



## Improved dairy cattle mating plans at herd level using genomic information



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### ABSTRACT

From 2012 to 2018, 223 180 Montbéliarde females were genotyped in France and the number of newly genotyped females increased at a rate of about 33% each year. With female genotyping information, farmers have access to the genomic estimated breeding values of the females in their herd and to their carrier status for genetic defects or major genes segregating in the breed. This information, combined with genomic coancestry, can be used when planning matings in order to maximize the expected on-farm profit of future female offspring. We compared different mating allocation approaches for their capacity to maximize the expected genetic gain while limiting expected progeny inbreeding and the probability to conceive an offspring homozygous for a lethal recessive allele. Three mate allocation strategies (random mating (**RAND**), sequential mating (**gSEQE**) and linear programming mating (**gLPE**)) were compared on 160 actual Montbéliarde herds using male and female genomic information. Then, we assessed the benefit of using female genomic information by comparing matings planned using only female pedigree information with the equivalent strategy using genomic information. We measured the benefit of adding genomic expected inbreeding and risk of conception of an offspring homozygous for a lethal recessive allele to Net merit in mating plans. The influence of three constraints was tested: by relaxing the constraint on availability of a particular semen type (sexed or conventional) for bulls, by adding an upper limit of 8.5% coancestry between mate pairs or by using a more stringent maximum use of a bull in a herd (5% vs 10%). The use of genomic information instead of pedigree information improved the mate allocation method in terms of progeny expected genetic merit, genetic diversity and risk to conceive an offspring homozygous for a lethal recessive allele. Optimizing mate allocation using linear programming and constraining coancestry to a maximum of 8.5% per mate pair reduced the average coancestry with a small impact on expected Net Merit. In summary, for male and female selection pathways, using genomic information is more efficient than using pedigree information to maximize genetic gain while constraining the expected inbreeding of the progeny and the risk to conceive an offspring homozygous for a lethal recessive allele. This study also underlines the key role of semen type (sexed vs conventional) and the associated constraints on the mate allocation algorithm to maximize genetic gain while maintaining genetic diversity and limiting the risk to conceive an offspring homozygous for a lethal recessive allele.

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### Implications

Our results showed that the use of complete genotyping information (i.e., genomic breeding values, genomic coancestry and carrier status for recessive genetic defects) improves mate allocation in terms of expected genetic merit of the progeny, genetic diversity and risk to conceive an offspring homozygous for a lethal recessive allele. Similar conclusions could be drawn regarding the use of female genomic

information instead of pedigree information. The type of semen (sexed or conventional) used affects mate allocation.

### Introduction

The Montbéliarde is a French dual-purpose breed with 628 000 cows in France in January 2018. From 2012 to 2018, 223 180 Montbéliarde females were genotyped and the number of newly genotyped females increased at a rate of about 33% each year. Genotyping coupled with genomic evaluation leads to genomic estimated breeding values (**GEBV**) with better accuracy than pedigree index. Furthermore, it provides measures of genomic inbreeding, which is expected to be more

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accurate than pedigree inbreeding since it does not rely on pedigree recording accuracy and completeness. In addition, carrier status for identified major genes and genetic defects is available for nearly all genotyped individuals.

All this information is important when planning the matings for the upcoming year. Technically, the aim of mating plans is to maximize the expected genetic level of a female progeny while minimizing expected inbreeding and probability to conceive an offspring homozygous for a lethal recessive allele. Pryce et al. (2012), Sun et al. (2013) and Carthy et al. (2019) found that relying on genomic coancestry is better than using pedigree coancestry to constrain genomic inbreeding. In 2015, Cole (2015) proposed a formula inspired by a method developed by Pryce et al. (2012) to assign a score for each potential mating in order to rank them and choose the best combination of matings. This score includes the genetic merit, the expected pedigree inbreeding of the potential progeny and the probability to conceive an offspring affected by a lethal recessive allele.

However, to our knowledge, no study has been performed yet on data collected from actual herds, accounting for practical constraints on herd size, use of conventional or sexed semen or risk of dystocia in heifers. Sexed semen has a higher probability to produce a replacement heifer than conventional semen. So, mating plans should account for this when computing the expected level of the progeny compared to matings with conventional semen.

Our objective was to compare different mating optimisation approaches for their capacity to maximize expected genetic gain while limiting expected progeny inbreeding and the probability to conceive an offspring homozygous for a lethal recessive allele. All these methods were applied at herd level, on real data, using actual farmers' choices of reproducing strategies on their herd (females mated to sexed, conventional or beef breed semen) in order to reflect the farmers' actual potential gains on farm. The mating plans accounted for the practical situation of each herd and especially the prior choice of the farmer about the use of sexed semen. Because this choice is an input parameter of the mating algorithm and it likely affects the overall profit, the objective function defined to optimize mating plans did not account for the extra cost of the sexed semen and the associated reduced fertility.

## Materials and methods

### Data set

**Animals.** In this study, 9143 genotyped females were selected from 160 actual French Montbéliarde herds to test different mate allocation methods. All females belonged to herds with more than 20 females to be mated in September 2018 and with at least 80% of them being genotyped. Moreover, they were more than 9 months old on 31 August 2018, with known GEBV, with known actual farmer's choice of type of semen (sexed or conventional) to be used and with known pedigree and genomic coancestry with the potential male mates. Females which were planned to be inseminated with beef semen were excluded since their calf will not contribute to herd replacement. In France, the farmer's choice of type of semen (sexed, conventional or of beef breed) to use for each female of the herd is routinely collected by AI (Artificial Insemination) companies when planning the mating. On average, herds were composed of 57 females (30 heifers and 27 cows) and the largest herd had 128 females to mate (71 heifers and 57 cows), all with purebred semen (sexed or conventional semen type).

Actual potential male mates were 54 genotyped Montbéliarde bulls from the Umotest breeding company (Ceyzériat, France) with semen available from the 2018 AI bull list: 45 young bulls with GEBV and 9 older bulls with estimated breeding values (EBV) taking into account daughter performances.

Table 1 shows the number of potential male and female mates per category: heifers and cows, young and old bulls, sexed semen or conventional semen to actually use. Males were genotyped with the

**Table 1**

Number of actual potential bulls provided by U MOTEST breeding company per semen type category and number of actual females (cows and heifers) to be mated to the males according to semen type.

Animals	Number of potential mates	
	Sexed semen	Conventional Semen
Males <sup>1</sup>		
Young	15	33
Old	2	9
Females		
Heifers	2461	2402
Cows	2315	1965

<sup>1</sup> 3 young and 2 old males were available with both sexed and conventional semen.

BovineSNP50 (50 k), and females were genotyped with the BovineSNP50 (50 k) or the EuroG10K BeadChip (Illumina Inc., San Diego) and imputed to 50 K-SNP level using FImpute software version 2.2 (Sargolzaei et al., 2014).

### Data origin

Animals GEBV, pedigree-based EBV (PEBV) and pedigree were obtained from the French National Database (CTIG, Jouy-en-Josas, France). For pedigree mating models, PEBV was polygenic EBV (<https://interbull.org/ib/geforms>) of all the females or their parent average EBV when no PEBV was available (e.g., in heifers) and pedigree coancestry was used. For genomic mating models, GEBV (<https://interbull.org/ib/nationalgenofoms>) and genomic coancestry were used for all females.

In the Montbéliarde breed, four main recessive genetic defects are segregating in the male and female populations: **MTCP** (mitochondropathy; Brochard et al., 2018; Hozé et al., 2018), **MH1** (Michot et al., 2017) and **MH2** (Fritz et al., 2013) (two embryonic lethals) and **SHGC** (Caprine-like Generalized Hypoplasia Syndrome, Floriot et al., 2015). Since the end of 2007, the Montbéliarde breed has forbidden the use of new bulls carrying SHGC genetic defects and all bulls are SHGC-free. Consequently, even though SHGC allele is still segregating in the female population, no mating with one of the 54 bulls considered in this study can result in an SHGC-affected offspring. Therefore, only the MH1, MH2 and MTCP genetic defects were considered here. The true carrier status for the three genetic defects MH1, MH2 and MTCP was known for all potential mates. Allele frequencies for the genetic disorders in the population and the subpopulation of the data set are provided in Table 2.

For pedigree mating models, the probability for a given couple to conceive an offspring which is homozygous for a lethal recessive allele was calculated considering that the carrier status of the bulls was known and the carrier status of the females could be inferred in probability through their pedigree information. This method developed by Brochard et al. (2018) is further explained in Supplementary Material S1. In brief, the method considers that even if a female is not genotyped, the probability that she carries a recessive allele can be calculated through her family information. The carrier status of her parents (if they were genotyped) or, of her grand-parents (if they were genotyped) or, at least the allele frequency in the population, allows for the

**Table 2**

Allele frequencies (%) for the three genetic disorders MH1, MH2 and MTCP in the Montbéliarde population and in the sub-population of the data set (9143 females and 54 males).

Population	MH1	MH2	MTCP
Montbéliarde population	6.6	5.1	8.2
Data set population	6.4	4.8	8.1

The MH1 and MH2 are haplotypes leading to embryonic loss, and the MTCP haplotype leads to mitochondropathy when homozygous.

calculation of the probability for the cow to carry the recessive allele for each genetic defect.

#### Coancestry calculation

For each potential mating between bull  $i$  and female  $j$ , the expected pedigree inbreeding of the progeny is given by their coancestry coefficient (Malécot, 1948) which is equal to one half of the corresponding off-diagonal element of the pedigree-based relationship matrix ( $\mathbf{A}$ ):  $a_{ij}' (= a_{ij}/2)$ ,  $a_{ij}' (= a_{ij}/2)$ .  $a_{ij}'$  reflects the inbreeding coefficient and therefore the expected loss of heterozygosity in the genome of the offspring of each potential mating, compared to a situation without inbreeding.

Genotyping provides the exact genotypes for all the markers for each animal. Therefore, the relationship between two individuals can be calculated assuming allelic frequencies in the founder population are known. It is also equal to the expected inbreeding coefficient of the future progeny. This relationship coefficient between  $i$  and  $j$  is calculated as (VanRaden, 2008)

$$g_{ij} = \frac{\sum_m (x_{im} - 2p_m) \times (x_{jm} - 2p_m)}{2 \sum_m p_m (1 - p_m)}$$

with  $x_{im}$  (respectively,  $x_{jm}$ ) the genotype score of animal  $i$  (respectively,  $j$ ) for marker  $m$ , coded 0 (homozygote), 1 (heterozygote) or 2 (alternative homozygote) and  $p_m$  the frequency of the second allele of marker  $m$  in the founder population. However, the frequencies in the founder population are unknown, and we used the following indirect procedure to estimate coancestry coefficients.

The expected proportion of the genome which is homozygous in the offspring of animals  $i$  and  $j$  can be calculated from the covariance between genotype scores of the parents using  $p_m = 0.5$  (see additional file from Eynard et al. (2015) for derivation) as follows:

$$g'_{ij} = \frac{g_{ij}/2 + 1}{2} = \frac{\left( \frac{\sum_m (x_{im} - 1) \times (x_{jm} - 1)}{N} \right) + 1}{2}$$

with  $N$  the number of markers. These values were computed using an in-house software.

Since  $a_{ij}'$  is the expected inbreeding of the future progeny conditional on the pedigree, i.e., the expected loss of heterozygosity in the genome under RAND, whereas  $1 - g'_{ij}$  reflects the total expected heterozygosity in offspring, they do not directly compare. However, they are linearly related, and this relationship is used here to estimate the coancestry. Heterozygosity of the future progeny of animals  $i$  and  $j$  ( $hg_{ij} = 1 - g'_{ij}$ ) is proportional to one minus the expected inbreeding of the progeny. Let us denote  $ha_{ij} = 1 - a_{ij}'$  the heterozygosity of the future progeny of animals  $i$  and  $j$ . For each potential mating between  $i$  and  $j$ ,  $ha_{ij}$  and  $hg_{ij}$  were computed. Then, the vector  $\mathbf{hg}$  was regressed on the vector  $\mathbf{ha}$  with a fixed intercept of zero and a slope  $\alpha$ . Finally, the adjusted genomic coancestry ( $g_{ij}''$ ) was calculated as follows:  $g_{ij}'' = 1 - hg_{ij}/\alpha = 1 - (1 - g'_{ij})/\alpha$ . This value  $g_{ij}''$  was then used in the optimization process and denoted as  $F_{ij}$ . The adjustment quality may depend on pedigree depth. Therefore, this regression was calibrated on all the animals with a pedigree depth of at least 8.5 equivalent-complete generations, as defined and computed by Pedig software (Boichard, 2002). For a given individual, the number of equivalent-complete generations is defined as the sum of all  $0.5^k$  terms over all ancestors,  $k$  being the number of generations between the individual and the ancestor. This sample included 53 males and 8506 females, with 10.0 and 9.7 equivalent-complete generations. These figures are very similar to the overall figures in the Montbéliarde breed ([http://idele.fr/fileadmin/medias/2019\\_varume\\_BL.pdf](http://idele.fr/fileadmin/medias/2019_varume_BL.pdf), p19).

#### Mating programs

**Objective function.** In France, the mating plans are proposed by technicians (from an AI or breeding company) based on the prior choice of semen type as specified by the farmer for each cow. Based on this information, matings are planned by choosing a bull with available semen of the specified type to be used on a particular cow. A criterion is needed in order to rank potential matings and to find the best combination of them at a herd level. Therefore, for each potential mating of a male  $i$  with a female  $j$ , an economic score was calculated by adapting the formula from Pryce et al. (2012) and Cole (2015) as follows:

$$\text{Score}_{ij} = \left( \frac{NM_i + NM_j}{2} + \lambda F_{ij} + \sum_{r=1}^{n_r} p(aa)_r \times v_r \right) \times \text{prob}(\varphi) + \left( \sum_{r=1}^{n_r} p(aa)_r \times v_r \right) \times \text{prob}(\sigma)$$

where  $NM_i$  and  $NM_j$  are the (Total) Net Merit indexes converted into euro units of male  $i$  and female  $j$ ,  $\lambda$  is the economic consequence of 1% increase of inbreeding,  $F_{ij}$  is the pedigree or genomic expected coancestry between male  $i$  and female  $j$ ,  $n_r$  is the number of recessive genes considered in the breed,  $p(aa)_r$  is the probability of the offspring to be homozygous for the recessive allele  $r$ ,  $v_r$  is the economic value (cost) associated with homozygosity at the deleterious allele of the recessive locus (assumed to be the same for male and female progeny) and  $\text{prob}(\varphi)$  (respectively,  $\text{prob}(\sigma)$ ) is the probability to get a female (respectively, a male) calf. This economic score represents a simplified expected economic profitability for the herd of an offspring conceived from the mating of a bull with a dam, due to its genetic level (Net Merit, expected inbreeding and genetic disorders), compared to the current female base population (i.e., Montbéliarde cows born between 2010 and 2012). Economic effects (as semen price) and technical effects (e.g., lower pregnancy rates associated with the use of sexed semen) were not accounted for here because semen type was already set by the farmer, was not optimized in the mating plan and was applied identically for all mating allocation method tested. Even though the formula of the economic score seems quite simple, it was shown to be pertinent when maximizing genetic gain while constraining inbreeding in the progeny and reducing the probability to conceive offspring affected by genetic disorders at a herd level (Pryce et al., 2012; Cole, 2015).

Since sexed semen increases the probability to get a female calf, a mating with sexed semen has a higher impact on the herd's future (e.g., its genetic and inbreeding levels) than a mating with conventional semen. This impact was accounted for in the economic score using a probability to conceive a female offspring  $\text{prob}(\varphi)$  equal to 0.9 with sexed semen and 0.5 with conventional semen. From a farmer's point of view, the value of a male calf does not depend on his Net Merit value nor on his inbreeding level since males are sold around 15 days old and carcass traits of young bulls are not accounted for in the Net Merit. Therefore, the economic impact of a male calf is limited to the cost associated with an offspring homozygous for any lethal recessive allele.

#### Overall constraints and technical assumptions

For all mate allocation methods used, some constraints were applied to the optimisation algorithm for biological or logistical reasons. First, all females must be mated exactly once. Second, females to be inseminated with sexed semen (according to the farmer's choice) could only be mated with 'sexed-semen' bulls, and similarly for conventional semen. Third, to be in line with farmers' practices to avoid difficult calvings, heifers to be inseminated with conventional semen could only be mated to a subset of males with calving ease EBV above a given threshold (corresponding to easy calving) according to the current Montbéliarde breed recommendations. When no mating was possible because the heifer's calving ease GEBVs were too low, the heifer could

only be mated to a set of eight bulls (out of 42) considered as bulls for Birth and Calving Ease traits.

In practice, farmers are limited in the number of semen doses per bull they can use for their herd due to logistical issues, e.g., not all farms can have an unlimited use of the best bull for Net Merit. Moreover, farmers are advised to use a diversified pool of bulls instead of having an intensive use of very few bulls. Here, a bull could be mated to up to 10% of the females of each herd to represent the current recommendations given by technicians. Note that this constraint is already very high because the top bull is likely to be the same in many herds, possibly leading to an overall 10% usage of one single bull in the whole population. When too many or too strong constraints were applied, the optimized mate allocation methods (described later) could not find any solution to mate all the females of a herd. In such a case, a dummy additional bull was added to the list of available bulls. This dummy additional bull was considered to have a Net Merit of 381.3€ (the worst Net Merit level among the 54 initial bulls), a coancestry of 6.985% with all the 9143 female (average coancestry of all the 54 male with all the 9143 female), to be free from any genetic defect considered here, to be available with sexed and conventional semen, to be useable with heifers in conventional semen and not to be limited in the number of planned matings. This strategy prevented the impossibility to fulfil all the constraints without giving a spurious advantage to such situations. It also corresponds to the actual situation where the AI technicians have some additional AI doses from bulls of lower genetic merit available. Unless specified, all the constraints described in this paragraph were applied and female genomic information was used when testing different mate allocation methods (Table 3).

#### Economic assumptions

In France, the Net Merit index (called ISU) is expressed in standardized units with a mean of 100 and SD of 20. A conversion was needed to transform the Net Merit EBV from an index scale to an economic scale. One SD of the Net Merit in the Montbéliarde breed is worth 100€ per lactation and per cow (adapted from Pinard and Regaldo, 2013). However, a cow with a higher Net Merit will generate benefits during her entire productive life. Assuming that the average productive life of a Montbéliarde cow is 2.88 lactations spread over 1 to 5 lactations (IDELE, 2017) leading to a survival rate of 72% from one lactation to

the next one. Assuming a discounting at 3% (as in Dezetter et al., 2017) and for simplicity an average age in first lactation of 3 years, the economic value associated with one SD of the Net Merit for the career of a cow was calculated as:

$$\sum_{i=4}^8 (0.72)^{i-4} * \frac{100 \text{ €}}{(1.03)^i} = 246\text{€}$$

Regarding the effect of inbreeding on performances, no economic value had been calculated yet in France. However, Dezetter et al. (2015) calculated the effect of 1% increase in inbreeding on several traits (milk yield, cell score, conception rate in heifers and cows). Using the economic values associated with these traits (adapted from Pinard and Regaldo, 2013), the economic loss associated with a 1% increase in inbreeding for an average productive life of a Montbéliarde cow was found to be 26.1€. This value was of the same order of magnitude as the values assumed by Cole (2015) of US \$25 and those found by Smith et al. (1998) US \$24 for the lifetime performance of dairy cows but it was larger than the range of values (AUS\$0 to AUS\$20) explored by Pryce et al. (2012).

Economic assumptions for the cost associated with an offspring affected by a genetic disease were 75€ for MH1 and MH2 (embryonic lethality) and 650€ for MTCP (Fritz and Malaval, personal communication). For MH1 and MH2, the economic value is between US\$40 and US\$120 used by Cole (2015) in his study for embryonic lethal haplotype in Holstein in the United States. Furthermore, the economic value associated with MTCP was higher than the values assumed by Cole (2015) because the mortality occurs between 4 and 6 months of age without preliminary signs.

#### Allocation methods

First, three mate allocation methods were compared for their capacity to maximize the expected genetic level while constraining the expected genomic inbreeding and the probability to conceive an offspring affected by a lethal recessive allele within the herds considered. The methods tested were RAND, gSEQ€ (Pryce et al., 2012; Sun et al., 2013; Cole, 2015) and mate allocation using gLP€ (Jansen and Wilton, 1985; Sun et al., 2013). In the random allocation method, males were allocated randomly to females and complied with the

**Table 3**  
Mate allocation scenarios description and constraints applied to mate allocation optimisation in Montbéliarde dairy cattle.

Heading	gLP€	RAND	gSEQ€	pLP€	gLP_NM	gLP€_all.sem	gLP€_coa8.5	gLP€_b5
Mate allocation optimization method <sup>1</sup>	LP	RAND	SEQ	LP	LP	LP	LP	LP
Female information source <sup>2</sup>	G	G	G	P	G	G	G	G
Matings optimization objective <sup>3</sup>	Score	None	Score	Score	Net Merit	Score	Score	Score
Bull semen type <sup>4</sup>	Actual	Actual	Actual	Actual	Actual	S & C	Actual	Actual
Maximum mate coancestry	None	None	None	None	None	None	None	None
Maximum bulls' matings per herd	10%	10%	10%	10%	10%	10%	10%	5%
One mating per female	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Female semen type <sup>5</sup>	Fixed	Fixed	Fixed	Fixed	Fixed	Fixed	Fixed	Fixed
Calving ease for heifer <sup>6</sup>	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes

RAND: mating method where mates were allocated randomly.

gSEQ€: mating method where mates were allocated sequentially using genomic information.

pLP€: mating method where mates were allocated using linear programming and pedigree information.

gLP\_NM: mating method where mates were allocated using linear programming and genomic Net Merit only.

gLP€\_all.sem: mating method where mates were allocated using linear programming and genomic information. All the 54 bulls are available with both types of semen (sexed and conventional).

gLP€\_coa8.5: mating method where mates were allocated using linear programming and genomic information. Coancestry between planned mates could not exceed 8.5%.

gLP€\_b5: mating method where mates were allocated using linear programming and genomic information. A threshold of 5% of mating per bull and per herd was set (instead of 10%).

gLP€: mating method where mates were allocated using linear programming and genomic information.

<sup>1</sup> RAND, random; SEQ, sequential; LP, linear programming.

<sup>2</sup> G: genome-based; P: pedigree-based.

<sup>3</sup> Score: mate allocation is optimized using economic score; None: no optimization; Net Merit: mate allocation is optimized using Net Merit only.

<sup>4</sup> S&C: all bulls have both sexed and convention semen straws available; Actual: bulls semen type availability corresponds to the actual one in 2018 mating season.

<sup>5</sup> Semen type (sexed or conventional) was already chosen by the farmer for each female.

<sup>6</sup> Heifers to be inseminated with conventional semen could only be mated with a subset of males with estimated breeding values leading to expected easy calving.

semen type constraints described above. In the sequential mate allocation method, females were considered sequentially, heifers before adult cows (but randomly within these categories), according to farmers' actual practices in the Montbéliarde breed in France. For the first female, the mating is planned to the bull with which she makes the best economic score. Then, the second female is considered and she is mated with the bull with which she has the best economic score, and so on. If the bull is already planned to be used with 10% of the females of the herd considered, the bull with the second best economic score is chosen etc. Linear programming method optimized all the matings jointly for a given herd and for specified constraints.

In a second step, the influence of (G)EBV accuracy and the balance between the Net Merit and the genomic expected inbreeding and the risk of conception of an offspring homozygous for a lethal recessive allele on mating was assessed. The influence of accuracy of the information used was tested using only pedigree information for females (pLP€) since genomic information for males is now always available, even for a farmer who does not genotype his females. Since PEBVs for females are not available for calving traits (only males are evaluated in France), in the pedigree mating model (pLP€), heifers planned to be inseminated with conventional semen were mated to a subset of 8 bulls with good Calving Ease and Birth GEBV, mimicking farmers current practices.

Balance between Net Merit and the other elements of the economic score was assessed reducing the objective function to  $Score'_{ij} = \frac{NM_i + NM_j}{2} \times \text{prob}(\varnothing)$ , where  $NM_i$  and  $NM_j$  are the Net Merit indexes in euro units of male  $i$  and female  $j$  (gLP\_NM).

In the third step, influence of three constraints on mate allocation was tested. The impact of the constraint on sexed or conventional semen availability for bulls was assessed (gLP€\_all.sem) assuming that all the 54 bulls are available with both types of semen. The addition of an 8.5% maximum threshold for the expected progeny genomic inbreeding was assessed (gLP€\_coa8.5). This limit was tested in case the economic constraint on expected inbreeding is not strong enough to prevent planned matings with more than 8.5% of expected inbreeding. The threshold of 10% of mating per bull and per herd was reduced to 5% (gLP€\_b5) to increase "within-herd" diversity.

Since there are stronger constraints (on ease at calving) for heifer matings than on cow matings and to avoid the excessive use of a bull with cows when he could be preferentially used with heifers, heifers were mated before cows in the sequential mate allocation strategy (gSEQ€).

Mate allocation methods were computed using R version 3.5.0 R Core Team (2018). They are summarized in Table 3. Linear programming optimization was performed using the 'Lp\_solve' package from Berkelaar et al. (2015).

## Results

To compare mate allocation methods, expected economic score, Net Merit and genomic inbreeding of the progeny and expected risk to conceive an offspring homozygous for a lethal recessive allele were calculated using genomic information and the complete formula for economic score. Scenarios were run only once. Values were averaged over all the 9143 matings in Tables 4 and 5 and over the 160 herds in Fig. 1.

Table 4 shows the average expected economic score, Net Merit and genomic inbreeding of the future progeny within strategy. It also provides, within strategy, the global and specific risk to conceive an offspring homozygous for a lethal recessive allele (MH1, MH2, MTCP or at least one of the 3), the highest expected genomic inbreeding among all planned matings and the number of situations where an additional dummy bull is necessary to allow for planning the mating of herds. The best average expected economic score was obtained with gLP€\_all.sem mate allocation strategy. The random mating was the worst strategy for expected economic score, expected Net Merit and global risk to conceive an offspring homozygous for a lethal recessive allele. Strategy gLP\_NM (mate allocation optimized only on expected Net Merit) led to the best average expected Net Merit (better by 8.4€ per mated female on average than gLP€ strategy) and the worst average and maximum expected genomic inbreeding (+2.1% and +16.6% respectively, compared to gLP€ strategy).

When mating females randomly (RAND) or when the information used to allocate mates was reduced (pLP€ and gLP\_NM) or when strong constraints were applied (gLP€\_b5), more than 75% of the herds had an average expected economic score smaller than the global average expected economic score in the gLP€ strategy (Fig. 1A). The within-herd average expected economic scores were similar across the 4 other strategies (gLP€, gSEQ€, gLP€\_all.sem and gLP€\_coa8.5), and they were evenly distributed above and below the global average expected economic score of the gLP€ strategy. For strategies RAND and gLP€\_b5, the within-herd average expected Net Merits were smaller than the global expected Net Merit of the gLP€ strategy in more than 75% of

**Table 4**

Average economic score (€), Net Merit (€), coancestry (%) and risk of conception of an offspring affected by a genetic defect (%) across all planned mating of 9143 females for 8 different mate allocation strategies and for all potential matings, in Montbéliarde dairy cattle.

Heading	FxB <sup>2</sup>	gLP€	RAND	gSEQ€	pLP€	gLP_NM	gLP€_all.sem	gLP€_coa8.5	gLP€_b5
Average economic score (€)	147.4	223.9	150	218.7	201.4	189.6	231.3	223.7	207.4
Average Net Merit (€)	392.1	437.1	390.9	436.3	436.6	445.5	441.3	436.5	412.3
Average genomic coancestry (%)	7.0	5.0	7.0	5.2	6.2	7.1	4.7	4.9	4.8
Maximum genomic coancestry (%)	33.2	14.6	31.9	16.5	13.6	31.2	14.6	8.5	14.6
Prob. of MH1 loss (%) <sup>1</sup>	0.36	0.1	0.29	0.13	0.26	0.5	0.08	0.09	0.1
Prob. of MH2 loss (%) <sup>1</sup>	0.31	0.05	0.27	0.06	0.07	0.04	0.02	0.06	0.04
Prob. of MTP loss (%) <sup>1</sup>	0.59	0	0.59	0.01	0.04	0.04	0	0.01	0
Prob. of loss from a genetic defect (%) <sup>1</sup>	1.3	0.15	1.15	0.2	0.37	0.58	0.11	0.16	0.14
Cases requiring dummy bull	0	0	0	0	7	0	0	8	197

gLP€: mating method where mates were allocated using linear programming and genomic information.

RAND: mating method where mates were allocated randomly.

gSEQ€: mating method where mates were allocated sequentially using genomic information.

pLP€: mating method where mates were allocated using linear programming and pedigree information.

gLP\_NM: mating method where mates were allocated using linear programming and genomic Net Merit only.

gLP€\_all.sem: mating method where mates were allocated using linear programming and genomic information. All the 54 bulls are available with both types of semen (sexed and conventional).

gLP€\_coa8.5: mating method where mates were allocated using linear programming and genomic information. Coancestry between planned mates could not exceed 8.5%.

gLP€\_b5: mating method where mates were allocated using linear programming and genomic information. A threshold of 5% of mating per bull and per herd was set (instead of 10%).

<sup>1</sup> Prob. of loss is the probability that an offspring is affected by one of the three deleterious genetic defects currently segregating in the Montbéliarde breed. MH1 and MH2 are haplotypes leading to embryonic loss and MTCP haplotypes leads to mitochondriopathy.

<sup>2</sup> FxB: All females mated with all bulls (all combinations between the 9143 females and the 54 bulls).

**Table 5**

Average Net Merit (for expected progeny and for bulls, in €), average expected couples coancestry and average risk to conceive an offspring affected by a genetic disease for gLP€ and gSEQ€ mating strategies, aggregated by type of semen to be used and females categories (heifers or cows).

Mate allocation method <sup>1</sup>	Net Merit (€)		Coancestry (%)	Risk of genetic disease (%)
	Progeny	Bulls		
<b>gLP€</b>				
Conventional semen				
Heifers	402	629	5.3	0.47
Cows	414	645	4.6	0.00
Sexed semen				
Heifers	476	673	5.1	0.07
Cows	452	676	4.8	0.03
<b>gSEQ€</b>				
Conventional semen				
Heifers	403	632	5.4	0.52
Cows	412	640	4.7	0.00
Sexed semen				
Heifers	492	704	5.5	0.02
Cows	433	638	5.0	0.23

<sup>1</sup> gLP€ = Mates allocated using linear programming and genomic information, all heifers and cows allocated at the same time, gSEQ€ = Mates allocated sequentially using genomic information, with heifer-group allocated before cow-group of females.

the herds but they were more or less evenly distributed in other strategies (Fig. 1B). Regarding expected inbreeding, the average expected genomic inbreeding level of the progeny was always higher in strategies RAND and gLP\_NM than in gLP€, gSEQ€, gLP€\_all.sem, gLP€\_coa8.5 and gLP€\_b5. In strategy pLP€, 75% of the herds had an average expected genomic inbreeding higher than 6%, whereas 75% of the herds in strategies gLP€, gSEQ€, gLP€\_all.sem, gLP€\_coa8.5 and gLP€\_b5 had an average expected genomic inbreeding smaller than 5.3% (Fig. 1C).

With strategy gLP€\_all.sem, the risk to conceive an offspring affected by one genetic disease was lower than 1% for all herds. In more than 75% of the herds, the latter risk was lower than 0.15% (Fig. 1D). In all strategies, some herds had a 0% risk to conceive an offspring affected by a genetic disease even if all the 160 herds tested had at least one female carrying at least one genetic defect. In strategies RAND, pLP€ and gLP\_NM, the average risk to conceive an offspring affected by a genetic disease per herd was higher than in the gLP€ scenario.

Table 6 provides the number of planned matings which are strictly identical between two strategies and the correlations between contributions of sires between two strategies. Random mate allocation (RAND) shared the smallest number of planned mating with all the other strategies, always below 7%. Conversely, gLP€ and gLP€\_coa8.5 strategies shared 99% of planned matings among all the 9143 females. Even if gLP€ and gSEQ€ strategies provided similar global results (Table 4 and Fig. 1), they only shared 65.5% of identical planned matings (Table 6). With respect to sire contributions, the correlations between strategies gLP€, gLP€\_coa8.5 and gSEQ€ were about 100%. The first and the second lowest correlations were obtained with RAND and gLP€\_b5 strategies, respectively (Table 6).

Table 5 shows that the use of the best bulls was always done through sexed semen for gLP€ and gSEQ€ strategies. As expected, the use of the best bulls between heifers and cows was more balanced in gLP€ strategy than in gSEQ€ strategy for sexed semen.

Within herd mate allocation, computing time was always faster than 5 s, in all the mate allocation strategies tested.

## Discussion

### Influence of the method

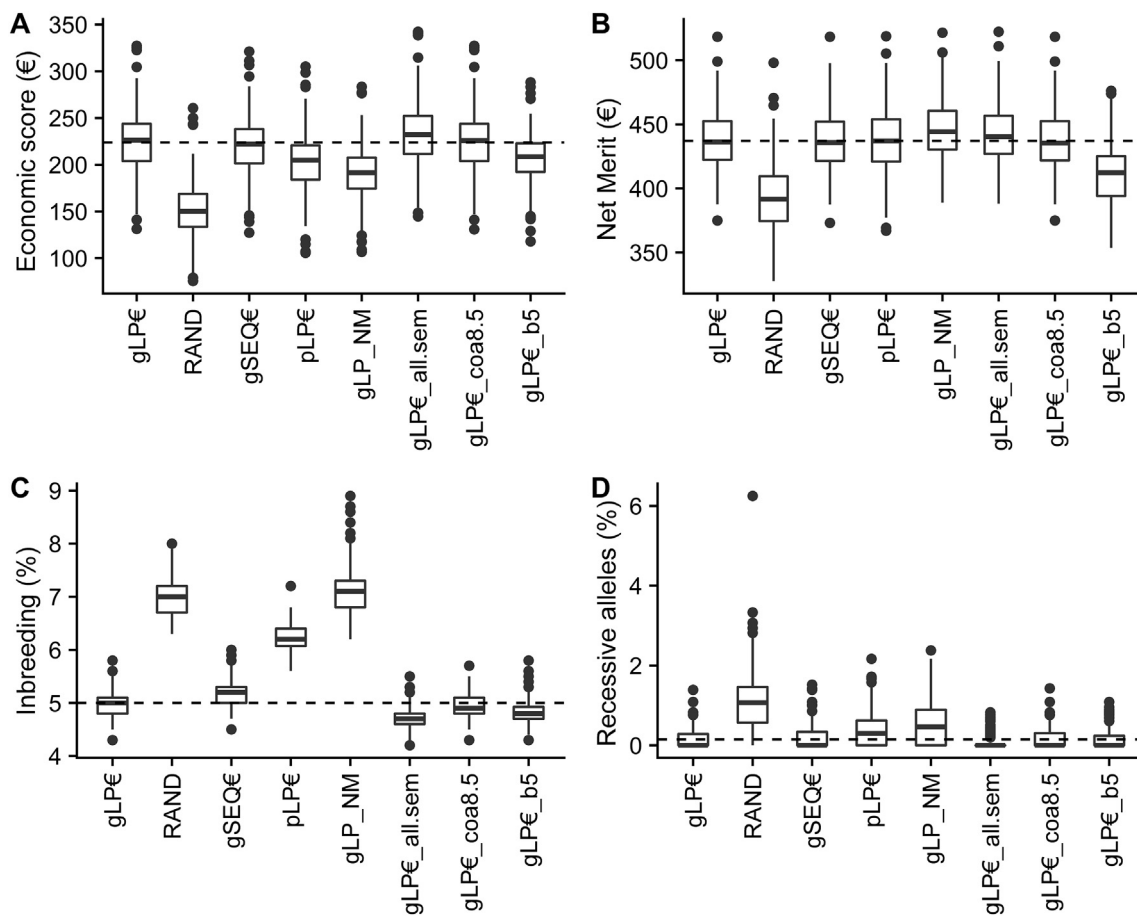
In contrast to the optimal contribution selection approach (Sonesson and Meuwissen, 2000), the method we used does not require to fix an

arbitrary maximum expected inbreeding in the progeny. However, the coancestry was managed through the expected economic effect of inbreeding depression in the offspring. Even though results for sequential and linear programming mate allocation methods were very similar for the average economic score of the 9143 females mated, linear programming always performed slightly better through better choices regarding average expected coancestry and expected probability to conceive an offspring affected by a genetic defect. Sun et al. (2013) and Carthy et al. (2019) also found that linear programming provided better results than gSEQ€. This is because linear programming considers all the potential matings at the same time to maximize the objective function, whereas for gSEQ€, matings are determined as being the best for each female sequentially which depends on the input order of the females into the algorithm because the number of matings per bull is limited. Since mating tools are developed to advise farmers regarding the best mating strategy to adopt, it is more acceptable for farmers that the solution provided by the software is the very best solution given all constraints without depending on the input order of females to mate. Finally, linear programming is better at dealing with all constraints since all constraints are accounted for simultaneously. For example, it automatically uses the bulls compatible for heifers to mate with heifers but does not prevent the use of such bulls with cows when it is possible.

Table 5 clearly shows that the linear programming method allowed finding the best combination of use of bulls with heifers or cows in order to maximize the use of the best bulls when sexed semen was used. This aspect is particularly important since the use of sexed semen considerably increases the probability to produce a heifer that could one day start a lactation, positively affecting the profitability of the herd. However, it is important to keep in mind that the use of sexed semen can have a substantial economic effects (sexed semen is usually more expensive than conventional semen) and technical effects (e.g., sexed semen can lead to lower pregnancy rates) on the herd (Hjortø et al., 2015; Kaniyamattam et al., 2016; De Vries et al., 2018; Bérodiér et al., 2019). These aspects were not addressed in this paper. Furthermore, this study was based on the farmers' decision regarding semen type to use for each female of his herd. In other situations, it may be important to extend the mate allocation methods considered here by including other economic aspects such as the type of semen to use for each female and the associated costs.

### Relative influence of the components of the objective function

As observed by Pryce et al. (2012), Sun et al. (2013) and Carthy et al. (2019), our study demonstrates that the use of genomic information (gLP€) leads to better results than the use of pedigree information (pLP€) to constrain the increase of inbreeding over time. Even though no large differences were observed for expected Net Merit of progeny, average expected genomic inbreeding was 1.2% points higher when optimization was performed with pedigree information than when it was performed with genomic information. Moreover, the risk to conceive an offspring affected by a recessive genetic defect was more than doubled when pedigree information was used as compared to when genomic information was used. These results support the recommendation of Sonesson et al. (2010) to fully use genomic information when animals are genotyped, especially to constrain rate of inbreeding. Carthy et al. (2019) tested a method proposed by Gengler et al. (2007) to impute genotypes of un-genotyped animals from a reference population and from the genotypes of their relatives. They compared three mating methods using imputed genomic information vs pedigree information to maximize genetic gain as well as the homogeneity of the expected progeny while constraining expected inbreeding. They found that constraining expected inbreeding was more efficient when imputed genomic information was used instead of pedigree information. Finally, it is important to notice that less than a quarter of the advised mating with the gLP€ strategy were conserved with the pLP€ strategy.



**Fig. 1.** Results of eight mate allocation strategies on 160 French dairy cattle herds for their capacity to maximize the expected economic score of the progeny (A), the expected Net Merit of the progeny (B), the expected genomic inbreeding of the progeny (C) and the probability to conceive an offspring affected by a genetic defect (D). The four criteria were averaged within strategy and within herd. Lower, middle and upper horizontal lines represent the first quartile, the median and the third quartile, respectively. The lower and upper vertical lines represent 1.5 times the interquartile range (IQR) from the first and third quartiles, respectively. Values smaller and larger than 1.5\*IQR were considered as outliers and are represented by dots. The dashed horizontal lines stand for the average progeny expected values in the gLP€ strategy, considering all females together. gLP€: mating method where mates were allocated using linear programming and genomic information; RAND: mating method where mates were allocated randomly; gSEQ€: mating method where mates were allocated sequentially using genomic information; pLP€: mating method where mates were allocated using linear programming and pedigree information; gLP\_NM: mating method where mates were allocated using linear programming and genomic Net Merit only; gLP€\_all.sem: mating method where mates were allocated using linear programming and genomic information. All the 54 bulls are available with both types of semen (sexed and conventional); gLP€\_coa8.5: mating method where mates were allocated using linear programming and genomic information. Coancestry between planned mates could not exceed 8.5%; gLP€\_b5: mating method where mates were allocated using linear programming and genomic information. A threshold of 5% of mating per bull and per herd was set (instead of 10%).

To the best of our knowledge, among the current French mating tools, genomic information is mainly used through GEBV. Therefore, genomic inbreeding or the risk to conceive an offspring affected by a genetic defect is scarcely managed. The influence of the components of the objective function was tested with strategy gLP\_NM, where the objective function was restricted to the expected Net Merit of the future progeny. This mating method provided the second worst average expected economic score after RAND, even though it led to the best expected Net Merit of the progeny. The average expected inbreeding for the 9143 mating was 2.1% points higher with the gLP\_NM strategy than with the gLP€ strategy. The expected genomic inbreeding per herd ranged from 6.2% to 8.9% with the gLP\_NM strategy, while it was restricted to 4.3% to 5.8% for the gLP€ strategy. For some herds, the average expected inbreeding reached higher levels than with a RAND strategy which is a likely consequence of a higher coancestry of the best females with the best bulls for Net Merit index. Finally, optimizing the matings on expected Net Merit only (gLP\_NM) also led to the second worst results regarding the risk to conceive an offspring affected by genetic defect. All these results advocate the use of the most accurate information available in mating advising tools. The use of the most complete optimization strategy is recommended in order to take expected Net Merit, genomic inbreeding and risk to conceive an offspring affected

by a genetic defect into account altogether, therefore maximizing the expected economic merit of the progeny for the farmer.

#### *Influence of constraints*

Less than half of the advised matings were identical between the gLP € strategy and the strategy where all bulls were available with both sexed and conventional semen (gLP€\_all.sem). This shows two important aspects. First, taking into account the type of semen to be used is essential to have the correct overview of the possible gains that can be made since the constraint on type of semen modified many suggested matings. Second, since the very best results (considering the economic gains, the Net Merit, the average inbreeding and the risk of conception of an offspring affected by a recessive genetic defect) were obtained with the gLP€\_all.sem strategy, it is crucial for a breeding company to try to provide as often as possible both sexed and conventional semen.

Inbreeding is known to have a negative impact on production traits, fertility traits and fitness traits in general (e.g., [Dezetter et al., 2015](#); [Howard et al., 2017](#); [Baes et al., 2019](#)). For simplicity, this inbreeding depression was assumed to have a linear effect even if at high levels of inbreeding (corresponding to close inbreeding); the inbreeding depression is known to have a stronger negative effect ([Howard et al., 2017](#);

**Table 6**

Percentage of identical matings between two mate allocation strategies (upper triangular matrix) and correlations between bulls' contributions across strategies (lower triangular matrix).

	gLPE	RAND	gSEQE	pLPE	gLp_NM	gLPE_all.sem	gLPE_coa8.5	gLPE_b5
gLPE		6.1	65.5	22.8	17.8	48	99	54.9
RAND	31.1		6.2	5.2	5.9	3.7	6.1	5.8
gSEQE	100	32.2		20.7	17.8	35.9	64.9	43
pLPE	88.8	33.8	88.8		16.3	13.6	22.7	14.6
gLp_NM	89.7	24.9	89.6	87.9		10.6	17.3	11.5
gLPE_all.sem	97.7	25.1	97.6	82.8	86.3		47.6	31.8
gLPE_coa8.5	100	31.3	99.9	88.7	89.5	97.8		54.5
gLPE_b5	82.6	45.2	83.1	71.6	74.8	79.2	82.5	

gLPE: mating method where mates were allocated using linear programming and genomic information.

RAND: mating method where mates were allocated randomly.

gSEQE: mating method where mates were allocated sequentially using genomic information.

pLPE: mating method where mates were allocated using linear programming and pedigree information.

gLp\_NM: mating method where mates were allocated using linear programming and genomic Net Merit only.

gLPE\_all.sem: mating method where mates were allocated using linear programming and genomic information. All the 54 bulls are available with both types of semen (sexed and conventional).

gLPE\_coa8.5: mating method where mates were allocated using linear programming and genomic information. Coancestry between planned mates could not exceed 8.5%.

gLPE\_b5: mating method where mates were allocated using linear programming and genomic information. A threshold of 5% of mating per bull and per herd was set (instead of 10%).

Baes et al., 2019). With a mating strategy constrained at 8.5% for the maximum coancestry between males and females (gLPE\_coa8.5), 99% of the planned mating were common between gLPE and gLPE\_coa8.5 strategies and only 8 females out of 9143 could not be mated because of their high coancestry levels with the proposed bulls. Currently, the Montb elarde AI technicians recommend a threshold for coancestry of 6.5%, but in a selected population, the average co-ancestry between males and females can be higher since both males and females are offspring of the same selected bulls of the former generations. The same mating strategy as gLPE\_coa8.5 was tested reducing the threshold from 8.5% to 6.25% of coancestry between parents (data not shown). The number of females that could not be mated because of the threshold strongly increased from 8 to 234 over a total of 9143 females, illustrating that the value associated with this constraint must be consistent with the potential mates available. Another constraint was tested within the gLPE\_b5 mating strategy: the number of matings per male and per herd was reduced from 10% to 5%. Reducing the number of matings per male led to the use of a larger number of bulls, to a low average expected inbreeding of the progeny (second lowest) and a lower risk to conceive an offspring affected by a genetic defect (second lowest). On the other hand, the gLPE\_b5 strategy could not find a mate for more than 2% of the females, and the average expected economic score and the average Net Merit were quite low compared to the gLPE strategy. Therefore, the gLPE\_coa8.5 strategy seems to be a good compromise between economic and practical efficiency since the average expected Net Merit, the average expected progeny inbreeding and the average risk to conceive an offspring affected by a genetic defect were very similar to the gLPE strategy while constraining the maximum expected inbreeding of the progeny.

### Perspectives

The mate allocation optimization was performed assuming that all farmers will select on the Net Merit index only, whereas the overall genetic goal may differ from farm to farm. However, the economic value associated with each trait of the Net Merit can vary, allowing each farmer to emphasize selection on some traits more relevant to his own farming system. Moreover, the economic score formula can be adapted to integrate new selection indices that may arise related to the development of genomic evaluation on new traits (Cole and Van Raden, 2018) as soon as an economic value can be associated with the new trait. For instance, Cole (2015) included polledness in the economic score calculation which illustrates that the inclusion of other genetic defects or genes of interest can be easily done.

Linear programming is an appealing approach to use in mating algorithm since it is fast, easy to implement and it always provides the same solution for a given data set.

In the future, it will be essential to account for the semen type category (sexed vs conventional) in mating algorithms since sexed semen influences the future of the herd beyond securing replacement and choosing the females to mate with sexed, conventional or beef breed semen (Ettema et al., 2017). Mainly for logistical issues (semen availability and semen type for each AI technician), the pool of bulls available for mating is reduced, for females to mate with sexed or conventional semen. This impacts genetic diversity and potential genetic gain. A possible recommendation to breeding companies is to limit the number of external constraints (such as semen type availability) applied to mating plans to let the optimization algorithm find a solution considering all aspects.

### Conclusions

Both for male and female selection pathways, using genomic information is more efficient than using pedigree information to maximize genetic gain while constraining the expected inbreeding of the progeny and the risk to conceive an offspring homozygous for a lethal recessive allele. This study underlines the key role of semen type (sexed vs conventional) and the associated constraints on the mate allocation algorithm to maximize genetic gain while maintaining genetic diversity. Linear programming algorithm was shown to be an attractive method for mate allocation since it is fast and it simultaneously takes into account all specific constraints of a herd in order to maximize the farmer's expected benefits.

### Ethics statement

Not applicable.

### Software and data repository resources

None of the data were deposited in an official repository. The data belong to the French farmers. Restrictions apply to the availability of these data, which are not publicly available.

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## Author Contributions

Marie Bérodiér carried out the simulations and drafted the manuscript. Theo Meuwissen, Peer Berg and Didier Boichard contributed to genomic relationship computations and interpretation. Mickaël Brochard conceived the study and provided all necessary data. Vincent Ducrocq supervised all analyses and contributed to the revision of the manuscript. All authors have read and approved the manuscript.

## Declaration of interest

Authors declare to have no conflicts of interest.

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## Appendix A. Supplementary material

Supplementary material to this article can be found online at <https://doi.org/10.1016/j.animal.2020.100016>.

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