Identification of informative cooperator herds for progeny testing based on yield deviations

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ABSTRACT

Several arguments exist for breeding organizations to focus on cooperative herds for progeny testing, but an efficient methodology addressing herd selection strategies is lacking. In this study, a new approach based on yield deviations (YD) to identify the most informative cooperator herds in terms of genetic differentiation was evaluated. Data comprised YD from 717,377 first-lactation cows from 2 regions in East and West Germany calving between January 2003 and January 2008. Daughters were ranked and classified within sire according to their YD for protein yield, fat yield, milk yield, and somatic cell score. Cows in created YD classes were merged with respective herd-calving year (HCY) characteristics. Cows of extreme YD classes (i.e., such classes including the most extreme daughter contributions), belonged to herds characterized by a high HCY production level, a low value for HCY somatic cell count, and a low HCY age at first calving (AFC). Cows with low extremes for YD in protein yield were associated with the lowest HCY production level, a high value for HCY somatic cell count, and a late HCY AFC. Ranks of HCY and ranks of herds considering HCY over the whole analyzed period were calculated by averaging YD percentages within HCY, and within herds, respectively. The YD percentages (in absolute values so that negative and positive daughter contributions were treated equally) were derived from the rank of the YD of a daughter within sire in relation to all daughters of a sire. A further partitioning of ranks of herds into quartiles revealed the following results: herds in the first quartile had the highest average protein yield, the highest intra-herd standard deviation for the national production index, and the lowest AFC. Correlations between herd rankings for different production traits ranged between 0.64 and 0.86, and were 0.65 for West Germany and 0.62 for East Germany between

HCY 2006 and the average herd rank of all calving years. Correlations between daughter yield deviations for the highest and the lowest herd quartile of 0.87 for protein yield disproved concerns regarding genotype by environment interaction between test and production environment. The suggested methodology to identify informative cooperator herds is easy to implement, holds for regions with small herd sizes, and thus, may help in implementing sustainable and competitive dairy cattle breeding programs.

Key words: progeny testing, cooperator herd, yield deviation, genotype $\times$ environment interaction

INTRODUCTION

Progeny testing (**PT**) in dairy cattle, as suggested by Henderson (1964) and by Skjervold and Langholz (1964), was established in Germany in the late 1960s. The original idea included a random mating system for young sires to generate a substantial pool of phenotypes for an unbiased EBV. This random mating system implied a random sample of herds used for PT (or even all herds within the active breeding population), and a random sample of cows within herds for inseminations with young sires. Apart from long generation intervals, PT in this form generated relatively high selection intensities, and highly reliable EBV for the male pathways of selection. The final improvement for those components was associated with a sustained selection response for traits under intensive selection pressure (König et al., 2007).

Further improvements to identify genetically superior sires could be put into effect by selecting special cooperator herds for PT. This idea was formulated by Hammond (1947), who suggested keeping and selecting animals in superior environments, so that animals can fully express their true genetic potential. Other studies also discussed possible genotype by environment interactions when differentiating between test environment and production environment (König et al., 2008), which underlines the importance of a broad testing scheme in a multitude of herds. As found in several studies

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(Hill, 1984; Garrick and Van Vleck, 1987), differences in test environments have been associated with differences in estimated variance components. The effect of heterogeneous variances across regions or herds on results of genetic evaluation for production traits has been discussed intensively (Van Vleck, 1963; Vinson, 1987; Boldman and Freeman, 1990). Former publications (Van Vleck, 1963), as well as more recent studies (Gernand et al., 2007), found higher additive genetic variances with an increasing production level in herds, and they gave recommendations for optimization of PT schemes. Simulation studies by Hill (1984) and Garrick and Van Vleck (1987) showed an increase of EBV with increasing intra-herd variances. The optimization of management and feeding strategies (Padilla and Keown, 1990), the milking technology and herd size (Weigel et al., 1993), as well as the skills of herdsman (Short et al., 1990) were identified as possible reasons for increased intra-herd variances. Since the unification of the 2 formerly separated German countries in 1990, the German dairy cattle population has been characterized by a dichotomy in housing and management conditions: in West Germany, family farms with herd sizes of around 30 to 100 cows are prevalent, whereas in East Germany, large-scale dairy farms with herd sizes of 200 to 2,000 cows are common. Also, in Germany, heterogeneity in variance components for production traits was found (König et al., 2005): the larger the farm, the larger the additive genetic variance. A reason for this could be that relationships between genotype and management (e.g., as arising from feeding according to the genetic potential) are higher in large farms.

Due to the increase of competition on the global semen market for dairy sires (Dekkers et al., 1996), some of the 14 different German breeding organizations refresh those ideas toward more selective PT in terms of test environments to achieve more accurate EBV. Additionally, higher accuracy to identify genetically superior sires among the total pool of test candidates will increase genetic gain as well as production level in the whole population. However, effective methods are lacking to identify those informative cooperator herds allowing the highest genetic differentiation. Some studies have focused on relatively simple aspects, such as the number of usable records (Meinert et al., 1997), or herd size and herd production level (Vierhout et al., 1999). Gernand et al. (2007) suggested cluster analyses to combine favorable effects of large herd size, high production level, and low age at first calving (AFC). Other studies (Brügemann, 2008; Dechow et al., 2008a) focused on genetic analyses and variance component estimation within herds. Brügemann (2008) found increasing additive genetic variances and heritabilities with increasing herd size and improving farm

management. In the study by Dechow et al. (2008a), intra-herd heritability was also negatively correlated with sire misidentification rates. Due to relatively large standard errors of estimates from intra-herd analyses, this approach is not applicable for small family farms as prevalent in West Germany.

As an alternative, we evaluated a strategy for selection of cooperator herds based on yield deviations (YD). The derivation and calculation of daughter yield deviations (DYD) and YD was reported by VanRaden and Wiggans (1991) for animal models, and by Mrode and Swanson (2004) for random regression models. Daughter yield deviations have been described as the most independent and most accurate measure of phenotypic performance of a bull, conceptually equivalent to average daughter records (VanRaden and Wiggans, 1991; Liu et al., 2004; Mrode and Swanson, 2004). Utilization of DYD for dairy cattle genetic evaluation and breeding objectives is quite common: DYD are used as controlling instruments at Interbull for validating trends in national genetic evaluations (Boichard et al., 1995), for the identification of preferential treatment (Powell et al., 1994), or for the identification of quantitative trait loci and derivation of SNP effects (Szyda et al., 2005; Neuner et al., 2008).

The specific goal of the present study was to investigate the association between YD and defined herd characteristics. Based on these findings, an approach using YD to select cooperator herds for PT is suggested.

MATERIALS AND METHODS

Data

The data consisted of 3,652,113 test-day records from 445,819 first-lactation cows in 26,651 herd-calving years (HCY) located in the German state Lower Saxony (northern part of West Germany), and of 2,244,185 test-day records from 271,558 first-lactation cows in 3,483 HCY located in Saxony (East Germany). Data from West Germany generally represent the typical family farm in this region with an average herd size of 16.7 cows in first lactation. Average herd size for large-scale dairy farms in East Germany comprised on average 68 cows in parity one. Cows calved between January 2003 and January 2008, and test-day records for all cows were available for this period. Furthermore, yield deviations for milk yield, fat yield, protein yield, and SCC for these cows were available. Yield deviations were calculated as lactation YD (i.e., based on the cow's performance adjusted for fixed and nongenetic random effects, and for genetic effects of the dam). Details for the calculation of YD and criteria for publication of YD are explained in Liu et al. (2004).

Table 1. Means and standard deviations (SD in parentheses) averaged over the first 5 test-day records for milk yield, fat content, protein content, SCC, calving interval, and age of first calving (AFC) for the regions West Germany and East Germany within calving years

Region and calving year	Calving year parameter						
	No. of cows	Milk (kg)	Fat (%)	Protein (%)	SCC ($\times 1,000$)	Calving interval	AFC
West Germany							
2003	64,293	26.57 (4.68)	4.05 (0.49)	3.31 (0.22)	167.26 (277.25)	417.28 (81.64)	29.64 (3.74)
2004	61,918	26.88 (4.71)	4.02 (0.48)	3.30 (0.21)	165.35 (269.83)	421.87 (86.60)	29.53 (3.85)
2005	55,079	27.57 (4.85)	3.99 (0.50)	3.30 (0.21)	167.83 (279.96)	424.30 (88.79)	29.19 (3.81)
2006	59,358	27.82 (4.78)	3.99 (0.49)	3.27 (0.20)	172.84 (292.55)	422.96 (86.07)	28.91 (3.70)
2007	25,019	28.05 (4.79)	3.96 (0.49)	3.26 (0.20)	176.43 (298.74)	417.89 (70.08)	28.49 (3.31)
East Germany							
2003	39,693	27.82 (5.21)	4.00 (0.51)	3.35 (0.22)	179.44 (308.71)	417.27 (81.29)	26.96 (2.75)
2004	40,178	28.26 (5.23)	4.00 (0.50)	3.32 (0.22)	176.99 (301.71)	421.92 (87.71)	26.75 (2.81)
2005	39,478	28.94 (5.29)	3.93 (0.51)	3.30 (0.22)	177.58 (301.38)	423.17 (88.39)	26.55 (2.78)
2006	37,786	29.40 (5.36)	3.92 (0.50)	3.28 (0.21)	193.51 (342.31)	424.17 (88.41)	26.32 (2.72)
2007	16,432	29.75 (5.24)	3.92 (0.49)	3.25 (0.21)	205.04 (358.23)	418.23 (71.37)	26.28 (2.61)

Records from cows that had their first herd test-day later than 60 d after calving (presumably due to herd changes) and records from cows without a second calving were excluded from the analyses. An additional requirement for keeping a cow record was a registered sire with more than 50 daughters, resulting in cows from 833 different sires. This strategy also excluded natural service sires. The final data set consisted of 265,667 cows in 22,668 HCY from West Germany, and of 173,567 cows in 3,410 HCY from East Germany. Means and standard deviations averaged over the first 5 test records for milk yield, fat content, protein content, SCC, calving interval, and AFC for both regions are shown in Table 1.

Methods

Ranking of Daughters Within Sire and Allocating Daughters to HCY. An initial, general analysis was conducted to verify possible associations between YD and respective HCY parameters. For this purpose, cows were classified in 7 different YD classes (Table 2). All cows were ranked within sire by the magnitude of their YD. Subsequently, the cows were assigned to different YD classes (e.g., the 10% of cows with the highest YD within their sire were assigned to class

“highest 10,” and the 20% with the highest YD within sire, from 0 to 20%, were assigned to class “highest 20”). Cow records in defined YD classes were merged with phenotypic observations of their remaining HCY contemporaries to calculate HCY parameters. These were (1) average HCY protein yield (average of first 5 test-day records), (2) average HCY SCS (average of first 5 test-day records), (3) average HCY calving interval, and (4) average HCY AFC.

A study focusing on the first 5 test-day records is in line with criteria for early selection strategies of young sires. Furthermore, genetic differentiation is less pronounced at the end of lactation due to a decrease in additive genetic variances (Gernand et al., 2007). Analyses were conducted separately for YD classification based on the following traits: (1) YD for milk yield, (2) fat yield, (3) protein yield, and (4) SCS.

Selection of Most Informative Cooperator Herds. For optimization of genetic differentiation, those herds are most informative that include a high fraction of cows with extreme genetic contributions (high or low; e.g., such cows classified in YD classes “highest 10%” and “lowest 10%”). In terms of the phenotypic expression of the genetic potential, average YD or YD with low extremes, as prevalent in YD class “average 40” within sire, are unfavorable. Our approach,

Table 2. Yield deviation (YD) classes used to analyze possible associations between YD and respective herd-calving year parameters

YD class	Range	Percentile
Lowest 10%	10% of daughters with lowest YD within sire	0 to 9
Lowest 20%	20% of daughters with lowest YD within sire	0 to 19
Lowest 30%	30% of daughters with lowest YD within sire	0 to 29
Average 40%	40% of daughters with low extremes for YD within sire (i.e., those cows between the lowest 30% and the highest 30%)	30 to 69
Highest 30%	30% of daughters with highest YD within sire	70 to 99
Highest 20%	20% of daughters with highest YD within sire	80 to 99
Highest 10%	10% of daughters with highest YD within sire	90 to 99

Figure 1. Example for ranking one specific herd-calving year (HCY) including 3 cows in first parity from 2 different sires: cows were ranked by extremeness of their yield deviation (YD) within sire (DYD = daughter yield deviation). Subsequently, absolute values of the percentages within sire were averaged for each HCY to create HCY ranks.

thus, focused on the identification of herds providing extreme YD within sire, treating negative and positive YD equally. Identification of cooperator herds based on this strategy does not focus on the success of a breeding organization with respect to the number of bulls in the national top list rather than a more accurate genetic differentiation.

For treating positive and negative daughter contributions equally, all cows within sire were ranked in percentages by extremeness of their YD, in a negative as well as in a positive direction. Hence, most extreme YD in both directions imply high values for daughter rank percentages. In the next step, HCY ranks were created by using the defined within-sire percentages and applying the following formula:

$$HCYrank_{jl} = \frac{\sum |perc_{ijkl}|}{n_{jl}},$$

where $HCYrank_{jl}$ is the rank of herd j in calving year l ; $|perc_{ijkl}|$ is the absolute value of the percentage score of cows i from herd j within sire k in year l ; and n_{jl} is the number of cows in herd j in calving year l . Furthermore, the rank of a herd, which considered all available HCY within the entire analyzed period, was calculated as follows:

$$Rank\ of\ herd_j = \frac{\sum |perc_{ijk}|}{n_j},$$

where $|perc_{ijk}|$ is the absolute value of the percentage score of cow i from herd j within sire k ; and n_j is the number of cows in herd j .

An example for calculating the HCY rank for one specific small HCY with 3 cows from 2 different sires in first lactation is given in Figure 1. As explained, at first, cows were ranked by extremeness of their YD within sire. A percentage score of -42.1% was assigned to cow A, which implies that this cow represents 42.1% of all cows below the DYD of the respective sire A. Cow B represents 80.7% of all cows above the DYD of sire A. Cow C has a percentage score of 21.2% , indicating that within all daughters of sire B that have a YD above the sires DYD, cow C represents the 21.2% most positive YD. Subsequently, absolute values of the percentage scores of all cows belonging to the HCY in this example are averaged to calculate the HCY rank of 48% :

$$HCYrank = \frac{|-42.1\%| + 80.7\% + 21.2\%}{3} = 48\%.$$

The procedure, as explained in Figure 1, was subsequently used to calculate the rank of a herd using cows from all HCY.

In the last step, herds were classified into quartiles according to their rank of herd. The lower the herd quartile, the more extreme the YD that were allocated. Low-quartile herds were suggested as a cooperator herd for PT with respect to genetic differentiation. For each herd quartile, means for the following herd characteristics were calculated:

- herd size (defined as the average number of first-lactation cows per HCY)
- protein yield (average of first 5 test-day records)
- intra-herd standard deviation for the German production index (**RZM**)
- AFC.

Figure 2. Mean herd-calving year parameters for test-day protein yield stratified by region for different yield deviation (YD) classes ranked by YD for protein yield and by YD for SCS. Different letters indicate significant differences at $P < 0.05$ within each region and trait combination.

Analyses were restricted to herds with at least 10 first-lactation cows in calving year 2006, and were conducted separately using YD for milk yield, fat yield, protein yield, and SCS. Spearman rank correlations were calculated between herd rankings for different traits, and between HCY ranks within the same trait.

Analysis of Genotype by Environment Interactions. Possible genotype by environment interactions ($G \times E$) for protein yield and SCC between high- and low-ranking herds were analyzed by correlating DYD of sires between the highest and lowest herd quartile. Data comprised 54,346 cows in the first herd quartile and 39,951 cows in the fourth herd quartile for West Germany, as well as 40,193 cows in the first herd quartile and 22,276 cows in the fourth herd quartile for East Germany. The DYD for a sire was the average of YD of his daughters in the respective herd quartile. Subsequently, Spearman rank correlations were calculated between sire DYD in different herd quartiles and different regions. The first analysis considered all sires, and was restricted in a second analysis to sires with at least 50 daughters in both environments. In the absence of $G \times E$, ranking of sires is expected to be similar in both environments.

RESULTS AND DISCUSSION

Associations Between YD and Herd Characteristics

Means for HCY test-day protein yield, HCY SCC, HCY calving interval, and HCY AFC, stratified by

region and YD classes for protein yield and SCC, are shown in Figures 2, 3, 4, and 5.

When ranking daughters according to YD for protein yield within sire, high YD were generally associated with a higher HCY production level for protein yield. This finding is also in line with the biological nature of traits (i.e., a positive association between the mean of the trait and the variance: a topic that has been investigated in dairy cattle from the perspective of heterogeneous intra-herd variances and selection proportions; Dong and Mao, 1988; Boldman and Freeman, 1990). High YD for protein yield were also found for a lower SCC, and a lower AFC within herds. We also observed a decrease in the HCY calving interval in West Germany with a more stringent allocation of YD, whereas no significant differences were found in East Germany. Cows with negative daughter contributions (i.e., YD classes “lowest 30%,” “lowest 20%,” and “lowest 10%”) were allocated to HCY characterized by a higher production level, a lower AFC, and a shorter calving interval compared with those of the YD group representing lower extremes in YD (average 40%). Daughters characterized by average genetic contributions were generally kept in herds having a low production level for protein yield, and a late AFC. A low production level in combination with a high AFC, a long calving interval, and a high SCC indicates a suboptimal management in those herds (Gernand et al., 2007). Similar trends were found when ranking daughters within sire according to YD for fat yield or YD for milk yield (results not shown). Hence,

Figure 3. Mean herd-calving year parameters for SCC stratified by region for different yield deviation (YD) classes ranked by YD for protein yield and by YD for SCS. Different letters indicate significant differences at $P < 0.05$ within each region and trait combination.

Figure 4. Mean herd-calving year parameters for calving interval stratified by region for different yield deviation (YD) classes ranked by YD for protein yield and by YD for SCS. Different letters indicate significant differences at $P < 0.05$ within each region and trait combination. No significant differences ($P < 0.05$) were found within East-Protein.

Figure 5. Mean herd-calving year parameters for age of first calving stratified by region for different yield deviation (YD) classes ranked by YD for protein yield and by YD for SCS. Different letters indicate significant differences at $P < 0.05$ within each region and trait combination.

these results are in line with results from previous studies using an approach based on variance components (Dodenhoff and Swalve, 1998; König et al., 2005; Gerber et al., 2008), indicating the better the testing environment, the better the phenotypic expression of the genetic potential.

When ranking daughters according to YD for SCS within sire, results from association analyses were completely different. Herd-calving year production level for test-day protein yield, test-day SCC, and HCY AFC were relatively equal for all created YD classes. Only HCY SCC was substantially higher for the lowest and the highest YD classes. Results for YD-SCS grouping showed the same patterns for East and for West Germany. Apparently, the genetic potential for SCC, being an indicator of mastitis resistance, is better expressed in an environment where the cow's immune system is under challenge. This is a desired effect in terms of a more accurate genetic differentiation for SCC and closely related susceptibility to mastitis (Philipsson et al., 1995), but difficult to combine with a maximization in genetic differentiation for production traits.

Selection of Cooperator Herds

Table 3 depicts average herd characteristics for the number of cows in first parity, test-day protein yield,

intra-herd standard deviation for the production index RZM, and AFC stratified by region and herd quartiles based on the rank of the herd for YD in protein yield. In West Germany, herd size was relatively equal for the first 3 herd quartiles, but herds allocated to the fourth quartile were substantially smaller. Test-day protein yield and intra-herd standard deviation of RZM decreased from the first to the fourth quartile. Cows in the first quartile produced an average of 100 g of protein per day higher than did cows in the fourth quartile. The difference in intra-herd standard deviation for RZM was 2.05 points when comparing these 2 quartiles. The second quartile was characterized by the lowest AFC, whereas the fourth quartile showed the highest AFC. Herd sizes, protein yield, and intra-herd standard deviation in RZM were higher, and AFC was lower for herd quartiles in East Germany when compared to the respective quartiles in West Germany. Interestingly, herds in East Germany allocated to the first quartile were smaller than the herds in the second and third quartile, but substantially larger than herds in the fourth quartile. Apart from that, trends for average protein yield and intra-herd standard deviation were similar to those in West Germany. Herds in the first quartile had the highest average protein yield, the highest standard deviation in RZM, and the second lowest AFC. These results support former arguments

Table 3. Mean herd characteristics and standard deviations (SD in parentheses) for number of cows in first parity, test-day protein yield, intra-herd standard deviation in the German production index RZM, and age of first calving (AFC) stratified by region for different herd quartiles¹ according to yield deviation (YD) selection for protein yield

Region and quartile	Herd characteristic				
	No. of herds	No. of cows in first parity	Protein (g)	Intra-herd SD for RZM	AFC
West Germany					
1	610	24.68 ^a (11.07)	943.86 ^a (73.98)	11.60 ^a (1.18)	29.10 ^{ab} (2.12)
2	610	25.31 ^a (12.32)	920.73 ^b (74.52)	10.99 ^b (1.10)	28.96 ^a (2.14)
3	610	24.40 ^a (13.04)	904.27 ^c (77.28)	10.58 ^c (1.23)	29.32 ^b (2.27)
4	611	18.32 ^b (7.73)	844.71 ^d (97.54)	9.55 ^d (1.40)	29.82 ^b (2.50)
East Germany					
1	126	82.62 ^a (73.92)	981.24 ^a (78.00)	12.41 ^a (1.09)	26.67 ^a (1.41)
2	127	109.61 ^b (100.99)	950.99 ^b (66.48)	11.95 ^b (0.85)	26.53 ^a (1.66)
3	127	100.20 ^{ab} (102.29)	912.13 ^c (63.69)	11.67 ^c (0.89)	26.72 ^a (1.45)
4	127	49.41 ^c (61.25)	848.36 ^d (94.62)	10.30 ^d (1.07)	27.97 ^b (1.95)

^{a-d}Different superscripts within regions indicate significant differences at $P < 0.05$.

¹Quartiles are based on the rank of the herd for genetic differentiation. The higher the quartile, the lower the genetic differentiation in herds based on yield deviations.

that potential cooperator herds for PT should have a high production level combined with a high intra-herd variance and a low AFC (Gernand et al., 2007). An early AFC combines several desired effects for improvements in breeding programs (i.e., a distinct genetic differentiation, and additionally, a decrease in generation intervals on the cow sire path of selection).

Progeny testing in extremely large herds may have some logistic advantages (e.g., an easier coordination of PT, especially in terms of conformation classification, or DNA sampling for genotyping in the near future), but a restriction only on herd size does not necessarily maximize genetic differentiation. Of course, a minimum for herd size should be a criterion to ensure a sufficient number of cows in contemporary groups with respect to a reliable genetic evaluation.

Rank Correlations Between Different Herd Rankings

Herd ranking based on YD for milk yield instead of YD for protein yield revealed almost identical results. The Spearman rank correlations between both alternatives were 0.84 and 0.86 for West and East Germany, respectively (Figure 6). Correlations between herd ranks for protein yield and those for fat yield were 0.64 for West Germany, and 0.69 for East Germany. However, correlations between herd ranks for protein yield and herd ranks for SCS were only 0.09 for West Germany, and slightly negative (−0.05) for East Germany.

Additionally, Spearman rank correlations between the herd rank for YD in protein yield in calving year 2006 and the average herd rank from all calving years (2003–2007) were calculated. Year 2006 was the most recent calving year including a substantial data pool, whereas data from calving year 2007 was substantially

decreased due to the criteria for publishing YD (Liu et al., 2004). Correlations were 0.65 for West Germany and 0.62 for East Germany. Those estimates of correlations suggest that an informative herd for a specific calving year will also be an informative herd in other calving years. Correlations between single years were in the range of 0.19 and 0.45, with correlations between consecutive years being higher than those between nonconsecutive years. Possible reasons for differences in herd rankings in different years are changes in farm management, disease issues, heat stress, or poor quality of roughage in some specific years so that animals cannot express their full genetic potential. However, from the practical and logistic point of view, we do not recommend an update in selection of cooperator herds in short intervals, or a herd selection based only on the information of one specific HCY.

Analysis of Genotype by Environment Interactions

Daughters of young bulls are supposed to be randomly distributed within the test region of an AI station. Hence, daughters are randomly distributed across herd sizes and production levels. Consequently, EBV of bulls should be unaffected by herd characteristics (Vinson, 1987). As there is a shift toward selective PT in those herds with higher intra-herd variances and a superior herd management, the question of $G \times E$ will arise. Genotype by environment interaction occurs when different genotypes are not equally affected by different environments (Falconer, 1952), and can result in differences in the ranking of genotypes. Thus, rank correlations between average DYD for protein yield and SCS in upper and lower herd quartiles for West and East Germany were calculated. Correlation coefficients

Figure 6. Spearman rank correlations between herd rank for protein yield (PY) and herd ranks for milk yield (MY), fat yield (FY), and SCS for 2 different regions in Germany.

are shown in Table 4. For protein yield, rank correlations ranged between 0.82 and 0.87 within and across different regions. Rank correlations for SCS between different quartiles ranged between 0.67 and 0.83. Rank correlations including only those sires with more than 50 daughters between herd quartiles within the same region and also across different regions, were in a range between 0.92 and 0.98 for both traits. Hence, according to the criteria suggested by Robertson (1959), correlations did not reveal any relevant $G \times E$ interaction between different herd conditions or regions. Results were also in line with those from Gerber et al. (2008), who found rank correlations in the range of 0.90 when comparing DYD of bulls in high-input and low-input production systems.

Several studies have focused on $G \times E$ (Van Vleck, 1963; Carabaño et al., 1990; Hayes et al., 2003). König et al. (2005) estimated genetic correlations for production traits between small herds from West Germany and herds from East Germany to be 0.90 and higher. Only when small family farms in West Germany were compared with large-scale dairy farms in East Germany with more than 150 cows in first lactation, correlations dropped to 0.79.

Economic pressure also will force dairy farmers in West Germany to increase herd size. Based on the genetic correlations above 0.95 estimated in this study, and considering the expected future herd structures in Germany, $G \times E$ should not be a problem. Currently selected cooperator herds for PT will be representative

Table 4. Spearman rank correlations between average daughter yield deviations in the first and fourth herd quartile for potential cooperator herds in two different German regions

Compared herd quartiles ¹	Trait	All sires		Sires with at least 50 daughters	
		Rank correlation	Sires (n)	Rank correlation	Sires (n)
1st quartile West/4th quartile West	Protein (kg)	0.87	785	0.98	84
	SCS	0.83		0.96	
1st quartile East/4th quartile East	Protein (kg)	0.82	791	0.97	60
	SCS	0.67		0.95	
1st quartile West/1st quartile East	Protein (kg)	0.87	141	0.97	36
	SCS	0.81		0.93	
1st quartile West/4th quartile East	Protein (kg)	0.82	137	0.92	24
	SCS	0.67		0.92	
4th quartile West/1st quartile East	Protein (kg)	0.86	142	0.97	38
	SCS	0.81		0.95	
4th quartile West/4th quartile East	Protein (kg)	0.82	138	0.94	26
	SCS	0.71		0.92	

¹Quartiles are based on the rank of the herd for genetic differentiation. The higher the quartile, the lower the genetic differentiation in herds based on yield deviations.

of the typical structure of German dairy cattle herds being competitive in the future.

Practical Considerations When Implementing Cooperator Herds

Using YD to identify informative cooperator herds for an accurate genetic differentiation among young bulls in PT schemes has 3 major advantages compared with selection strategies based on the intra-herd estimation of variance components (Brügemann, 2008; Dechow et al., 2008a). First, computing time for the suggested method is substantially lower. Second, YD are generally available when computing EBV in the process of national genetic evaluation. Hence, our algorithm could be incorporated as an additional feature in this routine process. Third, the YD-based approach is applicable also to small herds as prevalent in West Germany. In contrast, an intra-herd variance component estimation approach leads to inflated standard errors of estimates with decreasing herd size. The proposed method is also characterized by a high flexibility to data restrictions (e.g., focusing only on herds using a high quantity of young sires, or for created subsets within distinct regions).

Gernand et al. (2007) suggested a 2-step cluster approach to combine herd characteristics such as herd size, protein yield, and AFC for a selection of cooperator herds. This may be an applicable method, but it does not focus in detail on the aspect of optimizing genetic differentiation. Dechow and Norman (2007) used regression techniques to estimate herd-heritabilities more rapidly. Those estimates were moderately correlated with heritabilities estimated with an animal model. The regression technique can be seen as an alternative to stratify individual herds by heritability or additive genetic variance (Dechow et al., 2008b).

An adjustment procedure for heterogeneous variances (Reents et al., 1998) has been implemented in the estimation procedure of German EBV, which might have a slight effect on associations found between genetic contributions and herd characteristics. However, as the adjustment method depends on herd size, it will have a marginal effect only on the results for small herds as prevalent in West Germany.

Cooperator herds will be of major importance in the near future. Especially in the period of genome-wide selection (Meuwissen et al., 2001), program designs of existing breeding programs will be modified intensively. Schaeffer (2006) suggested using daughter records from cooperator herds as a substantial base to estimate SNP effects. Such a strategy especially is recommended for low-heritability traits to ensure sufficient reliabilities of genomic breeding values (VanRaden et al., 2009).

Several functional low-heritability traits have been incorporated in international breeding goals (Mark, 2004; Miglior et al., 2005). Additional traits such as claw health (König and Swalve, 2006), pathogen-specific mastitis resistance (de Haas et al., 2002; Sørensen et al., 2009), or other metabolic and reproductive diseases (Zwald et al., 2004) might become important in the future. For achieving high reliabilities of EBV in those low-heritability traits, larger numbers of daughters and larger contemporary groups are required, as compared with those needed for production traits (Lindhé and Philipsson, 1998; Willam et al., 2002). To date, recording systems for these major health problems are not implemented in Germany. In contrast, in Scandinavia, veterinary treatments are monitored on health cards by veterinarians (Philipsson and Lindhé, 2003). When starting such an attempt, it would be easier to concentrate on a certain number of cooperator herds. Testing bulls in special cooperator herds and contracting farmers also will secure sufficient test capacities and reduce costs for logistics (e.g., for type trait classification; Swalve and König, 2007).

One, albeit minor, disadvantage of our strategy exists in the current situation: selected contract herds based on yield traits are not necessarily the best herds for the genetic differentiation for SCS. We recommend a strategy that allows an accurate genetic differentiation for production traits, and using those informative and well-managed herds to generate an extensive high-quality data pool for functional health traits. When selecting cooperator herds with a high health status (e.g., low SCC), the disadvantage of reduced YD differentiation for SCC may be compensated for by recording mastitis. Genetic gain for animal health generally will increase when using direct health information compared with using selection strategies focusing on indicator traits recorded in the entire population (Philipsson, 1995; de Haas et al., 2002; Koenig et al., 2005). Another strategy to ensure an adequate within-herd variation in health traits would be to maintain a certain number of herds in PT that are characterized by only average herd ranks combined with more challenging environments like a higher average SCC.

CONCLUSIONS

The strategy to identify herds with maximized genetic differentiation based on YD is a practical method for selecting cooperator herds in dairy cattle breeding programs. In contrast to other herd selection procedures such as the estimation of intra-herd heritabilities, the YD approach is relatively easy to implement, requires less computing time, and is practicable even in the case of small herd sizes. However, the applied

theoretical selection strategy for finding cooperator herds implies that farmers are willing to participate in such a system. Financial compensation for participating farmers is necessary, especially when focusing on the accurate recording of additional and new health traits in cooperator herds. Ultimately, the presented approach can be seen as a substantial contribution to the design of competitive and sustainable dairy cattle breeding programs.

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