficult to ascertain. However, since at least 88% of all breeders from each line in selection were fingerprinted, the sample should represent reasonably well the genetic variation at the VNTR loci that was transmitted to the next generation. Within-line BS was larger in selected lines than in unselected lines PP and FF, probably because the successive generations of selection increased homozygosity. Similar BS difference between controls and Japanese quail lines under divergent selection for body weight [15,24] or turkey lines under selection on body weight, egg weight or shank length [25] were reported previously. Bandsharing BS_{PF} between the two origins of quail in the present work was 0.19, a low value which is comparable to that found between White Rock and White Leghorns, or between broilers and layers in poultry [4]. Our observations from BS values that IND lines were closer to the control lines than REC lines, and that lines AA and BB were more distant than lines DD and EE were already available from the principal component analysis of protein polymorphism data at 10 loci on the same sets of quail [14]. These two separate analyses with different types of markers concur to indicate that reciprocal recurrent selection appears to have had a more profound impact on the genome than individual selection. The results of the present study also offer clear experimental evidence from a genetic standpoint that reciprocal recurrent selection pulled away pure lines as intended [22], and that, on the contrary, within-line selection for the same trait moved the two IND lines in the same direction. Overall, it appears that known or expected relationships between these six quail lines were satisfactorily described by DNA fingerprinting.

Table V. Heterosis (H ± SE) and linear relationship (b ± SE) between heterosis in progeny and bandsharing of parents[1], in Japanese quail under reciprocal recurrent or within-line selection for early egg production

Selection method	Recurrent selection (REC)			Within-line selection (IND)		
Trait	H ± SE	H %	b ± SE	H ± SE	H %	b ± SE
Age at first egg (AFE), d	$-3.9^{***} \pm 0.5$	9.2	$0.027^{NS} \pm 0.133$	$-0.9^{NS} \pm 0.6$	2.3	$-0.536\,\dagger \pm 0.246$
Egg number after 65 days in test (EN1)	$8.8^{***} \pm 1.2$	18.8	$0.160^{NS} \pm 0\,427$	$3.6^{**} \pm 1.4$	6.7	$0.855^{*} \pm 0.354$
Egg number after 13 months (EN2)	$59^{***} \pm 14$	23 4	$-0.176^{NS} \pm 0.816$	$36^{*} \pm 16$	12.6	$0.523^{NS} \pm 0.576$
Egg weight (EW), g	$0.88^{***} \pm 0.13$	8.2	$-0.176^{NS} \pm 0.129$	$0.21^{NS} \pm 0.14$	1.9	$0.123^{NS} \pm 0.177$
Body weight at 34 days (BW), g	$22.8^{***} \pm 2.3$	12.8	$-0.249^{NS} \pm 0.147$	$4.0^{NS} \pm 2.7$	2.1	$0.555^{*} \pm 0.219$

[1] % BS difference between parental pairs = 100 (average BS from the two pairs of parents of purebred progeny − average BS from the two pairs of parents of crossbred progeny)/(average BS from the two pairs of parents of purebred progeny). It was obtained from each set of four parents which had all four (two purebred and two crossbred) combinations of progeny present in the egg laying test (14 REC and 8 IND sets, for 328 quail).

*** $P < 0.001$; ** $P < 0.01$; * $P < 0.05$; † $P < 0\ 10$; NS not significant.

4.2. Performance and bandsharing

Previously reported zootechnical differences between genetic types [19,20] were also obtained here, with higher egg production and weights in crossbreds and in one or both IND lines. However, the lack of a relationship between BS of parents and the performance of progeny observed for all five traits in the present study indicates that the interest of using BS directly as an indicator for planning matings in order to increase performance is dubious at least in the Japanese quail.

4.3. Heterosis and bandsharing

Expectedly [19,22], heterosis evaluated in the present work from individual matings was generally quite different under reciprocal recurrent and within-line selection: it was high for REC lines and intermediate or non-significant for IND lines. There was no relationship of parental BS difference under pure line and cross line matings with heterosis for the five zootechnical traits in the REC lines. On the contrary, heterosis for egg production and for body weight increased with the BS difference in the IND lines. In the literature, no report was found on BS and heterosis for animal populations under reciprocal recurrent selection. However, favorable associations between heterosis of progeny and BS of parents were reported previously for egg production traits in lines of chicken which had been under random or directional selection [5,8], and more generally, heterosis has been found to increase with genetic distance in laboratory animals [21]. The sharp difference between the two selection methods regarding the relationship between bandsharing and heterosis has not been reported before, and it has no straightforward explanation. However, it is possible that the relative importance of the various kinds of non-additive effects built up in crossbreds was different under the two methods of selection, with more dominance effects in crossbreds from within-line selection and more epistasis effects in crossbreds from reciprocal recurrent selection. Since BS, like dominance effects, is related to heterozygosity, this might then help explain the contrasted patterns of relationship with heterosis. In any case, empirical evidence indicates that planning crossbred matings from BS values to increase heterosis of progeny could be effective in poultry species under within-line selection, but the validity of BS as a predictor of heterosis remains to be tested in other farm animals.

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