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Performance comparison of crossbreed genotypes with different gene proportions of German Holsteins (GH) and purebred GH

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Abbreviations

ADR	Arbeitsgemeinschaft Deutscher Rinderzüchter e.V. Society of German Cattle Breeders r.a.
AFC	Age at first calving
AFS	Age at first service, Age at first mating
Ay	Ayrshire
BCS	Body Condition Score
BLE	Bundesprogramm Ökologischer Landbau in der Bundesanstalt für Landwirtschaft und Ernährung, Federal program for organic farming in the Federal Agency for Agriculture and Food
BMEL	Bundesministerium für Ernährung und Landwirtschaft, Federal Ministry of Food and Agriculture
BMELV	Bundesministerium für Ernährung, Landwirtschaft und Verbraucherschutz, Federal Ministry of Food, Agriculture and Consumer Protection
BOA	breed origin of the alleles
BRS	Bundesverband Rind und Schwein e.V., Federal association cattle and pig r.a.
BS	Brown Swiss
CB	all crossbreeds
CDCB	Council on Dairy Cattle Breeding
cm	centimeter
d	day
	Deutsche Demokratische Republik (DDR)
dl	day of life
dm	milking or lactation day
EBS	European Brown Swiss
et al.	et alii, and others
etc.	et cetera
EU	European Union
F1	first filial generation
F2	second filial generation
FAO	Food and Agriculture Organization
g	grams
GDR	German Democratic Republic (GDR)
GEBV	genomic estimated breeding values
GEH	Gesellschaft zur Erhaltung alter und gefährdeter Haustierrassen e.V. Society for the Conservation of Old and Endangered Breeds of Domestic Animals r.a.
GH	German Holsteins
GT	genotype
GUDP	Grønt Udviklings- og Demonstrationsprogram
h	hour, hours
h^2	heritability
HB	herd book
HF	Holstein Friesian
HO	Holstein
ICI	Inter-calving interval

JER	Jersey
kg	kilogram
l	liter
lb	Pound
lbs	Pounds
LEff	Lifetime efficiency
m	meter
max	maximum
MEff	Milking efficiency
min	minimum
min	minutes
mm	millimeter
MON	Montbéliarde, Montbéliard
MPT	Milk performance test
MY	milk yield
n	number
NO	Normande
NR, NRF	Norwegian Red, Nordic Red Cattle
NRC	Nordic Red Cattle
p	probability of error
p. n.	post natal
p. p.	post partum
pd	productive day
PEff	Production efficiency
PP	Productive period
PRCR	3 crossbreed animals of the ProCROSS breeding program, MON x (SRB x GH)
R1	First generation of backcross
RDC	Nordic Red Cattle
s, sec	seconds
SC	Somatic cell
SCC	Somatic cell content, Somatic cell count
SCS	Somatic cell score
SE	Standard error
SI	Simmental cattle
SMR	Schwarzbuntes Milchrind der DDR Black-pied Dairy Cattle of the GDR
SRB	Swedish Red Breed, also Swedish Red and White, Svensk Röd, Vit Boskap
Thous.	thousand
TMI	Total merit index
USA	United States of America
VR	Viking Red
vs.	versus
wl	week of life

1 Introduction

The cattle population in Germany has been gradually declining in recent years. Despite increased performance, the dairy cow population in particular has decreased with no end in sight expected for this trend.

In Germany Holsteins make up almost half the cattle population, being the dominant breed among dairy cattle. Because for many years breeding has favoured high yields over functional characteristics, alternative approaches are now being discussed. One option is crossbreeding with breeds that have a milk yield not too dissimilar to that of German Holsteins but are characterised by stable health and long Productive periods.

Breeding companies offer crossbreeding programmes that have proven successful in the US but do not necessarily guarantee the same performance in other breeding regions. In these programmes Holsteins are crossed with one or two breeds either as a two-way or rotational cross so that the crossbred herds contain cows with different genetic compositions.

An alternative would be hybrid breeding programmes as practised in pig breeding. The greatest heterosis effects can be achieved here because only purebred animals are crossed. The disadvantage of this method is that the female crossbred animals of the final stage cannot be used for further breeding.

The subject of the studies presented here is the health, fertility and milk production of German Holsteins and their crossbreeds with different proportions of genes from the breeds Montbéliarde, Jersey, Brown Swiss and Swedish Red located on four farming operations in north-eastern Germany. We also investigated whether the herd level influences the effectiveness of the crossbreeding.

When crosses are carried out to improve the functional characteristics, it should be taken into account that the heterosis effect is lost in subsequent generations. We therefore investigated the effects of backcrossing with one of the parental breeds or a third breed on the performance of dairy cows.

The comparison of the performance of the different genotypes will be used to make recommendations for crossbreeding with German Holsteins.

2 Literature overview

According to the Federal Statistical Office of Germany, in May 2022 there were 11 million cattle in Germany of which 3.8 million were dairy cows (Figure 1). The structural change is also making itself felt in cattle husbandry. The cattle population has been gradually declining since 2000 with the population in 2021 below that of 2015. (BMEL, 2022)

About 43% of German cattle are of the German Holstein breed (GH, black-pied and red-pied), 28% are Simmental dual-purpose cattle and the remaining approximately 29% are other dairy, dual-purpose and beef cattle breeds and crossbreeds. Among dairy cattle, 95% are German Holsteins, 3.8% are dairy cattle with dairy cattle crossbreeds while 7% of the total cattle population are crossbreeds of beef with dairy cattle (Figure 2). (BLE, 2022; BMEL, 2022; BRS, 2022)

There are 1.7 million herd-book German Holstein cows on approximately 13,350 breeding farms. They are the dominant breed in milk production and their breeding programme aims to implement the breeding objectives of producing a functional, long-lived and profitable milk cow with a high yield potential, stable health and good conformation. However, herd sizes, herd management and environmental conditions vary enormously across the different regions of Germany, which places high demands on dairy cows. (BRADE, W. AND BRADE, 2013; BRS, 2021b; DESTATIS, 2021; BMEL, 2022; BRS, 2022a; DESTATIS, 2022)

In 2021 the 1.6 million black-pied GH herd-book cows achieved an average milk production of 10,079 kg with a fat content of 4.05% and a protein content of 3.45% (BRS, 2022).

The production level in the dairy cattle population has increased enormously but certain functional traits have not followed this trend for a long time, such as the energy balance in early lactation and those functional traits required for an animal to achieve its actual output. Typical examples of these are found in the functional complexes of health (particularly metabolic diseases, disorders of mineral metabolism, lameness), fertility, behaviour or resource efficiency. (FISCHER, R., 2007; BREVES, 2019)

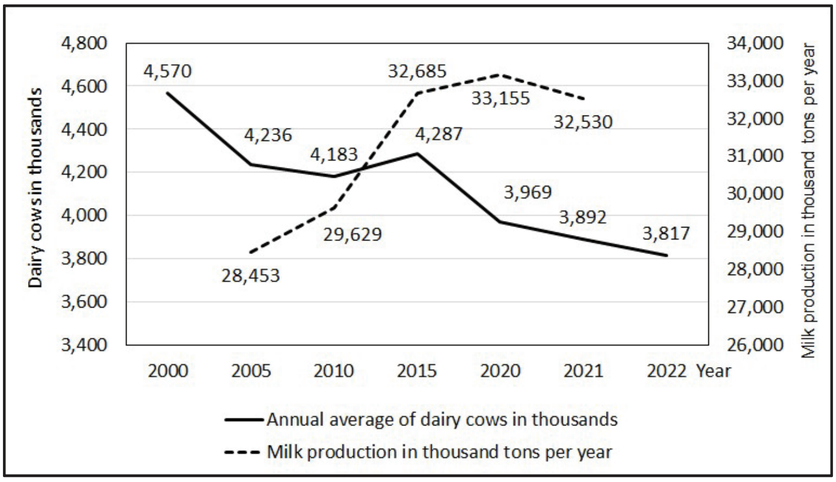


Figure 1: Development of the dairy cow population and milk production in Germany

Source: created by BMEL (2022)

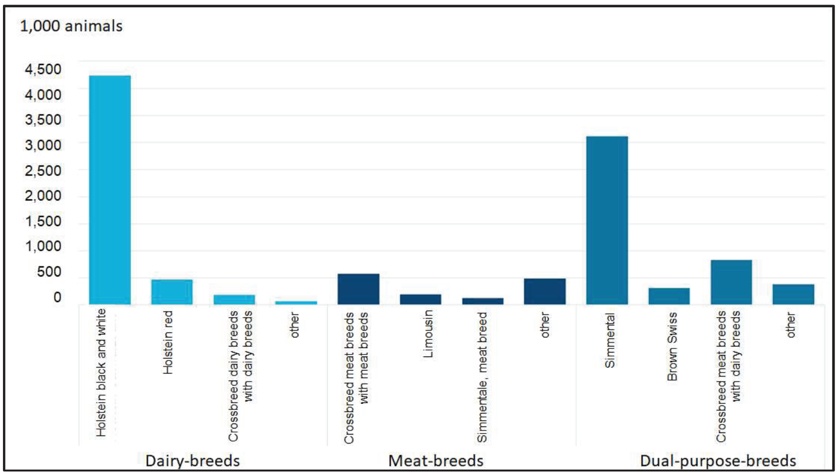


Figure 2: Cattle stocks by type of use and cattle breeds

Sources: BMEL (2022); Destatis (2022)

Along with the ethical dimension of early departure from the productive phase of an animal's life, the maximum physiological capacity for milk yield in the 4th to 5th lactation cannot be reached (Breves, 2019). The productive lifespan of dairy cows is on average about 3 years after the first calving or 2.8 lactations (Breves, 2019; De Vries, 2020). For the lifetime production, the breeding objective of more than 40,000 kg milk (BRS, 2021b) is therefore not achieved in German dairy operations.

Because many farms that produce milk with GH are completely satisfied with the production level (mean herd production of more than 12,000 kg milk per cow and year is no longer a rarity), crossbreeds are seen as an alternative to purebreeding to improve the functional characteristics (Swalve et al., 2008; Brade, W., 2020).

For Mertens et al. (2011) the growing importance of crossbreeding in the dairy industry over the last ten years was a clear indication that there has been a need for action in Holstein breeding, particularly in the areas of health and reproduction. Nothing of this has changed.

Crossbreeding may be an alternative to selection within a breed but must not be mistaken as a "remediation option" for problems that have developed because of poor management. A strategy must also be defined for how to manage the heifers of the first-cross progeny if they are going to be used for breeding. Systematic crossbreeding should be considered a breeding variation, particularly for exceptionally well-managed farms. (Zollitsch et al., 2016; Brade, W., 2019a)

2.1 Definitions

2.1.1 Animal breeding terminology

There is no clear, biologically based definition of the term **breed**. In general, the term refers to a group of domesticated animals of the same species that resemble each other in their morphological, physiological and ethological traits, that is, their appearance or conformation, as well as their performance and behaviour and have a common breeding history. They are not, however, completely closed reproductive communities and genetic exchange between different breed populations is common. (Kräußlich, 1997; Baumung, 2005; Willam and Simianer, 2017)

Fundamental terms in animal husbandry are defined in Regulation (EU) No. 652/2014 and the German Animal Breeding Act (TierZG 2019). **Breeding stock** thus refers only to animals and their ancestors that are entered or intended to be entered in a herd book for cattle of the same breed. In contrast, **livestock** of a breed are classified using certain traits that are based primarily on the conformation (such as colour, body, horns). (Kräußlich, 1997)

The combinations of all alleles on all of an animal's gene loci that control the expression of a trait form its **genotype** and the sum of all allelic effects of the gene loci involved determines the genetic make-up for the corresponding trait (WILLAM AND SIMIANER, 2017).

One of the most important parameters in animal breeding, the **heritability (h^2)**, measures the degree of agreement between the phenotype and the Breeding value and is defined as the ratio of additive genetic variance to the phenotypic variance (FALCONER, 1984).

A **population** is a group of interbreeding individuals; in agricultural livestock this is each group of animals that is in the same (pure) breeding programme (BAUMUNG, 2005). WILLAM AND SIMIANER (2017) define this term as a group of domesticated animals of the same species that resemble each other in their morphological, physiological and ethological traits and form an interbreeding community and a common **gene pool** (the totality of the genes in a generation); in animal breeding these are usually breeds or breeding populations (part of a breed such as Simmental in Germany). The **gene pool** depends on a range of factors such as selection and the inward and outward flow of individuals. As a rule, demarcation of a population is a matter of opinion. Populations are subject to changes that can lead to one population diverging genetically from other, initially similar populations to develop into a new species. The distribution of alleles therefore must not only be considered at the level of individuals but also within populations. (BRADE, W., 2006; WÜNSCHIERS, 2019; GRAW, 2020)

In the animal breeding definition, **selection** is the targeted choice of the best breeding animals to be the parents of the next generation, whereby breeders decide whether or not the animals will have progeny and how many as well as how long they will be used as parents in a breeding population. (WEISS, 2011; WILLAM AND SIMIANER, 2017)

Purebreeding involves animals within a population (breed, line) being mated, while avoiding mating between closely related individuals as far as possible (BAUMUNG, 2005; BRADE, W., 2006; WILLAM AND SIMIANER, 2017).

Crossbreeding is understood as mating between individuals from different lines, breeds or populations (BAUMUNG, 2005).

Inbreeding is the mating of animals that are more closely related than the average of the population to which they belong (WILLAM AND SIMIANER, 2017). Inbreeding is said to occur if the parents have at least one common ancestor (BRADE, W., 2006). The **inbreeding coefficient**, a measure of the degree of inbreeding, is defined as the probability that two alleles at any given locus are identical by descent and the likely proportion of the loci of an individual that contain genes that are identical by descent (FEDDERSEN, 2020). **Inbreeding depression** develops because of continued inbreeding and refers to the reduction in the mean phenotypic value for traits, particularly those related to reproduction or efficiency (FALCONER, 1984). They occur if recessive genes encounter one another due to increased homozygosity (BRADE, W., 2006).

Heterosis is present when crossbred progeny deviate systematically in their performance from the average of the parental populations. Heterosis is defined as the deviation in the average progeny performance from the average of the parental populations. Because this refers to a complete mating system, it must be interpreted as a population parameter. (BAUMUNG, 2005; WILLAM AND SIMIANER, 2017)

FALCONER (1984) considers heterosis to be the opposite of inbreeding depression because crossbreeding improves traits that were reduced during purebreeding by inbreeding. Consequently, breeding is predestined to exploit the heterosis effects for traits relating to reproduction, health and efficiency, that is, traits with a low heritability.

2.2 Performance parameters in dairy cattle breeding

2.2.1 Fertility performance

Sexual maturity (puberty) is the developmental stage from the formation of the accessory sexual organs and traits up to the attainment of the ability to reproduce. In the male animal it is characterised by the formation of motile sperm, the first ejaculate, libido and the ability to mate. In sexually mature female animals, eggs are released from the ovaries and a regular oestrus cycle starts, meaning that the animal is potentially fertile. The onset of sexual maturity is controlled hormonally, is specific for each species and breed and is influenced by live weight and condition but also by the husbandry conditions. (SCHWARK AND FAHR, 1976; STEWART et al., 1980; FERRELL, 1983; SCHWARK, 1989; GELDERMANN et al., 2005; WILLAM AND SIMIANER, 2017; SCHULDT AND DINSE, 2020)

Breeding maturity is then reached when an animal is sufficiently physically developed for breeding use. A male animal that is ready for breeding produces enough ejaculate with many viable sperm whereas the ejaculate at the time of sexual maturity has a smaller volume and is less concentrated. A female animal is ready for breeding when her skeletal development has reached a point where there is sufficient room for foetal growth, thus reducing the risk of a difficult birth. In cattle breeding maturity is determined primarily by body weight and condition, the development of which is fundamentally influenced by the intensity of rearing. (ROSSOW, 2002; GELDERMANN et al., 2005; SUTTER, 2006; WILLAM AND SIMIANER, 2017; SCHULDT AND DINSE, 2020)

A **heifer** is a young female cattle from the first insemination (ADR, 2017).

A **first service** is the first time a heifer or a cow is inseminated after calving. Each insemination is considered a first service if the difference to the previous insemination is greater than 224 days (minimum gestation period 210 days + minimum calving to first service interval 15 days = 225 days). Each first service starts a breeding cycle. (ROSSOW AND JÄCKEL, 2004; ADR, 2017)

The start of the reproductive phase corresponds to reaching breeding maturity and the first cover, known as the **Age at first mating** or **Age at first service (AFS)**. It is determined as the difference between the date of the first service and the date of the birth (ADR, 2017).

A successful gestation is followed by the birth of the first progeny. This age of the female animal is referred to in cattle as the **Age at first calving (AFC)** (ADR, 2017; WILLAM AND SIMIANER, 2017).

The interval (number of days) from one birth to the next is referred to as the **Inter-calving interval (ICI)** (WILLAM AND SIMIANER, 2017).

2.2.2 Milk production traits

The quantitative **milk production** describes the quantity of milk, fat and protein that is produced by a cow during a lactation. For the purposes of comparison and mathematical and statistical analyses, a **standard** or **305-day lactation** is defined internationally. It includes the milk yield (MY), the average fat content and fat quantity as well as the average protein content and the protein quantity in the first 305 days of a lactation and can be extrapolated from the output in the first 100 days. The yields from several lactations are summarised in the lactation average. The yields of all lactations of a cow are summed to form the **lifetime production**, which is given in kg MY. (SCHWARK, 1989; WILLAM AND SIMIANER, 2017)

The efficiency of the milk production can be calculated relative to milking days (**Milking efficiency**, MEff, yield per milking day = lifetime production in kg MY/number of milking days over the lifetime), productive days (**Production efficiency**, PEff, yield per productive day = lifetime production in kg MY/Productive period in days) and days of life (**Lifetime efficiency**, LEff, yield per day of life = lifetime production/number of days of life (incl. rearing)). These parameters are used to characterise the efficiency of the animal usage. (WANGLER et al., 2009)

2.2.3 Health traits

The **culling age** of animals is given in years and includes the lifespan of an animal, which is closely related to the Productive period. The Productive period of dairy cows is a critical factor in the cost-effectiveness of dairy husbandry, which is why breeding long-lived and high-performance dairy cows is of such importance. (PUNSMANN AND DISTL, 2017)

The **culling reasons** for dairy cattle are usually allocated using the standard ADR code (ADR, 2017).

The **Productive period** is used as a parameter for milk production and describes the period (in days, months or years) from the first calving to the departure of the animal from the herd. A critical prerequisite for a long PP is optimal rearing of dairy cattle. (ROSSOW, 2002; WILLAM AND SIMIANER, 2017; SCHULDT AND DINSE, 2020)

The **Somatic cell count (SCC)**, also known as the **Cell count** (**CC**, Somatic cells (SC) per ml of milk) is a measure of udder health and is a suitable tool for making breeding decisions because it can be measured as part of the Milk performance test (MPT) and closely correlates with the incidence of mastitis (WILLAM AND SIMIANER, 2017). The Somatic cell count is defined as the number of somatic cells per ml of milk (ADR, 2017). The content of somatic cells per ml of milk can be stated in absolute figures (e.g. 250×10^3) or it can be log-transformed to obtain a normal distribution. Internationally, it is customary to convert the cell count to the linear Somatic cell score (SCS, Somatic cell count, SCC). In healthy udder quarters no pathological changes are visible or palpable and the milk they produce contains no pathogens and has a normal number of somatic cells. For the milk Somatic cell count, up to 100×10^3 somatic cells per ml of milk for an individual animal is defined as the normal physiological range while the Somatic cell count for bulk milk is a measure of the health of a herd (Table 1). In a herd with good udder health, at a random monitoring time at least two-thirds of the animals have a Somatic cell count $<100 \times 10^3$ per ml of milk and not more than 2% have a cell count $>400 \times 10^3$ per ml of milk. (WOLTER et al., 2002)

Table 1: Somatic cell count of bulk milk to monitor the mastitis situation

Somatic cell count (SCC) in thousands per ml milk	Categories of udder health
< 125	healthy
126 bis 250	suspicious
> 250	ill

Source: WOLTER et al. (2002)

According to MÖCKLINGHOFF-WICKE AND ZIEGER (2005), a herd with good udder health has a mean Somatic cell count of $\leq 150 \times 10^3$ cells per ml of milk; at a higher cell count, 5% of the milk yield is lost and if the cell count exceeds 350×10^3, 10% is lost. The threshold of 100×10^3 cells per ml of milk is used by STEENBECK (2016) and WEERDA AND VEAUTHIER (2020) to differentiate between a diseased and a healthy udder (Table 2).

Table 2: Definition of the Somatic cell count (SCC) classes in milk yield monitoring

Classes: SCC / ml milk	Definition
≤ 100,000 > 100,000 and ≤ 200,000 > 200,000 and ≤ 400,000 > 400,000	Udder healthy Borderline between healthy and subclinical Subclinical mastitis Ill, significant entry in herd bulk milk, milk quality limit
> 700,000	Udder diseased animals, with 3 consecutive MPT: chronic mastitis with poor prospects for recovery

Sources: STEENBECK (2016); AUGUSTIN (2021), MPT = Milk performance test

The milk monitoring and cattle breeding association of Mecklenburg-Vorpommern classifies udder health using thresholds of 100 × 10^3 somatic cells per ml of milk for animals with healthy udders and 700 × 10^3 for problematic animals. They also define a milk quality threshold of 400 × 10^3 SC per ml of milk, which, if exceeded, reduces the sale price by at least €0.01 per kilogram for the affected calendar month as defined in the Raw Milk Quality Ordinance dated 11 January 2021 (Federal Law Gazette, p. 47), (AUGUSTIN, 2021)

Above a cell count of 200 × 10^3 cells/ml it can be assumed that many of the cows are affected by subclinical mastitis. The range between 100 × 10^3 and 200 × 10^3 cells/ml can be considered a threshold range. A value above 400 × 10^3 cells/ml on average for the last three checks leads to rejection by the dairy factory. Cows with >700 × 10^3 cells/ml on three consecutive test days are classified as “animals with poor healing prognosis” and should be removed from the herd for the long term. (KRÖMKER AND FRIEDRICH, 2012; STEENBECK, 2016; WEERDA AND VEAUTHIER, 2020)

2.3 Breeding methods

Purebreeding and crossbreeding methods (Table 3) are based on exploiting additive genetic and non-additive genetic allelic effects (dominance and overdominance) as well as systematically exploiting genetic differences in the outputs between different populations (WILLAM AND SIMIANER, 2017).

Table 3: Breeding methods

Exploitation of additive allelic effects	
In open populations Purebreeding Improvement breeding Displacement breeding Combination breeding	In closed populations Inbreeding Line breeding Conservation breeding
Exploitation of non-additive allelic effects	
Continuous crossbreeding Rotational crossing Alternating crossing Three-way-rotation	Discontinuous crossbreeding Single-crossing Multiple-crossing Three-way-crossing Four-way-crossing Backcrossing

Source: according to WILLAM AND SIMIANER (2017)

2.3.1 Breeding methods to exploit additive allelic effects

2.3.1.1 Breeding in open populations

Purebreeding is a relatively simple and reliable breeding method because from generation to generation progeny are produced with predominantly stable production or no drops in the production level caused by recombination losses. It is the most used breeding method and was the foundation for the development of today’s livestock breeds. Breeders maintain **herd books** in which the pedigree and performance of bred animals are entered. **Crossbreeding** methods involve systematically mating animals from different populations. The objective is to combine different performance traits of the animals and to exploit crossbreeding effects, known as **heterosis**, in addition to these combination effects (Section 2.1.1). The prerequisite for crossbreeding is that the crossing partners are purebreds. (WILLEKE, 2006; WILLAM AND SIMIANER, 2017)

If the market changes quickly or the additive genetic variance is limited, animals from foreign populations can be crossed in. **Improvement breeding or crossing** involves selected female animals in a population being mated with male animals from a different population for a limited period. The fundamental characteristics of the starting population should be preserved and only certain desirable traits are imported. An example from cattle breeding is the improvement of Simmental with selected Red Holstein bulls. The objective of **displacement breeding or crossing** is continuous displacement of the gene pool of a local population by the gene pool of a new population. The most recent example in cattle breeding is the displacement of Black Pied Dairy Cattle (SMR) by Holstein cattle in the East German Federal States in the 1990s. In **combination breeding or crossing**, new breeds are bred from different foundation breeds, such as the SMR, which is a cross between German Black Pied Cattle (Deutsche Schwarzbunte), Jersey cattle and Holstein–Friesian cattle (BAUMUNG, 2005). In beef cattle breeding, a cross between the beef breeds Simmental and Charolais is established and has been maintained since 1993 under the breed designation Uckermarker (Uckermärker). (BRADE, W., 2006; WILLEKE, 2006; FREYER et al., 2008; MARTIN et al., 2008; WILLAM AND SIMIANER, 2017; RZB, 2020)

2.3.1.2 Breeding in closed populations

Inbreeding can be considered an intense form of purebreeding and, with stringent selection, enables relatively rapid genetic anchoring of desirable characteristics as well as reliable heredity. For rapid consolidation of a breed, inbreeding is used for a limited period. Inbreeding is of no significance in practical animal breeding as a breeding method due to the danger of inbreeding depression. A slow form of inbreeding is **line breeding**, a middle course between systematic inbreeding and purebreeding. It is no longer of interest in modern cattle breeding. **Conservation breeding** is used for endangered livestock breeds that are threatened with extinction with the aim of preserving the gene pool of the relevant population (WILLAM AND SIMIANER, 2017). These breeds are published each year in the “Red List” of endangered livestock breeds by the German Federal Office for Agriculture and Food. Currently, the German Black-pied Cattle breed and the parental Brown Swiss (Braunvieh) and Old Breed Red Cattle (Rotvieh Alter Zuchtrichtung) breeds are on the list (BLE, 2020).

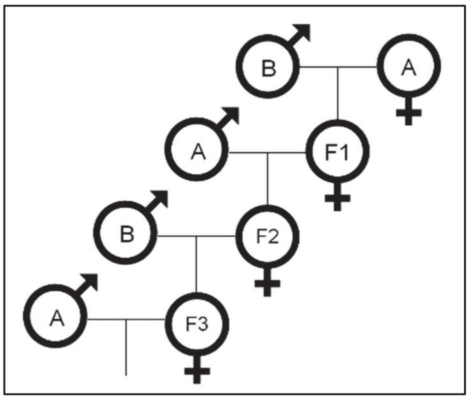
2.3.2 Exploitation of non-additive allelic effects

These crossbreeding methods produce inhomogeneous mixed populations with crossbred progeny in each generation having different genetic compositions to the parental breeds (BREM, 1997; WILLAM AND SIMIANER, 2017).

2.3.2.1 Continuous crossbreeding

With continuous crossbreeding the female animal is as a rule crossbred and the male is purebred, which means that the genetic compositions vary from generation to generation (BAUMUNG, 2005). There must also be purebred parental populations available for this breeding method (WILLAM AND SIMIANER, 2017).

With **criss-crossing** (Figure 3) the female crossbred animals are mated alternately with males from two parental breeds. With **rotational crossbreeding** (Figure 4) additional parental breeds are included so that sires from three or more breeds are crossed in rotation with females. The sires used are from the breeds with the smallest proportion of genes in the dams. (BREM, 1997; SWALVE, 2004; WILLAM AND SIMIANER, 2017)



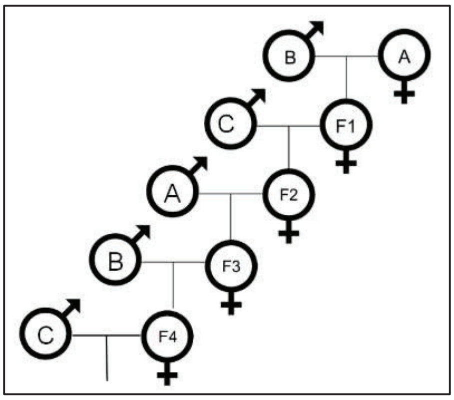


Figure 3: Alternating crossbreeding *Figure 4: Three-way rotation*

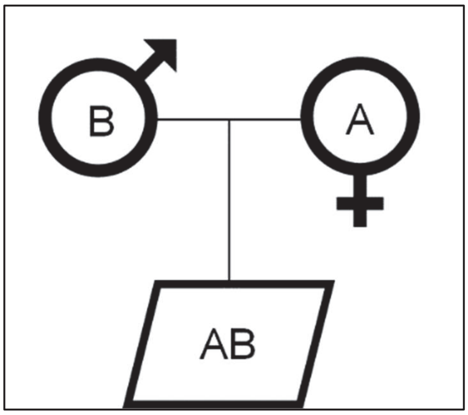
Source: according to BREM (1997) and WILLAM AND SIMIANER (2017)

2.3.2.2 Discontinuous crossbreeding or terminal crossing

With discontinuous crossbreeding, the strategy changes with each generation. The crossbred animals contain a specific proportion of the genes of the starting population and are not intended for further breeding. In cattle breeding, this breeding method is used only for producing beef cattle from milk (dam) and beef (sire) breeds. (WILLAM AND SIMIANER, 2017)

The simplest method from an organisational perspective is **simple crossbreeding** (Figure 5, also known as utility crossbreeding, F1 cross-breeding, two-way crossbreeding, two-breed crossbreeding or two-line crossbreeding) in which two complementary populations (breeds, lines) are combined for use as livestock that are not bred further. Both the maternal and paternal effects and the individual heterosis are exploited in this method. An example from practical cattle breeding is the mating of the Belgian Blue or Uckermarker (Uckermärker) breeds with dairy cows with low milk production to produce animals for fattening. (BREM, 1997; WILLAM AND SIMIANER, 2017)

With **backcrossing**, the female F1 crossbred progeny are mated again with one of the two parental breeds (Figure 6, WILLAM AND SIMIANER (2017)). In practical cattle breeding female crossbred progeny from GH and another milk or dual-purpose breed (F1) are inseminated with sperm from GH sires. The R1 progeny from these backcrosses are reared for milk production and mated with GH or crossed again.



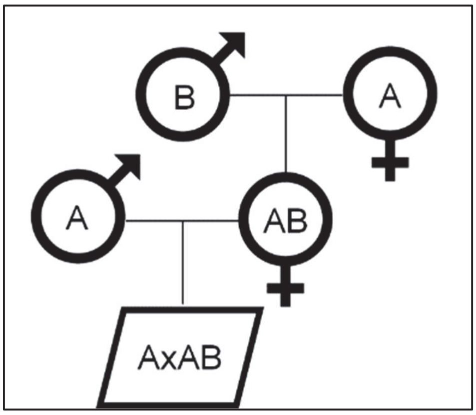


Figure 5: Simple crossbreeding *Figure 6: Backcrossing*

Sources: according to BREM (1997) and WILLAM AND SIMIANER (2017)

If the female F1 crosses are crossed with another breed, this is referred to as **three-breed crossbreeding** (Figure 7, BREM (1997); WILLAM AND SIMIANER (2017)). In practical cattle breeding these are the crosses from the ProCROSS programme described in Section 2.5.3.5.

This paper investigates breeds crossbred with GH, for which crossbred generations the proportions of the parental breed genes can be calculated from this crossbreeding strategy (Table 4).

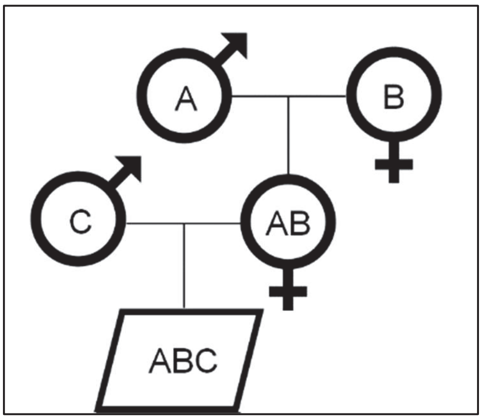


Figure 7: Three-breed crossbreeding

Sources: according to BREM (1997) and WILLAM AND SIMIANER (2017)

Table 4: Breed proportions (in %) for the crosses between GH and two other parental breeds by crossbreeding method

Generation	Crossing scheme	Gene parts in %		
		GH	Breed B	Breed C
Crossbreeding with 2 breeds				
Simple crossbreeding				
F1	B x GH	50.00 %	50.00 %	
Backcrossing				
R1	GH F1	75.00 %	25.00 %	
R2	GH x R1	87.50 %	12.50 %	
R3	GH x R2	93.75 %	6.25 %	
Alternating crossbreeding				
F2	GH x F1	75.00 %	25.00 %	
F3	B x F2	37.50 %	62.50 %	
F4	GH x F3	68.75 %	31.25 %	
Crossbreeding with 3 breeds				
3-breed crosses				
F2	C x F1	25.00 %	25.00 %	50.00 %
Backcrossing				
R1	GH x F2	62.50 %	12.50 %	25.00 %
R2	GH x R1	81.25 %	6.25 %	12.50 %
R3	GH x R2	90.63 %	3.13 %	6.25 %
Rotational crossbreeding				
F3	GH x F2	62.50 %	12.50 %	25.00 %
F4	B x F3	31.25 %	56.25 %	12.50 %
F5	C x F4	15.63 %	28.13 %	56.25 %
F6	GH x F5	57.81 %	14.06 %	28.13 %

GH = German Holsteins, source: according to WILLAM AND SIMIANER (2017)

2.4 Cattle breeds

Breeds that are of interest in the crossbreeding programmes with German Holsteins are described below. The cattle breeds described here are classified by the breeding and usage orientations, as in Table 5, that have become established in performance breeding. (KRÄUẞLICH, 1997)

Table 5: Classification of selected milk and dual-purpose breeds by breeding and usage orientation

Dairy cattle breeds
- Holstein Friesian or Holstein
- Scandinavian Red Breed
- Jersey

Dual purpose breeds, dairy and meat
- Simmental without crossing with Red Holsteins
- Brown Swiss without crossing
- Normande

Source: according to KRÄUẞLICH (1997)

2.4.1 Dairy cattle breeds

2.4.1.1 Holstein–Friesian, Holstein

German Black Pied Lowland Cattle (Deutsches Schwarzbuntes Niederungsrind, DSN) were bred in the bountiful marshlands and lowlands along the North Sea coastline from the Netherlands to Denmark. As a result of crossing with the English Shorthorn, the black–white colouring prevailed among the original, predominantly red–white cattle. (GROTHE, 1993; SAMBRAUS, 2011; BRADE, W. AND BRADE, 2013)

In the 17th century German migrants took their native black–white high-yield Friesian and Holstein varieties with them to their new homeland. In the US and Canada, a breed with very high milk yield, but producing milk with a low fat content, was bred from the imported animals with the first breeders' association founded in 1871. The cattle, now known as Holstein–Friesian (HF), made their way back to Germany through Canada and the US with the first herd book opened in 1876. In the 1960s this new breed prevailed over the black-pied lowland cattle in the Federal Republic of Germany. In the early 1980s the Red Holstein was heavily crossbred into the population of German Red Pied cattle. The displacement crossbreeding with HF in the former West Germany was also practised widely after 1989 in the east of Germany. Since the end of the 1970s the breed has been listed internationally by herd book organisations as **Holstein–Friesian (HF)**, although in the US and Canada it was decided to drop the "Friesian" part of the name and refer only to **Holstein (HO).** (GROTHE, 1993; BRADE, W. AND BRADE, 2013; ELFRICH AND ROESICKE, 2015)

German Holsteins (GH) are large-framed, long-legged and flat-muscled cattle with black-pied and red-pied colouring and usually have white udders, a white tail tip and white legs below the tarsal joints. An AFC between 25 and 28 months has proven to be positive for the subsequent development of the cow and her milk production. (BLE, 2022a)

The black-pied Holsteins are the largest breed block in Germany and are distributed across the whole country but predominantly in the north and west (SCHICHTL, 2007).

The breeding objective for GH is an economical, high-yielding dairy cow with a high lifetime production that can be used for many lactations due to her stable health, robustness and high fertility and has outstanding development potential with high feed consumption capacity and optimal feed conversion (BRS, 2021b).

Table 6: Average production for all German Holsteins test-day cows 2016

	Black and White	Red Holsteins
Milk yield, kg/year	9,224	8,271
Fat, %	4.04	4.20
Protein, %	3.39	3.44

MPT = Milk performance test, source: ADR (2016) according to BLE (2022)

Figure 8: Bull Foreman (born on April 17, 2020) and a half-sister, German Holsteins breed
Sources: KeLeKi and Schulze (2022)

2.4.1.2 Scandinavian Red Holstein, Nordic Red Cattle

The Nordic countries have the world's largest population of red dairy cows, about 273,000 cows, including Finnish Ayrshire (135,000), Swedish Red (SRB, 104,000) and Danish Red (34,000), that belong to a joint breed selection system that also incorporates Holsteins. (Iso-Touru et al., 2016; Guillenea et al., 2022; NAV, 2022)

The breeding history of the Scandinavian breeds is not uniform, which is why a highly genetically heterogeneous breed is combined under the name Nordic Red Cattle (RDC). It includes the Nordic dairy cattle population of four dairy breeds: HO, RDC, Jersey (JER) and Finncattle (FIC). HO and RDC are the most important dairy breeds with HO cows predominating in Denmark and Sweden and RDC cows predominating in Finland. Herds with JER cows are only found in Denmark and southern Sweden while indigenous FIC cows are only found in Finland. Crossbreeding is used for all primary breeds, both between different strains and between breeds. The latter applies particularly for the Danish RDC population, which is a synthetic breed comprising old Red Danish, Swedish Red, Brown Swiss and Red Holstein. (Lidauer et al., 2014)

Swedish Red (SRB)

Swedish Red (SRB, also known as Swedish Red and White, Svensk Röd, Vit Boskap) is a medium-sized dairy cattle breed that arose in Sweden from a cross between the dairy Shorthorn and Scottish Ayrshire. The breed is successfully used around the world for crossbreeding with Holsteins to improve fertility, calving and udder health. The breed is red with white markings and is widespread in Sweden. Cows weigh about 550 kg and produce about 7,500 kg milk per year. SRB is a hardy cattle breed and is also used for meat production. (Eriksson, 2003; Staff, 2021)

The breeding objectives for dairy cows in the Nordic countries have long included functional traits, both for the Nordic Red Ayrshire breeds (including SRB) and Holsteins (Berglund, 2008). The SRB breeding programme includes heavy weighting toward health, calving ease and reproductive performance. The stillbirth rate for heifers is 3.6% and for multiparous cows it is 2.5%. The breeding objective has also contributed to a lower mortality rate for SRB compared to Swedish Holsteins. (Jönsson, 2015; CRV, 2021)

In studies by Bieber et al. (2020), SRB cows under organic production conditions achieved the second-highest performance after Swedish Holsteins in a national average (Table 7).

Table 7: Average performance of SRB cows under organic production conditions

	Swedish Red Breed
Milk yield, kg/year	8,283
Fat, %	4.33
Protein, %	3.46

Source: BIEBER et al. (2020)

Figure 9: Swedish Red bull and cow

Sources: STAFF (2021); K.I. SAMEN (2022)

Viking Red (VR)

The breeding organisation Viking Genetics (VG) refers to the red-pied Scandinavian breed as Viking Red (VR) and promotes the breed as a crossbreeding partner in the ProCROSS breeding programme (Section 2.5.3.5) using rotational crossbreeding. About 200,000 cows in Denmark, Sweden and Finland that were tested by the Nordic Cattle Genetic Evaluation (NAV), a partner organisation of VG, achieved an annual milk production of 9,562 kg with a fat content of 4.35% and a protein content of 3.5%. Along with high milk production, the cows are characterised by a high genetic level for health and reproductive traits (VIKINGGENETICS, 2020).

The VR breed resulted from combination crossbreeding of Swedish Red, Finnish Ayrshire and Danish Red, a breed that was bred from the old Angeln cattle breed. (GEH, 2016; HAZEL LOESCHKE AND HEINS, 2019)

Norwegian Red (NRF)

The milk production of the Norwegian Red (NRF) breed exceeded 12,000 kg in 2020 with the most productive cows producing more than 16,000 kg. The average fat and protein content of the milk, referring to the total cow population across all lactations, was 4.3% fat and 3.5% protein in 2020. The health and reproductive performance of the cows, which has been the focus of the breeding programme for the breed since 1978, must be highlighted. The breed is described as long-lived. In 2020 only 2% difficult births and 3% stillbirths were recorded. The frequency of mastitis and other diseases is very low in NRF cows and heifers. A high percentage of the bulls is genetically polled. NRF cows are medium-sized and adult cows weigh approximately 610 kg. (BURNSIDE, 2007a; OTTEN, 2007; GENO, 2021b)

There are 270,000 NRF cows in Scandinavia, making it the largest cattle population. A different breeding strategy is used from the SRB because in Norway greater value is placed on health and fertility than in Sweden. Consequently, it is the only breed with a simultaneously positive genetic trend for milk production, health and fertility. (TIMMERMANS, 2007)


Figure 10: Norwegian Red bull and cow
Source: GENO (2021)

2.4.1.3 Jersey

The breed originated on the Channel Island of Jersey and has been known for its high-fat milk since the 18th century (SAMBRAUS, 2011).

Jersey (JER) is a small-framed, delicate-limbed cattle breed. The colour of the hide varies from fawn to cream but also to light red and almost black. The muzzle is dark with a lighter border and the animals have remarkably large, dark eyes ("doe eyes"). The horns are curved with sharp tips. It is a one-sided dairy breed that is characterised by good persistence of milk production and the animals are also easy calvers and long-lived. The early-maturing Jerseys produce the highest herd yields for milk, fat and protein relative to body weight of all cattle breeds. (ELFRICH AND ROESICKE, 2015; MÜLLER, 2018; BLE, 2022)

JER cows show lower yield losses at higher temperatures compared to HF and are correspondingly less sensitive to heat stress (WEST, 2003). Cows of the JER breed are regarded as having correct feet and legs with good claw health and a healthy, easily milkable udder of a quality and functionality that enables high daily yields over many lactations (ELFRICH AND ROESICKE, 2015). The breeding objective of the **German Jersey** is to produce early-maturing and robust dairy cattle with a live weight of more than 400 kg and a milk yield of 7,000 kg (305-day production), 6.00% fat and 4.25% protein with a hip height of 125–133 cm. (RINDERALLIANZ GMBH AND MRV, 2021b).

Table 8: Average performance of all Jersey test-day cows 2016

	Jersey
Milk yield, kg/year	6,428
Fat, %	5.42
Protein, %	3.98

MPT = Milk performance test,
Source: ADR (2016) quoted at BLE (2022)


Figure 11: Jersey bull and cow
Source: VDJ (2022)

2.4.2 Milk-focused dual-purpose breeds

2.4.2.1 Simmental

KÜNZI AND STRANZINGER (1993) consider the red and fawn spotted cattle of the Bernese Oberland to be the basis for the first herd books of the Simmental. Bones found in archaeological digs in Bern provide evidence that cattle with a similar skeletal structure to Simmental cattle were kept in this region as early as the third to fifth century (WENGER, 1972).

The spotted coat of this breed with its medium to large frame shows all colour gradations from reddish brown to light gold on a white background. An important identifying feature of the breed is the white head, which may have eye rings or pigment around the eyes. The breed is genetically polled (BLE, 2022).

Advantages of Simmental cows are the very low Somatic cell count in the milk compared to all other breeds with an average lifetime production of 30,000 kg, extremely flat lactation curves and regular fertility over at least four lactations, all while maintaining outstanding musculature (GRUPP, 2001a, b, 2003). The optimal Simmental cow is characterised by its strong forehand and health even during peak lactation and has stable feet and legs due to the strong musculature on the back and hindlegs (DIEPOLD, 2019). The male calves are exceptionally well suited for fattening (BRÄHMIG, 2011).

Breeding of Simmental goes back more than 150 years. **German Simmental (SI)**, a fit and high-yield dual-purpose breed, are primarily bred in the south of Germany; it currently makes up 27% of the German cattle population. The breeding objective is sustainable improvement in the cost-effectiveness of milk production with a balanced consideration of meat production and above all the fitness traits. The polled gene is heavily selected for in both suckler herds and milk production. Adult SI cows reach a hip height of 140–150 cm and a chest circumference of 210–240 cm with a weight of 650–850 kg. With on average fewer than 180 × 10^3 somatic cells per ml of milk, they have outstanding udder health. (ASR, 2022; BMEL, 2022)

Table 9: Average performance of all Simmental cows

	Simmental
Milk yield, kg/year	7,400
Fat, %	4.2
Protein, %	3.5

MPT = Milk performance test, source: BLE (2021)

Figure 12: Simmental dual-purpose bull and cow
Sources: AID (1996); ASR (2022)

In France, the population is made up of French Simmental and **Montbéliarde** (**MON**, also Montbéliard) (BRADE, W., 2006).

MON have been bred for cheese production in France since the 19th century, which is why the milk has an outstanding fat to protein ratio. The original breeding regions were the mountains of eastern France in the Franche-Comté region before the breed spread across all French highland regions. The harsh climate of the mountains encouraged adaptability, meaning that the breed can handle the coldest and hottest weather conditions. It currently makes up the second-largest proportion of the French cattle population. As a dual-purpose breed, it has good meat quality with a low fat content and a high beef yield. Due to its milk qualities and functional traits (fertility, longevity, high adaptability), MON cattle are exported to many countries. With crossbreeding, MON improve milk and meat yields as well as fitness and fertility. The breeding objective includes high milk fat and protein production from forage, good mastitis resistance and a relative low fat to protein ratio with high persistence. The ideal pelvis structure, sloped rump and high tail head make the MON the most prolific breed with exceptionally easy calving. The aim is a Conception rate at first service of 55%. The tough feet and legs and the udder quality should guarantee long-lived cows with several lactations. (FCE, 2015; CRV, 2021)

In 2014 approximately 627, 000 MON cows were kept on 19,700 farms in France. 435,500 cows were measured in milk test days and 26,600 are listed in the herd book. Adult cows weigh 650–800 kg with a hip height of 145–150 cm. Young bulls reach carcass weights of 350–380 kg while adult bulls weigh 1,000–1,200 kg. (FCE, 2015)

KOÇ (2011) compared performances of the MON and HF breeds under Mediterranean conditions. MON cows had significantly lower 305-day milk yields compared to HF cows (5,956.5 ± 84.73 vs. 6,655.3 ± 109.57 kg MY) but higher milk components (fat and protein content: 3.55% ± 0.07%, 2.93% ± 0.04% vs. 3.26% ± 0.10%, 2.85% ± 0.06%). The better udder health of the MON cows was demonstrated by the Somatic cell count (138×10^3 vs. 199×10^3 cells/ml of milk). The AFC of the MON heifers is 31.7 months on average, which is higher than that of the HF with 30.3 months, while the ICI was 392 days on average, which is lower than that of the HF (400 days).

Table 10: Average performance of all Montbéliarde test-day cows 2014

	Montbéliarde
Milk yield, kg/year	8,278
Fat, %	3.84
Protein, %	3.44

MPT = Milk performance test, source: FCE (2015)

Figure 13: Montbéliarde bull and cow
Source: FCE (2015)

2.4.2.2 Brown Swiss

The ancestors of the Brown Swiss, which are shorthorn or long-nosed cattle, came from the Caucasus and the Middle East to Central Switzerland. The cattle were mixed there with Alemann cattle and spread from there as far as Tyrol. (ENGELER, 1947; ELFRICH AND ROESICKE, 2015)

In the second half of the 19th century a few bulls and cows were exported to the US where they formed the basis of the breeding of the Brown Swiss (KÜNZI AND STRANZINGER, 1993).

Since 1966, the European Brown Swiss has been specifically bred by crossing with bulls from North America to develop a milk-focused dual-purpose breed (Brown Swiss) with a yield per year of 8,000 to 10,000 kg milk with 4.18% fat and 3.57% protein. Adult cows have a hip height of approximately 142–154 cm with a weight of more than 600 kg. Fattening ability and carcass quality satisfy economic requirements for both extensive and intensive cattle fattening methods. (ELFRICH AND ROESICKE, 2015; BRADE, W., 2019a; BRS, 2021c)

The **German Brown Swiss (BS)** is a milk-focused dual-purpose breed that is distributed primarily in the alpine country and the alpine foothills of southern Germany (BRS, 2021c; ADB, 2023). In Bavaria, the breed makes up more than 10% of the dairy cow population (ETTLE, 2017). Breeding is carried out jointly with Austria (BRADE, W., 2006).

The uniformly brown to greyish brown cattle with their black, lightly bordered muzzle and lightly bordered eyes have light-coloured horns with dark tips. Along with the milk yield with high protein content and an exceptional udder, breeding also considers high fertility, longevity, udder health, healthy feet and legs, and good fattening properties of the bull calves. The German Brown Swiss Working Group characterises the profile of the breed with 8,000–9,000 kg milk and a fat and protein content totalling 7%–8%. (BLE, 2022; ADB, 2023)

The lifetime production of Brown Swiss cows in studies by PUNSMANN et al. (2018b) was on average 22 ,127 kg milk, 924 kg fat and 789 kg protein with a Lifetime efficiency of 8.34 kg milk, 0.35 kg fat and 0.30 kg protein per day of life.

Table 11: Average performance of all Brown Swiss test-day cows 2016

	Brown Swiss
Milk yield, kg/year	7,531
Fat, %	4.26
Protein, %	3.60

MPT = Milk performance test, source: ADR (2016) quoted at BLE (2022)

Figure 14: Brown Swiss bull and cow
Source: RBW (2021)

2.4.2.3 Normande

The French milk-focused dual-purpose breed **Normande** (**NO**, Normande cattle) is synonymous with milk with high levels of components, resistance to metabolic and udder diseases, and good functionality (feet and legs, udder, fertility). It is characterised by high meat yields with outstanding meat properties as well as a calm nature. The average milk yield is 7,400 kg with 4.1%–4.6% fat and 3.7% protein. The cattle appear stocky with reddish brown to black brindling on a white background, typically with a broad, light head, while the eyes are surrounded by a dark ring. On average, an NO cow weighs between 650 and 750 kg, is about 145 cm high with a chest depth of 75 cm. The original breeding regions are Normandy and Brittany. The breed is recommended for crossbreeding with Holstein due to the high proportion of kappa casein. (Servais, 2011; R&S Vertriebs GmbH, 2020; Spanring and Gastegger, 2020; TwoPlus, 2020)

Figure 15: Normande bull and cow
Sources: Valren (2017); R&S Vertriebs GmbH (2020)

2.5 Crossbreeding in dairy cattle breeding

In the history of cattle breeding, it can be seen for almost all breeds that phases of purebreeding alternate with phases of crossbreeding over longer or shorter periods. Very often in the purebreeding phases, formal criteria are prioritised with economic traits at the expense of breeding progress. (Lederer, 2005)

In dairy cattle breeding, purebreeding is the dominant breeding method. The reasons for this are biological: Dairy cows have only a very low reproductive rate and a long generational interval, and the individual animal has a relatively high value because the production animal is also usually the breeding animal. In addition, the Holstein breed is a high-yield breed for which it is difficult to find crossbreeding partners with a similar production level. (Swalve et al., 2008)

The reasons for crossbreeding may be the need for traits that are difficult to reconcile, if at all, with purebreeding and in this case combination effects are exploited. Position effects indicate the importance of which population the sires and dams represent. (Baumung, 2005)

Systematic crossbreeding of German Black Pied Cattle started as early as 1920 and was continued after 1960 with the breeding of Black Pied Dairy Cattle of the GDR (SMR). The average milk yield dropped in the F1 generation (JER × DSR = genotype (GT) 18) from 3,664 kg to 3,310 kg. In the F2 generation (HF × GT 18), the average increased to 3,596 kg. (FREYER et al., 2008; BRADE, W., 2014)

Avoiding inbreeding depression is one of the major benefits of crossbreeding. Breeding new synthetic breeds is, however, laborious. Because new breeds have higher genetic variation, a higher selection limit must be reached than for the pure breeds from which they originate. The homozygosity of desired traits requires selection spanning many years. It therefore seems sensible to establish crossbreeding systems similar to the methods used in hybrid pig breeding. To be able to exploit heterosis effects, the parental breeds or purebred lines must be continuously improved using additive genetics. In the production stage, a consistent genetic composition and the possibility of increasing internal stocks must be assured. (HILL, 1971)

Exploiting additive genetic effects to improve very specific performance and conformation traits was a priority in cattle breeding at the start of the second half of the 20th century. The European Brown Swiss population was thus refined for rapid adaptation to market requirements using Brown Swiss from North America. In dairy cattle breeding, displacement of the European black-pied dual-purpose type by the heavily milk-focused Holstein–Friesian from the US and Canada started. This was due to the low yields from backcrosses, high prices for crossbred progeny on the breeding animal market and not least the professional marketing by the US insemination stations. (LEDERER, 2005)

In principle, there are two fundamental reasons for introducing crossbreeding: to import properties that are not or only barely present in the local breed and to exploit heterosis effects. Crossbreeding cannot, however, resolve problems of management or feeding. (BAUMUNG, 2005; ZOLLITSCH et al., 2016)

Crossbreeding is carried out in tropical countries to combine the robustness, heat tolerance, disease tolerance and/or resistance, and environmental adaptability of the indigenous cattle with the superior milk production and more rapid rates of growth of temperate breeds and to minimise the negative consequences of inbreeding depression in the livestock sector. Crossbreeding provides the opportunity to breed highly productive cattle but must be monitored to preserve adapted indigenous breeds. (MEKONNEN et al., 2020)

RINELL AND HERINGSTAD (2018) collected data about crossbreeding between Norwegian Red (NRF) and Israeli Holstein to see how the daughters behave when they are reared under different environmental conditions to their sires. The focus lay particularly on health and fertility. The results showed that the crossbred cows have better fertility and reduced susceptibility to postpartum disorders.

In dairy cows crossbreeding thus improves not only productive and physiological reactions, it can also reduce the effects of environmentally induced heat stress (HERNÁNDEZ RIVERA et al., 2019).

Over the last 40 years, Holsteins have become the leading breed internationally due to the superior milk yield. Selecting for high milk production and a large frame for high feed consumption capacity stands in opposition to fertility and health, which has led to a steep decline in the functional traits. Although in recent years there have been efforts to increase these functional traits using selection in the HO breed, the low heritability makes breeding difficult. Another problem is inbreeding that has risen in the US to over 8% with the establishment of genomic selection, which is a higher level than if first cousins are mated. From 2014 to 2018 the degree of inbreeding has increased annually by 0.35%. Heterosis effects counteract inbreeding depression, which can be taken advantage of when crossbreeding. This assumes, however, that the highest-ranking sire is used when crossbreeding to increase the frequency of and thus the certainty of inheriting the desired genes. (HAZEL LOESCHKE AND HEINS, 2019)

In 2020 the World Holstein Friesian Federation (WHFF) published data on the rise of inbreeding since 1980. Average inbreeding coefficients for HO for each of 10 cohorts of the 12 largest populations and in the US and Australia are shown in Table 12.

Table 12: Average inbreeding coefficients of Holstein populations (at least 87% HO genes) for the cohorts 1980 to 2009 by breeding region

Birth cohorts	Average inbreeding coefficient		
	12 largest populations	USA	Australia
1980 – 1989	0.11	0.19	-
1990 – 1999	0.19	0.19	0.14
2000 – 2009	0.10	0.11	0.11
2010 – 2019	0.19	0.26	0.04

Source: WHFF (2020)

From 2010 to 2019 the level of inbreeding in all herds in the WHFF increased from 2.5% to 8.5%. The greatest increase was recorded in Italy, the US and Canada with 0.25% to 0.26% per year, which is classified as “problematic” but is below the value that HAZEL LOESCHKE AND HEINS (2019) state for the US. In Germany, the degree of inbreeding for GH increased moderately in the same period by 0.15% per year and in the 12 largest populations it increased by 0.19% per year. According to a recommendation from the Food and Agriculture Organization of the United Nations (FAO), inbreeding should not be more than 1% over four years. The WHFF therefore surveys the member breeding organisations from 26 countries every four years for the degree of inbreeding in female cattle with a genetic composition of at least 87% Holstein to be able to make corrections if necessary (FEDDERSEN, 2020).

The COUNCIL ON DAIRY CATTLE BREEDING (CDCB) publishes information on the gradual change in the genetic base regularly at five-year intervals. The estimated Breeding value of bulls and cows in April 2020 revealed the latest change in the genetic base. Holstein breeding in the US currently has an inbreeding level of 8.09%, which is about 1.8% above the maximum recommended value. From 2000 to 2019 the annual increase in inbreeding rose from +0.12% to +0.4%, which is in part due to the use of genomic estimated Breeding value that enables early and reliable selection of the best bulls. Breeding companies argue that a high level of inbreeding of 10% and more is unproblematic because most of the recessive genes that cause inbreeding depression are eliminated. Random mutations in the HO breed could also lead to a high ongoing genetic diversity. (HANSEN, 2020)

As well as reducing the level of inbreeding, rotational crossbreeding with two to four breeds can exploit heterosis effects if purebred bulls are mated each time with the female progeny. The percentage of the heterosis effect that can be seen in crossbreeding varies greatly with the number of breeds that are included in the rotation. In all cases it is essential that the crossbreeding partners are not related to each other. The average percentage of the heterosis effect expressed over the first four generations of 2-breed, 3-breed and 4-breed crossbreeding systems is 72%, 91% and 97% respectively, which means that switching from two to three breeds increases the average percentage of the heterosis effect by 19%, whereas the addition of a 4th breed only brings an additional increase of 6% (Table 13). If crossbreeding with three breeds is carried out in a defined rotational system, the heterosis effect remains at 86% and for four breeds it remains at 93%. Finding more than three breeds that are appropriate for a particular environment or management system is difficult, however. Because for 2-breed crosses the heterosis effect is lower over the generations than for 3-breed and 4-breed crosses (Table 13), three breeds is most likely the optimal number in a fixed rotation for most crossbreeding systems. (LÓPEZ-VILLALOBOS, 1998; HEINS et al., 2006)

Table 13: Heterosis effects for generations of crossbreeding programs when using 2, 3 and 4 unrelated breeds

Generation	Heterosis effect in %		
	2 breeds	3 breeds	4 breeds
1	100	100	100
2	50	100	100
3	75	75	100
4	63	88	88
5	69	88	94
6	66	84	94
7	67	86	94
8	67	86	93
9	67	86	93

Source: HEINS et al. (2007)

In New Zealand crossbreeding effects aimed at milk production as well as fertility, and Productive period in particular, are achieved using a high proportion of crossbred cows (rotational crossbreeding Jersey × Holstein) (BUCKLEY et al., 2014; BRADE, W., 2021).

Efficient breeding programmes require a certain population size. Thanks to their functional traits, some breeds with low numbers could be interesting crossbreeding partners for highly productive breeds with the aim of exploiting heterosis. A simulation model showed that implementing a genomic rotational crossbreeding strategy may be an attractive option to encourage the use of a breed with low numbers such as the Angler. (STOCK et al., 2021; STOCK, 2022)

Results from overseas cannot simply be transferred to Central Europe, however. The use of crossbreeding programmes assumes testing of the performance under current production conditions. (SWALVE, 2004; SWALVE et al., 2008)

Crossbreeding provides an opportunity to achieve a short-term reduction in the level of inbreeding in the Holstein breed while also ensuring an improvement in the stress sensitivity, fertility and Productive period (BRADE, W., 2019a).

For dairy cattle, crossbreeding is only useful if traits such as fertility and Productive period are priorities. However, only breeds with production traits that are not too dissimilar to the parental population can be considered. Otherwise, possible heterosis effects cannot compensate for the reductions in the milk production level due to additive genetic differences. Sires that are amongst the best in their population for the particular traits must be selected as crossbreeding partners, which assumes an established breeding programme. (SWALVE, 2004; SWALVE et al., 2008; ZOLLITSCH et al., 2016)

The additive genetic merit of a crossbreeding partner would have to be at least 90% of the Holstein merit in milk yield according to MCALLISTER et al. (1994). Based on the situation at the time, only the Ayrshire breed reached this level.

MCALLISTER (2002) considers breeds to be crossbreeding partners if they achieve a performance level of ≥ 75% of that of the Holstein. Performance in which they clearly exceed Holstein, such as fitness, must also be considered. The author recommends combinations of two-breed, three-breed and four-breed crosses to form mixed populations. These populations can achieve high performance levels but have high resource requirements.

Crossbreeding can greatly increase the income of dairy cattle farms, particularly in management systems that place high demands on functional traits. By improving functional traits and increasing longevity, for 3-breed crosses a heterosis effect of at least 10% relative to the total merit can be expected. The prerequisite for crossbreeding to be beneficial in the long term is that the genetic gain within the parental breeds is not reduced. If the crossbred cow population makes up less than 50% of the total population and young bulls can be tested by their crossbred progeny, this prerequisite can be satisfied. (SØRENSEN et al., 2008)

2.5.1 Crossbreeding programmes in dairy cattle breeding

When describing crossbreeds, the sires that the dams are mated with are named first, e.g. crosses of Simmental bulls with German Holsteins dams: SI × GH.

Breeding decisions only ever reveal their effects in the long term and can often only be judged as wrong or right after several generations (ZOLLITSCH et al., 2016).

The steady increase in crossbred animals on dairy farms led MERTENS et al. (2011) to perform an economic evaluation. Economic benefits were seen due to the heterosis effects in the F1 generation compared to the HF breed. The calculated evaluation of the subsequent generations could not be validated by data from experience but suggested a decline due to weaker heterosis effects. The economic outcome is not only affected by the differences between the parental breeds and the crossbreeds but also by the variation in performance within the breeds, which varies enormously between herds primarily due to the management system. When using Scandinavian Red Pied cattle, subject to more reliable data, the greatest economic effect is achieved in the F1 generation.

SCHAEFFER et al. (2011) compared the performance of purebred Holsteins with crossbreeds (Norwegian Red, Swedish Red, Brown Swiss, Jersey). For the 305-day milk yield, as expected the Holstein cows dominated but the fat and protein yields of the crossbred progeny were superior. There were no significant differences for the Somatic cell count and milkability nor for temperament. Crossbred cows showed high values for fertility caused by heterosis (calving to first service interval, stillbirth rate and calving ease).

In studies conducted by HEINS et al. (2007), the milk yields of different 2-breed crosses between Holstein (HO) and Brown Swiss (BS), Normande (NO), Montbéliarde (MON), and Swedish Red (SRB) were compared to the yields of 3-breed crosses – BS × (MON × HO), MON × (SRB × HO), SRB × (NO × HO). The milk production traits of the various 2-breed and 3-breed crosses did not deviate significantly from each other except for the crosses with NO influence, which were significantly lower. The 3-breed crosses with 50% MON genes tended to have the highest milk components, which is why the agriculturalists involved in the studies wanted to continue breeding with these crosses in their herds.

For about 10 years crossbred bulls have also been in demand on the breeding market. Heterosis on the male side plays a critical role here. Crossbred bulls achieve high Conception rates and highly reliable heritability, e.g., of milk components and conformation. However, they are more suitable for use in large herds in which utility crossbreeding is carried out using a 50% hybrid vigour effect for the fertility. For example, the highest-ranking bulls that are a cross of 75% HO and 25% JER are used heavily in New Zealand for this purpose. However, this strategy is not without controversy because the heterosis effect decreases when used in breeding programmes compared to the use of pure breeds. Further problems are seen when breeding with crossbred bulls in the spread of crossed progeny and their heterogeneity. (DEBERGH, 2012)

In December 2021 in Denmark, Finland and Sweden the Nordisk Avlsværdi Vurdering (NAV, Nordic Cattle Genetic Evaluation) breeding association started to calculate the genomic Breeding values for crossbred dairy cows with genes from the breeds RDC, JER, HO and MON. Genotyped crossbred cows receive the genomic Breeding values for almost the same traits as purebred cows, including all subindices for yield, conformation and udder indices. However, the Breeding value estimation does not include the performances of the crossbred progeny themselves, meaning that the Breeding values are based exclusively on genomic information. The aim is to estimate the suitability of purebred bulls for use in the crossbreeding programme. (FOGH et al., 2021)

2.5.2 Two-breed crossbreeding with Holstein

2.5.2.1 Holstein, German Simmental

Because the dual-purpose Simmental (SI) is the second-most important cattle breed in Germany, crosses with German Holsteins (GH) were analysed for their performance. Male SI × GH crosses are exceptionally well suited to fattening. Female F1 animals are superior to GH for fertility (ICI between 1st and 2nd calving: 374.3 days vs. 394.4 days) but inferior for milk yield (6,728.8 kg vs. 7,037.8 kg MY in 305 days in the 1st lactation). (BRADE, W., 2019a)

In the quantifiable characteristics, F1 crossbred animals (SI × GH) are superior to SI but not GH. The heterosis effects are 19.75 kg for fat, 16.7 kg for protein and 276 kg for the (uncorrected) milk volume, each referring to a complete lactation. With a genetic composition of 50% SI genes, a slightly more positive heterosis effect is expected. (NOLTE, 2019)

Cows from an alternating crossbreeding programme with SI × GH did not show any differences in the AFC but the calving to first service, calving to conception and Inter-calving intervals were shortened as the proportion of Simmental genes increased. For the Productive period, F1 cows (SI × GH) were superior by 16% over the average for purebred GH and SI cows. Regarding health status and disease susceptibility and frequency, no effect was detected with an increased proportion of SI genes. The expected reduced output for the milk volume (−2,200 kg MY lifetime production) was not compensated by improved fertility performance. (DIEPOLD, 2019)

2.5.2.2 Holstein, Jersey

The superiority in Productive period and improved fertility of the Jersey (JER) recommend the breed as a crossbreeding partner for HF. Furthermore, there is sufficient genetic distance between the breeds to enable heterosis effects. In a crossbreeding trial, North American JER sires were generated using embryonic imports and mated with black-pied Holsteins. In the first 90 days the milk yield corresponded to that of purebred Holsteins (2,122 kg vs. 2,391 kg milk). The benefits of the crosses lay specifically in better calving ease and the proportion of stillbirths was also considerably lower (4.9% vs. 10.9%). (BRADE, E. et al., 2007)

MALTECCA et al. (2006) reported of possibly better calf health due to an improvement in the calving ease and thus a reduction in the losses in HO herds by crossing with JER. No differences between JER × HO calves vs. HO calves were identified for respiratory diseases, and the number of days with diarrhoea tended to be lower in the crossbred animals at 7 days of age.

In Northern Ireland and New Zealand, JER crossbred cows fed low and moderate quantities of concentrate showed superior reproductive performance while in New Zealand heterosis effects were also seen in the productivity. (BUCKLEY et al., 2014; MCCLEARN et al., 2020)

Australian studies recommend crosses between HF and JER due to the high fertility (First-service Conception rates 52%, Conception rates of 68% vs. 42%, 54% for HF) for seasonal calving. (AULDIST et al., 2007)

In Argentina US Holsteins are crossed with Canadian JER and Guernsey, a breed similar to JER (LITWIN AND MANCUSO, 2014).

2.5.2.3 Holstein, Nordic Red Cattle, Norwegian Red

CLASEN et al. (2019) analysed data from 103,307 pure HO cows and 14,832 F1 crosses (Nordic Red Cattle (NRF) sires and HO dams). In the first lactation, the crosses were superior to the HO in terms of the milk volume but not the protein quantity. In the first and second lactations, the crosses showed better udder health (up to 15% lower incidence of mastitis), fertility and health (stillbirths, losses). These results were confirmed independently of the herd level regarding the average milk production.

A study by BUCKLEY et al. (2014) reviewed data analyses of the reproductive performance and Productive period from Ireland, New Zealand and the United States. NRF were best suited to seasonal production with pasture grazing. The high fertility and long lifespan of this breed was also confirmed in the crosses of NRF × HF.

In the two-way rotational crossbreeding programme of the Norwegian breeding organisation Geno, HO and NRF were alternately crossed. The crossbred animals are characterised by outstanding fertility, calving ease and longevity, produce equally high quantities of fat and protein as HO and are resistant to udder and limb diseases. (GENO, 2021a)

2.5.2.4 Holstein, Montbéliarde, Normande

Crossbred cows of HO and Montbéliarde (MON) had improved uterine health compared to HO cows, possibly as a result of heterosis and/or breed complementarity, as well as a less pronounced reduction in feed intake during the last few days of gestation. (MENDONÇA et al., 2014)

HEINS et al. (2010) investigated the calving behaviour of HO cows compared to crosses (MON × HO) in two herds in Minnesota. Crosses of MON × HO (n = 138) had calves weighing 48.3 kg on average, which were significantly heavier than those of the purebred HO (n = 277, 43.3 kg), and thus tended to have a higher, but not significantly so, proportion of difficult births (9.4% vs. 5.9%). The stillbirth rate was the same at 4.3% vs. 4.1%.

In studies by HAZEL LOESCHKE et al. (2013), in the first 150 days of the first lactation F1 crosses of MON and HO had significantly higher body condition scores (BCS as defined by EDMONSON et al. (1989)) of 3.30 vs. 2.74 and live weight (551 vs. 528 kg), even though the cows did not differ in terms of their dry matter intake. The authors suspect that the higher but not too high body condition of the crosses positively affected the fertility because they conceived again earlier than the HO.

As the studies progressed, MON × HO crossbred cows showed no differences to the purebred HO cows regarding fat and protein production from the first to the fifth lactation. The Conception rate at first service was overall 21% higher than in the HO. The crosses had a higher live weight (611 vs. 572 kg) with a similar frame to the HO while the condition was evaluated as “better” (BCS 3.36 vs. 2.87). (HAZEL LOESCHKE et al., 2014)

Crosses of HO with MON in 1,137 herds and with Normande (NO) in 1,033 herds were compared to purebred Holstein, Normande and Montbéliarde for inbreeding and breed differences. In these herds, crossbred cows made up about 13% of the total number of animals analysed. For all traits (milk, fat and protein quantity, Somatic cell count, Conception rates, Inter-calving-to-conception interval), beneficial heterosis effects were found in the F1 generation but these declined with the backcrosses. (DEZETTER et al., 2015)

F1 crosses of HO with the breeds NO, MON and Swedish Red (SRB) calved significantly more often a second, third and fourth time, had a lifespan on average that was 300 to 400 days longer, and achieved a significantly higher total fat and protein quantity than purebred HO. The crossbreeds were also superior in terms of the profitability. The lowest rates of difficult births and stillbirths in heifers and cows were seen for the crosses of SRB sires with HO dams, the highest for the HO, and the differences in the means were significant (heifers 5.5% and 7.7% vs. 16.4% and 15.1%, cows: 2.1% and 4.7% vs. 8.4% vs. 12.7%). A comparison of crosses between HO sires and dams of the various breeds indicated the same superiority of the breed combination HO × SRB. (HEINS et al., 2007; HEINS et al., 2012)

2.5.2.5 Holstein, Brown Swiss

The reasons given by BRADE, W. (2019a) for selecting the Brown Swiss (BS) breed as a crossbreeding partner for HF included a noteworthy milk production predisposition that combines a high milk protein content with an ideal protein composition as well as high lifetime production in comparison. Lower ICI in the F1 crosses is considered evidence of improved fertility. (BRADE, W., 2019a)

BS × HF crosses achieved lower milk production in the first lactation than HF comparison animals but a higher fat and protein production (DECHOW et al., 2007; BRADE, W., 2019a).

2.5.2.6 TwoPlus

The TwoPlus breeding programme combines the Holstein (HO) breed with the highest milk production and Norwegian Red (NRF), a breed with low production costs, in rotational crossbreeding (Figure 16). F1 heifers from the NRF × HO cross are mated with purebred HO sires and their progeny (F2) are mated with purebred NRF sires. The crossbreeding programme eliminates the effects of the increasing level of inbreeding resulting from purebreeding of HO and improves the fertility while production remains the same (Table 14). The crossbred herds will become increasingly homogeneous due to the rotation, the danger of inbreeding depression will be kept low and the heterosis effect will correspond permanently to 67% of the effect achieved in the first generation. Crosses of NRF and HO have the same fat and protein performance as purebred HO, are easy calvers with low stillbirth rates and are stable in terms of metabolic and udder diseases. Adult crosses achieve similar live weights but a higher body condition than HO. (BERRY et al., 2007; BUCKLEY et al., 2007; BURNSIDE, 2007b, a; GLOVER et al., 2010)

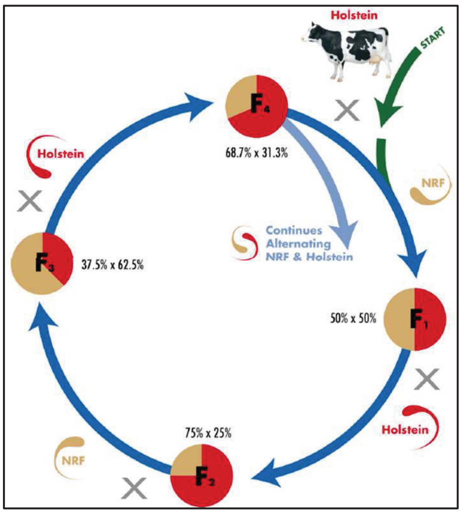


Figure 16: Rotation scheme for the TwoPlus breeding programme

Source: BURNSIDE (2007)

Table 14: Performances of the Holstein (HO) and Norwegian Red (NRF) breeds and differences between the NRF × HO crosses and HO

Parameter	Holstein, HO	Norwegian Red, NRF	NRF x HO
Number of cows	3,600	419	697
Non-return-rate	76.6 %	81.8	+5.2
Gestation period in days	279	277	-2
Age at first calving in days	485	478	-7
Stillbirth 1st calving 2nd calving	 14.5 % 5.9 %	 9.2 % 1.6 %	 -5.3 % -4.3 %
Performances in 1st lactation 305-day milk yield in kg 305-day amount of fat in kg 305-day amount of protein in kg	 9,882 332 294	 9,521 334 291	 -361 +2 -3

HO = Holstein, NRF = Norwegian Red, source: GLOVER et al. (2010)

2.5.3 Three-breed crossbreeding with Holstein

2.5.3.1 Holstein, Montbéliarde, Scandinavian Red

Three-breed crossbreeding was carried out with the F1 animals from the 2-breed crossbreeding described in Section 2.5.2. In the 305-day yields in the first lactation the crosses with 25% HO genes were superior to the F1 crosses (50% HO) on average but no statistically confirmed differences were identified (9,314 vs. 9,189 kg MY). (HEINS et al., 2007)

2.5.3.2 Holstein, Jersey, Scandinavian Red

Holstein, Jersey, Norwegian Red

MCCLEARN et al. (2020) see positive effects in pasture-based production systems for HF herds when crossed with JER in terms of the efficiency of the milk production. HO herds with poor reproductive performance and low milk components benefit from crosses with JER. Cows from the three-way cross of HO, JER and Norwegian Red (NRF) showed the highest milk components in the comparison of the genotypes and HO had the highest total milk yield. However, for herds with high fertility performance, the authors do not recommend crossing with JER or a three-way cross.

With high fertility performance, particularly calving ease, increased fat and protein content and a high feed efficiency, the breeding organisation GENO (2021a) promotes 3-breed rotational crossbreeding with NRF × HO × JER.

Danish Holstein, Danish Red, Danish Jersey

To investigate the influence on the Productive period, CLASEN et al. (2017) compared Danish Holstein with their crosses from systematic rotational crossbreeding with Danish Red and Danish Jersey. From the first to the fifth lactation, the highest number of days from calving to culling were observed for the crosses. Data from 73,741 cows confirm the heterosis effect regarding health, which is why crossbreeding is considered an effective tool for improving the longevity of Danish dairy cows.

2.5.3.3 Holstein, Montbéliarde, Jersey

Three-breed crosses of MON × (JER × HO) were smaller but heavier on day 150 post-partum (pp) than purebred HO (hip height 138 cm, live weight 537 kg vs. 141 cm, 528 kg) while the BCS was accordingly significantly higher (3.29 vs. 2.74). The 305-day milk yield of the crosses was, however, significantly lower (8,735 vs. 9, 200 kg). (HAZEL LOESCHKE et al., 2013)

2.5.3.4 VikingGoldenCross

VikingGoldenCross is a 3-breed rotational crossbreeding programme that combines Viking Holstein, Viking Red and Viking Jersey. The crossbred cows are healthy, fertile and suitable for long distances and thus for pasture grazing. The concept has become established in New Zealand, Australia, Great Britain, Ireland and other countries and is particularly well suited to herds with seasonal calving. (VIKINGGENETICS, 2023)

2.5.3.5 ProCROSS

ProCROSS (PRCR) is a breeding method developed by Coopex Montbéliarde, a French insemination centre, and VikingGenetics, a breeding co-operative owned by 20,000 farmers in Denmark, Sweden and Finland. This breeding programme uses rotational crossbreeding with the breeds Holstein (HO), Montbéliarde (MON) and Viking Red (VR) or Swedish Red (SRB) (Figure 17, Figure 18, Figure 20). In the first generation HO cows are mated with MON and the F1 cows are then mated with VR. The third generation is inseminated with HO again. Heifers are preferably mated with VR to produce smaller calves. Otherwise, the order plays a less important role. An important argument for crossbreeding is to improve the fitness of Holstein cows using the heterosis effect. Positive effects are also expected for milk yield and feed intake. Along with heterosis, combination effects are exploited while inbreeding depression is avoided. It can be assumed that the level of heterosis over the course of the rotations from the fourth generation on stabilises at 86% (Figure 19). The HO breed is used in the breeding programme because of its high milk yield while MON is characterised by robustness and good physical condition. This is combined with the calving ease, health and longevity of the VR breed. ProCROSS is used in Scandinavia and France in 500 and 400 farms respectively while in Germany 100 farms use the method. (SERVAIS, 2012; PETER AND MEILI, 2020; VIKINGGENETICS, 2021)

In 2008 a working group from the University of Minnesota started a 10-year study on the ProCROSS breeding programme. The studies were conducted in high-performance herds with a starting population of 3,550 HO heifers of which 150 were maintained as purebred HO. In each herd at least 100 HO were mated in equal number either with highest-ranking sires of the VR or MON breeds to initiate a 3-breed rotational crossbreeding system in both directions. In accordance with rotational crossbreeding, HO sires were used to service the F2 cows (Figure 18). (HEINS et al., 2010; HAZEL LOESCHKE et al., 2013, 2014; HAZEL LOESCHKE et al., 2017b, a; HAZEL LOESCHKE AND HEINS, 2019; SHONKA-MARTIN; HAZEL LOESCHKE; et al., 2019; HAZEL et al., 2020b, a; HAZEL LOESCHKE et al., 2021)

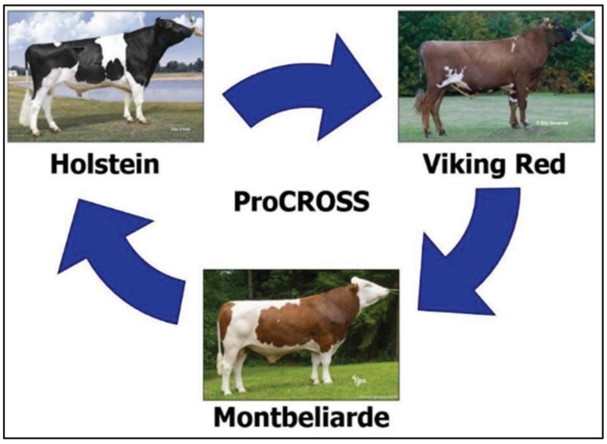


Figure 17: Breeds in the ProCROSS rotational crossbreeding system
Source: HAZEL LOESCHKE et al. (2019)

The motivation behind the crossbreeding programme with the three breeds is the superiority of 2-breed crosses of MON × HO and VR × HO compared to purebred Holsteins in terms of fertility, health and milk components. The F1 cows calved for the first time between late 2010 and early 2014. For all genotypes, the same AFC (23.7 to 23.9 months) and similar calving traits were observed. The stillbirth rate revealed the better vitality of the crosses, however (MON/VR × HO 5% vs. HO 9%). The Conception rate at first service for the crossbred cows was 7% higher in the first lactation than the HO cows. Due to lower losses, 71% of the crosses calved a second time while the rate for HO was 63%. In the 305-day milk yield, the MON × HO were at the same level as the HO (10,954 vs. 10,970 kg MY) while VR × HO was significantly lower with 10,537 kg MY. The Somatic cell count did not show any significant differences. However, the F1 crosses showed greater longevity, living 96 to 219 days longer than HO, and consequently achieving superior lifetime production of on average 1,174 to 8,118 kg MY (Table 15). (HAZEL LOESCHKE et al., 2017b, a; HAZEL et al., 2020a; HAZEL LOESCHKE et al., 2021)

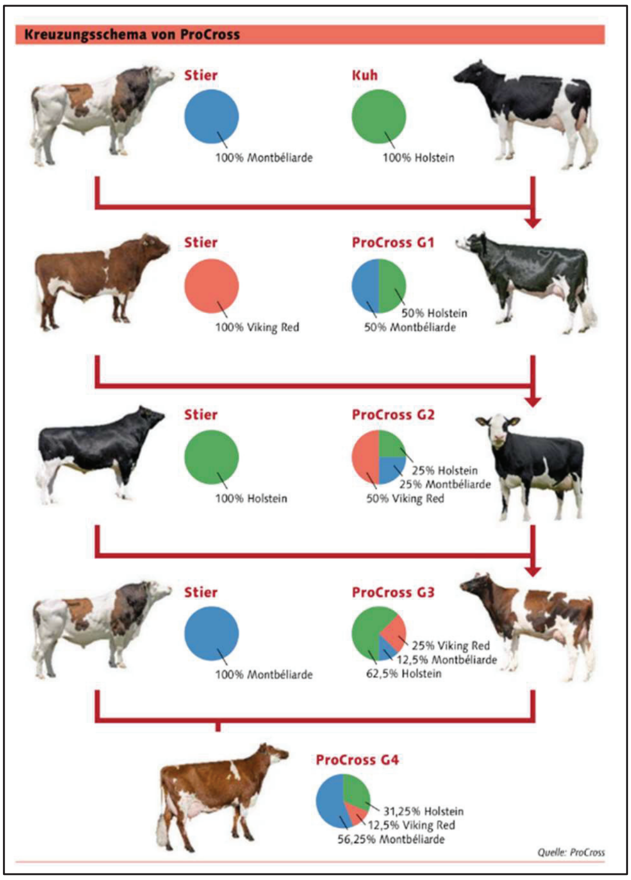


Figure 18: Proportions of the breeds in the ProCROSS crossbreeding system
Source: PETER AND MEILI (2020)

Table 15: Age and performance of F1 crossbred cows of Montbéliarde and Viking Red with Holsteins compared to Holstein cows

Parameter	HO n = 640	MON x HO n = 358	VR x HO n = 376
Days of life	886	1,105	982
Amount of milk in kg	32,774	40,892	33,948
Fat in kg	1,199	1,521	1,310
Protein in kg	1,002	2,810	2,397

HO = Holstein, MON = Montbéliarde, VR = Viking Red, n = number, Source: HAZEL LOESCHKE et al. (2021)

SHONKA-MARTIN et al. (2019); HAZEL LOESCHKE et al. (2019) compared crossbred cows from the ProCROSS rotational crossbreeding programme with purebred HO cows for dry matter intake, body weight, composition, BCS and production during the first 150 days of the first, second and third lactation (Table 16). The cows received the same total mixed ration twice daily and were housed in free-stall barns. The mean wither height of the crossbred cows was 3.5 cm less than that of the HO while there were no differences detected for the mean hip height (145.2 vs. 146.4 cm). The mean BCS was higher for the multiparous ProCROSS cows (3.25) than for the HO cows (3.06). The lower dry matter intake of the ProCROSS cows (3,360 kg vs. 3,592 kg from day 1 to 150 of lactation) led to lower feed costs with a similar fat and protein content (445 kg vs. 441 kg).

Table 16 lists the performance traits for the ProCROSS 3-breed crosses compared to the HO. All 3-breed crossbred cows had a smaller frame size and better condition than the HO cows.

Regarding the udder shape, the genotypes differed in rear teat width, which was assessed in favour of the crossbred cows. The gestation length is three to four days longer for the MON breed than for HO, which is why, as expected, it is also increased in the crosses with MON genes. The crosses calved for the first time significantly earlier than the HO heifers. As expected, the stillbirth rate of the crosses was lower by about half and the Conception rate at first service in all lactations was significantly higher than for HO. During the 1st lactation the seven herds that were analysed had relatively low health treatment costs across all breeds. Differences between the genotypes were seen, however, in the 2nd and 3rd lactation in which the ProCROSS crosses needed 14% to 25% lower total costs for treatments on average. For all genotypes relative low losses were recorded in the 1st lactation. The culling rate for the ProCROSS crosses was, however, significantly lower from the 2nd lactation on than for the HO cows. A significantly higher percentage of ProCROSS cows achieved a Productive period of at least 45 months, and thus a longer lifespan, but this could not be statistically confirmed. Due to their longer lifespan, the 3-breed crosses had a higher lifetime fat and protein production, even though the HO had superior milk yield in the first three lactations compared to the crosses. (HAZEL LOESCHKE AND HEINS, 2019)

Table 16: Comparison of the performance between Holstein cows and cows from the ProCROSS crossbreeding program by sire

Parameter	HO	Difference for ProCROSS	
		Sire MON	Sire VR
Number of heifers	1,073	462	505
Age at first calving in month	23.2	-0.3***	-0.5***
Number of cows	1,138	541	533
Gestation period (days)			
1st gestation	276	+4***	+3***
2nd / 3rd gestation	278	+3***	+2***
Stillbirth			
1st calving	9 %	4***	5***
2nd / 3rd calving	3 %	1	0
Conception rate at 1st service			
1st. lactation	43 %	+9***	+8***
2nd lactation	35 %	+7*	+12***
3rd lactation	35 %	+7	+13***
Number of cows	1,186	502	537
Total health treatment cost ($)			
1st lactation	43	-12***	-7*
2nd lactation	68	-21***	-20***
3rd lactation	92	-25***	-14****
Survival to 1st calving	86.7 %	+2	+3*
Lived to at least 45 months (after 1st calving)	18.0	+15.3***	+6.7***
Lifetime			
Number of cows	250	117	109
Fat + protein production (kg)	2,132	+307*	+385
Days in the herd	850	+176**	+117

HO = Holstein, MON = Montbéliarde, VR = Viking Red,
* significantly (p ≤ 0,10), ** significantly (p ≤ 0,05); significantly *** (p ≤ 0,01) from Holstein
Source: according to HAZEL LOESCHKE et al. (2019); HAZEL LOESCHKE et al. (2021)

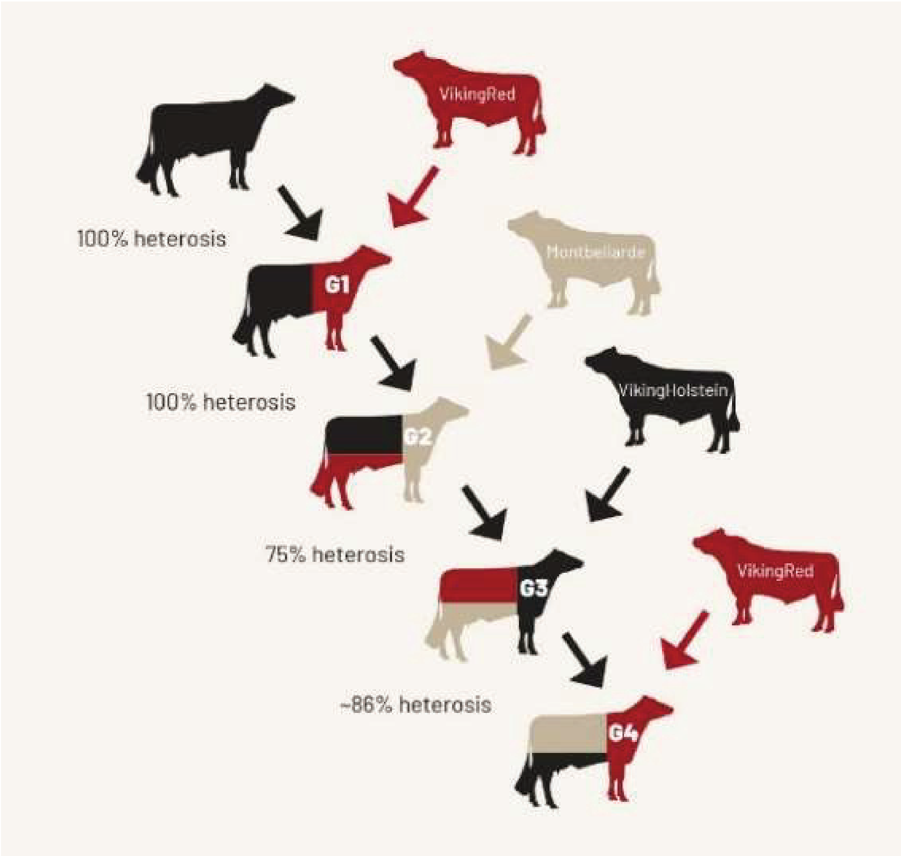


Figure 19: Crossbreeding method for the ProCROSS breeding programme with heterosis effects in the generations

Source: (VIKINGGENETICS, 2021)

Figure 20: Four generations of ProCROSS cows in a herd of the University of Minnesota, sires of the cows (from left to right): Montbéliarde (Micmac), Holstein (Clover), Viking Red (SRB, Peterslund), Montbéliarde (Urbaniste)

Source: HAZEL LOESCHKE et al. (2019)

3 Materials and methods

The performance and health of crossbreds with German Holstein were analysed in collaboration with four farming operations in Mecklenburg-Vorpommern and Brandenburg with farms A, B and C using a conventional farming system and farm D using an organic farming system.

3.1 Subject of the research

All crossbreeds were performed in the first generation using German Holstein cows. When stating the genotype of the crosses and in the crossbreeding plan, the sire is named first in each case.

Table A1 shows the animal stocks at the end of 2020 (farms A, B, D) and 2015 (farm C) as well as the proportions of the crosses in the herds for all years analysed. The largest herd was on farm D with 613 female cattle from 6 months of age, followed by farms C (626), B (340) and A (298). The average percentage of crosses was 11% (A and B), 18% (C) and 41% (D) of the female cattle stock.

In the analysis period, for the Milk performance tests for farms A and C about two-thirds of all cows tested were in the 1st and 2nd lactation (65.8% and 69.4%, Table A2) while on farms B and D it was about half of all the test-day cows (47.7% and 52.8%). Cows with more than three lactations were analysed on the test days at a rate of 15.9% (farm A) and 14.2% (farm C) while on farm B the rate was 34.2% and on farm D 29.8%.

3.2 Data acquisition, processing, evaluation and presentation of the results

Pedigree and performance data (health, fertility, milk yield) were collected using the management software Herde and HerdePlus from dsp-Agrosoft GmbH with the four study farms providing their databases.

The crosses were made with cows from the breed German Holsteins (GH) and another breed as a 2-breed cross (F1) or backcrosses (F2, F3). Three-breed crosses were performed as combination or backcrosses (F2, F3, F4, Table A3). The farms used the breeds Montbéliarde (MON, farms A, B), Jersey (JER, farms C, D), Brown Swiss (BS, farms A, C, D) and Swedish Red (SRB, farms A, B, C, D) as crossbreeding partners. The genotype MON50SRB25 (MON × (SRB × GH)) is examined separately under the name ProCROSS (PRCR) because this genetic composition is promoted internationally by the CRV breeding association. Due to the high diversity, all other variants of the genotypes with proportions of GH and two other breeds are combined and analysed as “3-breed cross” or “3-breeds”. Their genetic compositions are shown in Table A3.

The genotypes are grouped by the mating breed that makes up the largest proportion after GH. The crosses listed in Table A3 are compared to German Holsteins in the genotype comparison of the entire sample. Minima and maxima for the years of birth and the number of genotypes evaluated in the farms are listed in Tables A4 and A5.

Only female animals that were mated with purebred sires were included in the evaluation. Breeding values for selected sires (also known as bulls) with a high number of 50% daughters in the total random sample are, if present, listed in Table A6. These sires and others were also used in the ancestral generations. The complete pedigree of the purebred GH and the crosses is available up to the 5th generation but is not shown here due to the large volume of data.

In Table 17 the parameters that are used to compare the performances of the genotypes are defined. Data were only recorded for parameters for which a completed lifetime production for the animals was available in sufficient number (Tables A7, A8).

The udder health was recorded for all cows using the Somatic cell count for the cohorts 2005 to 2017 (farms A, B, C) and 2007 to 2021 (farm D) for which there were at least 20 data sets from the test days in the sample.

Performances as the genetic contribution of a breed decreases due to backcrossing with GH are shown using the example of MON, SRB and BS and, for the SRB crosses, the F1 backcross with SRB as well (Tables A9 to A11). The sample size included data from farm A only for the comparison of the MON crosses, farm B only for the BS crosses and from all farms for the SRB crosses.

Using the example of the parameters Age at first calving and Lifetime efficiency, we analysed whether it was predominantly the breed of the sire that influenced the performance of the daughters or his genetics or Breeding value, independent of breed. For this purpose, crosses with 50% genes from the breeds MON, JER, BS and SRB as well as the ten highest-ranking sires in both parameters in the current studies with the best-performing daughters were tested among each other and compared to purebred GH for any significant differences (Tables A12 to A15).

Using Excel 2016 and 2019 MSO from Microsoft (Version 2207), the data were prepared statistically and shown in diagrams and tables.

The differences in the performance parameters between the German Holsteins, which are represented on all farms and in all cohorts, and their crosses were analysed using linear mixed models, also known as hierarchical linear models or multi-level models. The year of birth of the animal was included as a control variable in the statistical model. Unlike linear regressions or covariance analyses, linear mixed models take into account the dependence between the performances of the animals on the same farm as a result of the feeding and rearing conditions. This two-level structure (farm: higher level, animal: lower level) is considered in the models used. When calculating the same parameters using different samples from the overall population, this results in different animal numbers and values for the same genotype.

Significances are defined as significant $p<0.05$, highly significant $p<0.01$ and extremely significant $p<0.001$.

Table 17: Abbreviations and definitions of the parameters used in the analysis

Parameter	Abb.	Definition
Days of life	dl	Days from birth to cull, herd life
Productive days	pd	Days from first calving to cull
Milking or lactation days	dm	Days a cow is milked
Fertility		
First breeding age	AFS	Age at first breeding in months
Age at first calving	AFC	Age at first calving in months
Inter-calving interval	ICI	Interval between two calvings in days
Health		
Age at cull	AC	Interval: birth to culling in months or years
Productive period	PP	Interval: first calving to culling in years
Number of lactations	NL	Number of lactations started
Reasons of culling		According by ADR
Milkability		Low milkability, poor milkability
Claws and limbs		Musculoskeletal disorders
Low performance		Insufficient milk yield
Infertility		Non-pregnancy despite occupancy
Metabolic disease		Metabolic disorders
Other		Other reasons and illnesses
Somatic cell count	SCC	Number of somatic cells in thousand / ml milk, indicator of udder health
Classes, (thousand / ml milk)		According to udder health report (MPT)
≤ 100	< 100	Udder healthy
> 100 and ≤ 200	100-200	Subclinical mastitis
> 200 and ≤ 400	200-400	Significant drop in performance
> 400	> 400	Endangering the ability to deliver the milk
Milk yield		
Lifetime milk production		Lifetime milk in kg/cow
Milking efficiency	MEff	kg milk per milking or lactation day
Production efficiency	PEff	kg milk per day from first calving to culling
Lifetime efficiency	LEff	kg milk per day of life

Abb. = Abbreviation, p. n. = postnatal, ADR = Arbeitsgemeinschaft Deutscher Rinderzüchter e.V.,
MPT = Milk performance test
Sources: WANGLER and HARMS (2009); STEENBECK (2016); ADR (2017); MSD (2018)

4 Presentation of the results

4.1 Performances of the herds on the study farms

The performance level for the herds is shown for farms A, B and D using the 2020 calendar year (Table 18). For farm C there are data available from January to December for 2015. The largest herd was on farm C with 374 dairy cows, followed by farm D with 329 cows and farms B and A with 236 and 232 dairy cows, respectively (Table A1).

In the herds on farms A, B and C the average AFS is between 15.0 and 15.7 months and the AFC is between 25.1 and 25.4 months. On farm D the heifers were mated for the first time on average at 19.0 months and accordingly calved for the first time at 27.6 months on average.

There were no differences seen for the ICI between the herds on the study farms (403 to 410 days).

Regarding the milk production level, farms A and C were comparable with 30, 847 to 33, 258 kg MY lifetime production per cow. Farm B achieved the highest value for this parameter with 36,242 kg MY per cow while farm D achieved the lowest value by far with 19,093 kg. In the efficiency of the milk yield, farms A and C with 17.2 and 16.9 kg MY per day of life (dl), 30.3 and 28.3 kg MY per productive day (pd) and 33.3 and 33.0 kg MY per milking or lactation day (dm) were ahead of farm B with 16.0 kg MY per dl, 24.9 kg MY per pd and 28.8 kg MY per dm Farm D performed worst in all efficiency parameters (10.4 kg MY per dl, 19.2 kg MY per pd, 22.3 kg MY per dm).

Similar average values were also observed for farms A and C for the Productive period of 2.8 and 3.0 years as well as 3.0 and 3.2 lactations. On farm B the cows were used on average for 4.9 years and 3.8 lactations while on farm D the values were only 2.5 years and 2.8 lactations.

Analogous to the PP, the mean culling age of the herds on farm C in 2020 was 6.2 years, which was considerably higher than the herd means on farms A, B and D (A 4.7 years, B 5.2 years, D 4.8 years).

Regarding the reasons for culling, the high percentage of “other reasons and diseases” cited by farms B and D of 23% and 22%, respectively, as well as by farm C of 26% was noteworthy, with only 4% of culling being assigned to this category on farm A. In contrast, 47% of the culling on farm A was due to “low performance” (performance) and 30% was due to “poor milkability” (milkability) with these categories named on the other three farms at rates of 3%, 8%, 10% or 28%. Infertility was cited by farm A as the reason for culling in 4% of instances while on farm B this was the reason for 15% and on farms C and D for 30% and 23% of instances, respectively. Culling due to “metabolic diseases” totalled 1% to 6% of the reasons across all farms.

Udder health is analysed using the number of somatic cells (SC) per ml of milk given in the udder health report in the test-day records. The annual averages for farms A and D are 277.1 × 10^3 and 273.5 × 10^3 SC per ml of milk. These herds achieved the highest proportion of cows with healthy udders, that is, cows with an average of <100 × 10^3 SC per ml of milk, with 47.8% and 48.9% of the herds, respectively. The milk quality was on average compromised in 15.0% and 14.0% of the cows (>400 × 10^3 SC per ml of milk). On farms B and C, average scores of 362.6 × 10^3 and 319.4 × 10^3 SC per ml of milk were measured, with 39.8% and 37.0%, respectively, of the tested cows having healthy udders while 22.8% and 18.7% had >400 × 10^3 SC per ml of milk.

Table 18: Mean milk, fertility and health parameters of the herds on the study farms in the last year that could be fully analysed (January to December)

Parameter	**Average**			
Farm	**A**	**B**	**C**	**D**
Year	**2020**	**2020**	**2015**	**2020**
Fertility				
First breeding age (months)	15.3	15.0	15.7	19.0
Age at first calving (months)	25.1	25.3	25.4	27.4
Inter-calving interval (days)	403	406	405	410
Milk yields				
Lifetime milk production (kg milk), dl	30,847	36,242	33,258	19,093
Lifetime efficiency (kg milk / dl)	17.2	16.0	16.9	10.4
Production efficiency, kg milk / pd)	30.3	24.9	28.3	19.2
Milking efficiency (kg milk / dm)	33.3	28.8	33.0	22.3
Health				
Age at cull (years)	4.7	6.2	5.2	4.8
Productive period (years)	2.8	4.9	3.0	2.5
Number of lactations	3.0	3.8	3.2	2.8
Percentage of culls by reasons				
Age	1 %	10 %	-	-
Low performance	47 %	-	8 %	28 %
Infertility	4 %	15 %	30 %	23 %
Udder diseases	-	18 %	15 %	22 %
Milkability	30 %	10 %	-	3 %
Claws and limbs	10 %	8 %	16 %	2 %
Other reasons and illnesses	4 %	23 %	26 %	22 %
Metabolic diseases	2 %	3 %	6 %	1 %
Somatic Cells, (thousand per ml milk)	277.1	362.6	319.4	273.5
Share < 100 thousand	47.8 %	39.8 %	37.0 %	48.9 %
Share > 400 thousand	15.0 %	22.8 %	18.7 %	14.0 %

dl = day of life, pd = productive day, dm = milking day

4.2 Performance comparison of German Holsteins (GH) vs. crosses with 50% GH genes

Crosses with 50% MON genes start breeding earlier than GH and their crosses with JER, BS and SRB, and thus both the mean AFS and mean AFC are consequently lower, but this is not significant due to the wide spread of the data (Figure 21, Table 19; Table A7). The AFS and AFC of 15.1 and 25.8 months for MON50 contrasts with 16.4 and 16.5 months for the AFS and 26.1, 26.2 and 26.3 months for the AFC for BS50, SRB50 and GH, respectively. The highest means for the AFS and AFC of 18.1 and 28.8 months on average are seen for JER50 but absolute maximum values are seen for GH with 36.4 and 43.8 months.

The highest mean ICI of 418.3 days is seen for GH, followed by JER50 (375.4 days), MON50 (381.8 days), and BS50 and SRB50 (395.9 and 392.3 days). The ICI is another parameter with a very high spread within the genotypes. Nevertheless, the differences between GH vs. JER50, BS50 and SRB50 are significant while the difference between MON50 and GH is approaching the significance level.

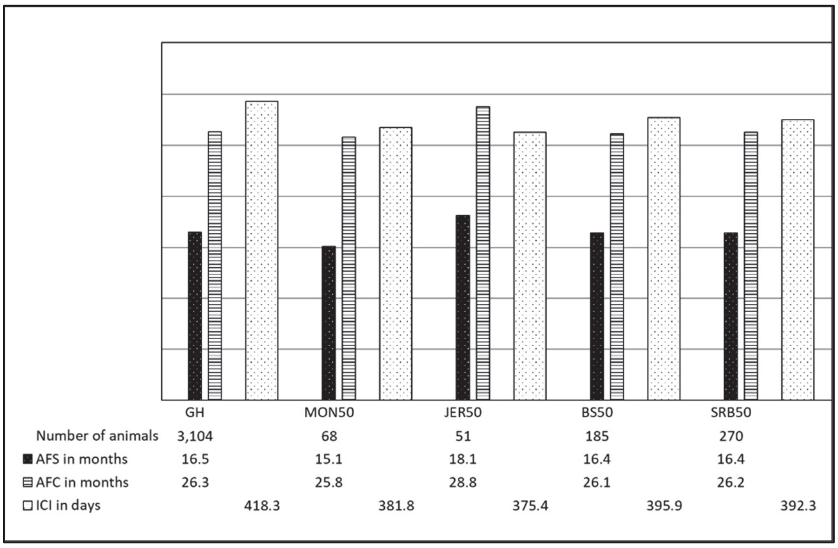


Figure 21: Fertility performance for German Holsteins (GH) vs. MON50, JER50, BS50 and SRB50

MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed,
AFS = Age at first service, AFC = Age at first calving, ICI = Inter-calving interval

Table 19: Significance of the fertility performance for German Holsteins (GH) vs. MON50 vs. JER50 vs. BS50 vs. SRB50

	Significance at p<0.05			
Genotype	**GH**	**JER50**	**BS50**	**SRB50**
Age at first service in months				
MON50	0.101	0.338	0.743	0.556
JER50	0.591		0.412	0.523
BS50	0.690			0.792
SRB50	0.879			
Age at first calving in months				
MON50	0.978	0.372	0.778	0.931
JER50	0.290		0.199	0.798
BS50	0.697			0.250
SRB50	0.883			
Inter-calving interval in days				
MON50	0.051	0.379	0.929	0.708
JER50	**0.002**		0.318	0.679
BS50	**0.001**			0.438
SRB50	**0.000**			

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, numbers in the Genotype indicate the proportion of genes in %, n=number of animals

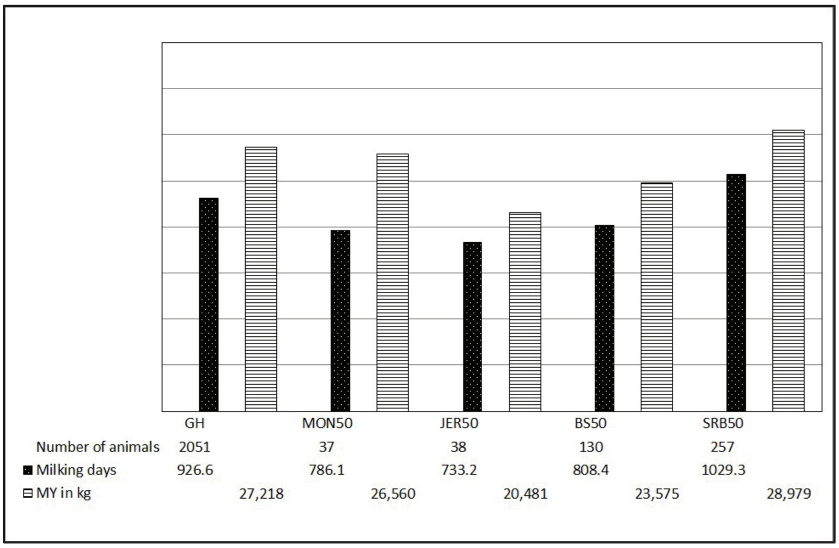


Figure 22: Milk yields of German Holsteins (GH) vs. MON50, JER50, BS50 and SRB50

MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed,
MY = milk yield, numbers in the Genotype indicate the proportion of genes in %

Table 20: Significance of the milk yields for German Holsteins (GH) vs. MON50 vs. JER50 vs. BS50 vs. SRB50

	Significance at p<0.05			
Genotype	**GH**	**JER50**	**BS50**	**SRB50**
Number of milking days				
MON50	0.653	0.962	0.975	0.500
JER50	0.611		0.978	0.403
BS50	0.538			0.490
SRB50	0.718			
Amount of milk in kg				
MON50	0.818	0.878	0.752	0.755
JER50	0.665		0.881	0.429
BS50	0.446			0.633
SRB50	0.891			

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, numbers in the Genotype indicate the proportion of genes in %, n=number of animals

The highest average lifetime production was achieved by the crosses with 50% SRB genes (SRB50) with 28,979 kg MY in 1, 029 dm, but only isolated GH cows achieved more than 100,000 L MY (Figure 22, Table A7). Purebred GH followed with 27,218 kg MY and 927 dm on average for the lifetime production while MON50 were in third place with 26,560 kg MY and 786 dm. BS50 yielded an average of 23,575 kg MY but were milked for longer on average than MON50 and JER50 with 808 dm. The lowest mean MY (20,481 kg) is milked from JER50 cows in 733 dm, which is also the lowest mean for the dm. The differences are not significant (Table 20).

The efficiency of the milk production is indicated by the parameters Milking efficiency (MEff) in kg MY per dm , Production efficiency (PEff) in kg MY per productive day (pd) and Lifetime efficiency (LEff) in kg MY per day of life (dl) (Figure 23, Table 21, Table A7).

When examining the efficiency of the milk yield, the MON50 crosses performed best across all three parameters but this was not significant (30.8 kg MY per dm, 27.3 kg MY per pd, 13.4 kg MY per dl). GH followed in second place (28.1 kg MY per dm, 24.7 kg MY per pd, 12.9 kg MY per dl). JER50 and SRB50 were at the same level for MEff and PEff (27.4 and 27.0 kg MY per dm; 23.3 and 23.7 kg MY per pd), with BS50 achieving approximately 1 kg MY less per dm and pd (26.0 kg MY per dm; 22.4 kg MY per pd) with the low MEff significant compared to GH with p<0.05. In the LEff the BS50 and SRB50 crosses were similar to GH (12.1 and 12.5 kg MY per dl) while the JER50 crosses performed worst with 10.6 kg MY per dl.

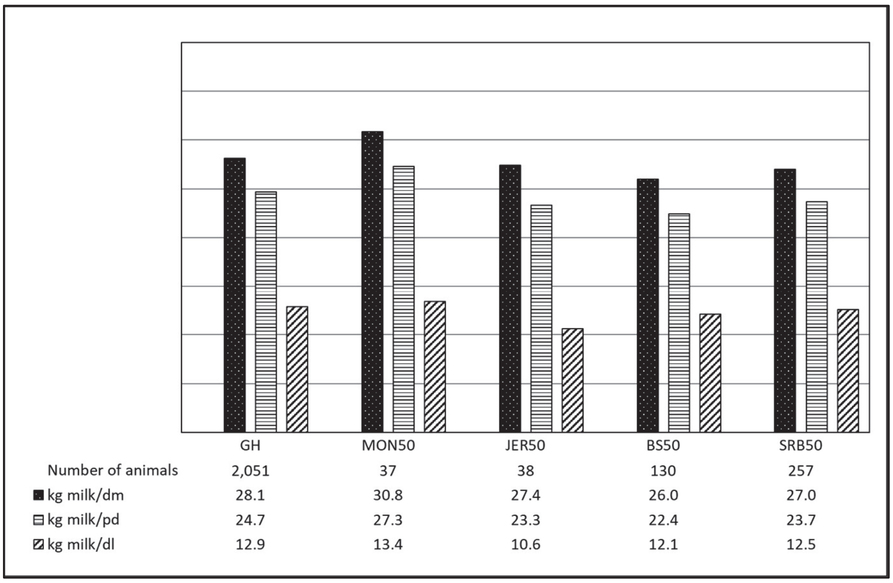


Figure 23: Efficiency of the milk yield of German Holsteins (GH) vs. MON50, JER50, BS50 and SRB50

MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, dl = day of life, pd = productive day, dm = milking day, numbers in the Genotype indicate the proportion of genes in %

Table 21: Significance of the efficiency of the milk yields for German Holsteins (GH) vs. MON50 vs. JER50 vs. BS50 vs. SRB50

Genotype	**Significance at p<0.05**			
	GH	**JER50**	**BS50**	**SRB50**
Milking efficiency in kg milk per milking day				
MON50	0.752	0.717	0.125	0.363
JER50	0.419		0.218	0.252
BS50	**0.022**			0.663
SRB50	0.106			
Production efficiency in kg milk per productive day				
MON50	0.932	0.142	0.254	0.223
JER50	0.067		0.442	0.940
BS50	0.135			0.433
SRB50	0.136			
Lifetime efficiency in kg milk per day of life				
MON50	0.719	0.948	0.792	0.993
JER50	0.658		0.837	0.706
BS50	0.385			0.929
SRB50	0.596			

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, numbers in the Genotype indicate the proportion of genes in %, n=number of animals

A first calving was recorded for 73.0% to 80.6% of the analysed animals with 19.4% to 27.0% of the analysed heifers therefore being culled (Table 22). An exception was the JER50 crosses for which only 5.3% of the heifers were culled prior to first calving.

Table 22: Percentage of animals up to the 1st calving

Genotyp	Number of animals	Number of animals at the 1st calving	Number of animals with 1st calving in %
GH	3,782	2,917	77.1
MON50	74	54	73.0
JER50	57	54	94.7
BS50	260	206	79.2
SRB50	434	350	80.6

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, numbers in the Genotype indicate the proportion of genes in %

The cows with the longest lives were those from the GH breed with 13.5 years recorded in this analysis (Table A7) but on average the JER50 and SRB50 crossbred cows reached the highest age at departure from the herds (5.2 and 5.1 years, Figure 24, Table A7). GH and BS50 follow with 4.0 years and MON50 with 3.7 years on average.

Due to the late breeding age, the Productive period and the number of started lactations decrease for the JER50 (2.5 years PP, 2.7 lactations) to the same level as the BS50 (2.7 years PP, 2.8 lactations). Regarding the PP and the number of lactations, the SRB50 crosses (3.4 years PP, 3.3 lactations) perform better than GH (2.9 years PP, 3.1 lactations), BS50 (2.7 years PP, 2.8 lactations) and MON50 (2.5 years PP, 3.2 lactations). The differences between the parameters for age and production are not significant (Table 23).

To compare the health of GH and their crosses, the Somatic cell count (SCC), given as the average total of 10^3 cells per ml of milk, as well as the proportion of cows that have “healthy udders”, or <100 × 10^3 SC per ml of milk, and “compromised milk quality”, or >400 × 10^3 SC per ml of milk, are analysed using the test-day records (Figure 25, Table 24, Table A7). On average GH, BS50 and SRB50 are at the same level (310.1 to 329.5 × 10^3 SC per ml of milk), for JER50 more than 100 × 10^3 SC more on average were measured while the MON50 cows had the highest mean of 557.1 × 10^3 SC per ml of milk.

For the proportions of the classes, the best values were achieved for JER50 with on average 49% of the cows having healthy udders and the quality of the milk compromised in only 16% (>400 × 10^3 SC per ml of milk). GH, BS50 and SRB50 are at a similar level with the MON50 crosses again performing worst for udder health. There were no significances in this analysis.

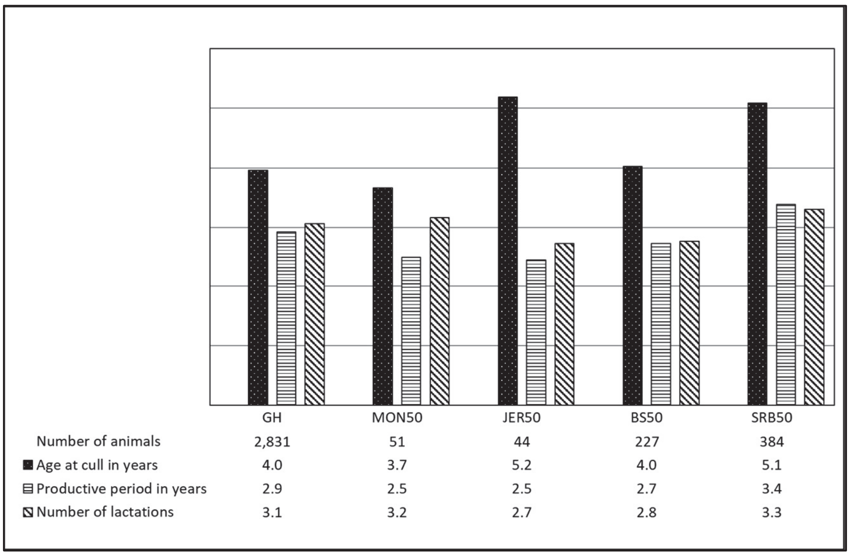


Figure 24: Age and Productive period on departure and number of lactations of German Holsteins (GH) vs. MON50, SRB50, BS50 and JER50

MON = Montbéliarde, SRB = Swedish Red Breed, BS = Brown Swiss, JER = Jersey

Table 23: Significance of the parameters age and Productive period on departure and number of lactations of German Holsteins (GH) vs. MON50 vs. JER50 vs. BS50 vs. SRB50

Genotype	Significance at p<0.05			
	GH	**JER50**	**BS50**	**SRB50**
Age at cull in years				
MON50	0.997	0.135	0.562	0.241
JER50	0.052		0.173	0.509
BS50	0.396			0.423
SRB50	0.118			
Productive period in years				
MON50	0.745	0.761	0.998	0.506
JER50	0.450		0.696	0.431
BS50	0.679			0.298
SRB50	0.612			
Number of lactations				
MON50	0.574	0.662	0.344	0.642
JER50	0.979		0.618	0.465
BS50	0.481			0.921

GH = German Holsteins, MON = Montbéliarde, BS = Brown Swiss, SRB = Swedish Red Breed, numbers in the Genotype indicate the proportion of genes in %

For 3,500 animals, of which 693 were 2-breed crosses and 2,807 were GH, the reasons for culling were stated by the farms (Table 25). For up to about one-third of the total sample, the reasons cited were “other culling reasons” (GH: 32.0%; MON50: 17.6%; JER50: 20.5%; BS50: 32.3%; SRB50: 37.9%) which are not included in the analysis by genotype. On the farms “other reasons” was cited for between 15.0% and 44.4% for all animals.

For GH low yields (17.3%) and infertility (17.2%) were cited most as the reasons for culling, followed in third place by milkability (11.1%). Udder diseases (7.9%) only reached fifth place after claw and limb disorders (8.6%). 39.2% of MON50 are culled due to poor milkability with a further 17.6% culled due to low yields. Advanced age, infertility and locomotor diseases follow with 7.8% each. The most common reasons for culling BS50 are infertility and udder diseases (17.7% and 15.9%) followed by low yields (14.2%). Infertility and low yields are the most common reasons cited for culling JER50 while for SRB50 the reasons are, in order, low yields, udder diseases and infertility. For almost all genotypes 2.8% to 4.5% are culled due to metabolic disorders although this reason was not recorded for MON50. No JER50 cows were culled due to milkability and age. Age reasons were cited for culling for only 0.4% to 3.1% of GH, BS50 and SRB50 but for MON50 the rate was 7.8%.

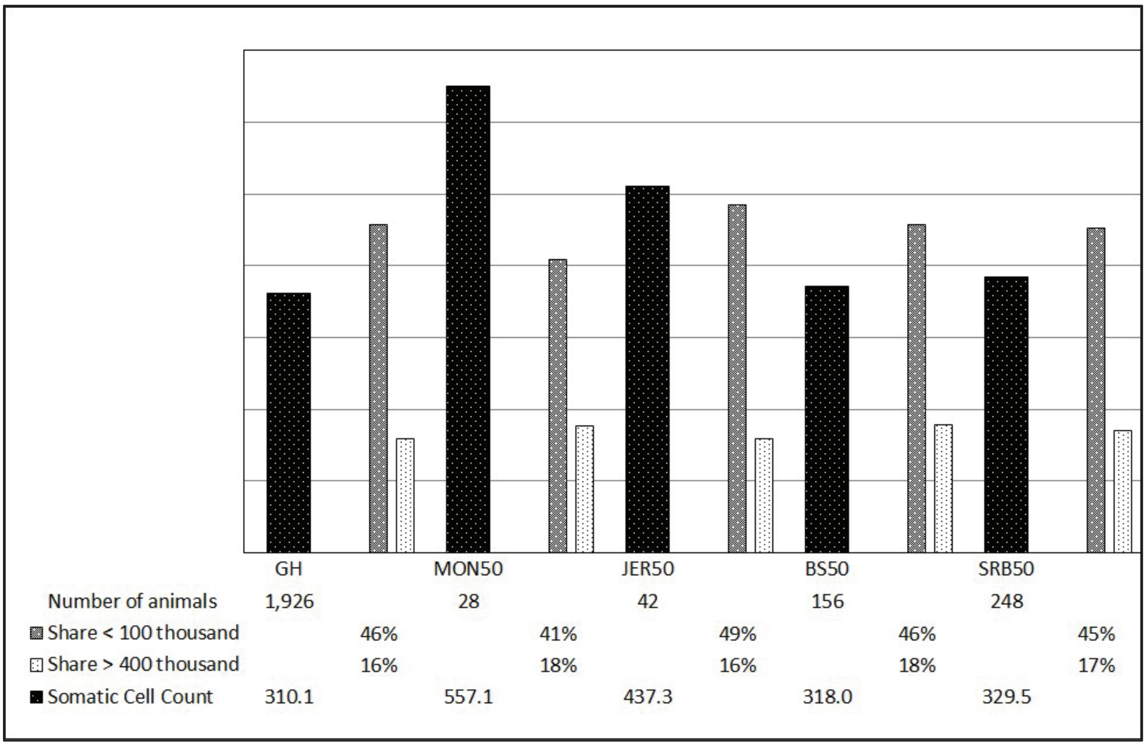


Figure 25: Somatic cell counts per ml of milk for German Holsteins (GH) vs. MON50, JER50, BS50 and SRB50

MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed

Table 24: Significance of the Somatic cell counts per ml of milk for German Holsteins (GH) vs. MON50 vs. JER50 vs. BS50 vs. SRB50

Genotype	**Significance at p<0.05**			
	GH	**JER50**	**BS50**	**SRB50**
Somatic Cell Count, total in thousand per ml milk				
MON50	0.201	0.680	0.206	0.268
JER50	0.860		0.354	0.757
BS50	0.860			0.506
SRB50	0.861			
Somatic Cell Count, share < 100 thousand per ml milk				
MON50	0.096	0.576	0.147	0.280
JER50	0.246		0.278	0.440
BS50	0.986			0.660
SRB50	0.330			
Somatic Cell Count, share > 400 thousand per ml milk				
MON50	0.612	0.236	0.696	0.770
JER50	0.057		0.087	0.882
BS50	0.918			0.093
SRB50	0.775			

GH = German Holsteins, MON = Montbéliarde, BS = Brown Swiss, SRB = Swedish Red Breed, numbers in the Genotype indicate the proportion of genes in %

Table 25: Culling reasons for German Holsteins (GH) vs. MON50 vs. JER50 vs. BS50 vs. SRB50

		Percentage of culls by reasons							
	n	**Age**	**Udder diseases**	**Low milk yield**	**Claws and limbs**	**Milkability**	**Metabolic diseases**	**Infertility**	**Other**
Farm									
A	1,547	4.0%	1.8%	31.8%	9.8%	24.0%	2.7%	10.9%	15.0%
B	586	7.0%	13.3%	4.1%	5.8%	3.6%	1.7%	20.1%	44.4%
C	493	0.0%	14.2%	8.9%	9.9%	0.4%	2.8%	37.1%	26.6%
D	2,089	0.0%	12.3%	15.9%	7.1%	1.9%	2.9%	15.4%	44.4%
Total	**4,715**	**2.2%**	**9.2%**	**18.9%**	**8.1%**	**9.2%**	**2.7%**	**16.8%**	**32.9%**
Genotype Farm									
GH A, B, C, D	2,807	3.1%	7.9%	**17.3%**	8.6%	11.1%	2.8%	**17.2**%	32.0%
MON50 A, B	51	7.8%	2.0%	**17.6%**	7.8%	**39.2%**	0.0%	7.8%	17.6%
JER50 C, D	44	0.0%	**18.2%**	**25.0%**	2.3%	0.0%	4.5%	**29.5%**	20.5%
BS50 A, C, D	226	0.4%	**15.9%**	**14.2%**	10.6%	4.9%	4.0%	**17.7%**	32.3%
SRB50 A, B, C, D	372	1.9%	13.2%	**16.9%**	8.3%	6.2%	3.2%	12.4%	37.9%
Total	**3,500**	**2.6%**	**10.6%**	**17.5%**	**8.0%**	**11.8%**	**3.1%**	**18.0%**	**28.4%**

GH = German Holsteins, MON = Montbéliarde, BS = Brown Swiss, SRB = Swedish Red Breed, numbers in the genotype indicate the proportion of genes in %, n = number of culled animals

4.3 Performance comparison of German Holsteins (GH) vs. crosses of different genotypes

GH are compared below to “all crossbreeds” (CB), crosses with >75% GH genes (GH >75), the ProCROSS genotype (PRCR, MON × (SRB × GH)) and crosses between GH and two other breeds with varying proportions of genes (3-breed crosses, 3-breeds) (Tables A3, A4).

The average AFS and AFC of all genotypes analysed here were quite high at 15.6 to 17.1 months and 26.6 to 26.9 months, respectively (Figure 26, Table 26, Table A7). GH heifers were on average 16.5 months old at first service and calved on average at 26.3 months and thus earlier than crosses with >75% GH genes (26.9 months) and somewhat later than CB (26.1 months). Although the differences in the AFC are relatively small, they are highly significant with $p<0.001$. Larger differences were calculated for the means of the ICI. The 418.3-day ICI of the GH was significant vs. CB (389.8 days, $p<0.05$) and the 3-breed crosses (387.0 days, $p<0.001$). The lowest mean ICI was observed for the PRCR crosses with 371.8 days.

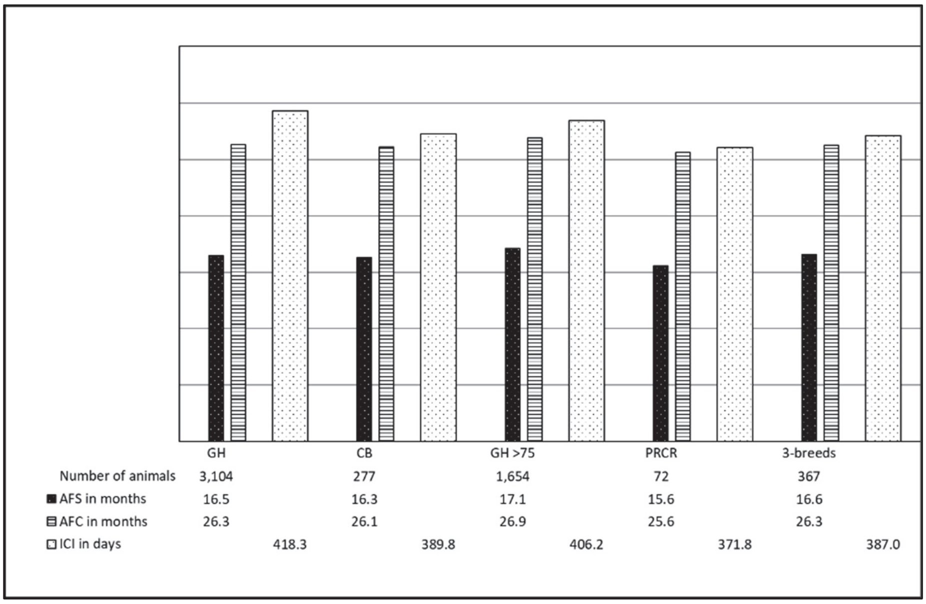


Figure 26: Fertility performance for German Holsteins (GH) vs. “all crossbreeds” (CB)

GH = German Holsteins, CB = all crossbreeds

Table 26: Significance of the fertility performance for German Holsteins (GH) vs. “all crossbreeds”, GH >75, ProCROSS and 3-breed crosses

Parameter	Significance GH vs. at p<0.05			
	All crossbreeds	**GH > 75%**	**ProCROSS**	**3-breeds**
AFS in months	0.113	0.436	0.381	0.840
AFC in months	**0.001**	**0.001**	0.400	0.727
ICI in days	**0.049**	0.558	0.122	**0.000**

AFS = Age at first service, AFC = Age at first calving, ICI = Inter-calving interval, GH = German Holsteins,

In the comparison of the lifetime milk yields, the highest means were seen for the purebred GH (927 dm, 27, 218 kg MY); compared to GH >75 the number of milking days was significantly higher; compared to the 3-breed crosses the milk yield was higher (Figure 27, Table 27, Table A7). GH >75 with 534 dm and 13, 266 kg MY was clearly below the comparison genotypes. PRCR achieved similarly high mean dm as the other 3-breed crosses (761 vs. 722 dm) but had a higher lifetime production regarding the MY (23,668 vs. 19, 354 kg).

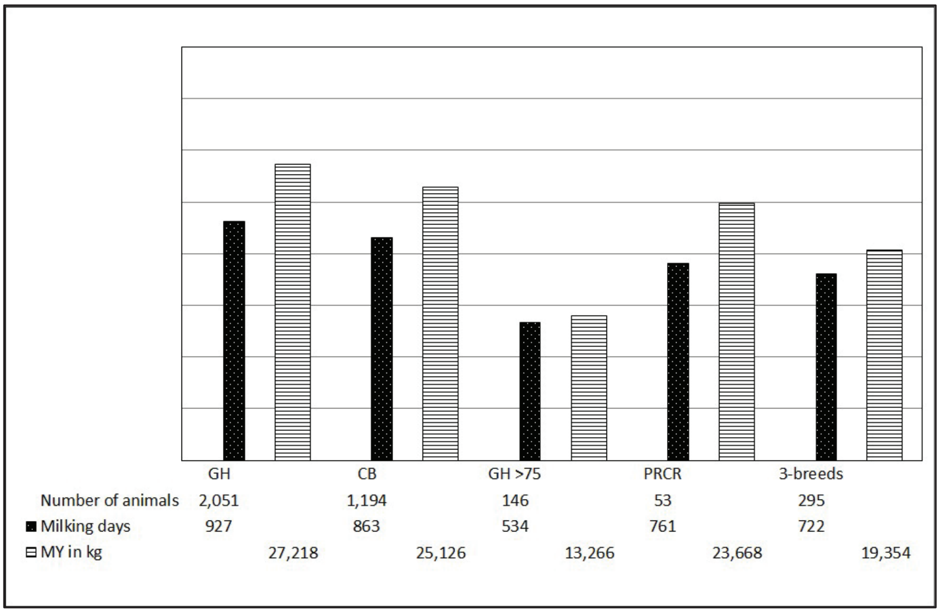


Figure 27: Milk production for German Holsteins (GH) vs. "all crossbreeds" (CB), GH >75, ProCROSS (PRCR) and 3-breed crosses

GH = German Holsteins, CB = all crossbreeds

Table 27: Significance of the milk production for German Holstein (GH) vs. "all crossbreeds", GH >75, ProCROSS and 3-breed crosses

Parameter	Significance GH vs. at p<0.05			
	All crossbreeds	GH > 75%	ProCROSS	3-breeds
Milking days	0.885	**0.035**	0.749	0.195
Milk in kg	0.772	0.191	0.432	**0.009**

GH = German Holsteins

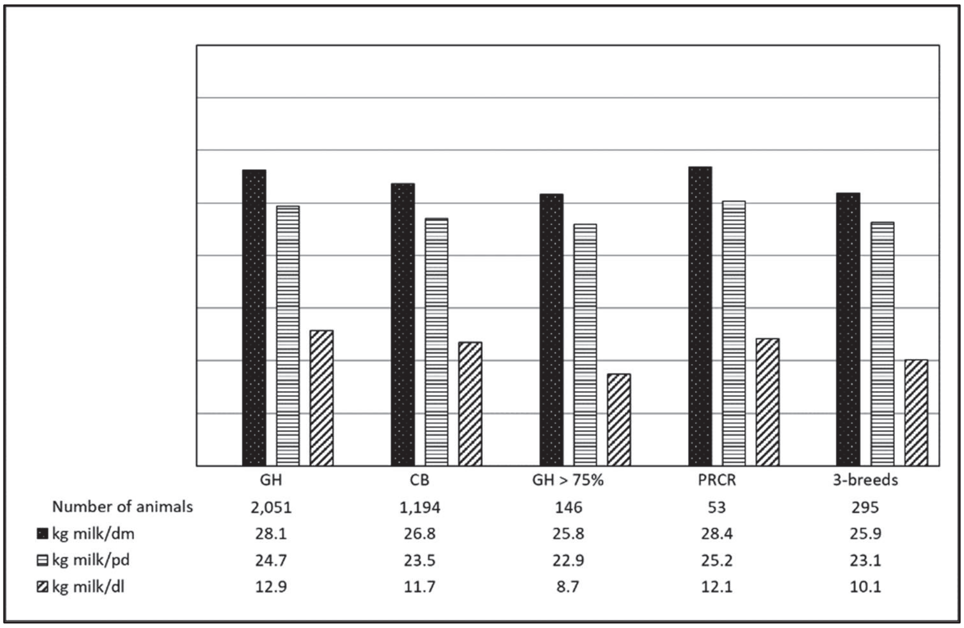


Figure 28: Efficiency of the milk production for German Holsteins (GH) vs. "all crossbreeds" (CB), GH >75, ProCROSS (PRCR) and 3-breed crosses

GH = German Holsteins, CB = all crossbreeds

Table 28: Significance of the efficiency of the milk production for German Holsteins (GH) vs. “all crossbreeds”, GH >75, ProCROSS and 3-breed crosses

Parameter	Significance GH vs. at p<0.05			
	All crossbreeds	GH > 75%	ProCROSS	3-breeds
Milk per milking day	**0.000**	**0.001**	0.096	**0.000**
Milk per productive day	0.069	**0.000**	**0.000**	**0.042**
Milk per day of life	0.175	**0.001**	0.199	**0.000**

milk = amount of milk in kg, GH = German Holsteins

Regarding the milk Production efficiency, the GH were significantly better than the 3-breed crosses (p<0.05, Figure 28, Table 28, Table A7). For MEff and LEff, the GH are comparable to the PRCR genotype (28.1 vs. 28.4 kg MY per dm, 12.9 vs. 12.1 kg MY per dl). The PRCR genotype was significantly superior to the GH for the PEff (25.2 vs. 24.7 kg MY per pd, p<0.001). The worst performer across all values was GH >75.

For the culling age, GH and CB are comparable (4.0 and 3.9 years, respectively; Figure 29, Table 29, Table A7) and are followed by PRCR and the other 3-breed crosses (3.7 and 3.4 years). The means of the PP were analogous. For the number of lactations, the PRCR were on the same level as CB (2.9 lactations) but the other 3-breed crosses achieved fewer (2.6 lactations). With 2.6 years on average, the GH >75 were culled the earliest, achieved the lowest PP (1.5 years) and the lowest number of lactations (2.4).

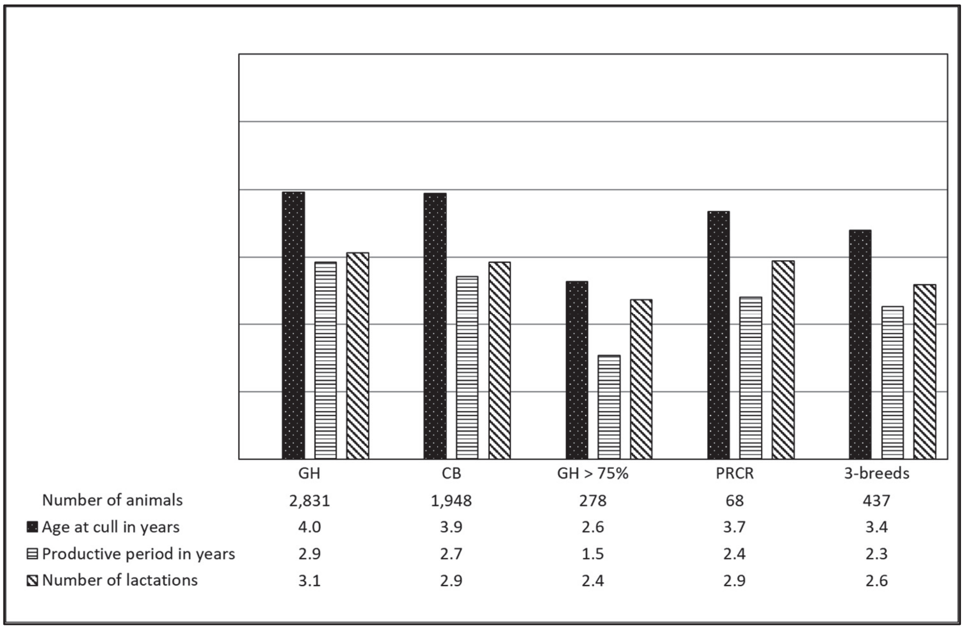


Figure 29: Age and Productive period on departure and number of lactations of German Holsteins (GH) vs. “all crossbreeds” (CB), GH >75, ProCROSS (PRCR) and 3-breed crosses

GH = German Holsteins, CB = all crossbreeds

Table 29: Significance of age and Productive period on departure and number of lactations of German Holsteins (GH) vs. “all crossbreeds”, GH >75, ProCROSS and 3-breed crosses

Parameter	Significance GH vs. at p<0.05			
	All crossbreeds	GH > 75%	ProCROSS	3-breeds
Age at cull in years	0.207	0.867	0.450	0.791
Productive period in years	0.901	**0.002**	0.932	0.190
Number of lactations	0.804	0.124	0.313	0.495

GH = German Holsteins

For udder health, there were no differences observed between GH and the comparison genotypes (Figure 30, Table 30, Table A7). The PRCR crosses were an exception. For the SCC, they had on average approximately 100 × 10^3 more cells per ml of milk and achieved an average proportion of 43% of cows in the class “healthy udders” or <100 × 10^3 SC per ml of milk, the lowest value, which was even significant vs. GH. The highest proportion of cows with healthy udders was achieved by GH >75 with 53% on average and the class >400 × 10^3 SC per ml of milk was seen on average in only 13%.

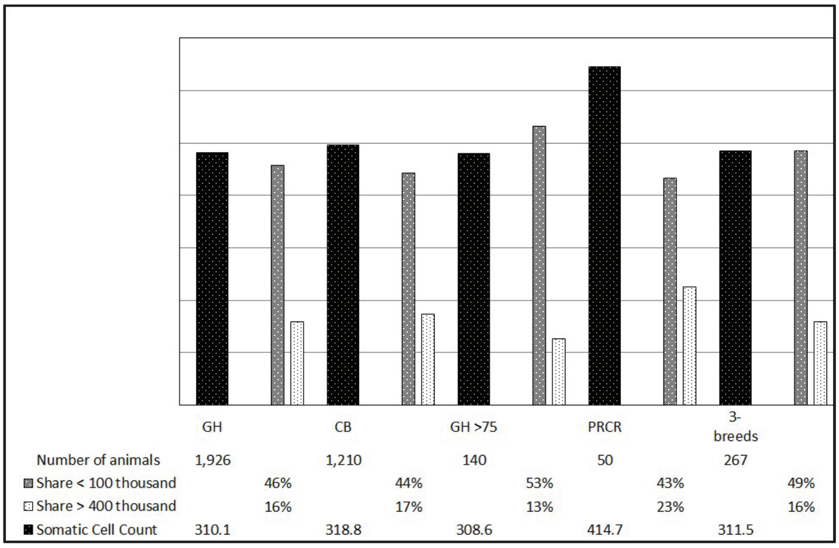


Figure 30: Somatic cell count in 10^3 cells per ml of milk for German Holsteins (GH) vs. “all crossbreeds” (CB), GH >75, ProCROSS (PRCR) and 3-breed crosses

GH = German Holsteins, CB = all crossbreeds

Table 30: Significance of the Somatic cell count per ml of milk for German Holsteins (GH) vs. “all crossbreeds”, GH >75, ProCROSS and 3-breed crosses

Parameter	Significance GH vs. at p<0.05			
In thousand / ml milk	All crossbreeds	GH > 75%	ProCROSS	3-breeds
Share < 100	0.478	0.645	**0.006**	0.920
Share > 400	0.218	0.458	0.352	**0.013**
SCC	0.137	0.844	0.053	0.394

SCC = Somatic Cell Count, GH = German Holsteins

4.4 Performance comparison of German Holsteins (GH) vs. crosses with MON, BS and SRB with different genetic compositions

This performance comparison was done with GH vs. MON, BS and SRB crosses as well as backcrosses in the F2 generation with GH (MON25, BF25, SRB25) and SRB (SRB75) and backcrosses with GH in the F3 generation (MON12.5, BS12.5, SRB12.5, Table 31). The MON crosses were located on farm A, the BS crosses on farm D; they were compared to GH with the same cohorts on the corresponding farms. SRB crosses were located on all farms and they were compared to the GH from the total sample.

With an increasing percentage of GH genes, for the MON and BS backcrosses the AFS, AFC and ICI increase (Figure 31, Tables A9, A10). The AFS increases as the percentage of GH genes increases, for MON crosses from 15.1 to 15.5 months. The GH on this farm were first serviced on average at 15.1 months and thus at the same age as the F1 crosses (MON × GH).

For the BS crosses this increase in the AFS from the F1 generation to the F2 and F3 is in part significant. GH were on average serviced later on farm D than the BS crosses (AFS 18.6 vs. 17.2 to

18.5 months, Table A10). The mean ICI of GH on farm A corresponds to the average of all MON crosses (400.4 vs. 383.7 to 428.4 days). On farm D the average ICI of 432.8 for the GH is higher than that of the BS crosses (405.0 to 422.4 days).

The increase in the AFS and AFC as the percentage of GH genes increases was also seen in the SRB crosses (Figure 32, Table A11) but the same AFS of 16.3 months on average was observed for SRB50 and SRB25 crosses. The AFS and AFC of the GH of 16.5 and 26.3 months were at the same level as the SRB crosses. The mean ICI of the GH was higher than CB.

There is fertility performance data available for 10 SRB75 crosses. The AFS and AFC are considerably higher than for the comparison genotypes but not significantly so. The mean ICI of 355.1 days is less than the mean ICI for the SRB crossbreeds with a higher percentage of GH genes (390.6 to 402.4 days) and significantly less than that of the GH (418.0 days).

Table 31: Number of animals and cohorts of German Holsteins (GH), crosses with GH and their backcrosses on the study farms

Genotype		**Farm**	**n**	**Year of birth**	
Abb.	**Crossbreed**			**min**	**max**
Montbéliarde (MON)					
GH		A	1,403	2009	2018
MON50	MON x GH	A	67	2009	2019
MON25	GH x MON50	A	26	2011	2019
MON12.5	GH x MON25	A	25	2015	2019
Brown Swiss (BS)					
BS					
GH		D	775	2002	2016
BS50	BS x GH	D	257	2002	2013
BS25	GH x BS50	D	139	2004	2016
BS12.5	GH x BS25	D	51	2007	2016
Swedish Red Breed (SRB)					
GH		A, B, C, D	3,782	2001	2019
SRB75	SRB x SRB50	A, B, D	11	2008	2015
SRB50	SRB x GH	A, B, C, D	434	2001	2017
SRB25	GH x SRB50	A, B, D	344	2003	2019
SRB12.5	GH x SRB25	A, B, D	114	2005	2019

GH = German Holsteins, Numbers in the genotype indicate the proportion of genes in %, Abb. = abbreviation, n = number of animals, min = minimum, max = maximum

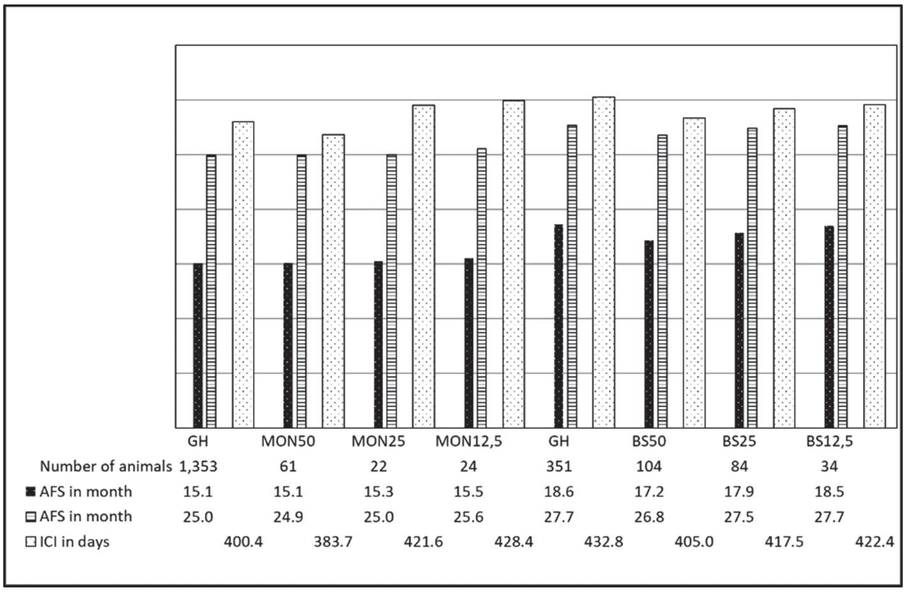


Figure 31: Fertility performance for German Holsteins (GH) vs. MON (Montbéliarde) and BS (Brown Swiss) crosses with 50%, 25% and 12.5% GH genes on farms A and D

AFS = Age at first service, AFC = Age at first calving, ICI = Inter-calving interval
Significance: AFS MON12.5 vs. GH, MON50 ($p < 0.05$), GH vs. BS50, BS25 ($p < 0.001$), BS50 vs. BS25, BS12.5 ($p < 0.05$)
AFC GH BS50 ($p < 0.001$), GH vs. BS2;5 ($p < 0.05$); BS50 vs. BS25 ($p < 0.05$), BS50 vs. BS12.5 ($p < 0.001$); ICI GH vs. BS50 ($p < 0.01$)

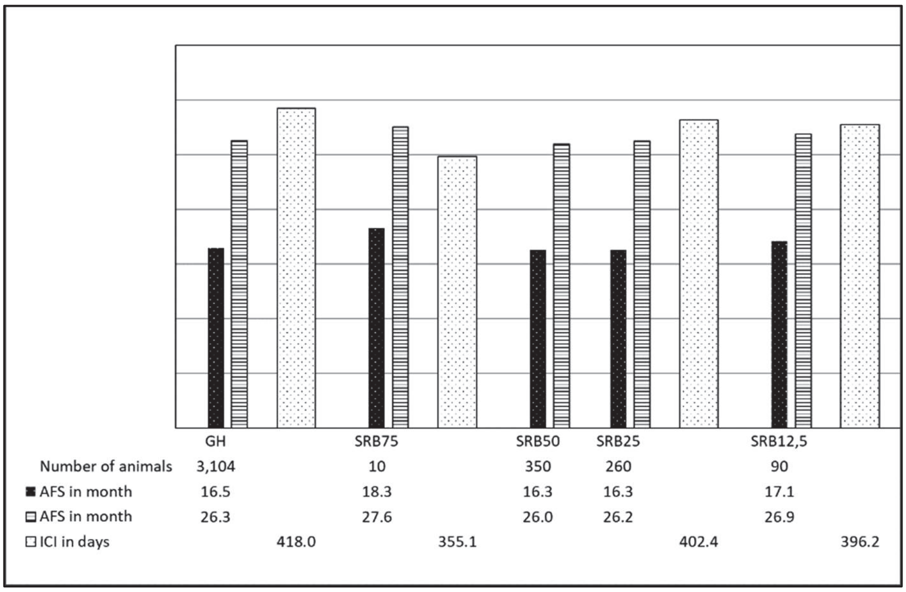


Figure 32: Fertility performance for German Holsteins (GH) vs. SRB (Swedish Red) crosses with 75%, 50%, 25% and 12.5% GH genes

AFS = Age at first service, AFC = Age at first calving, ICI = Inter-calving interval
Significance: AFS SRB75 vs. SRB50, SRB25 ($p < 0.05$); ICI GH vs. SRB75 ($p < 0.05$)

Although the lifetime production of MON crosses and GH cows on farm A differed in terms of the milk yield, this difference was not significant (Figure 33, Table A9). With 27,020 kg the MON50 had on average a higher milk yield than the GH (25, 604 kg MY) but the two genotypes only differed slightly in the average number of milking days (795.7 vs. 775.9 dm). The worst performers were the six cows with the MON12.5 genotype (18, 572 kg MY, 560.7 dm). On farm D (Figure 33, Table A10) the GH produced significantly more milk than the BS50 and BS12.5 crosses (24, 356 vs. 18, 173 and 13, 455 kg MY). What is noteworthy is the different number of milking days for the GH, which is also significantly higher (956.2 vs. 765.9 and 543.0 dm). BS12.5 cows had considerably lower values for both parameters, with a significant difference compared to BS25.

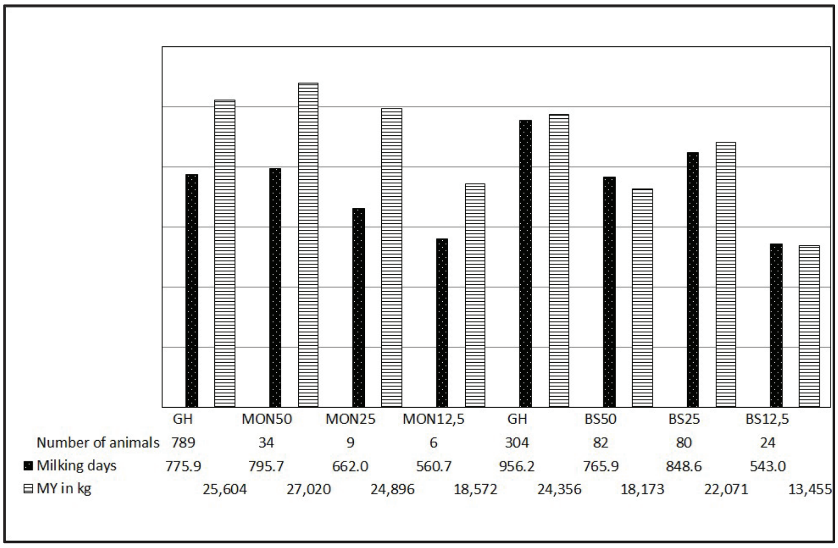


Figure 33: Milk production for German Holsteins (GH) vs. MON (Montbéliarde) and BS (Brown Swiss) crosses with 50%, 25% and 12.5% GH genes on farms A and D

Significance: milking days GH vs. BS50, BS25, BS12.5 ($p < 0.05$), BS25 vs. BS12.5 ($p < 0.05$); milk in kg GH vs. BS50, BS12.5 and BS50 vs. BS25 ($p < 0.05$)

Crosses of SRB and GH did not show any trend depending on the genetic composition of the cross (Figure 34, Table A11). Purebred GH produced 26, 503 kg MY over 903.7 milking days. As the percentage of GH genes increased, values of 26, 049 kg MY (SRB50), 29, 684 kg MY (SRB25) and 21, 215 kg MY (SRB12.5) were recorded whereas the eight cows with 25% GH genes produced only 18, 719 kg MY. Similar results were seen for the average number of milking days (dm) with no influence of the genetic composition apparent.

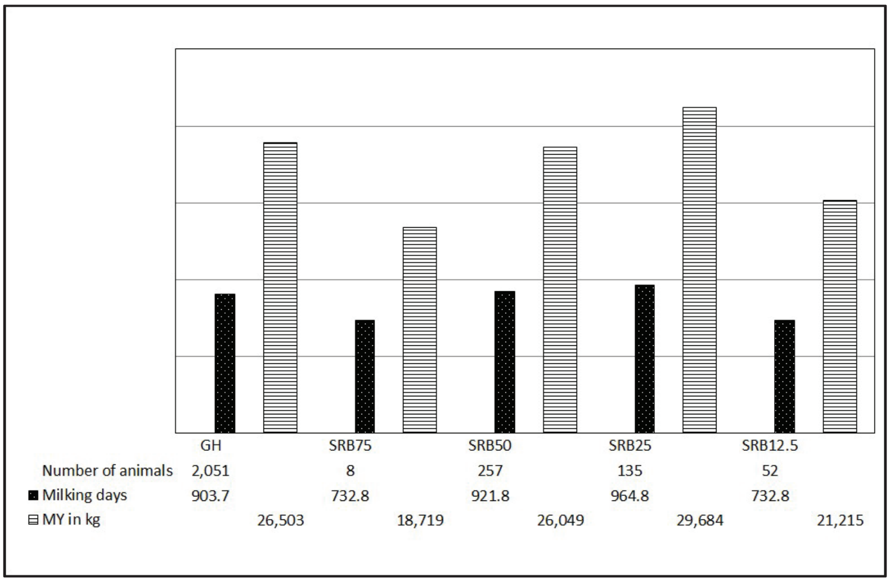


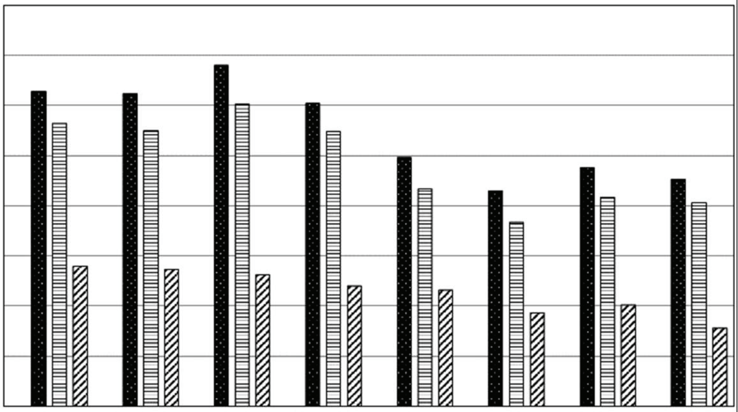
Figure 34: Milk production for German Holsteins (GH) vs. SRB (Swedish Red) crosses with 75%, 50%, 25% and 12.5% GH genes

The means for the backcrosses do not provide any information about the efficiency of the milk production depending on the percentage of GH genes.

The highest values for the production and Lifetime efficiency (LEff) for the milk production were seen for the GH with significant differences for GH vs. BS crosses, with the exception of BS25 for MEff and PEff (Figure 35, Figure 36, Tables A9, A10, A11).

For MEff the MON crosses of the three generations were equivalent with MON25 performing more efficiently by 2.6 kg MY per dm, but this was not significant. F2 backcrosses with GH (25% MON, BS and SRB genes) each had higher means for the efficiency parameters than the F1 crosses with 50% genes with this being significant for BS50 vs. BS25.

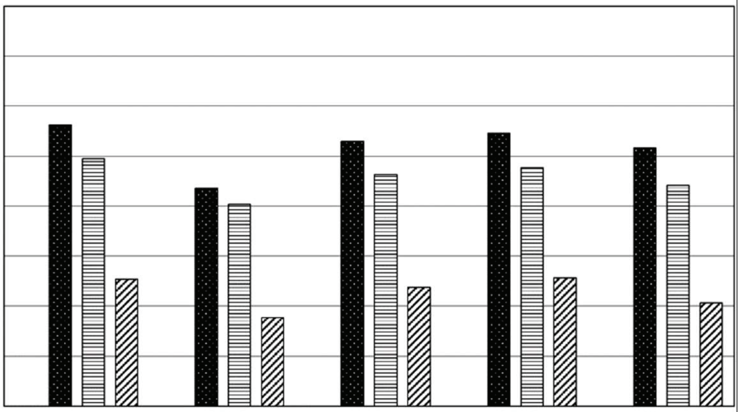
The eight SRB75 cows are inferior to the GH with the difference being significant for MEff and PEff (28.1 vs. 21.8 kg MY per dm, 24.7 vs. 20.2 kg MY per pd, 12.7 vs. 8.8 kg MY per dl). These values are also lower than the efficiency values for the cows with lower percentages of SRB genes, significantly so for the MEff.



	GH	MON50	MON25	MON12,5	GH	BS50	BS25	BS12,5
Number of animals	789	34	9	6	304	82	80	24
■ kg milk/dm	31.4	31.1	34.0	30.2	24.8	21.4	23.8	22.6
⊟ kg milk/pd	28.2	27.5	30.1	27.4	21.7	18.3	20.8	20.3
▨ kg milk/dl	14.0	13.7	13.1	12.0	11.6	9.3	10.1	7.8

Figure 35: Efficiency of the milk production for German Holsteins (GH) vs. MON (Montbéliarde) and BS (Brown Swiss) crosses with 50%, 25% and 12.5% GH genes on farms A and D

Significance: MEff: GH vs. BS50, BS25, BS12.5 ($p < 0.05$), BS50 vs. BS25 ($p < 0.05$), LEff: GH vs. BS50, BS25, BS12.5 ($p < 0.05$), BS25 vs. BS12.5 ($p < 0.05$)



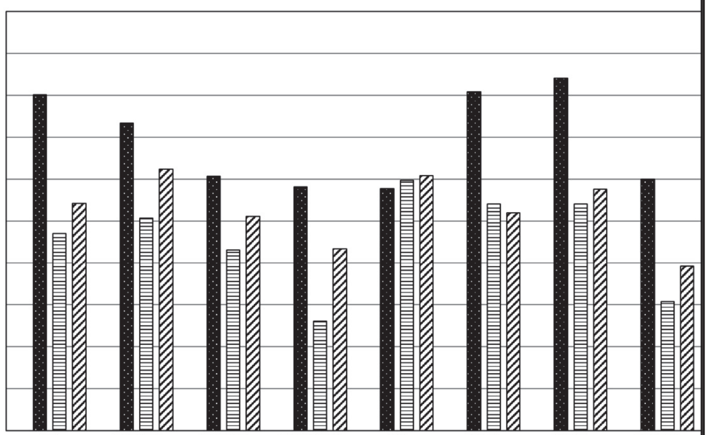
	GH	SRB75	SRB50	SRB25	SRB12,5
Number of animals	2,051	8	257	135	52
■ kg milk/dm	28.1	21.8	26.5	27.3	25.8
⊟ kg milk/pd	24.7	20.2	23.1	23.9	22.1
▨ kg milk/dl	12.7	8.8	11.8	12.8	10.3

Figure 36: Efficiency of the milk production for German Holsteins (GH) vs. SRB (Swedish Red) crosses with 75%, 50%, 25% and 12.5% GH genes

Significance: MEff GH vs. SRB75, SRB50 ($p < 0.001$), SRB75 vs. SRB50, SRB25, SRB12.5 ($p < 0.05$), PEff GH vs. SRB75, SRB12.5 and SRB75 vs. SRB25 ($p < 0.05$)

Age at cull, PP and number of lactations decline with an increasing percentage of GH genes for the MON crosses (Figure 37, Tables A9, A10). On farm A the GH cows were culled with the highest average age of 4.0 years followed by MON50 with 3.7 years on average. On farm D the highest culling age was reported for the BS25 (4.2 years) and the BS50 cows also left the herd with a relatively high average age of 4.0 years.

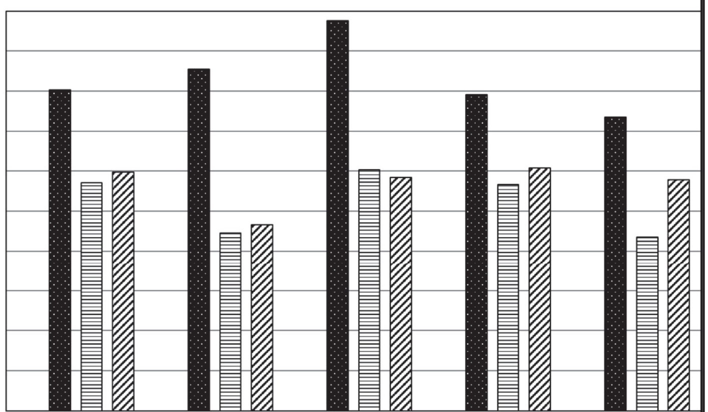
Cows with a high percentage of SRB genes were older than GH on average, with 4.0 and 4.9 years, but not significantly so (Figure 38, Table A11). For the PP and the number of lactations, GH and the SRB50 and SRB25 crosses were at a similar level of 2.8 to 3.0 years and 2.9 to 3.0 lactations, respectively. Cows with 75% and 12.5% SRB genes had a Productive period of 2.2 years, which is considerably but not significantly lower.



	GH	MON50	MON25	MON12,5	GH	BS50	BS25	BS12,5
Number of animals	950	47	14	12	641	163	117	40
■ Age at cull in years	4.0	3.7	3.0	2.9	2.9	4.0	4.2	3.0
⊟ Productive period in years	2.4	2.5	2.2	1.3	3.0	2.7	2.7	1.5
▨ Number of lactations	2.7	3.1	2.6	2.2	3.0	2.6	2.9	2.0

Figure 37: Age and Productive period on departure for German Holsteins (GH) vs. MON (Mont-béliarde) and BS (Brown Swiss) crosses with 50%, 25% and 12.5% GH genes on farms A and D

Significance: Age at cull: GH vs. Mon12.5 ($p < 0.01$), GH vs. BS50, BS25 ($p < 0.001$), BS12.5 vs. BS50, BS25 ($p < 0.05$); Productive period: MON12.5 vs. GH, MON50 ($p < 0.05$), BS12.5 vs. GH, BS50, BS25 ($p < 0.001$); Number of lactations: MON50 vs. MON12.5; BS12.5 vs. GH, BS25 ($p < 0.05$)



	GH	SRB75	SRB50	SRB25	SRB12,5
Number of animals	2,831	9	384	278	82
■ Age at cull in years	4.0	4.3	4.9	4.0	3.7
⊟ Productive period in years	2.9	2.2	3.0	2.8	2.2
▨ Number of lactations	3.0	2.3	2.9	3.0	2.9

Figure 38: Age and Productive period at cull as well as number of lactations for German Holsteins (GH) vs. SRB (Swedish Red) crosses with 75%, 50%, 25% and 12.5% GH genes

For the crosses, the higher percentage of MON, BS and SRB genes had a negative impact on udder health (Figure 39, Figure 40, Tables A9, A10, A11). The higher Somatic cell count is, however, only significant for BS50 and BS12.5 crosses vs. GH. The comparison was similar for the proportion of cows with healthy udders on test days (increasing proportion) and the proportion of cows in the class >400 × 10^3 SC per ml of milk (decreasing proportion). However, the results for the SRB75 cows did not correspond to those of all the other crosses. For this cross, a mean SC count of 271.7 × 10^3 SC per ml of milk was recorded along with the lowest proportion of test-day cows with healthy udders (35%) and the highest proportion of test days with >400 × 10^3 SC per ml of milk.

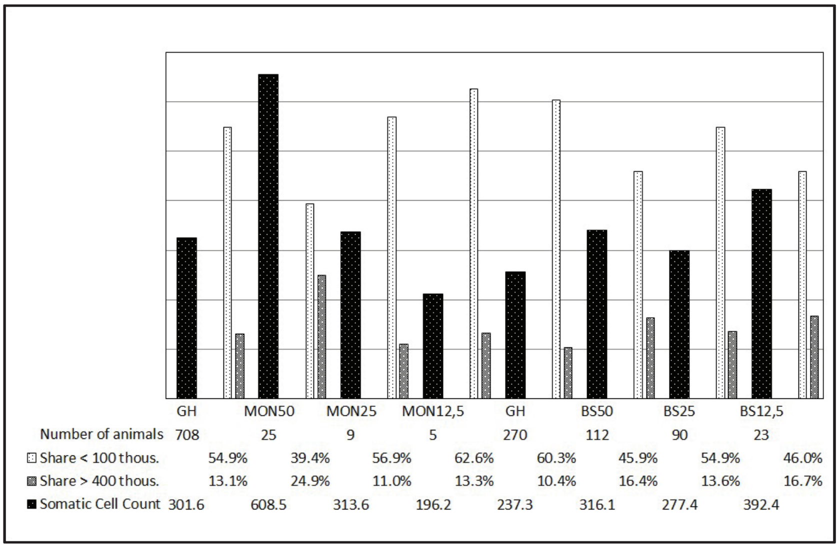


Figure 39: Somatic cell count per ml of milk for German Holsteins (GH) vs. MON (Montbéliarde) and BS (Brown Swiss) crosses with 50%, 25% and 12.5% GH genes on farms A and D

thous. = thousand

significance: SC in thousand / ml milk: GH vs. BS50 ($p < 0.05$); SC < 100 thousand / ml milk; GH vs. MON50 ($p < 0.001$), GH vs. BS12.5 ($p < 0.01$), BS50 vs. BS25 ($p < 0.05$), SC > 400 thousand / ml milk: GH vs. BS50 ($p < 0.01$)

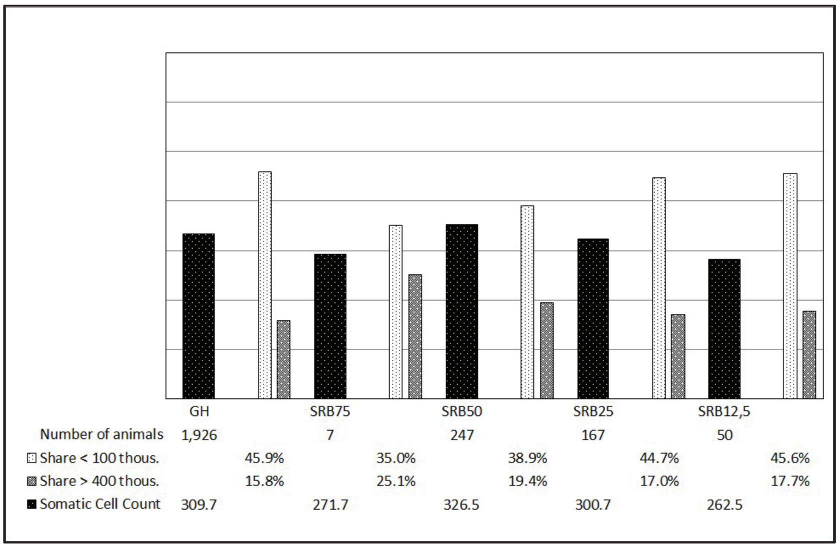


Figure 40: Somatic cell count per ml of milk for German Holsteins (GH) vs. SRB (Swedish Red) crosses with 75%, 50%, 25% and 12.5% GH genes

thous. = thousand

4.5 Age at first calving and Lifetime efficiency of daughters of the breeds MON, JER, BS and SRB and daughters of selected sires of these breeds

In the following comparison of the performance, the genotype of the dam is disregarded. The comparison group includes all GH with their sires not considered separately here.

The influence of the sire's breed was investigated using the F1 daughters of MON, JER, BS and SRB bulls (Table 32). For the comparison of the performance of the daughters of selected sires, the sires were ranked by the average performance of their F1 daughters. The ten highest-ranking sires with the highest-performing daughters (lowest mean Age at first calving, highest mean Lifetime efficiency) were compared to each other and to purebred GH (Table 33).

Table 32: Number of GH analysed and F1 daughters and sires of the Montbéliarde, Jersey, Brown Swiss and Swedish Red breeds for fertility and milk production (Age at first calving and Lifetime efficiency)

	Age at first calving		Lifetime efficiency	
Breed	Number of daughters	Number of sires	Number of daughters	Number of sires
GH	3,783		3,782	
MON	165	3	130	3
JER	57	4	51	3
BS	428	13	95	13
SRB	578	17	149	17

GH = German Holsteins, MON = Montbéliarde, JER = Jersey; BS = Brown Swiss; SRB = Swedish Red Breed

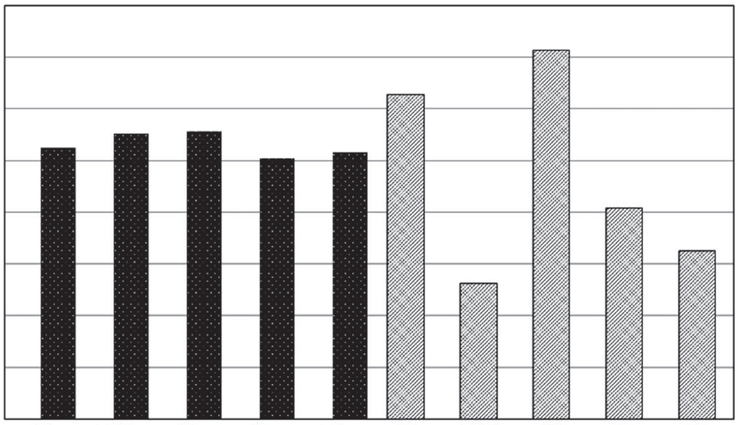
Table 33: Number, name and breed of the sires with the best-performing daughters

Number	Name	Breed	Number	Name	Breed
1	Triomphe	MON	17	Hucos	BS
2	Helux	MON	19	Juwel	BS
4	Plumitif	MON	22	Peterslund	SRB
5	Paul	JER	28	A Linne	SRB
6	Brazo	JER	31	Langbo	SRB
7	Rampant	JER	37	Gunnarstorp	SRB
9	Eagel	BS	38	Tuima	SRB
14	Agenda	BS			

MON = Montbéliarde, JER = Jersey; BS = Brown Swiss; SRB = Swedish Red Breed

The AFC of F1 heifers of the MON and JER breeds is on average 1.4 and 1.6 months higher than the AFC of the comparison sample of GH and 1.8 to 2.6 months higher than the SRB and BS daughters (Figure 41, Table A12). Due to the large spread from 20.3 months for the minimum and 37.6 months for the maximum for the GH (sf = 1.42) and 21.9 to 35.7 months (sf = 1.43–1.86) for the crosses, the differences are not significant. For the fertility, the F1 daughters of BS sires have a mean AFC of 25.2 months, which is lower than that of the SRB daughters (25.8 months) and GH (26.2 months).

JER F1 daughters achieve the highest efficiency with 13.6 kg MY per dl followed by purebred GH with 13.1 kg MY per dl. BS F1 daughters with 12.0 kg MY per dl performed better than the SRB F1 daughters (11.6 kg MY per dl). For the Lifetime efficiency, the F1 daughters of the MON breed performed the worst with 11.3 kg MY per dl. Except for the JER daughters, the crosses are significantly inferior to the GH ($p<0.01$). Significance was also demonstrated for the LEff between the F1 daughters of JER vs. MON and SRB ($p<0.05$, Table A12).



Breed of sires	GH	MON	JER	BS	SRB	GH	MON	JER	BS	SRB
Number of daughters	3,783	165	57	428	578	3,782	130	51	95	149
■ AFC in month	26.2	27.6	27.8	25.2	25.8					
▨ kg milk/dl						13.1	11.3	13.6	12.0	11.6

Figure 41: AFC in months and Lifetime efficiency in kg MY per day of life for purebred German Holsteins (GH) vs. daughters of the breeds Montbéliarde (MON), Jersey (JER), Brown Swiss (BS) and Swedish Red (SRB) with 50% GH genes

AFC = Age at first calving, dl = day of life; significance: LEff in kg milk / dl: GH vs. daughters of MON ($p < 0.01$), daughters of BS ($p = 0,01$), daughters of SRB ($p < 0.001$)

The mean AFC of the GH was 26.0 months and thus significantly higher than that of the daughters of the sires Triomphe (25.0 months, MON, $p<0.001$), Brazo (23.8 months, JER, $p<0.001$), Rampant (24.2 months, JER, $p<0.01$), Gunnarstorp and Tuima (24.5 months, SRB, $p<0.05$). A comparable average AFC was observed for the daughters of the sires Helux (26.1 months, MON) and A Linne (26.1 months, SRB). Although the daughters of the sires Plumitif (25.5 months, MON), Agenda (25.3 months, BS) and Langbo (25.4 months, SRB) have lower AFC values, the difference to the GH is not significant. Comparing the average values for the AFC between the crossbred daughters reveals significant differences between the MON sire Helux as well as the SRB sire A Linne and the JER sires Brazo ($p<0.01$) and Rampant ($p<0.05$) (Figure 42, Table 34, A13, A14).

For the Lifetime efficiency (LEff) there is a significant difference between the daughters of the sires Peterslund (12.0 kg MY per day of life (dl), SRB) vs. GH (13.7 kg MY per dl, $p<0.01$) and the Triomphe and Plumitif daughters (13.9 and 15.3 kg MY per dl, MON, $p<0.05$). The lower LEff for the daughters of the JER sire Paul of 11.8 kg MY per dl and the SRB sire Peterslund (12.0 kg MY per dl) are not significant. The same is true of the highest LEff of the Rampant daughters and the LEff of the remaining daughters (Figure 43, Table 35, A13, A15).

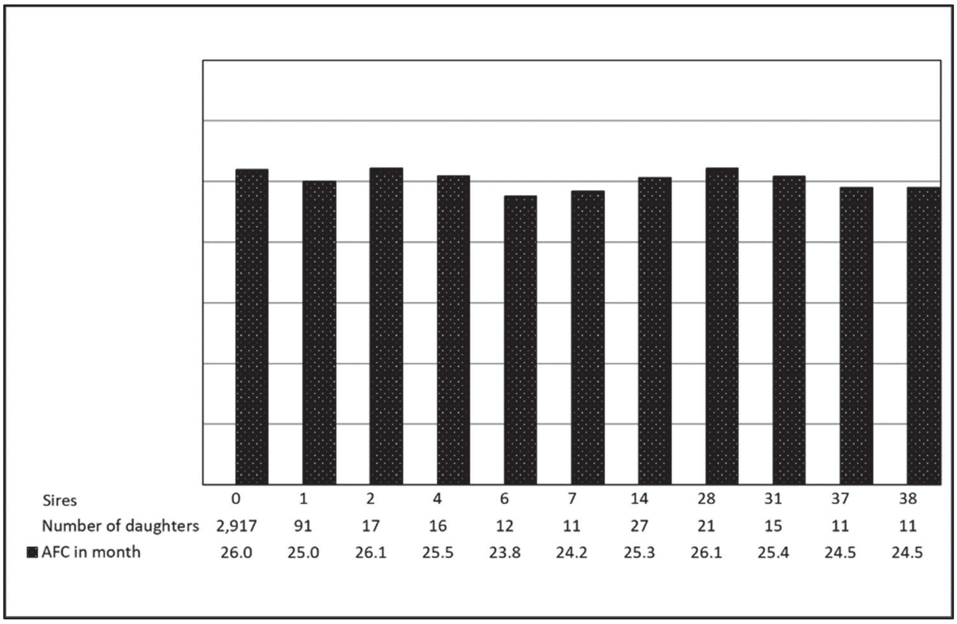


Figure 42: AFC in months for daughters of the breeds German Holsteins (sire 0), Montbéliarde (sires 1, 2, 4), Jersey (sires 6, 7), Brown Swiss (sire 14) and Swedish Red (sires 28, 31, 37, 38)

AFC = Age at first calving

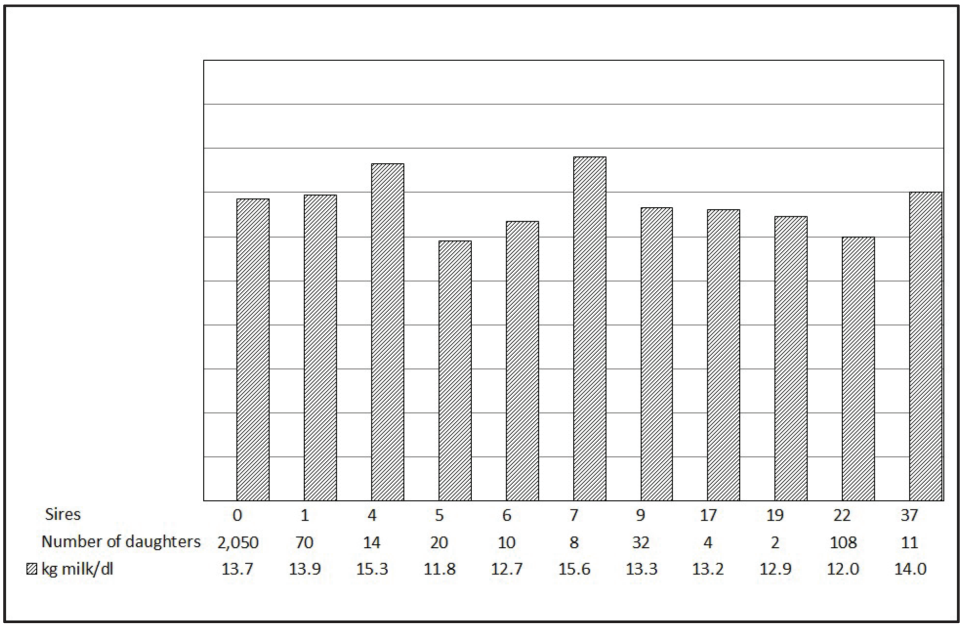


Figure 43: Lifetime efficiency in kg MY per day of life of daughters of the German Holsteins breed (sire 0), Montbéliarde (sires 1, 4), Jersey (sires 5, 6, 7), Brown Swiss (sires 9, 17, 19) and Swedish Red (sire 37)

dl = day of life

Table 34: Ranking of the sires by the average Age at first calving in months of their F1 daughters

	Sire			F1-daughters	
Rank	Name	Number	Breed	Number	Average AFC
1	Brazo	6	JER	12	23.8
2	Rampant	7	JER	11	24.2
3	Gunnarstorp	37	SRB	11	24.5
4	Tuima	38	SRB	11	24.5
5	Triomphe	1	MON	91	25.0
6	Agenda	14	BS	27	25.3
7	Langbo	31	SRB	15	25.4
8	Plumitif	4	MON	16	25.5
9		0	GH	2,917	26.0
10	Helux	2	MON	17	26.1
11	A Linne	28	SRB	21	26.1

MON = Montbéliarde, JER = Jersey; BS = Brown Swiss; SRB = Swedish Red Breed = AFC = Age at first calving in months

Table 35: Ranking of the sires by the average Lifetime efficiency in kg milk / dl of their F1 daughters

	Sire			F1-daughters	
Rank	Name	Number	Breed	Number	Average
1	Rampant	7	JER	8	15.6
2	Plumitif	4	MON	14	15.3
3	Gunnarstorp	37	SRB	11	14.0
4	Triomphe	1	MON	70	13.9
5		0	GH	2,050	13.7
6	Eagel	9	BS	32	13.3
7	Hucos	17	BS	4	13.2
8	Juwel	19	BS	2	12.9
9	Brazo	6	JER	10	12.7
10	Peterslund	22	SRB	108	12.0
11	Paul	5	JER	20	11.8

GH = German Holsteins, MON = Montbéliarde, JER = Jersey; BS = Brown Swiss; SRB = Swedish Red Breed

4.6 Influence of the herd level on the performance differences between GH and crosses (GH vs. BS50 and SRB50)

Using the example of the crosses with 50% GH as well as 50% BS and SRB genes (genotypes BS50 and SRB50), the extent of the influence of the herd level on the performance differences is analysed (Table 36, A17, A18). The performances on farms A, B and C correspond to the average level. Because the performances on farm D for the milk yield and the Lifetime efficiency are significantly lower than on the other three farms, this herd is assigned a lower production level.

Independent of the herd level, the crosses are only superior to purebred GH for the fertility (AFC and ICI).

With lower milk yield and high AFC (farm D), the cross of GH with BS and SRB appears to be disadvantageous overall (Table 36, A17, A18). Only AFC and ICI are highly significantly below GH or trending (BS50 ICI) below GH. For the milk production the purebred GH are significantly superior to the crosses. What is noteworthy is the worse health of the crosses with a tendentially lower Productive period (2.9 to 2.7 years) and the tendentially to highly significantly worse udder health (261 × 10^3 vs. BS50 316 × 10^3 and SRB50 339 × 10^3 SC per ml of milk).

With an average production level, the crossbreeds achieved better yields than the purebred GH (Table 36, A17, A18).

However, these differences are only significant for the ICI vs. BS50 on farm C, and for the AFC and the proportion of milk samples with <100 × 10^3 somatic cells per ml of milk the differences are approaching certainty (Table A17).

On farm A (mean production level, Table 36, A18) the cows with the SRB50 genotype tend to have a longer Productive period than the GH while their mean ICI is significantly lower. The Somatic cell count as a measure of udder health is on average lower for the SRB crosses than for GH (GH 309 × 10^3 vs. SRB50 256 × 10^3 SC per ml of milk). For the proportion of cows with healthy udders, the GH cows with 52.3% in the class with <100 × 10^3 SC per ml of milk are ahead of the crosses (49.6%) but neither are verified.

On farm B (mean production level, Table 36, A18) the AFC of the SRB50 crosses tends to be lower than that of the GH while the ICI is highly significantly lower than that of the GH. The superiority of the SRB50 for milk yield (42,941 vs. 32,567 kg MY) and Productive period (5.0 vs. 3.5 years) is significant. Furthermore, they have a higher Lifetime efficiency of 15.1 vs. 13.2 kg MY per day of life, but this is not statistically confirmed. The health trait "mean number of somatic cells per ml of milk" is in favour of GH (GH 312 × 10^3 vs. SRB50 414 × 10^3 SC per ml of milk) but again this is not significant. The proportion of milk samples with <100 × 10^3 SC per ml of milk of 49.2% for GH is above the average for the SRB50 of 47.3%. The proportion of samples with >400 × 10^3 SC per ml of milk for the crosses of 20.8% tends to be higher than for the GH with 14.4%.

Table 36: Mean yields of GH vs. BS50 and SRB50 on farms with moderate (A, B, C) and low (D) herd level

Herd level	Medium			Low
Farm Parameter	A	B	C	D
All Genotypes, n =	**2,144**	**825**	**673**	**2,623**
Age at first calving (month)	25.2	26.3	25.9	27.5
Inter-calving interval (days)	400.6	424.9	404.6	415.9
Lifetime milk production (kg milk)	29,171	32,824	24,578	19,766
Lifetime efficiency (kg milk / dl)	14.5	13.2	12.9	9.8
Productive period (years)	2.8	3.5	2.4	2.5
Somatic Cells (thousand / ml milk)	316	317	350	291
German Holsteins, n =	**1,661**	**757**	**483**	**881**
Age at first calving (months)	25.2	26.3	26.0	27.7
Inter-calving interval (days)	403.5	429.5	413.0	429.0
Lifetime milk production (kg milk)	29,171	32,567	24,679	23,879
Lifetime efficiency (kg milk / dl)	14.5	13,2	13,0	11,4
Productive period (years)	2.8	3.5	2.4	2.9
Somatic Cells (thousand / ml milk)	309	312	361	261
BS50, n =			**88**	**169**
Age at first calving (months)			25.6	26.8
Inter-calving interval (days)			385.4	405.0
Lifetime milk production (kg milk)			26,501	18,173
Lifetime efficiency (kg milk / dl)			13.4	9.3
Productive period (years)			2.7	2.7
Somatic Cells (thousand / ml milk)			329	316
SRB50, n =	**57**	**21**		**346**
Age at first calving (months)	25.0	25.5		27.2
Inter-calving interval (days)	381.1	393.3		399.9
Lifetime milk production (kg milk)	32,226	42,941		19,843
Lifetime efficiency (kg milk / dl)	14.4	15.1		9.6
Productive period (years)	3.4	5.0		2.7
Somatic Cells (thousand / ml milk)	256	414		339

GH = German Holsteins, BS = Brown Swiss, SRB = Swedish Red Breed, numbers in the Genotype indicate the proportion of genes in %, n = number of animals, dl = day of life

5 Discussion

In Germany, the dairy industry is one of the most important agricultural sectors. The total number of dairy cows in Germany has dropped considerably over the last 25 years despite increasing milk production. While in 1995 there were 5.2 million cows across Germany, by 2021 the population had fallen to below 3.9 million animals. And this trend appears to be continuing. (FEDERAL STATISTICAL OFFICE OF GERMANY, 1995; BMEL, 2022)

As described in Section 2, crossbreeding is carried out on farms that keep dairy cows to improve the fertility and health of the herds while retaining the production level of the German Holsteins (GH). It is therefore of interest if crosses can meet this requirement, but this will only become apparent in cattle breeding after many years because of the long generational interval and the long Productive period that is desired.

These studies were performed with data from four farms in Mecklenburg-Vorpommern and Brandenburg that started crossbreeding in 2003 to 2006 and had in some cases ceased milk production when this paper was written (farms A and C).

The crosses made up on average 11% to 42% of the cow stock on the study farms when the last data were collected with 63% on farm D in 2020. On all farms GH were crossed with Swedish Red (SRB). Montbéliarde (MON) was used on farms A and B. Brown Swiss (BS) was the crossbreeding partner for GH on farms A, C and D while Jersey (JER) was used on farms C and D.

Using the Herde and HerdePlus management software from dsp-Agrosoft GmbH, the data were collected and analysed considering the effect of the cohort and farm.

5.1 Performance comparison of German Holsteins (GH) vs. crosses with 50% GH genes

5.1.1 GH vs. MON × GH

In the current studies MON50 crosses were on average the youngest F1 heifers at first service with 15.1 months. The average for the GH is 16.5 months but the differences in the means vs. GH are not significant for either the AFS or the AFC. The mean ICI for the GH tends to be higher with 418.3 days than the ICI of the crosses with 50% MON genes (381.8 days, p= 0.051).

Because the Montbéliarde (MON) breed belongs to the population of Simmental cattle (SI) (Section 2.4.2.1), comparing the results from our study with the performances of this breed and the German Simmental (SI) is logical.

As in our study, the ICI of the F1 crosses of SI and GH were below the mean of the purebred GH cows. A comparison of GH, SI and their F1 crosses revealed that the purebred GH had the lowest AFC, however. (SCHICHTL, 2007)

In contrast, cows with a high percentage of SI genes did not differ from GH in terms of the AFC in studies conducted by DIEPOLD (2019).

In studies by PENASA (2009) and PENASA et al. (2010), HO × MON crosses had an ICI over an average of five calvings that was 10.2 days below that of the parent generation (Irish purebred HO, MON), which is attributed to a heterosis effect.

Dairy HO × SI crossbred cows showed better reproductive performance in the comparison with HO cows (ICI 381 vs. 445 days, Conception rate 37.3% vs. 33.6%). There were no differences seen for the AFC and calving ease, however. These results are reflected in the better condition of the crossbred animals (BCS 3.63 vs. 2.94). There were no differences between the genetic groups in terms of the body weight (p>0.05). (KNOB et al., 2016)

Backcrossing to increase the proportion of SI genes in a crossbred herd (GH × SI in alternating crossbreeding) on the Teaching and Research Farm of the Faculty of Veterinary Medicine

Oberschleißheim of the Ludwig-Maximilians-Universität Munich, also had a positive, shortening effect on the ICI. Over five years the average ICI decreased from 434 to 401 days (DIEPOLD, 2019).

The positive effective of crossbreeding of MON × GH on the AFS and AFC and the shortening of the ICI was also confirmed by MALCHIODI et al. (2011) and MALCHIODI et al. (2014).

Regarding milk production, in our studies we observed a high mean for the MON crosses, higher than the milk yields for JER and BS crosses. The Productive period (2.5 years) and culling age (3.7 years) are below the means of the other F1 crosses. The high milk yield with a lower age leads to the highest average efficiency, relative to age (13.4 kg MY per dl), but this is not significant. Relative to the milking days, the MON50 crossbred cows with 30.8 kg were the only genotype to exceed the economic threshold of ≥ 30.0 kg MY defined by WANGLER AND HARMS (2009). MON crosses are mostly on farm A, which recorded for its herds the highest efficiency for milk production of all four study farms. Although as part of the statistical analysis the data were corrected for the farm effect, it could be inferred that the management system plays a critical role for the efficiency parameters.

In studies conducted by HOUDEK (2019) in seven herds in Minnesota, US, crosses of MON × HO were equal to purebred HO in the 305-day milk yield in the 1st to the 3rd lactations.

In the quantifiable characteristics of milk production, the F1 crossbred animals investigated by SCHICHTL (2007) are superior to purebred SI but not GH. The heterosis effects are 276 kg for the (uncorrected) milk volume, referring to a complete lactation.

OUWELTJES (2012) assumed the heterosis effect because his studies showed that the 305-day milk yields for HO and crosses of SI × HO did not differ significantly, even though the purebred SI were inferior to the HO by 943 kg and the sires' Breeding values lead him to expect better performance for the purebred daughters.

NOLTE (2019) evaluated data from animals crossbred between SI and GH with different genetic compositions. As expected, the purebred GH cows yielded the highest milk volumes while the crossbred animals with 50% SI genes lay in the range of the average of the parental animals.

Health traits are examined in our study using the age at culling, the Productive period and the SC per ml of milk. The F1 MON crosses performed worst in this regard. While the PP was still the same as the average of the other genotypes, the mean SCC was very high, more than 100×10^3 SC per ml of milk higher than for BS50, which had the second highest value. Accordingly, the MON50 crosses achieved the lowest percentage of milk samples with $<100 \times 10^3$ SC per ml of 41% whereas the other genotypes achieved 45% to 49%.

In contrast, MALCHIODI et al. (2011) reported a lower SCC but the difference between the means of the HO and the MON × HO was not significant.

In other studies crossing with SI resulted in improvements in a GH herd for fitness and udder health (reduction in SC) but the milkability worsened. The crosses were superior to GH cows in terms of metabolic stability and udder health. (GRUPP, 2001b, 2003; SCHICHTL, 2007; BAADEN, 2012)

NOLTE (2019) found in a genotype comparison that, despite higher milk production, cows with 10% SI genes had the second-lowest Somatic cell counts. Particularly high SC counts were observed in a group with 50% SI genes, but the values barely differed from those of purebred GH cows.

For two-thirds of all 1,435 SI cows analysed by HANEMANN (2014) on 35 farms in Bavaria, at least one claw disorder was diagnosed. However, F1 cows from a cross between Polish HF dams with MON sires showed a trend toward better functional traits compared to purebred Polish HO cows (PUPPEL et al., 2017). In studies by DIEPOLD (2019), F1 cows with 50% SI genes also achieved the highest age at the time of culling (2,415 days) and had a PP that was 16% longer than the average recorded for purebred German Holsteins.

Crossbred HO × SI cows had a higher survival rate in the 2nd lactation than HO cows (83% vs. 92%). On average the percentage of cows that ended the 1st, 2nd and 3rd lactation was higher in the crossbred cows than the HO cows. (KNOB et al., 2016)

Under subtropical conditions, crosses of SI × HO showed the best performances for reproduction (Conception rate, calving to conception interval, Inter-calving interval) and health (disease rate). For the AFC, the SI × HO crosses were equal to the HO (24.8 vs. 24.6 months). (NASR et al., 2021)

5.1.2 GH vs. JER × GH

JER heifers in this genotype comparison clearly reach breeding maturity later than GH (18.1 vs. 16.5 months). As adult animals the JER crosses are characterised by high fertility, as evidenced by the ICI, which is significantly lower than that of the purebred GH and clearly lower than the average (JER50 375.4 days vs. GH 418.3 days).

A similar result was seen for the fertility of JER animals in crossbreeding experiments in Saxony in which F1 animals (JER × GH) had significantly shorter calving to first service intervals and ICI compared to GH (385.3 vs. 400.5 days) (BRADE, W., 2014).

Crosses between Polish HF and JER achieved a mean ICI of 403 days, a better result than HF with a 446-day ICI on average (ADAMCZYK et al., 2018).

The lower milk production of the JER50 in our studies in terms of the yield (20,481 kg MY) and efficiency (10.6 kg MY per dl) corresponds to expectations because here only the milk yield and not the fat and protein yields are compared. The high average culling age of 5.2 years is explained by the low culling rate of the heifers up to the 1st calving (5.3% vs. 22.9% GH vs. 23.0% CB) because the Productive period is only average at 2.5 years. Regarding the udder health, the JER50 with 437.3 × 10^3 SC per ml of milk take the second-last place with only the MON50 crosses performing worse with a mean of 557.1 × 10^3 SC per ml of milk.

PRENDIVILLE et al. (2010) observed that F1 daughters of HF × JER had higher milk production (p<0.001) and higher milkability (p<0.01) compared to the mean of the parental breeds, which corresponds to a heterosis effect of +1.0 kg milk per day (+5.8%). For the absolute milk production they were below the HF but significantly above purebred JER (HF 18.0 kg/day vs. JER 14.2 kg/day vs. F1 JER × HF 17.1 kg/day).

Purebred Polish HF achieved an average age of 6.3 years with 28,933 kg milk and an efficiency of 20.2 kg milk per milking day. For crosses of JER × HF, a lower mean age of 6.1 years and a lifetime production of 27,340 kg milk were recorded but the milk yield per milking day was the same as the HF. (ADAMCZYK et al., 2018)

An Irish study compared the milk production and fertility performance of purebred Holstein (HO), Friesian (FR) and JER cows and their respective crosses in 40 commercial dairy cattle herds with spring calving. HO × FR cows, HO × JER cows and FR × JER cows calved earlier than their purebred parents and had shorter ICIs. The milk yield was, as expected, the highest for the HO (5, 217 kg), moderate for FR (4,591 g) and lowest for JER (4,230 kg). (COFFEY et al., 2016)

Breed effects for production traits fall in favour of HO for the milk yield in Irish dairy cows (1st to 5th lactation). For the ICI, crosses of HO × FR and HO × JER were superior to purebred HO. (PENASA, 2009; PENASA et al., 2010)

In the late 1990s in New Zealand crossbreeding was performed resulting in a proportion of 18% (HO × JER). Under the market values for milk and beef that prevailed at the time, rotational crossbreeding herds of HO × JER were more profitable than purebred herds. (HO × JER 505 NZ$/ha vs. HO 398 NZ$/ha) (LÓPEZ-VILLALOBOS; GARRICK; HOLMES; et al., 2000)

In a genotype comparison by SCHWAGER-SUTER et al. (2001) JER × HO crosses also proved to be more efficient than purebred cows.

AULDIST et al. (2007) compared the reproductive performance and milk production as well as live weight and body condition during early lactation of purebred HO cows with JER × HO crosses with 25, 50 or 75% HO genes in four Australian herds. The HO cows had a daily milk yield in early lactation that was higher by 2.2 kg compared to the crosses. The daily yields of milk fat and protein did not differ during the study period between the HO and JER × HO cows. The better fertility of the crosses was demonstrated by the higher Conception rates.

The better reproductive performance of JER crosses compared to HO was also confirmed by ANDERSON et al. (2007). The incidence of lameness in JER × HO cows was also 13.0 percentage points lower than for HO cows and the culling rate was 5.1 percentage points lower.

HEINS et al. (2008) observed a significantly lower milk yield (4,388 vs. 4,644 kg) from day 4 to 150 of lactation for JER × HO cows than for purebred HO cows. The fat and protein production during the first 150 days of lactation was not significantly different between the crosses (302 kg) and the HO cows (309 kg), however.

Crossbred cows of JER × HO and HO × JER had a significantly higher likelihood of developing mastitis compared to purebred HO and JER cows in a study by OLSON et al. (2011). On the other hand, the AFC did not differ significantly.

In adult three-year-old HO × JER crossbred cows, DAL PIZZOL et al. (2014) observed a lower SC count at the time of calving ($p<0.0001$) with a lower daily milk yield (F1 HO × JER vs. HO: 30.81 ± 0.25 vs. 33.24 ± 0.29 kg/day).

Both previously cited conclusions drawn by OLSON et al. (2011) and DAL PIZZOL et al. (2014) regarding the SC count contradict studies conducted by PRENDIVILLE et al. (2010) in which no difference was observed in the udder health between HF, JER and F1 cows (HF × JER).

HEINS et al. (2011) identified a trend toward a higher SCS (3.79) for JER × HO cows during the 1st and 2nd lactation compared to purebred HO cows (3.40); however, JER × HO cows developed clinical mastitis significantly less often (−23.4%) during the 3rd lactation.

CHAWALA et al. (2013) investigated genetic parameters and breed effects in the development of clinical lameness in HF, JER and dairy cows crossbred from both breeds. JER cows had a significantly lower incidence (6.0%, $p<0.05$) than HF cows (6.8%) but a similar incidence to that of the crossbred cows (6.1%). The sires' estimated Breeding values for clinical lameness were between −5% and 8%, whereby the JER sires had the lowest values. The heritability of the disease was estimated as 0.016, meaning that the influence of the selection of sire on the disease rate is very low. The use of JER bulls had a positive effect, however, and can be an alternative to increase the genetic resistance to lameness in New Zealand dairy cows. The cause is likely to be the heterosis effect.

Breed complementarity and heterosis that can be achieved by crossbreeding led to superior performance and consequently to higher expected profitability in cows that were crosses of the breeds HO, Friesian and JER compared to the purebred parents in each case. In these studies the SC count of the JER crosses was also higher than the average of the parental breeds. (COFFEY et al., 2016)

In a comparison of JER × HF cows and HF cows by VANCE et al. (2013) the crossbred animals had improved fertility performance that was demonstrated by higher Conception rates and shorter calving to conception intervals. The genotype had no influence on the fat and protein content with expected high milk yields for the HF cows and high milk components for the crosses. The crosses also had a higher SC count per ml of milk in this genotype comparison. (VANCE et al., 2012; VANCE et al., 2013)

5.1.3 GH vs. BS × GH

AFS and AFC for Brown Swiss (BS) crosses in the studies described here of 16.4 and 26.1 months respectively are at the same level as the GH (16.5 and 26.3 months) with no significant differences. The average ICI of the BS50 genotype is significantly lower than that of the GH (395.1 vs. 418.3 days).

The mean ICI of F1 crosses of GH and BS was also considerably below the mean ICI of purebred GH in a study by FREYER et al. (2008) (F1 367 vs. GH 398 days).

Under subtropical conditions Brown Swiss (BS) × HO crosses calved at 24.2 months on average and HO heifers at 24.6 months, meaning that the fertility of the heifers was also comparable (NASR et al., 2021).

This confirms crossbreeding results for F1 crosses of GH and BS which nevertheless showed better condition at calving with the same AFS (14.2 and 14.3 months) and AFC (both 24.5 months) compared to GH. There were no differences for the ICI (1st to 2nd calving) (DOBMAIER, 2012).

This cross was also investigated by BLÖTTNER (2012). The BS crosses were ready to breed again after calving earlier than the purebred GH cows with a significant difference seen after the 2nd and 3rd calving. (BLÖTTNER et al., 2011a; BLÖTTNER, 2012)

BS × HO crosses did not conceive more quickly after the 1st calving than HO in a genotype comparison by MALCHIODI et al. (2014).

The milk production of the BS50 in our studies was low for milk yield and Lifetime efficiency but not significantly so with only the JER50 performing worse.

In the milk production in the 1st lactation, BS × GH crosses observed by DOBMAIER et al. (2012) were superior to purebred GH and BS, but the GH had better Milking efficiency than the crosses. FREYER et al. (2008) ranked the milk production of F1 cows of BS × GH (7,525 kg) between that of GH (7,894 kg) and BS (6,440 kg).

Cows of a utility crossbreed of BS and GH had a milk yield that was 0.6 kg/day less in the 1st lactation and 1 kg/day less in the 2nd lactation compared to purebred GH. The longer and wider teats of BS crosses were associated with slower milk flow and longer milking times but also with fewer treatments for udder diseases. (DOBMAIER, 2012; FISCHER, B., 2012)

A comparison of BS × HO crosses (n = 55) and purebred HO cows (n = 50) showed significant superiority of the HO in the first three lactations for the milk yield. The Somatic cell count in the milk did not differ significantly. (BLÖTTNER et al., 2011a, b; BLÖTTNER, 2012)

In contrast, crossbreeding between BS and HO seemed to have a positive effect on milk yield and Somatic cell count in studies by DECHOW et al. (2007).

In studies by PUNSMANN et al. (2018c) the most common reason for culling purebred BS was cited as infertility with 25%, followed by unknown reasons and advanced age with a mean Productive period of 2.5 years. The Productive period of 2.7 years for the BS50 cows was also in this range in the genotype comparison we performed.

5.1.4 GH vs. SRB × GH

SRB50 have an average heifer fertility but are significantly superior to GH for the ICI. The lifetime production of milk is higher than GH but not significantly so. For the Lifetime efficiency they correspond to the GH but again this is not statistically confirmed. For the Somatic cell count, the cows with the SRB × GH genotype were at the level of the GH. The culling age of 5.1 years is more than 1 year higher than that of the GH cows. For this genotype, the Productive period of 3.4 years is above average but the difference is not significant.

SRB were superior to Nordic Holstein regarding fertility performance in studies conducted by MUUTTORANTA et al. (2019) from the 1st to the 3rd calving. They were returned to breeding earlier after calving and conceived again more quickly. Crossbreeds of both breeds also showed this superiority for MALCHIODI et al. (2014).

FERRIS et al. (2014) emphasised the high fertility and Productive period of the Norwegian Red (NR), which were both considerably higher up to the 4th lactation in their studies compared to HF.

In terms of milk yield, Italian crosses of SRB × HO were significantly below the purebred HO (32.35 vs. 35.21 kg milk/day). MON × HO cows also had higher milk yields than the cows with 50% SRB genes. Although for the SC count the SRB crosses were inferior to the HO, this difference was not significant. (MALCHIODI et al., 2011)

F1 crosses of Polish HF and SRB showed positive effects for fertility, milk components and udder health. An SC count that was 38.94% lower confirmed greater resistance to mastitis. (SOLARCZYK et al., 2021)

EZRA et al. (2016) compared the performances from the 1st to the 3rd lactation of Israeli HO cows to crosses of HO and NR. HO were significantly superior to the crosses in the 305-day milk yield, the fat and protein content, and the persistence. There were no differences determined for the SC count. The better fertility and health of the crosses were demonstrated by the higher Conception rates and lower rates of metritis.

The aim of a study conducted by BEGLEY et al. (2009) was to investigate potential differences in the udder health using the SCC and the rate of mastitis between HF, NR and NR × HF cows on Irish commercial dairy farms. The mean of all available SCS records over lactation values of 2.15, 2.04, and 2.12 were obtained with the HF, NR, and NRX cows, corresponding to mean SCC values throughout lactation of 223,000, 174,000 and 202,000 cells/ml, respectively. The mean SCC and the proportion of animals that developed mastitis among the crosses (10.4% mastitis rate) was significantly higher than that of the purebred NR (6.0% mastitis rate) but below that of the HF (11.9% mastitis rate). The results confirmed the superiority of NR regarding udder health and suggest that improvements in these traits result from crossbreeding with NR.

5.1.5 Summary for GH vs. crosses with 50% GH genes

Studies of Polish F1 cows resulting from crossbreeding of HF with sires from other breeds (Norman, Norwegian Red, Danish Red, Brown Swiss, Montbéliarde and Simmental) showed a tendency toward better functional traits than purebred Polish Holstein cows. (PUPPEL et al., 2017)

A summary comparison of the performances of German Holstein with F1 crosses in our studies reveals a more differentiated picture (Table 37).

MON50 heifers start breeding one month earlier at 15.1 months on average and accordingly calve for the first time earlier than the other genotypes in this comparison. The fertility data for the heifers are not statistically confirmed, however. The calving interval for the F1 MON crossbred cows is average as is milk production in terms of the yield. The LEff was unexpectedly high because in this comparison high milk yield was calculated with a moderate Productive period. It is nevertheless too low overall because the crosses do not reach the economic threshold for a dairy cow herd as defined by WANGLER AND HARMS (2009) of 15.0 kg milk per day of life. When evaluating the health data (culling age, Productive period, SCC), this genotype performs worst. Crossbreeding MON into GH herds therefore cannot be recommended.

For fertility of the heifers, the JER50 crosses are considerably worse than GH and the other F1 crosses. For JER50 a very high AFS of 18.1 months on average was observed. Most JER50 crosses were on farm C (n = 47) with only ten animals on farm D. Because the mean AFS in 2015 on farm C was 15.7 months, this cannot explain the high average for the F1 JER crosses. The Jersey breed is early to mature and has a small frame and relatively low body weight (Section 2.4.1.3, ELFRICH AND ROESICKE (2015); BLE (2022)). F1 heifers have a lower body mass increase than black-pied (BRADE, W., 2014) and the other crosses that were kept on farm C. If live weight played a critical role for the start of breeding, this could explain the high means for the AFS and AFC of the JER crosses.

The BS50 genotype has equivalent fertility performance and health parameters to the average of the F1 crosses. In terms of the culling age and the Productive period, they are also in the middle of the results observed for the F1 crosses. The SC count of 318.0×10^3 is the lowest among the F1 crosses but is above that of the GH and SRB50.

From the perspective of US milk producers, crosses of JER and BS live longer than purebred HO (WEIGEL AND BARLASS, 2003). This was confirmed by CLASEN et al. (2017) and they therefore recommend crosses of Danish HO with Danish Red and Danish JER to improve the longevity of Danish dairy cows. Regarding the culling age, our studies confirm this. A recommendation to crossbreed with JER and BS cannot be made, however, because the F1 cows are unsatisfactory regarding the other parameters.

The highest milk yield is shown in Table 37 for the F1 crosses with SRB. The heifers show an average fertility while for the ICI the SRB50 cows, like all the other F1 crosses, are significantly superior to the GH. The highest mean Productive period (3.4 years) and an equally high mean culling age of 5.1 years, similar to that of the JER F1 animals (5.2 years), indicate stable health and performance traits. The mean SC count is equivalent to the GH and BS50 cows as is the proportion of 45% of the milk samples with $<100 \times 10^3$ SC per ml. The SRB breed can therefore contribute to improvements in the performance of GH herds, particularly the health and longevity.

Table 37: Overview of the mean performance of GH vs. crosses with 50% GH genes

Genotype		Fertility			Milk yield		Health		
		AFS	AFC	ICI	Milk	LEff	AC	PP	SCC
	n	months	months	days	kg	kg milk / dl	years	years	thous. / ml milk
GH	3,782	16.5	26.3	418.3	27,218	12.9	4.0	2.9	310.1
MON50	74	15.1	25.8	381.3	26,560	13.4	3.7	2.5	552.1
JER50	57	18.1	28.8	375.4	20,481	10.6	5.2	2.5	437.3
BS50	260	16.4	26.1	395.1	23,575	12.1	4.0	2.7	318.0
SRB50	434	16.4	26.2	392.3	28,979	12.5	5.1	3.4	329.5

n = Number of animals, AFS = Age at first service, AFC = Age at first calving, ICI = Inter-calving interval, LEff = Lifetime efficiency, AC = Age at cull, dl = day of life, PP = Productive period, SCC = Somatic Cell Content, thous. = thousand, GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, Numbers in the genotype indicate the percentage of genes
Significance: ICI: GH vs. JER50, BS50, SRB50 ($p < 0,01$)

5.2 Performance comparison of German Holsteins (GH) vs. crosses of different genotypes

The breeding association VikingGenetics promotes “crossbreeding as an effective tool to improve fertility” (VIKINGGENETICS, 2022). The ProCROSS breeding programme, described in Section 2.5.3.5, is considered separately in our studies with the PRCR genotype (MON × (SRB × GH)) that corresponds to the genotype of the crossbreeding programme.

The fertility of the heifers of all crossbreeds (CB) is comparable to that of GH (Table 38). However, the calving interval for the crossbred cows is significantly lower (ICI 389.8 vs. GH 418.3 days) with the PRCR cows showing the best performance (371.8 days) followed by the 3-breed crosses (387.0 days). Because the PRCR genotype contains 50% MON genes, the early start to breeding conforms to expectations. It must be pointed out here though that the mean calving interval for GH satisfies the breeding objective.

Table 38: Overview of the mean performance of GH vs. crosses with different genotypes

Genotype	n	Fertility			Milk yield		Health		
		AFS months	AFC months	ICI days	Milk kg	LEff kg milk / dl	AC years	PP years	SCC thous. / ml milk
GH	3,782	16.5	26.3	418.3	27,218	12.9	4.0	2.9	310.1
CB	2,469	16.3	26.1	389.8	25,126	11.7	3.9	2.7	318.8
GH > 75	412	17.1	26.9	406.2	13,266	8.7	2.6	1.5	308.6
PRCR	82	15.6	25.6	371.8	23,668	12.1	3.7	2.4	414.7
3-breed crossess	479	16.6	26.3	387.0	19,354	10.1	3.4	2.3	311.5

n = Number of animals, AFS = Age at first service, AFC = Age at first calving, ICI = Inter-calving interval, LEff = Lifetime efficiency, AC = Age at cull, dl = day of life, PP = Productive period, SCC = Somatic Cell Content, thous. = thousand, GH = German Holsteins, CB = all crossbreeds, PRCR = ProCROSS (MON50SRB25), The highest milk production was achieved, as expected, by the GH. Regarding milk yield, LEff and culling age, the PRCR cows performed better than the other 3-breed crosses but did not reach the level of the GH. The udder health in turn is clearly better in the 3-breed crosses than in PRCR and is comparable to that of GH, GH >75 and CB.

From this analysis, we cannot recommend crossbreeding with GH because the lifetime production and health parameters are inadequate.

The poor performance of the genotypes with more than 75% GH genes is also a drawback. In this analysis, the backcrosses with GH show that a decrease in performance must be expected when the heterosis declines. If crossbreeding is carried out in a herd, the subsequent breeding in the following generations must also be taken into account. Crosses beyond the F2 generation with a 3rd breed cannot be recommended.

A German practitioner reported that ProCROSS heifers started breeding as early as 13 to 14 months while Holstein heifers from the same herd were only ready to breed at 15 months; the crossbred cows could also be easily milked with the milking robot and had a milk yield that is higher than the herd average (32 vs. 31 kg milk per day, VIKINGGENETICS (2020)). The difference between GH and PRCR is confirmed in our studies for AFS and AFC but not for the milk yield.

Milk producers in Italy started crossbreeding Holstein as early as the late 1990s. Results from milk testing on six farms showed benefits for fertility and milk components but the crosses were inferior to the Holstein in terms of the milk yield. The number of days open for the ProCROSS crosses in the 1st (F1: SRB × HO) and 2nd generation (MON × F1) was 97 to 133 days on average and for the HO the value was 128 to 174 days on average. For the milk yield, means for HO of 8, 967 to 11, 252 kg were recorded on the farms with the crosses producing below this with 8, 019 to 10, 271 kg. This agrees with our results. (SCHRÖPFER, 2010)

The milk energy output (Mcal/day) of ProCROSS crosses is also below that of purebred Holstein in the long-term studies conducted by SHONKA-MARTIN; HEINS; et al. (2019). However, regarding feed conversion they achieved superior results to the Holstein (+5.5% efficiency in feed conversion).

Danish dairy farmers saw benefits in the crosses regarding functional traits and in a survey 55% described themselves as satisfied with the 3-breed crosses. 50% to 60% saw benefits with longevity, health, and feet and legs and up to 30% saw benefits with fertility, profitability and vitality. (SCHRÖPFER, 2010)

In terms of the lactation performance, BRÄHMIG (2011) was barely able to demonstrate any effects for the F1 generation (BS × GH) and only slight effects for the R1 generation (backcross, GH × F1). For the fat and protein content, the F1 generation showed a heterosis effect of 2.83% and 1.89% respectively but the differences in performance between the crosses and the purebred parental breeds were not significant. Although the F1 and R1 generations showed better lactation performance for the milk components compared to the purebred parental generation, the GH cows were superior to all other genotypes when every other quantifiable characteristic was considered. As expected, for the F1 generation exceptionally good values were reported for the Somatic cell count compared to the purebred generation. The improvement here was −19.79%, which corresponds to -56×10^3 SC per ml of milk. The fertility traits calving to first service interval, delay period and calving to conception interval (−10.94%, −9.97%, −10.61%) and thus the ICI (−2.07%) were all clearly improved in the F1 generation but not in the backcrosses.

The higher potential of crosses of MON × (SRB ×HO) regarding fertility was also confirmed by MALCHIODI et al. (2014). The crossbred cows conceived again more quickly and had higher Conception rates after the 1st insemination than the HO, which shortened the ICI.

5.3 Performance comparison of German Holsteins (GH) vs. crosses with MON, BS and SRB with different genetic compositions

On farm A MON were mated with GH and backcrossed with GH, while on farm D there are data available for BS × GH and their F1 and F2 daughters from backcrosses with GH. The performances of the crosses were compared to those of purebred GH from the same cohorts on the corresponding farm. SRB crosses and their backcrosses with GH and SRB were located on all farms and they were compared to the GH from the total sample (Table 39).

The positive effect of crossbreeding on the fertility is reduced with each backcross and the AFS, AFC and ICI increase as the proportion of GH genes rises. For the BS crosses this increase in the AFS from the F1 generation to the F2 and F3 is in part significant.

On farm A, where the MON crosses were located, the heifers analysed here were inseminated for the first time at 15.3 months on average, which is significantly earlier than on the other farms (Table A8). The AFS increases from 15.1 to 15.5 months as the percentage of GH genes increases, whereby the GH were inseminated on average at 15.1 months and thus at the same age as the F1 crosses.

On farm D with BS crosses the AFS is overall very high (mean AFS in 2020: 19.0 months, Table 18: Mean milk, fertility and health parameters of the herds on the study farms in the last year that could be fully analysed (January to December) while the average for all heifers on this farm was 18.3 in the study period, which is significantly higher than the averages on all the other farms. The GH were on average bred later than all the BS crosses, although the difference is insignificant (AFS 18.6 vs. 17.2 to 18.5 months).

For the SRB crosses, the means of the fertility parameters for the backcrosses with GH do not increase as clearly as for the above MON and BS crosses. The AFS, AFC and ICI of the GH of 16.5 and 26.3 months were at the same level as for the SRB crosses. For the backcrosses of F1 animals with SRB (SRB75), no clear conclusion can be drawn for the AFS and AFC due to the lack of significance, even though the means are considerably higher. The ICI for crosses with 75% SRB genes is significantly lower than that of purebred GH.

In terms of the milk production, a clear statement can be made only for the BS crosses compared to the GH, thanks to a significant difference, with all BS crosses producing clearly less milk but not when comparing the crossbred generations. SRB crosses are equal (SRB50), superior (SRB25) or inferior (SRB75, SRB12.5) to the GH with no trend seen for the percentage of GH or SRB genes. The milk yield of the MON crosses drops with backcrossing to GH. Although for the MON50 a higher lifetime production was determined, due to the lack of statistical certainty there is no clear picture here either.

Similar results are obtained when comparing the efficiency of the milk production. GH perform best or are equivalent (GH vs. SRB25). A clear trend as the proportion of GH genes increases is not apparent or, as is the case for MON backcrosses, is not statistically certain.

The culling age and Productive period suggest that the increasing proportion of GH genes has an effect or there is a possible decline in the heterosis in the backcrosses. The culling age, Productive period and number of lactations decrease from the F1 to the F3 generation for the MON crosses, in part significantly. However, the BS crosses do not confirm this picture and for the SRB crosses the changes are not statistically certain.

Table 39: Mean performances of GH vs. crosses of different genotypes with 75%, 50%, 25% and 12.5% GH genes

Genotype		Fertility			Milk yield		Health		
	n	AFS months	AFC months	ICI days	Milk kg	LEff kg milk / dl	AC years	PP years	SCC thous. / ml milk
GH	1,353	15.1	25.0	400.4	25,604	14.0	4.0	2.4	301.6
MON50	61	15.1	24.9	383.7	27,020	13.7	3.7	2.5	608.5
MON25	22	15.3	25.0	421.6	24,896	13.1	3.0	2.2	313.6
MON12,5	24	15.5	25.6	428.4	18,572	12.0	2.9	1.3	196.2
GH	351	18.6	27.7	432.8	24,356	11.6	2.9	3.0	237.3
BS50	104	17.2	26.8	405.0	18,173	9.3	4.0	2.7	316.1
BS25	84	17.9	27.5	417.5	22,071	10.1	4.2	2.7	277.4
BS12,5	34	18.5	27.7	422.4	13,455	7.8	3.0	1.5	392.4
GH	3,104	16.5	26.3	418.0	26,503	12.7	4.0	2.9	309.7
SRB75	10	18.3	27.6	355.1	18,719	8.8	4.3	2.2	271.7
SRB50	350	16.3	26.0	390.5	26,049	11.8	4.9	3.0	326.5
SRB25	260	16.3	26.2	402.4	29,684	12.8	4.0	2.8	300.7
SRB12,5	90	17.1	26.9	396.2	21,215	10.3	3.7	2.2	262.5

n = Number of animals, AFS = Age at first service, AFC = Age at first calving, ICI = Inter-calving interval, LEff = Lifetime efficiency, AC = Age at cull, dl = day of life, PP = Productive period, SCC = Somatic Cell Content, thous. = thousand, GH = German Holsteins, MON = Montbéliarde, BS = Brown Swiss, SRB = Swedish Red Breed, Numbers in the genotype indicate the percentage of genes
Significance: AFS: MON12.5 vs. GH, MON50 ($p < 0.05$), GH vs. BS50, BS25 ($p < 0.001$), BS50 vs. BS25, BS12.5 ($p < 0.05$), SRB75 vs. SRB50, SRB25 ($p < 0.05$); AFC: GH vs. BS50 ($p < 0.001$), GH vs. BS2;5 ($p < 0.05$); BS50 vs. BS25 ($p < 0.05$), BS50 vs. BS12.5 ($p < 0.001$); CI: GH vs. BS50 ($p < 0.01$), GH vs. SRB75 ($p < 0.05$); Milk in kg: GH vs. BS50, BS12.5, BS50 vs. BS25 ($p < 0.05$)
LEff: GH vs. BS50, BS25, BS12.5 ($p < 0.05$), BS25 vs. BS12.5 ($p < 0.05$);
AC: GH vs. MON12.5 ($p < 0.01$), GH vs. BS50, BS25 ($p < 0.001$), BS12.5 vs. BS50, BS25 ($p < 0.05$);
PP: MON12.5 vs. GH, MON50 ($p < 0.05$), BS12.5 vs. GH, BS50, BS25 ($p < 0.001$); SC in thousand / ml milk: GH vs. BS50 ($p < 0.05$)

In a study of the effect of increasing the proportion of SI genes, backcrossing resulted in a lower milk yield in the daughter generations in the culling year (DIEPOLD, 2019).

DECHOW et al. (2007) investigated the performances of BS and HO as well as their crosses and backcrosses. The BS × HO F1 crosses were superior to purebred BS in terms of milk, fat and protein yield and equivalent to purebred HO. The calving to first service interval was significantly lower after the 1st and 2nd calving compared to all purebred animals and after the 3rd calving it was lower than that of HO but equivalent to that of BS. As a result of the backcrossing with BS, all performances decreased significantly. The authors ruled out mating of sires with lower Breeding values and assumed that the cause was recombination losses.

Crosses of HO with MON in 1,137 herds and with Normande (NO, 1,033 herds) were compared to purebred Holstein to identify any inbreeding and breed differences. The crosses made up 13% of the cow population in each case. HO was genetically superior to the crosses in the 305-day milk yield (MON × HO: +951 kg MY, +40 kg fat, +17 kg protein, NO × HO: +2,444 kg MY, +102 kg fat, +54 kg protein) but inferior for fertility with −0.27% to −0.44% lower Conception rates. For all traits, positive heterosis effects were seen in the F1 generation that were lost in the backcrossed cows, which indicates recombination losses. (DEZETTER et al., 2015)

5.4 Age at first calving and Lifetime efficiency of daughters of the breeds MON, JER, BS and SRB and daughters of selected sires of these breeds

To determine whether the sire's breed or the Breeding value of the bull is critical for the increased performance of F1 generation crosses, without considering the sire's breed, the ten bulls with the highest average performance by their daughters for the parameters AFC for fertility and LEff for milk production were selected. The genotype of the dams was not considered. This was contrasted with the ranking by performance of the F1 daughters of all sires of the breeds MON, JER, BS and SRB as well as purebred GH.

In the ranking by AFC, the 428 F1 daughters of the 13 BS sires were in 1st place with 25.2 months followed by the 578 F1 daughters of the 17 SRB sires with 25.8 months (Table 41, Figure 41, Table A13). The GH came in 3rd place while places 4 and 5 were taken by the F1 daughters of MON and JER bulls.

For the mean Lifetime efficiency, the 51 JER F1 daughters of three bulls took 1st place with 13.6 kg MY per dl, ahead of GH with 13.1 kg MY per dl while BS and SRB had a significantly lower yield (12.0 and 11.6 kg MY per dl). The 130 MON F1 daughters of three bulls came in last with 11.3 kg MY per dl (Table 40, Figure 41, Table A14).

The F1 daughters of the JER bulls Brazo and Rampant with 23.8 and 24.2 months mean AFC took the first places, ranking ahead of the SRB bulls Gunnarstorp and Tuima each with 24.5 months. The daughters of two additional SRB bulls have mean AFC values of 25.4 (Langbo) and 26.1 months (A Linne), therefore coming 7th and 11th, and thus last, respectively. The 5th place is taken by the daughters of the MON bull Triomphe, but other daughters of MON sires came in at places 8 and 10. Among the ten best sires with low AFC, only one BS bull (Agenda) was successful with his daughters coming in 6th.

Eight daughters of the JER bull Rampant achieve the highest mean Lifetime efficiency (15.6 kg MY per dl), followed by 14 daughters of the MON bull Plumitif (15.3 kg MY per dl). These cows were the only F1 daughter group on average that were above the threshold for efficient lifetime production of 15.0 kg MY per dl as defined by WANGLER AND HARMS (2009). The SRB bull with the most efficient daughters is the bull Gunnarstorp and he was again in 3rd place for the Lifetime efficiency. The second SRB bull (Peterslund) ranked second last for efficiency but in terms of the fertility was not one of the ten sires with the best daughters.

With ranking of the fertility (AFC) weighted by the number of F1 daughters, the 23 daughters of the two best JER bulls were in 1st place (Table 41). In the comparison of all F1 daughters, without screening the individual sires, the F1 progeny of the JER breed took the 5th and thus last place for this parameter (Table 40).

Table 40: Ranking of German Holsteins and daughters of the breeds Montbéliarde, Jersey, Brown Swiss and SRB by Age at first calving and the Lifetime efficiency

Breed	Number of Sires	Number of Daughters	Average	Ranking
Age at first calving in months				
GH		3,783	**26.2**	**3**
MON	3	165	**27.6**	**4**
JER	4	57	**27.8**	**5**
BS	13	428	**25.2**	**1**
SRB	17	578	**25.8**	**2**
Lifetime efficiency in kg milk per day of life				
GH		3,782	**13.1**	**2**
MON	3	130	**11.3**	**5**
JER	3	51	**13.6**	**1**
BS	13	95	**12.0**	**3**
SRB	17	149	**11.6**	**4**

GH = German Holsteins, MON = Montbéliarde, JER = Jersey; BS = Brown Swiss; SRB = Swedish Red Breed

Table 41: Ranking weighted by number of daughters of German Holsteins and F1 daughters of selected sires of the breeds Montbéliarde, Jersey, Brown Swiss and SRB by Age at first calving and Lifetime efficiency

Breed	Age at first calving: Number of Sires	Age at first calving: Number of Daughters	Age at first calving: Ranking	Lifetime efficiency: Number of Sires	Lifetime efficiency: Number of Daughters	Lifetime efficiency: Ranking
GH		2,917	**5**		2,050	**2**
MON	3	124	**2**	2	84	**1**
JER	2	23	**1**	3	38	**4**
BS	1	27	**2**	3	38	**3**
SRB	4	58	**4**	2	119	**5**

GH = German Holsteins, MON = Montbéliarde, JER = Jersey; BS = Brown Swiss; SRB = Swedish Red Breed

At weighted 2nd place are the daughters of the MON and BS sires, which took places 3, 8 and 10 (MON) as well as 6 (BS) in the ranking of the sires (Table 41). F1 daughters of all MON bulls only achieve 4th or the second-last place in the assessment by breed.

In the weighted ranking of the bulls, the F1 daughters of the SRB bulls take the second-last place. In the individual assessment, although the bulls Gunnarstorp and Tuima took places 3 and 4 they only have 11 daughters each. The bulls Langbo with 15 daughters and A Linne with 28 daughters take the lower places 7 and 11, thus lowering the weighted mean rank. For the overall evaluation of the breed, the SRB take out 2nd place with a total of 578 daughters (Table 41).

Again in the ranking of the Lifetime efficiency, there is no agreement in the ranking by breed and by the weighted number of daughters of the sires of a breed.

When selecting the crossbreeding partners for GH, the Breeding value of a bull should therefore play the critical role and not his breed. The Breeding values of the sires are not currently estimated across breeds and/or based on the performances of the crossbred progeny. Genomic estimated Breeding values can also be accessed early for female cattle but not currently for crossbred heifers and dairy cows, which makes timely selection difficult.

In New Zealand, a genetic evaluation across breeds and selection of bulls that were used in crossbreeding were carried out already 20 years ago. The crossbred daughters themselves were not included in the evaluation, however. (LÓPEZ-VILLALOBOS; GARRICK; BLAIR; et al., 2000)

Bayern-Genetik GmbH promotes a TYP Breeding value that readily enables farm managers to pursue individual farm breeding objectives in purebreeding and crossbreeding and to breed a cow with the correct balance and no extremes (BAYERN-GENETIK GMBH, 2023). The insemination association Besamungsverein Neustadt a.d. Aisch e.V. offers daughter-proven Simmental sires for crossbreeding (BSN, 2023). However, the information that is provided indicates that again the sires are not tested on the basis of their crossbred daughters.

The VikingGenetics and VikingDanmark breeding associations have been calculating the genomic estimated breeding values (GEBV) using the Nordisk Avlsvaerdi Vurdering (NAV, Nordic Cattle Genetic Evaluation) since December 2021 for dairy cattle crosses from Denmark, Finland and Sweden. Initially only genotyped two-breed and three-breed crosses between Red Danish, Jersey and Holstein were assigned a GEBV but from 2022 crosses with Montbéliarde also received a GEBV. The GEBVs are developed based on the work done at Aarhus University, VikingGenetics and VikingDanmark as part of the GUDP project DairyCross (Grønt Udviklings- og Demonstrationsprogram, Green Development and Demonstration Programme of the Danish Ministry of Food, Agriculture and Fisheries). The objective of the project is to implement GEBVs for crossbred animals and thus to help when selecting crossbreeding partners in practical dairy cattle breeding in northern Europe. Furthermore, modules are being developed for insemination planning software that contains the genomic information of the crossbred animals to maximise the diversity of the crossbreeding. The project will also be used as a basis for choosing the design of purebred dairy cattle lines for generating efficient crossbred progeny. (FOGH et al., 2021; FOGH et al., 2022; THOMASEN et al., 2023)

In the US studies are being conducted to determine whether GEBVs can be estimated based on reference populations of purebred bulls by weighting the breed proportions (STEYN et al., 2021). In April 2019, the US Council on Dairy Cattle Breeding expanded its genomic evaluation system to include crossbred dairy cows. (WIGGANS et al., 2019)

To be able to determine GEBVs for crossbred heifers and cows, EIRÍKSSON et al. (2022) tested whether the effects of marker alleles in crossbred animals depend on the breed origin of the alleles (BOA). They were able to determine that combining estimated marker effects from purebred evaluations based on BOA can generate a reliable GEBV for crossbred dairy cows.

Implementing GEBVs. for female crosses enables farmers to select genomically tested crossbred and purebred heifers in a herd on an equal basis (EIRÍKSSON et al., 2021; FOGH et al., 2021; EIRÍKSSON et al., 2022; FOGH et al., 2022; THOMASEN et al., 2023).

In Bavaria, the results of performance tests including crosses have been published but only for the slaughter performance of juvenile Simmental and Brown Swiss bulls (LKV BAYERN, 2022). Mating recommendations for crossbreeding with dairy cattle are primarily given for utility crossbreeding with beef cattle breeds (BERKEMEIER AND HILBK-KORTENBRUCK, 2019).

Under the search term “crossbreeding”, RINDERALLIANZ GMBH (2023), one of the largest breeding companies in Germany, and the PHÖNIX GROUP (2023), which is made up of seven German and French cattle breeding organisations, have only published a bull catalogue for beef cattle.

5.5 Influence of herd management on the differences in the performance between GH and crossbreeds

5.5.1 Performance levels of the herds on the study farms

It should be pointed out here that the data used in our studies originate from functional farms. The authors had no influence on the quality and quantity of the data collection with the management software. Despite statistical analysis using a linear mixed model, it therefore seems useful to consider the performance level of the farms when discussing the results. The performance level is evaluated using the herd performances for the calendar year 2020 for farms A, B and D as well as 2015 for farm C, the last calendar years, that is, from January to December, that could be assessed.

The fertility performance of the animals on farms A, B and C correspond to the recommendations from the literature (Table 42). The AFS is slightly increased at 15.0 to 15.7 months. On farm D in 2020 very high average AFS and AFC values of 19.0 and 27.4 months were recorded. The farm management seems to prefer breeding late because an AFS of 16.7 to 19.3 months and an AFC of 26.3 to 28.7 months was also recorded for previous years (2007 to 2019). The ICI is 403 to 410 days on all four study farms, which corresponds to common practice and the target values for GH (Table 42).

The breeding objective for GH aims at a lifetime production of 40,000 kg milk (RINDERALLIANZ GMBH AND MRV, 2021a). Profitable herds should produce on average 30,000 g milk with a Productive period of more than 3 years (Table 42). These herd performances are achieved on farms A, B and C. However, the Productive period on farm A of 2.8 years is below the target value. Because on these farms the average proportion of crosses is less than 20% of the stock, the target values for GH can be used as a performance guideline.

Table 42: Target values for the performance parameters for the German Holsteins breed

Identification number	Target value (herd average)
Fertility	
First breeding age	14 – 15 months
Age at first calving	24 – 28 months
Calving interval	341 – 430 days, depending on performance
Milk yield	
Milking efficiency	30 kg milk / milking day
Production efficiency	25 kg milk / productive day
Lifetime efficiency	15 kg milk / day of life
Amount of milk	30,000 kg / cow
Health	
Productive period	≥ 3.0 years
Somatic Cell Content	> 75% with < 100 thousand / ml milk
Culls	Heifers: 1st – 3rd MLP < 5% up to 6 months of age: < 7%

MPT = Milk performance test
Sources: MAIER (2006); WANGLER AND HARMS (2009); STEINHÖFEL (2011); HARMS et al. (2014); ADR (2017); MSD (2018); BRS (2021); RINDERALLIANZ GMBH AND MRV (2021)

Farm D uses organic production methods. Results from a study in Bavaria showed that it is possible for organic farms to achieve a milk yield that is equally as high as that achieved on conventional farms (HEINE, 2022). With a Productive period of 2.5 years and a herd average of 19,093 kg milk in 2020, on farm D only low performances are realised (Table 18). In 2015 a mean lifetime production of 22,953 kg milk was achieved and the Productive period was 2.5 years. It is apparent from the herd management software that by 2019 the lifetime production had declined steadily to 19,651 kg milk in a 2.3-year Productive period and increased again slightly in 2020. The reason behind this is not the subject of our study.

Although SUNDBERG et al. (2009) found differences in herd structure and cow performances between organic and conventionally operated farms, meaningful interactions between the production system and breed were not identified for any of the traits examined. These results also justify comparing the performances of various genotypes in conventional and organic farming as in the current studies.

5.5.2 Culling reasons

From the documentation of the culling reasons, subjective assessment by herd management appears to play a larger role than the objective health state of the animals or their performances.

Thus, “other reasons” ranked highly with 32.9% on average for the entire sample with farms B and D ranking ahead with 44.4% each. On farm A only 15.0% of cows were culled for “other reasons” while “low yield” (31.8%) was cited particularly frequently. The information provided by farm C appears to be the most reliable, corresponding to the information in the literature for dairy cattle breeding in Germany and the individual Federal States.

In Germany the most commonly cited reasons for culling dairy cows are infertility, udder diseases and claw/limb disorders (Figure 44) and this has not changed for years. That “other reasons and diseases” or “other” is very commonly noted (30%) coincides with the reasons provided in our own studies for GH (32%) and CB (34%). The proportion of animals culled due to “advanced age” and “metabolic diseases” are also very similar. Infertility is cited for 17% (GH) and 16% (CB) in our studies and follows the category “Low performance” ahead of “Udder and Claw/limb disorders” and thus is in the same order as seen in the information for Germany. (BRADE, W. et al., 2008; LKV BAYERN, 2019; LKV SACHSEN-ANHALT, 2019; BRADE, W., 2020; HOEDEMAKER et al., 2020; RÖMER, 2020; BAUER, 2021; BAUER et al., 2021; BRS, 2022; LKV BADEN-WÜRTTEMBERG, 2022)

For GH and CB, “Low performance” is the most cited reason for culling (17% and 21%). Because this reason was stated frequently (farm A: 31.8%, farm D: 15.9%) on both farms, where 77% of the animals evaluated here are located, this aspect is rather an indicator of the influence of the management than of the genotype. A similar pattern is seen for the milkability, which is only cited by farm A as a frequent culling reason (24%), however.

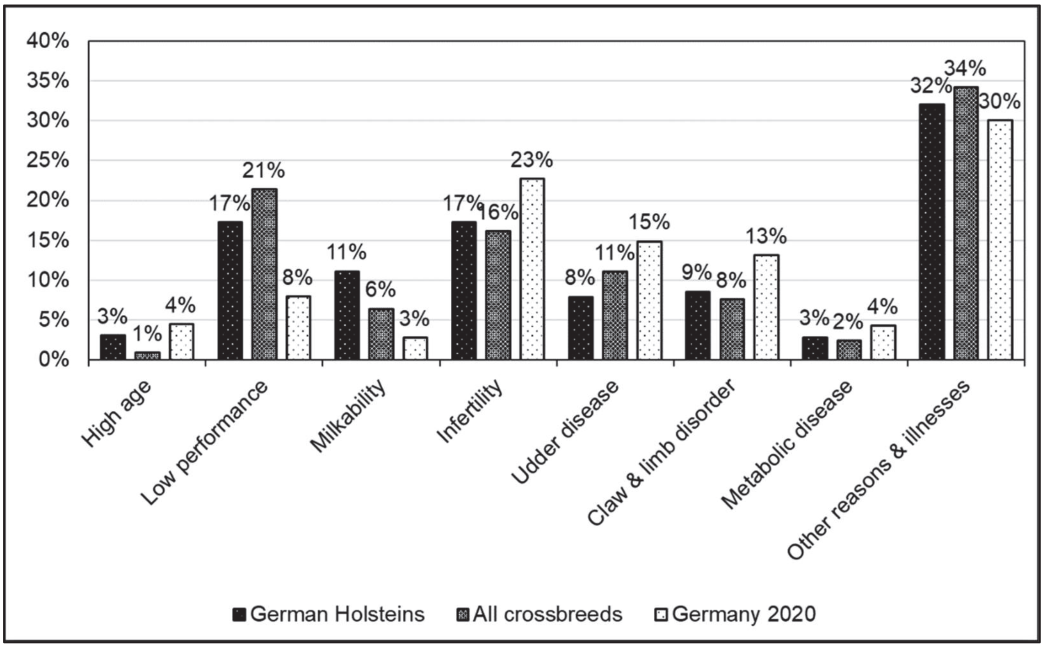


Figure 44: Reasons for culling German Holsteins and “all crossbreeds” compared to test-day cows in Germany in 2020 (BRS, 2022)

For the MON50 cows, udder diseases rank in second-last place with 2.0% but because metabolic diseases were not named at all as a culling reason this reason only is ranked lower. Culling due to infertility and claw and limb disorders as well as age reasons rank at the same level with each reported at 7.8% (with 4 cows of 51 disposals, Table 25) The most common reason was milkability (39.2% or 20 of 51 disposals, Table 25). Most MON50 crosses were located on farm A (67 of 74 animals or 47 of 51 culled animals). Milkability was cited as the reason for 24.0% of the disposals for all genotypes from this farm and in 2020 it was the reason for 30% of the total disposals from the herd on this farm (Table 18, A16). Similar results are seen for the category “udder diseases”: in the total sample from farm A this reason was named for 1.8% of the disposals, for the MON50 it was cited for 2.0% of disposals (Table 25, A16). In 2020 this reason was not even noted in the herd software (Table 18). These proportions are low compared to the other farms and genotypes.

Another example are the JER50 crosses, which were located primarily on farm C (47 of 57 animals culled, Table 18, A16). For this genotype, the most common reason cited for culling with 29.5% is infertility while in the total sample the rate is 37.1% and on farm C in 2015 it was also the most cited reason for culling at 30%.

DONAT et al. (2015) report similar limits regarding the quality of documentation and deficits in the recording of health data in an analysis of data collected on metabolic disorders in farming operations in Thuringia that do not permit scientific analysis of routine data from the herd management, which is possibly a problem across all of Germany.

5.5.3 Influence of the herd level on the performance differences between GH vs. BS50 and SRB50

The extent to which the herd level affects the performance differences between GH and their crosses is analysed using the example of the BS50 and SRB50 genotypes. BS crosses are located on farms A, C and D and F1 crosses of SRB × GH are on all farms analysed in our study. However, data with sufficiently high numbers to permit analysis for the BS50 genotype are only available from farms C and D and for the SRB50 genotype from farms A, B and D.

Independent of the herd level, that is, on all farms, the crosses are only superior to the purebred GH for fertility (AFC and ICI).

On the organically operated farm D, the heifers calved on average at 27.5 months in our studies. For the total sample from the farm, a mean milk yield of 19,766 kg with a mean Productive period of 2.5 years is achieved, generating a Lifetime efficiency of 9.8 kg MY per day of life (Table 36). The herd is therefore assigned a “low production level”. The crosses of the BS50 and SRB50 genotypes are inferior to GH in this herd for milk production and health parameters, with the Productive period approaching significance, while the lifetime production and Lifetime efficiency as well as the udder health are either approaching significance or are highly significant (Table A17).

Moderate performances are reported for the herds on farms A, B and C because in terms of the Lifetime efficiency they fall below the guideline of 15.0 kg MY per day of life (WANGLER AND HARMS, 2009) but in terms of milk yield and efficiency they are significantly above the level on farm D. For this performance level, crossbreeding GH with BS and SRB has a positive effect, in some cases significantly so. For both milk yield and Lifetime efficiency as well as the Productive period, the crosses achieved higher means than the GH on the same farm. For udder health, there is no obvious superiority or inferiority of a genotype. While the BS50 crosses on farm C and the SRB50 on farm A achieved better values than the purebred GH, this is not the case on farm B (SRB50). However, the differences between the means are not significant.

In studies by MERTENS et al. (2011) the economic impact of crossbreeding in dairy cattle breeding was influenced not only by the differences in the parental breeds and the crossbreeding generations but also by the variation in performance within the breeds, which varies enormously between the herds primarily due to the management system.

JUSZCZAK AND ZIEMINSKI (1994) conclude from a comparison of crosses of Polish HF with red-pied and Ayrshire that the production conditions play a critical role and must be considered when evaluating performances.

With an increasing production level, the inferior performance of JER crosses compared to purebred GH increased for the milk yield (BRADE, W., 2014). In studies conducted by PUNSMANN et al. (2018a) on the performance of purebred Brown Swiss, a higher absolute herd level was associated with greater longevity and a longer Productive period. For LEMBEYE et al. (2016) the breed effects also increased as the production level rose.

This was also confirmed by KROGMEIER (2009) who recorded a decline in the Productive period with an increasing herd level for the milk yield. In his studies in Bavaria on the Productive period of Brown Swiss and Simmental for the cohorts 1994 to 1999, long-lived cows were found more often on smaller farms with below-average milk yield.

However, other results from a performance comparison of HO and Norwegian Red × HO crosses showed that the crossbred cows were superior to the Holstein across most traits, regardless of the management level. The crosses conceived again more quickly after calving, had higher 305-day milk yields in the 1st and 2nd lactations and were less susceptible to mastitis. The survival rate in the 2nd and 3rd lactations also revealed the superiority of the crosses. The consequently longer Productive period was attributed primarily to the higher fertility, greater calving ease and fewer stillbirths in the crosses. The authors assume that the crosses are beneficial, independent of the management level. (CLASEN et al., 2018; CLASEN et al., 2019)

KARGO et al. (2012) also came to this conclusion having studied the heterosis effects in Danish Jersey herds with different management levels. The results showed an increase in the additive genetic variance with increasing production level but the heterosis was lowest for the milk production traits (305-d milk, fat and protein yields) at a lower intensity and approaching the highest at a moderate level.

5.6 Crossbreeding in dairy cattle breeding – pro and contra

5.6.1 Crossbreeding in dairy cattle breeding – pro

Holstein cattle dominate in milk production. However, the breed does have room for improvement, for example, in its fitness traits. The low heritability of traits such as fertility or Productive period mean that only limited genetic progress can be expected using selection within a purebred population. (BRADE, W. AND BRADE, 2007)

Crossbreeding provides the opportunity to exploit position effects between breeds or lines as well as heterosis effects. In poultry and pig breeding, this crossbreeding method has long been established. For dairy cattle, crossbreeding can only be recommended unreservedly if useful traits such as fertility and Productive period are priorities. (SWALVE, 2004)

Crossbreeding can result in economic benefits in dairy cattle if less importance is placed on volume in milk pricing and if traits unrelated to milk production such as disease resistance play an important role in the breeding objective (SWAN AND KINGHORN, 1992).

Increasing fitness and fertility is a primary concern in crossbreeding of dairy cattle. It can provide an alternative method for improving the reproductive performance of dairy cows, which is of critical importance for agricultural income (LINDNER, 2008; SWALVE et al., 2008; MERTENS et al., 2011; GONI et al., 2015; BRADE, W., 2020).

Dairy farmers in the US report that benefits of crossbreeding are improved fertility, ease of calving and longevity as well as improved fitness of the crossbred calves. Problems with the sale of slaughter cattle, insufficient uniformity of crossbred animals, poor milk volume performance and problems when selecting bulls are some of the drawbacks of crossbreeding. (WEIGEL AND BARLASS, 2003)

In a 10-year study at the University of Minnesota, HAZEL LOESCHKE AND HEINS (2019) demonstrated the benefits of the ProCROSS 3-breed rotational crossbreeding programme. The influence of heterosis in crossbreeding vs. purebreeding was apparent for fertility, health and Productive period. All generations of the crossbred cows had lower stillbirth rates than the Holstein cows and conceived again earlier. Lower treatment costs for the crosses are indicative of more stable health. For rotational crossbreeding, the authors recommend selecting breeds with effective crossbreeding programmes that take into consideration traits that boost profitability. The breeds should complement one another regarding the most important traits and be adapted to the environmental conditions of the herds.

Crossbred animals experience less stress compared to Holstein under the same environmental conditions. This was demonstrated by the cortisol level measured in the hair of 210 animals (50% crosses, 50% Holstein) at the University of Udine (Italy). If cows are under stress, their cortisol level rises and this can be tracked over long periods in their hair. For 66% of Holstein cows, the values were higher than the normal cortisol level and thus in the critical range, while this was the case only for 37% of the crosses. 20% of the Holstein cows were considered clinically ill but only 10% of the crosses were. On average, the cortisol level of the crossbred animals was considerably lower than that of the Holsteins. (SCHRÖPFER, 2010)

A positive breeding-induced heterosis effect can be demonstrated when examining the SC count. For the German Holstein, crossbreeding may bring improvements in udder health (SCHICHTL, 2007). This could not be confirmed in our studies. Udder health tended to be significantly worse or was highly significantly worse than that of the GH cows except for the SRB crosses, which were equivalent to the purebred GH (Section 4.6).

MCALLISTER, J. (2002) reported clear effects for the longevity (21% heterosis). Again, this could not be confirmed in our studies with the Productive period of the crossbred animals also tending to be lower than that of the GH animals (Section 4.6), except for the SRB crosses again.

Because milk production in future will to some degree be subject to widely diverging requirements from consumers (e.g. price level, quality, preferred husbandry method) and generators (e.g. use of local advantages, availability of permanent pasture), it can be assumed that types of cows that satisfy site factors specific for each farm and profitable achievement of the production goal will increasingly be of interest. Another improvement in performance is indicated particularly with year-round indoor housing and conventional marketing of milk on cultivatable sites. Refinement of Holstein cattle lends itself to this. If there is less selection for high milk volume and the focus instead becomes a lower concentrate requirement (with longer Productive period), Jersey cattle (and Jersey crosses) have proven useful internationally for exploiting permanent pasture. Climate change will also play a role in future breeding programmes with heat stress becoming a problem even in countries with a moderate climate. Breed-related effects in the heat tolerance of various genotypes/breeds are already the subject of many studies. (BRADE, W., 2022)

Systematic crossbreeding can greatly increase the economic efficiency of dairy production systems, particularly in management systems that have high requirements for functional traits. Danish studies confirm the heterosis effects for the economically most important traits in milk production. The additional profit achieved is mainly due to a long Productive period and improved functional traits, except for mastitis, and is somewhat lower for milk production. Optimal crossbreeding strategies in dairy cattle herds require three breeds with a high genetic level in relation to the overall economic value that are used in a systematic rotational crossbreeding programme. Danish dairy farmers have recognised the value of this crossbreeding strategy. It is expected that greater use of such a breeding strategy will lead to improved wellbeing of the cows and improved economic efficiency of the dairy economy. (KARGO et al., 2008; SØRENSEN et al., 2008)

5.6.2 Crossbreeding in dairy cattle breeding – contra

However, the question arises of how to continue breeding with the crossbred animals so that the desired improvements are not lost in subsequent generations. Under intensive conditions, parameters such as uniformity of the frame are particularly important, which makes further breeding of crossbred animals less useful (SWALVE, 2004).

This is the case unless a farm opts to use utility crossbreeding in which progeny are bred to exploit heterosis, which requires that crossbreeding is always carried out with purebred animals or breeding stock must be repeatedly purchased, meaning that this method is not sustainable for the individual farm or the populations. It would require a specialised system with purebreeding farms that produce the F1 calves as a source of replacement heifers. (SWALVE, 2004; LEDERER, 2005; MEILI, 2010)

From the perspective of practical cattle breeding, it has not been possible to date to only work with F1 cows in a herd (NOLTE, 2019).

A compromise would be a 2-breed rotational cross. Limiting crossbreeding to two breeds is necessary because a breed is needed that has a milk production level not too dissimilar to Holstein. If this is not taken into consideration, although heterosis effects could be exploited, they would not compensate for the losses in the milk yield due to additive genetic differences. There are only very limited number of breeds available, however. (SWALVE, 2004)

Due to the steady increase in crossbred animals on dairy farms, MERTENS et al. (2011) carried out an economic evaluation. To improve functional traits (Productive period, fertility) in Saxony, the breeds Swedish red-pied and Norwegian red-pied as well as BS and SI are used as crossbreeding partners for GH. The calculations carried out using a calculation model show economic benefits for the F1 generation compared to the GH breed that are primarily due to the heterosis effects. For the underlying basic variant, when using the Scandinavian red-pied cattle, the greatest economic effect is achieved in the F1 generation. The authors point out that the body of data is not sufficiently reliable, however.

When evaluating the crossbreeding effects, the Productive period and the production level should be considered in addition to the absolute performance. In a comparison of crosses of Polish HF with red-pied (Rb) and Ayrshire (Ay), the three-breed crosses achieved the highest lactation performance. However, because the culling rates were also higher than for the purebred cows, lower lifetime production was reported. The genotype Ay × Rb did not exceed the purebred animals in the absolute lactation performance as much but had superior lifetime production due to the lower culling rates. (JUSZCZAK AND ZIEMINSKI, 1994)

5.6.3 Motivation for crossbreeding in dairy cattle breeding

Dairy farmers in the US reported that they achieved improvements in fertility, calving ease, longevity and milk components as a result of crossbreeding. The marketing of crossbred animals and bull calves were mentioned as problems along with insufficient uniformity within the dairy cow herd, which led to management problems. (WEIGEL AND BARLASS, 2003)

Rotational crossbreeding can be faster and more effective than purebreeding when trying to improve the functional traits of cows and develop robust dairy cattle systems. In France MAGNE AND QUÉNON (2021) identified motivations for crossbreeding dairy cattle: technical problems related to breeding highly specialised purebred cows, the conversion to more sustainable and robust dairy cattle systems and the desire to regain decision-making autonomy in managing farms. A small group of respondents named inbreeding in purebred cattle as a motivation for crossbreeding. In France Holstein is also mostly used as a foundation breed in crossbreeding with other breeds.

The herd managers on the study farms that provided the data used in this paper cited deficits in the functional traits of German Holstein as a reason for starting crossbreeding. The lower milk yield of the crosses was taken into account.

On farm A exploiting a wider range of dairy bulls was given as another reason for initiating crossbreeding. On farm B MON were also used for breeding after good experiences with SRB. The herd manager cited improvement in claw health and longevity as some of the positive effects as well as calving ease due to the sloped pelvis. The SRB have also brought greater calm to the herd.

On farm C bulls were being fattened, which is why breeding with the dual-purpose Brown Swiss was started to obtain male calves with a higher fattening performance. Higher income for F1 bull calves and F1 slaughter cows can be an advantage of crossbreeding because the heterosis also has a positive effect on growth performance and carcass yield. (BRADE, W., 2019b; LÜTKE HOLZ, 2019; LWK, 2020)

The objective for crossbreeding GH with SRB and Brown Swiss cited by the herd manager of farm D was better adaptation to the site and improvement in resistance, fertility, milk components and Productive period of the herd.

Other farms that had briefly bred SRB or JER into the GH herds did not achieve improvements in the Productive period and stopped crossbreeding because of the lower milk yield and worse milkability of the F1 animals. The large variability in the composition, particularly the frame, when crossing with JER was named as a reason for abandoning crossbreeding. (SCHENDEL, 2012; DINSE AND SCHULDT, 2016)

6 Conclusions

From our studies of crossbreeding with German Holsteins (GH), we can draw the following conclusions:

- F1 crosses of SRB × GH are equal to purebred GH for milk production (milk yield and Lifetime efficiency) as well as for fertility of the heifers (AFS, AFC) and udder health. Regarding the fertility of the cows (ICI), they perform significantly better, achieving considerably higher means for culling age and Productive period, meaning that the SRB breed can be recommended as a crossbreeding partner for GH.
- The breeds Montbéliarde, Jersey and Brown Swiss should not be used for crossbreeding with GH because the F1 daughters are inferior to purebred GH across almost all the traits examined here. For the fertility of the cows, which was examined here using the parameter Inter-calving interval, the crosses achieved significantly lower values. Because the mean ICI for the GH is in the range of the target values for the breed, this again does not support crossbreeding with the breeds indicated.
- Three-breed crosses are equal to GH for fertility and udder health but inferior for milk production (milk yield, Lifetime efficiency). A recommendation for crossbreeding with three breeds therefore cannot be made.
- The fitness and fertility of dairy cow herds can be improved by crossbreeding. Only F1 animals should be produced because a loss of performance can be expected with backcrossing.
- Because the production level in dairy cow herds affects the outcome, crossbreeding should only be considered with a moderate production level at a minimum. With a low herd level, positive effects due to crossbreeding cannot be expected.
- When selecting the crossbreeding partners for GH, the Breeding value of a bull should play a more critical role than his breed. It would be beneficial for crossbreeding to establish estimated Breeding values for purebred bulls based on the performance of their crossbred daughters and of genomic Breeding values for female crossbred animals, which Scandinavian breeding associations have already started doing.

7 Summary

Crossbreeding with German Holsteins is primarily carried out to improve functional traits. The current studies on the opportunities and limitations of crossbreeding were performed using data from four farms in two Federal States in north-eastern Germany that started crossbreeding in 2003 to 2006 and had in some cases ceased milk production when this paper was written (farms A and C). Only data from completed lifetime production of the animals were evaluated.

The crosses made up on average 11% to 42% of the cow stock on the study farms from the start to the end of data collection with 63% on farm D in 2020. On all farms German Holsteins (GH) were crossed with Swedish Red (SRB). Montbéliarde (MON) was used on farms A and B. Brown Swiss (BS) was the crossbreeding partner for GH on farms A, C and D while Jersey (JER) was used on farms C and D. Using the Herde and HerdePlus management software from dsp-Agrosoft GmbH, the data were collected and statistically analysed, considering the effect of the cohort and farm.

The performance of purebred GH in the trait complexes fertility (Age at first service, AFS; Age at first calving, AFC; Inter-calving interval ICI), milk performance (lifetime production: milking days, milk yield, efficiency) and health (culling age, Productive period, udder health) was compared to that of the various crossbred genotypes. We also tested the extent to which the herd level influenced the performance differences between the genotypes.

F1 crosses of SRB × GH are equal to purebred GH for milk production in terms of milk yield and Lifetime efficiency as well as for fertility of the heifers (AFS, AFC) and udder health. Because they performed significantly better regarding the fertility of the cows (ICI) and achieved considerably higher means for the culling age and Productive period, SRB is a suitable crossbreeding partner for GH.

F1 crosses of GH with the breeds Montbéliarde, Jersey and Brown Swiss are inferior to the purebred GH for almost all the traits examined here. Only the ICI of these genotypes is significantly lower, which cannot be assessed as a benefit of the crosses because the GH has a mean ICI of 418 days and is thus in the range of the target values for this breed.

Three-breed crosses are equal to GH in fertility and udder health but considerably inferior for milk production (Milk yield, Lifetime efficiency). Cows with the genotype MON × (SRB × GH), which corresponds to that of the ProCROSS breeding programme, confirm the very good fertility but their milk yield is only average. In terms of udder health (Somatic cell count), they are below the means of almost all crossbreeds examined with only the F1 crosses with MON and JER performing worse. A recommendation for crossbreeding with three breeds therefore cannot be made.

With an increasing proportion of GH genes in the backcrosses, either clear conclusions cannot be drawn (Milk yield: SRB, BS) or the declining heterosis effect, which is described in the literature, leads to a drop in performance (fertility: MON, BS, SRB, milk yield: MON). Genotypes with >75% GH genes perform worse in heifer fertility as well as milk production and Productive period compared to purebred GH while they are equal in the cow's fertility and udder health.

The fitness and fertility of dairy cow herds can be improved by crossbreeding. Only F1 animals should be produced because a decline in the performance can be expected with backcrossing.

Because the production level in dairy cow herds critically affects the outcome, crossbreeding should only be considered with a moderate production level at a minimum. With a low herd level, positive effects due to crossbreeding cannot be expected.

It would be beneficial for crossbreeding to develop Breeding value estimates for potential sires based on the performance of their crossbred progeny and to establish genomic Breeding values for female crossbred animals.

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Attachment of tables and pictures

List of tables

Table A1: Livestock, replacement rate of the year 2020 (Farms A, B, D) and 2015 (Farm C) as well as proportion of crossbreeds in the total herd of female cattle from 6 months of age in the study farms

Farm Year	A	B	C	D
Average number of animals in the last fully evaluable year				
Year	2020	2020	2015	2020
Total	298	340	626	613
Dairy cattle	232	236	374	329
Heifers from the 6th month of life	66	104	252	284
Proportion of crossbreeds in the total stock from 6 months of age				
2001				3 %
2002				7 %
2003				14 %
2004	6 %			25 %
2005	3 %	2 %		24 %
2006	2 %	3 %	1 %	32 %
2007	8 %	3 %	1 %	36 %
2008	5 %	3 %	4 %	38 %
2009	4 %	4 %	12 %	38 %
2010	3 %	6 %	17 %	41 %
2011	5 %	7 %	21 %	43 %
2012	7 %	9 %	26 %	49 %
2013	8 %	12 %	30 %	52 %
2014	11 %	12 %	33 %	54 %
2015	14 %	13 %	35 %	55 %
2016	18 %	16 %		58 %
2017	21 %	20 %		57 %
2018	21 %	25 %		63 %
2019	26 %	27 %		61 %
2020	28 %			63 %
Average	11 %	11 %	18 %	41 %

Table A2: Number of evaluated cows and Milk performance tests (MPT) as well as proportion of MPT by farms and lactations

Farm	A	B	C	D
Years	2006 – 21	2007 – 21	2008 - 16	2007 – 21
Number of cows	1,751	768	825	2,278
Number of MPT	49,607	25,633	22,172	39,474
Lactation	Proportion records			
1st	37.7%	26.4%	41.8%	29.1%
2nd	28.1%	21.3%	27.6%	23.7%
3rd	18.3%	18.1%	16.4%	17.4%
4th	9.4%	14.1%	8.8%	12.3%
5th	4.0%	9.2%	4.0%	6.8%
6th	1.7%	5.5%	1.3%	4.9%
7th	0.7%	3.1%	0.1%	2.8%
8th	0.2%	1.4%	0.0%	1.4%
9th	0.0%	0.5%		0.7%
10th		0.3%		0.7%
11th		0.1%		0.1%
1st and 2nd	65.8%	47.7%	69.4%	52.8%
>3	15.9%	34.2%	14.2%	29.8%

MPT = Milk performance test

Table A3: Crossbreeding schemes and gene shares of the breeds in the evaluated genotypes

Genotype	Crossbreed	n	Gene shares of the breeds in %				
			GH	MON	JER	BS	SRB
GH > 75	Various	412	> 75.0	0 – 12.5	1.6 – 12.5	1.6 – 18.8	1.6 – 15.6
GH < 75	Various	162	12.5 – 71.9	12.5 – 62.5	12.5 – 37.5	6.3 – 75.0	3.1 – 87.5
MON50	MON X GH	74	50.0	50.0			
MON25	GH X MON50	26	75.0	25.0			
MON12.5	GH X MON25	25	87.5	12.5			
JER50	GH x JER	57	50.0		50.0		
JER25	GH x JER50	18	75.0		25.0		
BS50	GH x BS	260	50.0			50.0	
BS25	GH x BS50	145	75.0			25.0	
BS12.5	GH x BS25	51	87.5			12.5	
SRB75	SRB X SRB50	11	25.0				75.0
SRB50	GH x SRB	434	50.0				50.0
SRB25	GH x SRB50	344	75.0				25.0
SRB12.5	GH X SRB25	114	87.5				12.5
MON50SRB25, PRCR	MON x SRB50	82	25.0	50.0			25.0
3-breed-crosses		479					
MON75SRB12.5	MON x PRCR	17	12.5	75.0			12.5
MON50SRB12.5	MON x SRB25	24	37.5	50.0			12.5
MON25SRB12.5	GH x MON50SRB25	57	62.5	25.0			12.5
BS50SRB25	BS x SRB50	95	25.0			50.0	25.0
BS50SRB12.5	BS x BS50SRB25	45	37.5			50.0	12.5
BS25SRB12.5	GH x BS50SRB25	75	62.5			25.0	12.5
SRB50MON25	SRB x MON50	23	25.0	25.0			50.0
SRBBS25	SRB x BS50	88				25.0	50.0
SRB12.5BS6.25	GH x SRBBS25	35	81.25			6.25	12.5
SRBJER	SRB x JER50	20	25.0		25.0		50.0

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, PRCR = ProCROSS,
n = number of animals

Table A4: Minimum and maximum of the dates of birth as well as number of evaluated genotypes in the farms

Genotype	Dates of birth		Number of animals				
			Farm				Total
	min	max	A	B	C	D	
Total	25/01/01	27/11/19	2,144	825	659	2,223	6,251
GH	26/01/01	23/01/19	1,661	757	483	881	3,782
All crossbreeds	25/01/01	27/11/19	483	68	176	1,742	2,269
GH > 75	17/06/05	07/10/19	45	9		358	412
GH < 75	22/11/06	20/11/19	66	2	5	89	162
MON50	06/08/09	27/11/19	67	7			74
MON25	16/11/11	02/09/19	26				26
MON12.5	04/03/15	07/10/19	25				25
JER50	05/09/02	01/10/09			47	10	57
JER25	23/11/06	23/04/12				18	18
BS50	07/06/02	29/09/13	3		88	169	260
BS25	13/08/04	28/04/16			6	139	145
BS12.5	18/03/07	11/10/16				51	51
SRB75	07/07/08	12/10/15	1	1		9	11
SRB50	25/01/01	14/05/17	57	21	10	346	434
SRB25	26/04/03	11/06/19	29	14		301	344
SRB12.5	17/06/05	07/03/19	20	7		87	114
PRCR	01/12/08	11/07/19	70	12			82
3-breed crosses	10/07/04	12/07/19	119	2	20	338	479

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, PRCR = ProCROSS (MON50SRB25), numbers in the genotype indicate the proportion of genes in %, min = minimum, max = maximum

Table A5: Minimum and maximum of the dates of birth as well as number of evaluated 3-breed crosses in the farms

3-breed crosses	Dates of birth		Number of animals				
			Farm				Total
Genotype	min	max	A	B	C	D	
MON75SRB25	21/04/12	12/07/19	17				17
MON50SRB12.5	08/05/11	31/07/19	24				24
MON25SRB12.5	20/10/12	19/09/19	55	2			57
BS50SRB25	10/07/04	18/12/09				95	95
BS50SRB12.5	03/08/07	26/06/14				45	45
BS25SRB12.5	23/06/07	29/03/16				75	75
SRB50MON25	01/07/12	26/04/17	23				23
SRBBS25	10/09/05	30/07/13				88	88
SRB12.5BS6.25	01/10/10	23/04/18				35	35
SRBJER	31/03/10	18/07/11			20		20
Total	10/07/04	12/07/19	119	2	20	338	479

MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, numbers in the genotype indicate the proportion of genes in %, min = minimum, max = maximum

Table A6: Selected sires, year of birth, number of evaluated daughters and breeding values

Name of sire	HB-Nr.	Year	n	RZG	TMI	RZM	NTM	ISU	Yield	INEL	NM$	VV	BW
Breed Montbéliarde (MON)													
Triomphe	605773	2002	113					114		14			
Helux	606099	2005	25					121		29			
Jeremiah	606297	2014						142					
Plumitif	605576	1999	17		116								
Breed Jersey (JER)													
Paul	409180	2003	28			88							
Brazo ET	409192	1998	12	1107									
Rampant ET	409233	2001	11										
Skae Laban	409846	1993	6										
Breed Brown Swiss (BS)													
Agenda	10608299	2000	35	106									
Paydor	352.532	2005	30										
Eagel	10/608170	1997	58	112									
Etpat	360.027	1998	56		128								
Etrox	352.976	2006	26										
Extra PP	342.960	2004	11										
Hucos	340.840	1997	22		18								
Juwel	342.575	2003	15		125								
Payssli	435.070	2005	10										
Breed Swedish Red Breed (SRB)													
A Linne	599962	2004	29				-9		90				
Backgard	666708	1991	17										96
Gunnarstorp	598927	2002	11	131			25		98				
K Lens	598016	1999	23									103	
Orraryd	596823	1998	42	125									
Oscar SE	813185	2006	62										
Peterslund	597199	1997	138	117									
S Adam	598904	2002	15										

Name of sire	HB-Nr.	Year	n	RZG	TMI	RZM	NTM	ISU	Yield	INEL	NM$	VV	BW
Spyderman	813792	2008	19										
St Hallebo	598977	2010	17			301							
Stoepafors	594100	1994	42										
Superman	813791	2008	30								+531		
T Bruno	592064	1990	65										
Tuima	589020	2004	13										
Nero	588972	2011	18	101									
Walstad	593813	1996	15										

HB-Nr. = Herdbook number, Year = Year of birth, n = Number of evaluated daughters in the total sample

Breeding values:
RZG = Gesamtzuchtwert, Total Merit Index, (Germany, Austria)
TMI = Total Merit Index (Germany, Austria)
RZM = Relativzuchtwert Milch (Relative breeding value of milk, Germany, Austria)
NTM = Nordic Total Merit-Index (Scandinavia)
ISU = Index Synthèse UPRa (France)
Yield = Breeding value for milk production (Scandinavia)
INEL = INdex Economique Laitier (France)
NM$ = Net Merit (ST genetics, USA)
VV = Veislinė vertė (Lithuania)BW = Breeding Worth (New Zealand)

Table A7: Statistical parameters of selected performances of German Holsteins (GH) and crossbreeds with different gene shares in the total sample

Genotype/ Breed	Statistical parameters				
	Number	Average	SE	min	max
Age at first service in months					
GH	3,104	16.5	0.7	10.1	36.4
All crossbreeds	1,654	16.3	0.7	10.9	36.3
GH > 75%	277	17.1	1.1	10.9	27.3
GH < 75	111	18.2	1.3	13.0	25.4
MON50	68	15.1	0.1	13.1	17.4
MON25	22	15.3	0.2	13.9	17.0
MON12.5	24	15.5	0.2	14.3	17.2
JER50	51	18.1	3.2	13.7	25.8
JER25	9	19.6	2.0	16.5	22.0
BS50	185	16.4	0.5	12.9	21.9
BS25	90	17.8	0.3	14.4	25.0
BS12.5	34	18.5	1.7	12.1	25.1
SRB75	6	19.8	1.8	16.0	26.8
SRB50	270	16.4	0.7	12.9	29.7
SRB25	220	16.3	1.0	13.4	27.9
SRB12.5	82	17.3	1.3	12.8	28.1
PRCR	72	15.6	0.6	12.6	19.0
3-breeds	301	16.6	0.7	10.9	32.3
Age at first calving in months					
GH	2,917	26.3	0.5	20.3	43.8
All crossbreeds	1,900	26.1	0.5	20.0	45.3
GH > 75%	298	26.9	0.9	20.0	37.0
GH < 75	107	27.5	1.0	23.6	34.4
MON50	54	25.8	1.0	23.4	32.9
MON25	18	25.0	0.4	22.9	30.3
MON12.5	17	25.6	1.1	23.8	29.0
JER50	54	28.8	4.0	23.1	40.5
JER25	16	28.6	1.7	24.8	33.6
BS50	206	26.1	0.5	22.3	31.5
BS25	124	27.4	0.2	23.7	34.2
BS12.5	39	27.7	2.1	21.1	34.2
SRB75	10	28.3	1.6	25.0	35.7
SRB50	350	26.2	0.6	22.1	34.8
SRB25	260	26.2	0.8	22.3	42.4
SRB12.5	90	27.1	1.0	23.1	37.0
PRCR	67	25.6	0.8	21.9	30.5
3-breeds	366	26.3	0.6	20.0	41.3
Inter-calving interval in days					
GH	1,729	418.3	6.3	293.7	1, 022.0
All crossbreeds	791	389.8	6.6	276.0	697.0
GH > 75	70	406.2	11.2	356.0	521.0
GH < 75	35	397.7	11.3	325.0	496.7
MON50	28	381.8	6.7	332.0	446.5
MON25	6	421.6	39.2	347.5	613.0
MON12.5	5	428.4	21.6	376.0	486.0

Genotype/ Breed	Statistical parameters				
	Number	Average	SE	min	max
JER50	30	375.4	6.5	309.0	446.0
JER25	6	469.0	0.44	359.0	531.5
BS50	73	395.9	8.3	276.0	630.0
BS25	54	417.0	8.1	335.0	697.0
BS12.5	12	422.4	16.5	351.0	521.0
SRB75	5	359.7	17.2	333.0	422.0
SRB50	193	392.3	6.3	315.0	696.0
SRB25	69	404.2	6.6	327.0	621.0
SRB12.5	23	392.1	15.1	316.0	502.5
PRCR	41	371.8	4.6	327.3	484.5
3-breeds	172	387.0	10.1	328.5	634.0
Number of milking days					
GH	2,097	926.6	73.6	16	3,576
All crossbreeds	1,286	862.7	111.6	9	3,592
GH > 75%	159	533.9	36.4	28	2,423
GH < 75	67	1,034.2	594.7	14	2,989
MON50	37	786.1	82.9	38	1,960
MON25	9	662.0	427.9	132	1,671
MON12.5	6	560.7	259.7	19	903
SRB75	8	506.3	124.2	30	870
SRB50	257	1,029.3	201.7	9	2,736
SRB25	135	943.2	202.2	17	2,410
SRB12.5	52	573.5	98.4	20	2,423
BS50	130	808.4	47.6	18	2,417
BS25	86	659.9	48.6	20	2,826
BS12.5	24	505.0	49.6	28	1,777
JER50	38	733.2	50.6	19	1,776
JER25	10	754.3	0.4	62	1,738
PRCR	53	761.5	52.6	41	1,968
3-breeds	321	786.2	112.6	14	3,592
Milk in kg					
GH	2,097	27,218	2,501	48	108,931
All crossbreeds	1,286	25,126	3,703	2	95,841
GH > 75%	159	13,266	1,538	92	63,720
GH < 75	67	32,097	19,771	2	95,841
MON50	37	26,560	3,206	890	76,778
MON25	9	24,896	11,897	3,716	69,570
MON12.5	6	18,572	4,532	317	29,369
SRB75	8	8,807	2,595	147	21,679
SRB50	257	28,979	6,486	106	82,344
SRB25	135	29,423	8,604	213	94,678
SRB12.5	52	14,381	1,924	92	63,720
BS50	130	23,575	3,982	54	69,067
BS25	86	19,427	2,489	70	84,100
BS12.5	24	12,512	2,542	319	46,981
JER50	38	20,481	9,851	57	58,405
JER25	10	18,057	0,429	1,214	49,405
PRCR	53	23,668	2,185	4,689	12,577
3-breeds	321	786,2	112,6	180	89,981

Genotype/ Breed	Statistical parameters				
	Number	Average	SE	min	max
Milk in kg per milking day					
GH	2,097	28.1	1.6	2.8	59.1
All crossbreeds	1,286	26.8	1.7	0.1	52.0
GH > 75%	159	25.8	2.4	2.0	29.2
GH < 75	67	25.9	2.0	0.1	38.6
MON50	37	30.8	1.0	16.8	42.2
MON25	9	34.0	5.9	24.3	48.7
MON12.5	6	30.2	3.1	16.7	37.7
SRB75	8	17.7	2.6	4.9	24.9
SRB50	257	27.0	2.1	1.4	47.9
SRB25	135	27.0	3.4	9.7	42.8
SRB12.5	52	25.0	2.5	2.0	33.0
BS50	130	26.0	2.9	0.9	40.3
BS25	86	25.8	2.5	2.0	37.7
BS12.5	24	22.7	1.0	11.4	32.2
JER50	38	27.4	2.6	3.0	41.5
JER25	10	23.3	0.4	18.3	28.4
PRCR	53	28.4	2.2	14.5	52.0
3-breeds	321	26.7	1.7	5.3	41.1
Milk in kg per productive day					
GH	2,097	24.7	1.4	2.8	66.0
All crossbreeds	1,286	23.5	1.5	0.07	37.5
GH > 75%	159	22.9	2.5	1.9	29.1
GH < 75	67	23.1	2.0	0.1	35.8
MON50	37	27.3	0.8	16.8	37.4
MON25	9	30.1	1.4	22.9	34.1
MON12.5	6	27.4	2.4	16.7	32.4
SRB75	8	17.2	2.1	4.9	24.1
SRB50	257	23.7	1.9	0.01	31.9
SRB25	135	23.7	2.6	2.3	33.3
SRB12.5	52	21.9	2.7	0.1	30.1
BS50	130	22.4	2.5	0.03	34.0
BS25	86	23.2	2.8	2.0	31.4
BS12.5	24	20.3	3.5	7.8	26.8
JER50	38	23.3	1.8	3.0	33.6
JER25	10	20.8	0.4	16.1	26.4
PRCR	53	20.6	4.0	14.5	37.5
3-breeds	295	23.3	1.4	5.0	36.1
Milk in kg per day of life					
GH	2,097	12.9	0.9	0.1	30.5
All crossbreeds	1,286	11.7	1.1	0.003	26.7
GH > 75%	159	8.7	1.4	0.1	19.0
GH < 75	67	9.4	1.8	0.003	22.7
MON50	37	13.4	1.2	1.2	26.2
MON25	9	13.1	6.0	4.2	25.0
MON12.5	6	12.0	2.6	0.4	17.3
SRB75	8	5.3	1.3	0.2	10.9
SRB50	257	12.5	1.7	0.1	23.1
SRB25	135	12.6	2.9	0.2	26.7

Genotype/ Breed	Statistical parameters				
	Number	Average	SE	min	max
SRB12.5	52	7.7	0.7	0.1	19.0
BS50	130	12.1	1.8	0.1	21.3
BS25	86	9.3	0.6	0.1	20.1
BS12.5	24	7.3	0.9	0.4	17.5
JER50	38	10.6	3.9	0.1	22.2
JER25	10	9.0	0.4	1.4	15.6
PRCR	53	11.6	1.4	0.7	21.5
3-breeds	321	11.3	1.3	0.2	26.0
Age at cull in years					
GH	2,831	4.0	0.2	0.01	13.5
All crossbreeds	1,948	3.9	0.3	0.01	13.5
GH > 75%	278	2.6	0.1	0.03	9.2
GH < 75	104	2.8	1.9	0.03	12.1
MON50	51	3.7	0.3	0.03	8.0
MON25	14	3.0	1.5	0.04	7.6
MON12.5	12	2.9	0.4	1.43	4.7
JER50	44	5.2	0.7	2.04	8.1
JER25	15	4.0	1.0	0.03	8.7
BS50	227	4.0	0.1	0.01	12.3
BS25	123	4.2	0.7	0.01	11.4
BS12.5	40	3.0	0.3	0.02	8.1
SRB75	9	3.5	0.6	1.17	5.5
SRB50	384	5.1	0.6	0.01	10.7
SRB25	278	3.4	0.6	0.01	9.8
SRB12.5	82	2.7	0.2	0.03	9.2
PRCR	68	3.7	0.4	0.01	8.2
3-breeds	371	3.4	0.4	0.02	13.5
Productive period in years					
GH	2,123	2.9	0.2	0.03	11.5
All crossbreeds	1,436	2.7	0.3	0.02	11.3
GH > 75%	176	1.5	0.1	0.02	7.1
GH < 75	62	3.3	1.9	0.1	9.5
MON50	37	2.5	0.3	0.1	6.0
MON25	9	2.2	1.5	0.4	5.6
MON12.5	8	1.3	0.4	0.1	2.7
JER50	44	2.5	0.7	0.1	5.8
JER25	14	2.1	1.0	0.1	6.6
BS50	179	2.7	0.1	0.1	9.9
BS25	101	2.2	0.7	0.1	9.2
BS12.5	30	1.5	0.3	0.1	5.8
SRB75	8	1.7	0.6	0.1	2.8
SRB50	302	3.4	0.6	0.0	8.6
SRB25	201	2.8	0.6	0.1	8.5
SRB12.5	62	1.7	0.2	0.0	7.1
PRCR	53	2.7	0.4	0.1	6.2
3-breeds	317	2.4	0.4	0.1	11.3
Number of lactations					
GH	2,098	3.1	0.2	1	10
All crossbreeds	1,286	2.9	0.2	1	10

Genotype/ Breed	Statistical parameters				
	Number	Average	SE	min	max
GH > 75%	159	2.4	0.5	1	5
GH < 75	67	3.5	1.7	1	9
MON50	37	3.2	0.3	1	6
MON25	9	2.6	1.4	1	6
MON12.5	6	2.2	0.3	1	3
JER50	38	2.7	0.9	1	6
JER25	10	2.3	0.4	1	4
BS50	130	2.8	0.2	1	8
BS25	86	2.2	0.7	1	8
BS12.5	24	1.9	0.3	1	6
SRB75	8	1.6	0.2	1	3
SRB50	257	3.3	0.4	1	8
SRB25	135	3.0	0.6	1	8
SRB12.5	52	2.4	0.6	1	6
PRCR	53	2.9	0.2	1	7
3-breeds	321	2.8	0.4	1	10
Somatic cell counts, total in thousand / ml milk					
GH	1,926	310.1	19.1	13.0	6,574.0
All crossbreeds	1,210	318.8	15.5	5.5	5,537.0
GH > 75%	140	308.6	48.8	21.0	2,599.3
GH < 75	46	284.2	44.4	25.3	1,563.7
MON50	28	557.1	177.6	27.3	4,262.0
MON25	9	313.6	109.0	26.9	1,064.6
MON12.5	5	196.2	76.4	42.0	469.7
JER50	42	437.3	109.0	43.3	1,877.3
JER25	9	237.2	0.3	66.8	605.0
BS50	156	318.0	21.2	43.8	1,781.0
BS25	95	274.9	38.2	29.6	2,511.9
BS12.5	23	392.4	394.9	45.9	2,599.3
SRB75	6	260.1	113.8	31.3	700.8
SRB50	248	329.5	36.1	23.3	1.955.0
SRB25	167	287.8	35.5	5.5	4,767.3
SRB12.5	50	248.9	46.8	14.0	2.166.0
PRCR	50	414.7	106.2	39.3	5,050.5
3-breeds	269	331.7	29.9	21.3	1,888.0
Content of somatic cells share < 100 thousand / ml milk					
GH	1,926	45.8%	7.5%	0%	100%
All crossbreeds	1,210	44.2%	4.5%	0%	100%
GH > 75%	140	53.2%	2.6%	0%	100%
GH < 75	46	49.5%	4.1%	0%	100%
MON50	28	53.9%	4.5%	0%	100%
MON25	9	40.9%	5.6%	20.0%	100%
MON12.5	5	56.9%	8.7%	36.7%	91.7%
JER50	42	46.0%	6.3%	0%	100%
JER25	9	40.6%	35.4%	28.2%	83.9%
BS50	156	57.2%	4.3%	0%	100%
BS25	95	45.7%	11.1%	0%	100%
BS12.5	23	55.3%	2.9%	0%	100%
SRB75	6	62.6%	10.8%	0%	92.6%

Genotype/ Breed	Statistical parameters				
	Number	Average	SE	min	max
SRB50	248	46.2%	16.7%	0%	100%
SRB25	167	45.2%	1.7%	0%	100%
SRB12.5	50	53.8%	3.8%	0%	100%
PRCR	50	36.0%	8.3%	0%	100%
3-breeds	269	45.4%	6.6%	0%	100%
Content of somatic cells share > 400 thousand / ml milk					
GH	1,926	15.9%	2.8%	0%	100%
All crossbreeds	1,210	17.4%	1.5%	0%	100%
GH > 75%	140	12.6%	1.7%	0%	100%
GH < 75	46	12.8%	2.9%	0%	100%
MON50	28	17.7%	11.3%	0%	100%
MON25	9	11.0%	3.6%	0%	30%
MON12.5	5	13.3%	6.9%	0%	36%
JER50	42	29.9%	7.8%	0%	100%
JER25	9	7.1%	33.9%	0%	26%
BS50	156	17.8%	2.2%	0%	100%
BS25	95	14.0%	2.3%	0%	100%
BS12.5	23	16.7%	4.1%	0%	100%
SRB75	6	20.8%	13.0%	0%	100%
SRB50	248	17.1%	1.4%	0%	100%
SRB25	167	13.1%	1.7%	0%	29.6%
SRB12.5	50	21.0%	11.0%	0%	36.4%
PRCR	50	22.5%	8.4%	0%	100%
3-breeds	269	18.9%	2.9%	0%	26.3%

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, PRCR = ProCROSS (MON50SRB25), numbers in the genotype indicate the proportion of genes in %, n = number of animals, SE = standard error, min = minimum, max = maximum

Table A8: Statistical parameters of selected performances of German Holsteins (GH) and crossbreeds with different gene shares in the total sample

Farm	Number	Statistical parameters				Significance at p < 0,05		
	n	Average	SE	min	max	Farm B	Farm C	Farm D
Age at first service in months								
Farm A	2,037	15.3	0.03	10.1	26.9	0.000	0.000	0.000
Farm B	716	16.2	0.1	11.1	36.4		0.008	0.000
Farm C	612	15.9	0.1	12.9	21.0			0.000
Farm D	1,393	18.3	0.1	10.9	36.3			
Age at first calving in months								
Farm A	1,783	25.2	0.04	21.4	33.4	0.000	0.000	0.000
Farm B	613	26.3	0.1	20.3	43.8		0.007	0.000
Farm C	570	25.9	0.1	22.3	33.4			0.000
Farm D	1,851	27.5	0.1	20.0	45.3			
Inter-calving interval in days								
Farm A	1,062	400.6	1.6	294	674	0.000	0.310	0.000
Farm B	341	424.9	4.0	310	810		0.000	0.053
Farm C	283	404.6	3.7	276	666			0.010
Farm D	802	415.9	2.3	316	1,022			
Number of milking days								
Farm A	1,288	888.7	14.7	14	2,902	0.000	0.000	0.000

Farm	Number	Statistical parameters				Significance at p < 0,05		
	n	Average	SE	min	max	Farm B	Farm C	Farm D
Farm B	406	1,143.2	35.6	20	3,576		0.000	0.000
Farm C	387	788.1	23.6	16	2,204			0.616
Farm D	1,164	802.4	15.9	9	3,592			
Milk in kg								
Farm A	1,288	29,170.6	518.8	2	96,742	0.000	0.000	0.000
Farm B	406	32,824.2	1,128.1	322	108,931		0.000	0.000
Farm C	387	24,577.8	811.8	48	88,646			0.616
Farm D	1,164	19,765.8	449.6	70	89,981			
Milk in kg per milking day								
Farm A	1,288	31.3	0.2	0.1	59.1	0.000	0.000	0.000
Farm B	406	27.2	0.3	9.5	46.4		0.000	0.000
Farm C	387	29.3	0.3	3.0	48.5			0.000
Farm D	1,155	23.2	0.1	0.9	51.3			
Milk in kg per productive day								
Farm A	1,288	27.7	0.1	0.1	38.6	0.000	0.000	0.000
Farm B	406	23.2	0.2	9.5	35.5		0.000	0.000
Farm C	387	25.6	0.3	3.0	41.0			0.000
Farm D	1,155	20.5	0.1	0.9	66.0			
Milk in kg per day of life								
Farm A	1,288	14.5	0.2	0.003	28.2	0.000	0.000	0.000
Farm B	406	13.2	0.2	0.3	26.7		0.541	0.000
Farm C	387	12.9	0.3	0.1	30.5			0.000
Farm D	1,155	9.8	0.1	0.1	21.6			
Age at cull in years								
Farm A	1,547	4.3	0.1	0.01	11.2	0.367	0.000	0.000
Farm B	586	4.5	0.1	0.02	13.5		0.001	0.000
Farm C	493	4.0	0.1	0.01	8.8			0.000
Farm D	2,153	3.3	0.1	0.01	13.5			
Productive period in years								
Farm A	1,327	2.8	0.05	0.10	9.1	0.000	0.000	0.000
Farm B	433	3.5	0.1	0.10	11.5		0.000	0.000
Farm C	396	2.4	0.1	0.10	6.7			0.667
Farm D	2,153	3.3	0.1	0.01	13.5			
Number of lactations								
Farm A	1,288	3.1	0.04	1	9	0.000	0.000	0.000
Farm B	407	3.7	0.1	1	10		0.000	0.000
Farm C	387	2.6	0.1	1	7			0.646
Farm D	1,164	2.7	0.05	1	10			
Somatic cell counts in thousand / ml milk								
Farm A	1,186	315.6	13.4	16.0	6.574	0.957	0.053	0.151
Farm B	402	316.8	17.4	13.0	3.169		0.113	0.207
Farm C	375	350.4	12.0	32.7	1.833			0.000
Farm D	1173	290.9	10.8	5.5	5.537			
Somatic cell count, share < 100 thousand / ml milk								
Farm A	1,186	51.6%	0.8%	0.0%	100.0%	0.093	0.000	0.564
Farm B	402	49.0%	1.3%	0.0%	100.0%		0.000	0.040
Farm C	375	25.6%	1.2%	0.0%	100.0%			0.000
Farm D	1173	52.2%	0.8%	0.0%	100.0%			
Somatic cell count, share > 400 thousand / ml milk								

Farm	Number	Statistical parameters				Significance at p < 0,05		
	n	Average	SE	min	max	Farm B	Farm C	Farm D
Farm A	1,186	14.0%	0.5%	0.0%	100.0%	0.307	0.000	0.910
Farm B	402	15.0%	0.9%	0.0%	100.0%		0.000	0.364
Farm C	375	23.4%	1.1%	0.0%	100.0%			0.000
Farm D	1173	14.1%	0.6%	0.0%	100.0%			

n = number of animals, SE = standard error, min = minimum, max = maximum

Table A9: Statistical parameters of selected performances of German Holsteins (GH) and crossbreeds with different gene shares of the breed Montbéliarde (MON, Farm A)

Genotype	Number	Statistical parameters				Significance at p < 0.05		
	n	Average	SE	min	max	MON50	MON25	MON12.5
Age at first service in months								
GH	1,353	15.1	0.03	10.1	26.4	0.751	0.309	0.017
MON50	61	15.1	0.1	13.1	17.4		0.439	0.038
MON25	22	15.3	0.2	13.9	17.0			0.285
MON12.5	24	15.5	0.2	14.3	17.2			
Age at first calving in months								
GH	1,171	25.0	0.05	21.4	33.4	0.902	0.886	0.122
MON50	48	24.9	0.2	23.4	32.9		0.851	0.154
MON25	18	25.0	0.4	22.9	30.3			0.337
MON12.5	17	25.6	0.4	23.8	29.0			
Inter-calving interval in days								
GH	622	400.4	2.1	293.7	674.0	0.028	0.611	0.266
MON50	26	383.7	6.9	332.0	446.5		0.382	0.108
MON25	6	421.6	39.2	347.5	613.0			0.884
MON12.5	5	428.4	21.6	376.0	486.0			
Number of milking days								
GH	789	775.9	16.0	17	2,446	0.823	0.551	0.159
MON50	34	795.7	86.6	38	1,960		0.521	0.163
MON25	9	662.0	182.4	132	1,671			0.658
MON12.5	6	560.7	129.8	19	903			
Milk in kg								
GH	789	25,604.3	581.7	109	96,742	0.680	0.934	0.183
MON50	34	27,019.5	3,357.0	890	76,778		0.815	0.161
MON25	9	24,895.6	8,223.4	3.716	69,570			0.514
MON12.5	6	18,572.2	4,532.1	317	29,369			
Milk in kg per milking day								
GH	789	31.4	0.2	2.8	59.1	0.810	0.333	0.715
MON50	34	31.1	1.1	16.8	42.2		0.317	0.787
MON25	9	34.0	2.5	24.3	48.7			0.357
MON12.5	6	30.2	3.0	16.7	37.7			
Milk in kg per productive day								
GH	789	28.2	0.2	2.8	38.6	0.399	0.208	0.759
MON50	34	27.5	0.8	16.8	37.4		0.126	0.980
MON25	9	30.1	1.4	22.9	34.1			0.358
MON12.5	6	27.4	2.4	16.7	32.4			
Milk in kg per day of life								
GH	789	14.0	0.2	0.1	28.2	0.814	0.756	0.485
MON50	34	13.7	1.3	1.2	26.2		0.858	0.582
MON25	9	13.1	2.6	4.2	25.0			0.759

Genotype	Number	Statistical parameters				Significance at p < 0.05		
	n	Average	SE	min	max	MON50	MON25	MON12.5
MON12.5	6	12.0	2.6	0.4	17.3			
Age at cull in years								
GH	950	4.0	0.1	0.5	9.7	0.289	0.138	0.009
MON50	47	3.7	0.3	0.03	8.0		0.368	0.113
MON25	14	3.0	0.6	0.04	7.6			0.856
MON12.5	12	2.9	0.3	1.4	4.7			
Productive period in years								
GH	785	2.4	0.1	0.1	7.5	0.622	0.822	0.034
MON50	37	2.5	0.3	0.1	6.0		0.698	0.027
MON25	9	2.2	0.6	0.4	5.6			0.277
MON12.5	8	1.3	0.4	0.1	2.7			
Number of lactations								
GH	789	2.7	0.05	1	7	0.122	0.810	0.141
MON50	34	3.1	0.3	1	6		0.409	0.033
MON25	9	2.6	0.6	1	6			0.577
MON12.5	6	2.2	0.3	1	3			
Somatic cell counts in thousand / ml milk								
GH	708	301.6	18.4	16.0	6.574.0	0.133	0.916	0.244
MON50	25	608.5	196.7	27.3	4.262.0		0.199	0.061
MON25	9	313.6	109.0	26.9	1.064.6			0.395
MON12.5	5	196.2	76.4	42.0	469.7			
Somatic cell count, share < 100 thousand / ml milk								
GH	669	54.9%	1.1%	0.0%	100.0%	0.019	0.826	0.517
MON50	21	39.4%	6.6%	0.0%	100.0%		0.119	0.105
MON25	9	56.9%	8.7%	20.0%	100.0%			0.691
MON12.5	5	62.6%	10.8%	36.7%	91.7%			
Somatic cell count, share > 400 thousand / ml milk								
GH	503	13.1%	0.8%	0.0%	100.0%	0.070	0.583	0.977
MON50	21	24.9%	6.8%	0.0%	100.0%		0.062	0.234
MON25	6	11.0%	4.4%	0.0%	29.6%			0.775
MON12.5	3	13.3%	8.9%	0.0%	36.4%			

GH = German Holsteins, MON = Montbéliarde, numbers in the genotype indicate the proportion of genes in %, n = number of animals, SE = standard error, min = minimum, max = maximum

Table A10: Statistical parameters of selected performances of German Holsteins (GH) and crossbreeds with different gene shares of the breed Brown Swiss (BS, Farm D)

Genotype	Number	Statistical parameters				Significance at p < 0.05		
	n	Average	SE	min	max	BS50	BS25	BS12.5
Age at first service in months								
GH	351	18.6	0.1	13.0	28.9	0.000	0.000	0.190
BS50	104	17.2	0.1	13.3	21.9		0.019	0.000
BS25	84	17.9	0.3	14.4	25.0			0.203
BS12.5	34	18.5	0.4	12.1	25.1			
Age at first calving in months								
GH	468	27.7	0.1	22.0	38.1	0.000	0.018	0.225
BS50	129	26.8	0.1	22.4	31.5		0.014	0.000
BS25	118	27.5	0.2	23.7	34.2			0.651
BS12.5	39	27.7	0.4	21.1	34.2			
Inter-calving interval in days								
GH	276	432.8	4.8	322	1,022	0.008	0.398	0.128
BS50	36	405.0	11.2	329	630		0.379	0.489
BS25	52	417.5	8.5	335	697			0.793
BS12.5	12	422.4	16.5	351	521			
Number of milking days								
GH	304	956.2	29.2	25	3,070	0.003	0.349	0.000
BS50	82	765.9	56.5	24	2,417		0.366	0.053
BS25	80	848.6	71.5	20	2,826			0.013
BS12.5	24	543.0	95.0	28	1,777			
Milk in kg								
GH	304	24,355.7	842.0	468	86,934	0.003	0.393	0.000
BS50	82	18,173.4	1,656.7	144	69,067		0.142	0.160
BS25	80	22,071.2	2,059.2	70	84,100			0.013
BS12.5	24	13,455.4	2,666.0	319	46,981			
Milk in kg per milking day								
GH	304	24.8	0.2	14.3	51.3	0.001	0.030	0.021
BS50	82	21.4	0.8	0.9	32.0		0.021	0.140
BS25	80	23.8	0.7	2.0	35.0			0.322
BS12.5	24	22.6	1.0	11.4	32.2			
Milk in kg per productive day								
GH	304	21.7	0.2	7.3	36.6	0.131	0.160	0.171
BS50	127	20.6	0.7	0.0	34.0		0.850	0.775
BS25	80	20.8	0.6	2.0	31.4			0.657
BS12.5	24	20.3	1.0	7.8	26.8			
Milk in kg per day of life								
GH	304	11.6	0.2	0.5	20.8	0.001	0.024	0.000
BS50	82	9.3	0.5	0.1	20.3		0.347	0.207
BS25	80	10.1	0.6	0.1	20.1			0.049
BS12.5	24	7.8	1.0	0.4	17.5			
Age at cull in years								
GH	641	2.9	0.1	0.01	11.8	0.000	0.000	0.191
BS50	163	4.0	0.2	0.01	12.3		0.589	0.012
BS25	117	4.2	0.2	0.01	11.4			0.002
BS12.5	40	3.0	0.3	0.02	8.1			
Productive period in years								

Genotype	Number	Statistical parameters				Significance at p < 0.05		
	n	Average	SE	min	max	BS50	BS25	BS12.5
GH	307	3.0	0.1	0.0	9.7	0.371	0.218	0.000
BS50	130	2.7	0.2	0.1	9.9		0.986	0.000
BS25	95	2.7	0.2	0.1	9.2			0.001
BS12.5	30	1.5	0.3	0.1	5.8			
Number of lactations								
GH	304	3.0	0.1	1	9	0.067	0.463	0.000
BS50	82	2.6	0.2	1	8		0.300	0.059
BS25	80	2.9	0.2	1	8			0.011
BS12.5	24	2.0	0.3	1	6			
Somatic cell counts in thousand / ml milk								
GH	270	237.3	15.9	16.0	1,855.9	0.012	0.440	0.184
BS50	112	316.1	27.7	43.8	1,781.0		0.428	0.769
BS25	90	277.4	40.0	29.6	2,511.9			0.341
BS12.5	23	392.4	111.7	45.9	2,599.3			
Somatic cell count, share < 100 thousand / ml milk								
GH	264	60.3%	1.6%	0.0%	100.0%	0.000	0.301	0.009
BS50	101	45.9%	2.5%	0.0%	100.0%		0.022	0.991
BS25	82	54.9%	3.2%	0.0%	100.0%			0.212
BS12.5	19	46.0%	6.9%	0.0%	92.3%			
Somatic cell count, share > 400 thousand / ml milk								
GH	179	10.4%	1.0%	0.0%	87.5%	0.002	0.288	0.150
BS50	89	16.4%	2.0%	0.0%	100.0%		0.346	0.906
BS25	65	13.6%	2.8%	0.0%	100.0%			0.522
BS12.5	16	16.7%	4.9%	0.0%	83.3%			

GH = German Holstein, BS = Brown Swiss, numbers in the genotype indicate the proportion of genes in %, n = number of animals, SE = standard error, min = minimum, max = maximum

Table A11: Statistical parameters of selected performances of German Holsteins (GH) and crossbreeds with different gene shares of the breed Swedish Red Breed (SRB, Farms A, B, C, D)

Genotype	Number	Statistical parameters				Significance at p < 0.05			
	n	Average	SE	min	max	SRB75	SRB50	SRB25	SRB12.5
Age at first service in months									
GH	3,104	16.5	0.7	10.1	36.4	0.062	0.668	0.721	0.256
SRB75	6	18.3	1.1	16.0	26.8		0.042	0.047	0.234
SRB50	270	16.3	0.7	12.9	29.7			0.983	0.164
SRB25	220	16.3	0.8	13.4	27.9				0.186
SRB12.5	82	17.1	0.8	12.8	28.1				
Age at first calving in months									
GH	2,917	26.3	0.5	20.3	43.8	0.119	0.363	0.857	0.233
SRB75	10	27.6	0.9	25.0	35.7		0.052	0.112	0.428
SRB50	350	26.0	0.5	22.1	34.8			0.518	0.107
SRB25	260	26.2	0.5	22.3	42.4				0.236
SRB12.5	90	26.9	0.6	23.1	37.0				
Inter-calving interval in days									
GH	1,719	418.0	5.3	294	1.022	0.031	0.060	0.186	0.158
SRB75	5	355.1	28.9	333	422		0.229	0.116	0.198
SRB50	193	390.5	7.7	315	696			0.336	0.718
SRB25	69	402.4	10.0	327	621				0.716
SRB12.5	23	396.2	14.8	316	503				

Genotype	Number	Statistical parameters				Significance at p < 0.05			
	n	Average	SE	min	max	SRB75	SRB50	SRB25	SRB12.5
Number of milking days									
GH	2,051	903.7	150.3	16	3,576	0.479	0.896	0.691	0.327
SRB75	8	732.8	255.4	30	870		0.441	0.358	1.000
SRB50	257	921.8	164.7	9	2,736			0.787	0.297
SRB25	135	964.8	177.1	17	2,410				0.228
SRB12.5	52	732.8	191.1	20	2,423				
Milk in kg									
GH	2,051	26,502.8	5,306.5	48	108,931	0.319	0.917	0.520	0.341
SRB75	8	18,718.7	8,527.0	147	21,679		0.354	0.183	0.762
SRB50	257	26,048.6	5,734.3	106	82,344			0.481	0.395
SRB25	135	29,683.7	6,106.3	213	94,678				0.174
SRB12.5	52	21,214.8	6,534.5	92	63,720				
Milk in kg per milking day									
GH	2,051	28.1	1.7	2.8	59.1	0.000	0.000	0.123	0.003
SRB75	8	21.8	2.5	4.9	24.9		0.008	0.002	0.033
SRB50	257	26.5	1.8	1.4	47.9			0.15	0.423
SRB25	135	27.3	1.8	9.7	42.8				0.085
SRB12.5	52	25.8	1.9	2.0	33.0				
Milk in kg per productive day									
GH	2,051	24.7	1.5	2.8	66.0	0.012	0.128	0.336	0.038
SRB75	8	20.2	2.2	4.9	24.1		0.101	0.045	0.310
SRB50	257	23.1	1.5	0.0	31.9			0.408	0.316
SRB25	135	23.9	1.6	2.3	33.3				0.133
SRB12.5	52	22.1	1.7	0.1	30.1				
Milk in kg per day of life									
GH	2,051	12.7	1.5	0.1	30.5	0.080	0.453	0.934	0.129
SRB75	8	8.8	2.5	0.2	10.9		0.172	0.083	0.517
SRB50	257	11.8	1.7	0.1	23.1			0.470	0.313
SRB25	135	12.8	1.8	0.2	26.7				0.140
SRB12.5	5	10.3	1.9	0.1	19.0				
Age at cull in years									
GH	2,831	4.0	1.1	0.01	13.5	0.806	0.228	0.937	0.654
SRB75	9	4.3	1.4	1.2	5.5		0.573	0.771	0.592
SRB50	384	4.9	1.2	0.01	10.7			0.234	0.147
SRB25	278	4.0	1.2	0.01	9.8				0.722
SRB12.5	82	3.7	1.2	0.03	9.2				
Productive period in years									
GH	2,123	2.9	0.5	0.03	11.5	0.480	0.761	0.967	0.284
SRB75	8	2.2	0.9	0.10	2.8		0.387	0.509	0.956
SRB50	302	3.0	0.5	0.02	8.6			0.757	0.209
SRB25	201	2.8	0.6	0.10	8.5				0.331
SRB12.5	62	2.2	0.6	0.02	7.1				
Number of lactations									
GH	2,052	3.0	0.5	1	10	0.282	0.818	0.880	0.805
SRB75	8	2.3	0.7	1	3		0.342	0.263	0.391
SRB50	257	2.9	0.5	1	8			0.737	0.947
SRB25	135	3.0	0.5	1	8				0.730
SRB12.5	52	2.9	0.5	1	6				
Somatic cell counts in thousand / ml milk									

Genotype	Number	Statistical parameters				Significance at p < 0.05			
	n	Average	SE	min	max	SRB75	SRB50	SRB25	SRB12.5
GH	1,926	309.7	18.7	13.0	6,574.0	0.792	0.678	0.846	0.456
SRB75	7	271.7	143.4	31.3	700.8		0.709	0.845	0.952
SRB50	247	326.5	33.0	23.3	1,955.0			0.642	0.363
SRB25	167	300.7	39.8	5.5	4,767.3				0.601
SRB12.5	50	262.5	59.5	14.0	2,166.0				
Somatic cell count, share < 100 thousand / ml milk									
GH	1,819	46%	7%	0%	100%	0.283	0.093	0.722	0.932
SRB75	4	35%	12%	0%	93%		0.701	0.352	0.329
SRB50	236	39%	8%	0%	100%			0.204	0.197
SRB25	154	45%	8%	0%	100%				0.860
SRB12.5	43	46%	8%	0%	100%				
Somatic cell count, share > 400 thousand / ml milk									
GH	1,471	16%	3%	0%	100%	0.161	0.306	0.666	0.515
SRB75	3	25%	7%	0%	75%		0.396	0.226	0.292
SRB50	198	19%	3%	0%	67%			0.423	0.568
SRB25	107	17%	3%	0%	100%				0.805
SRB12.5	31	18%	4%	0%	100%				

GH = German Holstein, SRB = Swedish Red Breed, numbers in the genotype indicate the proportion of genes in %, n = number of animals, SE = standard error, min = minimum, max = maximum

Table A12: Statistical parameters of Age at first calving and Lifetime efficiency of German Holsteins (GH) vs. daughters with sires of the breeds Montbéliarde (MON), Jersey (JER), Brown Swiss (BS) and Swedish Red Breed (SRB)

Breed	Statistical parameters					Significance at p < 0.05			
	n	Average	SE	min	max	MON	JER	BS	SRB
Age at first calving in months									
GH	3,783	26.2	1.42	20.3	37.6	0.865	0.814	0.890	0.533
MON	165	27.6	1.86	21.9	32.9		0.766	0.817	0.582
JER	57	27.8	1.79	23.1	34.6			0.910	0.856
BS	428	25.2	1.75	22.3	34.4				0.724
SRB	578	25.8	1.43	22.1	35.7				
Lifetime efficiency in kg milk per day of life									
GH	3,782	13.1	0.75	0.1	43.8	0.002	0.640	0.010	0.000
MON	130	11.3	0.95	0.7	32.9		0.039	0.313	0.641
JER	51	13.6	1.17	0.1	40.5			0.121	0.045
BS	95	12.0	0.84	0.1	34.4				0.378
SRB	149	11.6	0.81	0.003	35.7				

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, Nr, = Nummer, = Anzahl Töchter, MW = Mittelwert, sf = Standardfehler, min = minimum, max = maximum

Table A13: Statistical parameters of Age at first calving and Lifetime efficiency of German Holsteins (GH) vs. daughters of selected sires of the breeds Montbéliarde (MON), Jersey (JER), Brown Swiss (BS) and Swedish Red Breed (SRB)

Sire					Statistical parameters			
Name	Farm	Breed	Nr.	n	Average	SE	min	max
Age at first calving in months								
GH	all	GH	0	2,917	26.0	0.7	20.3	43.8
Triomphe	A. B	MON	1	91	25.0	0.8	21.9	32.9
Helux	A	MON	2	17	26.1	0.9	23.6	27.5
Plumitif	A. B	MON	4	16	25.5	0.9	23.6	30.0
Brazo	C	JER	6	12	23.8	1.0	23.1	27.4
Rampant	C	JER	7	11	24.2	1.0	23.7	26.5
Agenda	C	BS	14	27	25.3	0.8	23.6	27.7
A Linne	A. D	SRB	28	21	26.1	0.9	22.8	30.6
Langbo	D	SRB	31	15	25.4	0.9	23.7	27.3
Gunnarstorp	A. B	SRB	37	11	24.5	1.0	22.5	25.7
Tuima	A	SRB	38	11	24.5	1.0	22.6	25.8
Lifetime efficiency in kg milk per day of life								
GH	all	GH	0	2,050	13.7	0.2	0.1	30.5
Triomphe	A, B	MON	1	70	13.9	0.7	0.7	26.2
Plumitif	A, B	MON	4	14	15.3	1.5	0.3	19.9
Paul	C, D	JER	5	20	11.8	1.3	2.3	23.1
Brazo	C	JER	6	10	12.7	1.8	0.1	18.4
Rampant	C	JER	7	8	15.6	2.0	10.4	22.2
Eagel	C	BS	9	32	13.3	1.0	0.3	21.3
Hucos	D	BS	17	4	13.2	2.8	11.5	18.3
Juwel	D	BS	19	2	12.9	3.9	8.3	17.2
Peterslund	all	SRB	22	108	12.0	0.6	0.3	23.1
Gunnarstorp	A, B	SRB	37	11	14.0	1.7	0.9	20.3

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, Nr. = number, n = number of daughters, SE = standard error, min = minimum, max = maximum

Table A14: Significances between averages of Age at first calving of German Holsteins (GH) vs. daughters of selected sires of the breeds Montbéliarde (MON), Jersey (JER), Brown Swiss (BS) and Swedish Red Breed (SRB)

Sire					Significance at $p < 0.05$									
Name	Farm	Breed	Nr.	n	1	2	4	6	7	14	28	31	37	38
GH	all	GH	0	2,917	0.000	0.873	0.345	0.001	0.007	0.099	0.849	0.339	0.029	0.026
Triomphe	A, B	MON	1	91		0.086	0.509	0.079	0.219	0.660	0.059	0.547	0.443	0.417
Helux	A	MON	2	17			0.431	0.009	0.029	0.251	0.994	0.422	0.071	0.065
Plumitif	A	MON	4	16				0.059	0.143	0.794	0.403	0.976	0.279	0.264
Brazo	C	JER	6	12					0.724	0.066	0.006	0.067	0.478	0.500
Rampant	C	JER	7	11						0.170	0.023	0.157	0.727	0.753
Agenda	C	BS	14	27							0.217	0.824	0.340	0.321
A Linne	A, D	SRB	28	21								0.394	0.059	0.054
Langbo	D	SRB	31	15									0.299	0.283
Gunarstorp	A, B	SRB	37	11										0.973
Tuima	A	SRB	38	11										

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, Nr. = number, n = number of daughters

Table A15: Significances between averages of lifetime efficiency of German Holsteins (GH) vs. daughters of selected sires of the breeds Montbéliarde (MON), Jersey (JER), Brown Swiss (BS) and Swedish Red Breed (SRB)

Sire					Significance at $p < 0.05$									
Name	Farm	Breed	Nr.	n	1	4	5	6	7	9	17	19	22	37
GH	A,B,C,D	GH	0	2,050	0.784	0.289	0.128	0.545	0.327	0.710	0.845	0.839	0.002	0.882
Triomphe	A, B	MON	1	70		0.393	0.142	0.506	0.403	0.642	0.798	0.804	0.029	0.973
Plumitif	A	MON	4	14			0.072	0.250	0.888	0.274	0.500	0.571	0.036	0.553
Paul	C, D	JER	5	20				0.696	0.099	0.331	0.655	0.788	0.899	0.304
Brazo	C	JER	6	10					0.256	0.729	0.874	0.950	0.715	0.588
Rampant	C	JER	7	8						0.296	0.467	0.535	0.072	0.517
Eagel	C	BS	9	32							0.952	0.915	0.222	0.751
Hucos	D	BS	17	4								0.958	0.674	0.807
Juwel	D	BS	19	2									0.813	0.806
Peterslund	A,B,C,D	SRB	22	108										0.262
Gunarstorp	A, B	SRB	37	11										

GH = German Holsteins, MON = Montbéliarde, JER = Jersey, BS = Brown Swiss, SRB = Swedish Red Breed, Nr. = number, n = number of daughters

Table A16: Reasons for culling aller Genotypen in the farms

Farm	n	Anteil Abgänge nach Abgangsgründen							
		High age	Udder disease	Low performance	Claw & limb disorders	Milkability	Metabolic disease	Infertility	Other
A	1,547	4.0%	1.8%	31.8%	9.8%	24.0%	2.7%	10.9%	15.0%
B	586	7.0%	13.3%	4.1%	5.8%	3.6%	1.7%	20.1%	44.4%
C	493	0.0%	14.2%	8.9%	9.9%	0.4%	2.8%	37.1%	26.6%
D	2,089	0.0%	12.3%	15.9%	7.1%	1.9%	2.9%	15.4%	44.4%

n = number of animals

Table A17: Performance comparison of GH vs. BS50 in farms with low (Farm D) and medium (Farm C) herd level

Herd level / Farm	Law / D			Medium / C		
Parameter	n	Average	p	n	Average	p
All genotypes	2,623			673		C vs. D
Age at first calving (months)	1,851	27.5		570	25.9	0.000
Inter-calving interval (days)	802	415.9		683	404.6	0.010
Milk, (kg)	1,164	19,766		387	24,578	0.000
Lifetime efficiency (kg milk / dl)	1,164	9.8			12.9	0.000
Productive period (years)	1,403	2.5		396	2.4	0.667
SCC (thousand per ml milk)		291			350	0.000
Share < 100	1,173	52.2 %		375	25.6 %	0.000
Share > 400		14.1 %			23.4 %	0.000
GH	881			483		
Age at first calving (months)	518	27.7		562	26.0	
Inter-calving interval (days)	326	429.0		309	413.0	
Milk, (kg)	354	23,879		364	24,679	
Lifetime efficiency (kg milk / dl)		11.4			13.0	
Productive period (years)	357	2.9		388	2.4	
SCC (thousand per ml milk)		261			361	
Share < 100	320	57.7 %		361	23.8 %	
Share > 400		11.8 %			24.1 %	
BS50	169		GH vs. BS50	88		GH vs. BS50
Age at first calving (months)	129	26.8	0.000	74	25.6	0.085
Inter-calving interval (days)	36	405.0	0.052	34	385.4	0.000
Milk, (kg)	82	18,173	0.002	45	26,501	0.563
Lifetime efficiency (kg milk / dl)		9.3	0.001		13.4	0.344
Productive period (years)	130	2.7	0.186	46	2.7	0.890
SCC (thousand per ml milk)		316	0.082		329	0.116
Share < 100	112	45.9 %	0.000	42	28.2 %	0.017
Share > 400		16.4 %	0.021		21.4 %	0.262

GH = German Holsteins, BS = Brown Swiss, n = number of animals, dl = day of life, SCC = Somatic cell count, significant $p < 0.05$

Table A18: Performance comparison of GH vs. BS50 in farms with low (Farm D) and medium (Farm C) herd level

Herd level / Farm	Low / D			Medium / A			Medium / B		
Parameter	n	Average	p	n	Average	p	n	Average	p
All genotypes	2.623			2.144		A vs. D	825		B vs. D
Age at first calving (months)	1,851	27.5		1,783	25.2	0.000	613	26.3	0.000
Inter-calving interval (days)	802	415.9		1,062	400.6	0.000	341	424.9	0.053
Milk, (kg)	1,164	19,766		1,288	29,171	0.000	406	32,824	0.000
Lifetime efficiency (kg milk / dl)	1,164	9.8		1,288	14.5	0.000	406	13.2	0.000
Productive period (years)	1,403	2.5		1,327	2.8	0.000	433	3.5	0.000
SCC (thousand per ml milk)	1,173	291		1,186	316	0.153	402	317	0.209
Share < 100		52.2 %			51.6 %	0.555		49.0 %	0.039
Share > 400		14.1 %			14.0 %	0.907		15.0 %	0.365
GH	881			1.661			757		
Age at first calving (months)	518	27.7		1,429	25.2		562	26.3	
Inter-calving interval (days)	326	429.0		874	403.5		309	429.5	
Milk, (kg)	354	23,879		1,047	29,171		364	32.567	
Lifetime efficiency (kg milk / dl)	354	11.4		1,047	14.5		364	13.2	
Productive period (years)	357	2.9		1,085	2.8		388	3.5	
SCC (thousand per ml milk)	320	261		966	309		361	312	
Share < 100		57.7 %			52.3 %			49.2 %	
Share > 400		11.8 %			13.5 %			14.4 %	
SRB50	346		GH vs. SRB50	57		GH vs. SRB50	21		GH vs. SRB50
Age at first calving (months)	266	27.2	0.000	53	25.0	0.351	21	25.5	0.088
Inter-calving interval (days)	132	399.9	0.000	42	381.1	0.000	19	393.3	0.000
Milk, (kg)	187	19,843	0.003	48	32,226	0.492	21	42.941	0.048
Lifetime efficiency (kg milk / dl)	187	9.6	0.000	48	14.4	0.599	21	15.1	0.140
Productive period (years)	232	2.7	0.062	48	3.4	0.084	21	5.0	0.013
SCC (thousand per ml milk)	179	339	0.003	47	256	0.123	21	414	0.138
Share < 100		44.4 %	0.000		49.6 %	0.459		47.3 %	0.709
Share > 400		17.5 %	0.000		13.4 %	0.947		20.8 %	0.095

GH = German Holsteins, SRB = Swedish Red Breed, n = number of animals, dl = day of life, SCC = Somatic cell count, significant $p < 0.05$

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(a)


(b)

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(a)


(b)

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(a)


(b)

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(a)


(b)

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(a)

(b)

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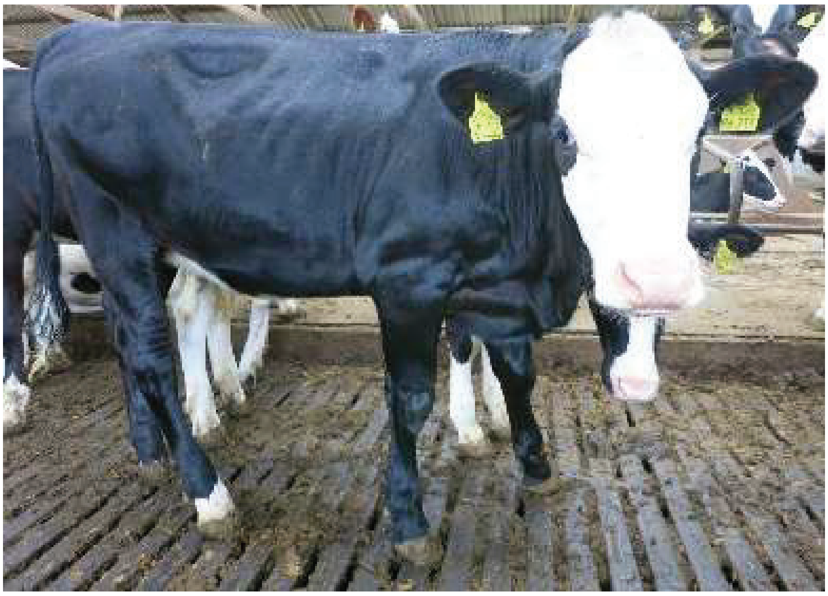
(a)

(b)



(b)

(c)

(c)


(d)

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