

# An Additive Relationship Matrix for the Sex Chromosomes

Mehdi Sargolzaei

L'Alliance Boviteq, St-Hyacinthe, QC, Canada  
and CGIL, University of Guelph, Guelph, ON, Canada

Larry Schaeffer

CGIL, University of Guelph, Guelph, ON, Canada

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## Summary

The derivation of additive relationships among animals for the sex chromosomes is presented, as well as a shortcut method for inverting the same matrix. A fast computational strategy is outlined for the calculation of inbreeding coefficients for this relationship matrix. The pedigree based methods of calculating inbreeding coefficients were correlated with inbreeding coefficients from genomic relationship matrices using SNP markers based on different numbers of chromosomes and for the X chromosome only via a simulation study. A relationship matrix for the X chromosome would be useful when the sex chromosome is to be analyzed separately, or for analyzing data on honey bees whose genetic inheritance is similar to the inheritance of the sex chromosomes.

## Introduction

The animal model for genetic evaluation utilizes the inverse of the numerator relationship matrix ( $\mathbf{A}$ ) due to Henderson's (1976) discovery of a fast method of computing the inverse. Relationships between parents, or inbreeding coefficients, are required for the direct inverse of  $\mathbf{A}$ . This led to several algorithms for computing inbreeding coefficients (Quaas, 1976; Tier, 1990; Golden et al., 1991; Meuwissen and Luo, 1992; Colleau, 2002; and Sargolzaei et al., 2005).

In most mammals, the sex chromosomes are X and Y and constitute 3 to 5% of the genome (Visscher, 2009). In humans there are an estimated 2000

genes on the X chromosome and about 18 on the Y chromosome. The genes on the X chromosome are associated with interleukin receptors, progesterone receptors, mature T-cell proliferation, immunoglobulin binding proteins, nerve growth factors, among others. Males carry XY and females carry XX. In males, except for the tips of X and Y, there is no recombination between X and Y during meiosis. We will assume there are no active alleles on the Y-chromosome.

All female progeny of a male receive the same set of alleles from the sire's X-chromosome, i.e. no variation from one progeny to the next. The X-chromosome from the dam, however, is a random sample of one of the two alleles at each gene from the dam's two X-chromosomes, i.e. every progeny receives a different set of alleles. Thus, it is possible to think of a separate numerator relationship matrix specifically for the sex chromosomes, which would differ from the traditional  $\mathbf{A}$  matrix for the autosomes. This inheritance mechanism is similar to that of breeding in the honey bee, where the drone is haploid, similar to a single X chromosome, and the female queens are diploid. Drones carry 16 chromosomes and queens carry 32 or 16 pair. Bienefeld, et al. (2007) described computations for obtaining relationships in bees as in this paper.

The purpose of this paper is to derive an appropriate relationship matrix for the sex chromosomes among individuals. Then to investigate the inverse of this matrix to see if it follows a pattern like the traditional  $\mathbf{A}$  matrix inverse, and then to describe a practical strategy for calculation of inbreeding coefficients for this relationship matrix. Simulation studies were made to compare inbreeding coefficients from genomic relationships to those from pedigree based methods.

## Derivation of Sex Chromosome Relationships

Begin with a gametic relationship matrix. Start with sire (1) and dam (2) and two progeny, one male (3) and one female (4). The first gamete (m) will be from the male parent and the second gamete (f) will be from the dam.

Animal	Gametes	1		2		3		4	
		m1	f1	m2	f2	m1	.5(m2+f2)	f1	.5(m2+f2)
1	m1	0	0	0	0	0	0	0	0
	f1	0	1	0	0	0	0	1	0
2	m2	0	0	1	0	0	.5	0	.5
	f2	0	0	0	1	0	.5	0	.5
3	m1	0	0	0	0	0	0	0	0
	.5(m2+f2)	0	0	.5	.5	0	1	0	.5
4	f1	0	1	0	0	0	0	1	0
	.5(m2+f2)	0	0	.5	.5	0	.5	0	1

Line m1 corresponds to the Y-chromosome of animal 1 (a male) while f1 is the X-chromosome sample from its dam. Individual 2 is female and hence m2 is the X-chromosome from its male parent, and f2 is the average of the two X-chromosomes of its dam. The male progeny from mating male 1 to female 2 is individual 3, which has inherited the Y-chromosome from male 1, and an average of the two X-chromosomes of female 2.

Thus, the general rules for forming further rows and columns are

1. The diagonals of the gametic matrix are all 1, except for any Y-chromosomes, which are 0. The row and column for a Y-chromosome are null vectors.
2. If the progeny is male it inherits the Y-chromosome from the sire and an average of the two X-chromosomes of the dam.
3. If the progeny is female, it inherits the X-chromosome completely from the sire, and an average of the two X-chromosomes of the dam.

To illustrate further, assume the following pedigrees of 6 individuals.

**Table 1**  
Example Pedigree.

ID	Sire	Dam	Gender
1	0	0	Male
2	0	0	Female
3	1	2	Male
4	1	2	Female
5	3	4	Male
6	3	4	Female

The gametic relationships for the sex chromosomes are as follows:

Animal	Gametes	1		2		3		4		5		6	
		m1	f1	m2	f2	m3	f3	m4	f4	m5	f5	m6	f6
1	m1	0	0	0	0	0	0	0	0	0	0	0	0
	f1	0	1	0	0	0	0	1	0	0	.5	0	.5
2	m2	0	0	1	0	0	.5	0	.5	0	.25	.5	.25
	f2	0	0	0	1	0	.5	0	.5	0	.25	.5	.25
3	m3	0	0	0	0	0	0	0	0	0	0	0	0
	f3	0	0	.5	.5	0	1	0	.5	0	.25	1	.25
4	m4	0	1	0	0	0	0	1	0	0	.5	0	.5
	f4	0	0	.5	.5	0	.5	0	1	0	.5	.5	.5
5	m5	0	0	0	0	0	0	0	0	0	0	0	0
	f5	0	.5	.25	.25	0	.25	.5	.5	0	1	.25	.5
6	m6	0	0	.5	.5	0	1	0	.5	0	.25	1	.25
	f6	0	.5	.25	.25	0	.25	.5	.5	0	.5	.25	1

where the columns of the matrix are formed from combinations of their ancestor columns, as follows:

$$\begin{aligned}
 m3 &= m1 \\
 m5 &= m3 = m1 \\
 f3 &= .5(m2 + f2) \\
 m4 &= f1 \\
 f4 &= .5(m2 + f2) \\
 f5 &= .5(m4 + f4) \\
 m6 &= f3 \\
 f6 &= .5(m4 + f4).
 \end{aligned}$$

The above matrix does not have an inverse due to the zero rows and columns for the Y-chromosomes. Also, the matrix is of order equal to twice the number of animals. Note that individual 6 is inbred while individual 5 is not inbred, at least at the sex chromosome level. The usual pedigree based inbreeding coefficients would be 0.25 for both individuals 5 and 6.

## Sex Chromosome Relationship Matrix

The gametic matrix can be reduced to a matrix of order equal to the number of animals, by summing the numbers within each 2 by 2 block and dividing by 2, as with a gametic matrix for autosomes. This gives the sex chromosome relationship matrix,  $\mathbf{S}$ , as

$$\mathbf{S} = \begin{pmatrix} .5 & 0 & 0 & .5 & .25 & .25 \\ 0 & 1 & .5 & .5 & .25 & .75 \\ 0 & .5 & .5 & .25 & .125 & .625 \\ .5 & .5 & .25 & 1 & .5 & .75 \\ .25 & .25 & .125 & .5 & .5 & .375 \\ .25 & .75 & .625 & .75 & .375 & 1.25 \end{pmatrix}.$$

This matrix is different from the traditional numerator relationship matrix for autosomes. The diagonals for males are always equal to .5. Because males have only one X chromosome there is half the usual genetic variability in males. For females the diagonals are equal to  $(1 + F)$  where  $F$  is the inbreeding coefficient.

## The Inverse of $\mathbf{S}$

The inverse can be easily computed as in Henderson's derivation. Let  $\mathbf{S}$  represent the sex chromosome relationship matrix, and partition it using the Cholesky decomposition as follows:

$$\mathbf{S} = \mathbf{L}\mathbf{L}' = \mathbf{T}\mathbf{D}\mathbf{D}'\mathbf{T}'$$

where  $\mathbf{D}$  is a diagonal matrix with the diagonals of  $\mathbf{L}$ . Let

$$\mathbf{B} = \mathbf{D}\mathbf{D}'$$

also a diagonal matrix whose diagonal elements are given by the following formulas. If the animal is female and the sire is known, then

$$b_i = 0.5 - 0.25(1 + F_d)$$

and  $F_d$  is the inbreeding coefficient of the dam (in this matrix), or if the sire is unknown, then

$$b_i = 0.5 - 0.25(-1 + F_d).$$

If the animal is male, then

$$b_i = 0.25 - 0.25(F_d),$$

and if both parents are unknown, then  $b_i = 1$  for females, and  $b_i = .5$  for males.

The inverse is then

$$\mathbf{S}^{-1} = \mathbf{T}'^{-1}\mathbf{B}^{-1}\mathbf{T}^{-1}.$$

Each row of  $\mathbf{T}^{-1}$  has, at most, 3 non-zero elements. For males the row consists of a 1 on the diagonal and -.5 on the off-diagonal for the dam of that animal. If the row is for a female animal, then the row consists of a 1 on the diagonal, a -.5 on the offdiagonal for the dam, and a -1 on the off-diagonal for the sire of that animal.

For the example pedigree,

$$\mathbf{T}^{-1} = \begin{pmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ 0 & -.5 & 1 & 0 & 0 & 0 \\ -1 & -.5 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & -.5 & 1 & 0 \\ 0 & 0 & -1 & -.5 & 0 & 1 \end{pmatrix},$$

and the diagonals of  $\mathbf{B}$  are

$$diag(\mathbf{B}) = \left( .5 \quad 1 \quad .25 \quad .25 \quad .25 \quad .25 \right).$$

The inverse of  $\mathbf{S}$  can be created using simple rules. Process each animal, where  $b_i$  has been computed and is known. Let  $\delta = b_i^{-1}$ , then add the following matrix into the corresponding appropriate positions in  $\mathbf{S}^{-1}$ .

	animal	sire	dam
animal	$\delta$	$-\delta$	$-.5\delta$
sire	$-\delta$	$\delta$	$.5\delta$
dam	$-.5\delta$	$.5\delta$	$.25\delta$

If the sire or dam are missing then remove the corresponding row and column from the above  $3 \times 3$  matrix before adding to  $\mathbf{S}^{-1}$ .

The complete inverse for the example pedigree is

$$\mathbf{S}^{-1} = \begin{pmatrix} 6 & 2 & 0 & -4 & 0 & 0 \\ 2 & 3 & -2 & -2 & 0 & 0 \\ 0 & -2 & 8 & 2 & 0 & -4 \\ -4 & -2 & 2 & 6 & -2 & -2 \\ 0 & 0 & 0 & -2 & 4 & 0 \\ 0 & 0 & -4 & -2 & 0 & 4 \end{pmatrix}.$$

### Calculation of Inbreeding

The above rules to create the inverse of  $\mathbf{S}$  require the inbreeding coefficients relative to the sex chromosomes only. The discussion here follows the work of Colleau (2002) and Sargolzaei et al. (2005) which described an indirect approach to obtain the relationships of a sire to its ancestors, progeny, mates and the mates' ancestors by tracing up and tracing down the pedigree once each. That algorithm requires a modification in order to accommodate the sex chromosomes and their mode of inheritance.

With the sex chromosomes, males are never inbred, only females can be inbred. For a female progeny, the inbreeding coefficient is equal to the sex chromosome relationship between the sire and dam, instead of half that relationship as for the autosomes.

Suppose we wish to calculate the inbreeding coefficients of the progeny of sire 3 in the example pedigree of Table 1. Let  $\mathbf{x}_i$  be a null column vector where the  $i^{th}$  element is set to 1. Then for sire 3,

$$\mathbf{S}\mathbf{x}_3 = \mathbf{s}_3,$$

where  $\mathbf{s}_3$  is the third column of  $\mathbf{S}$  which contains the relationships of sire 3 to all other animals.

Vector  $\mathbf{s}_3$  can be computed without constructing  $\mathbf{S}$  according to the indirect method of Colleau (2002) in two traces of the pedigree.

1. Trace the sorted (parents before progeny) pedigree upward to calculate

$$\mathbf{z} = \mathbf{B}^{-1}\mathbf{T}^{-1}\mathbf{s}_3,$$

by solving

$$\mathbf{T}'^{-1}\mathbf{z} = \mathbf{x}_3,$$

and

- Trace the sorted pedigree downward to arrive at  $\mathbf{s}_3$  that satisfies

$$\mathbf{T}^{-1}\mathbf{s}_3 = \mathbf{Bz}.$$

To illustrate the method, create a vector of all zeros except for the position of sire 3 which should contain 1.

### Step 1

Inbreeding coefficients of animals 1 to 4 are assumed to be 0 because parents of animals 1 and 2 are unknown. Then the  $b_i$  values of all animals can be calculated because the inbreeding coefficients of all parents are known. The starting numbers are

Starting vector for sire 3.

Animal	Sex	$b_i$	$\mathbf{x}_3$
1	M	0.5	0
2	F	1.0	0
3	M	0.5	1
4	F	0.25	0
5	M	0.25	0
6	F	0.25	0

Process from animal 3 upwards in the pedigree list contributing values to the  $\mathbf{x}_3$  vector to the sires and dams. For sire 3, the parents are 1 and 2. Thus, we would add  $0 \times x_3 = 0$  to sire 1's value,  $x_1$  and add  $.5 \times x_3 = .5$  to the dam's value,  $x_2$ . Then proceed to animal 2, whose parents are unknown, so nothing happens, and similarly to animal 1, whose parents are also unknown. The vector  $\mathbf{x}_3$  has been changed to  $\mathbf{z}$ .

Now multiply the vector  $\mathbf{z}$  elements by their corresponding  $b_i$  values giving the results below (equivalent to  $\mathbf{Bz}$ ):



After tracing up through the pedigree from sire 3.

Animal	Sex	$b_i$	$z_i$	$b_i \times z_i = w_i$
1	M	0.5	0	0
2	F	1.0	0.5	0.5
3	M	0.25	1	0.25
4	F	0.25	0	0
5	M	0.25	0	0
6	F	0.25	0	0

### Step 2

Now the pedigrees are traced from the top to the bottom of the pedigree list.

For animals 1 and 2 their parents are unknown so their  $w_i$  values do not change. For animal 3, its parents are 1 and 2. Animal 1, a male, contributes nothing to  $w_3$  while animal 2 (the dam) contributes  $.5 \times w_2$  to  $w_3$  which gives

$$w_3 = 0.25 + 0.25 = 0.5.$$

For animal 4 the parents are also animals 1 and 2, but because animal 4 is female, the sire (animal 1) contributes  $1 \times w_1$  and the dam (animal 2) contributes  $.5 \times w_2$  giving

$$w_4 = 0 + 0 + .25 = .25.$$

For animal 5, a male,

$$w_5 = 0(w_3) + .5(w_4) = 0.125,$$

and for animal 6, a female,

$$w_6 = 1(w_3) + .5(w_4) = 0.5 + 0.125 = 0.625.$$

At the end of the pedigree, then  $\mathbf{w} = \mathbf{s}_3$ .

After tracing down the pedigree from the top.

Animal	Sex	$b_i$	$\mathbf{s}_3$
1	M	0.5	0
2	F	1.0	0.5
3	M	0.5	0.5
4	F	0.25	0.25
5	M	0.25	0.125
6	F	0.25	0.625

The inbreeding coefficient of animal 6 is 0.25, which is the relationship between sire 3 and dam 4. The inbreeding coefficient of animal 5 is 0 because it is a male.

## Genomic Relationship Matrix for X-chromosome

Pedigree based relationships can be viewed as the probability of IBD between individuals within the recorded pedigree. The additive genomic relationship matrix ( $\mathbf{G}$ ) uses SNP markers to calculate relationships rather than pedigrees. Mendelian sampling is more accurately accounted for by SNP information compared to pedigree information only (Daetwyler et al., 2007). Both IBD and identity by state (IBS) are captured together in  $\mathbf{G}$ . IBS can also be interpreted as identical by descent from very past common ancestors. Therefore genomic relationships carry more information compared to traditional pedigree relationships. Several methods have been proposed to derive  $\mathbf{G}$  for autosomes (VanRaden, 2008, Leutenegger et al., 2003, Nejati-Javaremi et al., 1997). VanRaden (2008) calculated the additive genomic relationship matrix for autosomes as:

$$\mathbf{G} = \frac{\mathbf{Z}\mathbf{Z}'}{2\sum p_i(1-p_i)}$$

where  $\mathbf{Z}$  is mean adjusted genotype matrix with dimension of number of individuals by number of SNP. Instead of 0, 1, and 2,  $\mathbf{Z}$  contains  $-2p_i$ ,  $(1-2p_i)$  and  $(2-2p_i)$  for genotypes AA, AB and BB, respectively, and  $p_i$  is the frequency of allele B, and  $2p_i$  is the mean of genotypes for the  $i^{th}$  SNP. Allele frequencies should be calculated for the unselected based population.

Assuming the same allele frequencies in males and females,  $\mathbf{G}$  for X-chromosome can be obtained by modifying elements of  $\mathbf{Z}$  pertaining to the male X chromosome. For a male, the elements of  $\mathbf{Z}$  would be  $-p_i$  for the A allele and  $(1-p_i)$  for the B allele.

## Simulation Study

In order to compare autosome and sex inbreeding coefficients for X-chromosome inheritance, a simulation study was carried out. QMSim software (Sargolzaei and Schenkel, 2009) was modified to simulate XY inheritance pattern of males and females. Two populations were simulated. The

first population (P1) was similar to a dairy cattle population having 29 autosomes and 1 sex chromosome. Twenty discrete generations were simulated starting from a base population of 20 males and 400 females. Sires and dams were mated at random and each dam produced 2 progeny with probability of 0.5 of being male or female. The second population (P2) represented the honey bee situation with 16 chromosomes of the haplodiploid system. Base population consisted of 5 queens (representing 5 adjacent colonies) and 75 drones. Because the queen flies out of her nest for mating, drones from other nearby colonies have a chance to mate with the queen. Each queen mated with 15 drones at random and produced 1,000 drones and workers. Queens and drones were replaced with young progeny in each reproductive cycle. In total, 10 reproductive cycles were simulated. The length of chromosomes (in centiMorgan) in P1 and P2 was according to Arias et al. (2009) and Beye et al. (2006), respectively. In P1, the pseudo-autosomal part of X-chromosome was not simulated. Each chromosome was genotyped for 1,500 evenly spaced SNP. There was an average of 1 crossover per 100 centiMorgan, and equal allele frequencies in the base population were considered.

Inbreeding coefficients were computed as in the **A** matrix, as in the **S** matrix, and for different number of chromosomes for **G**. In P1, **G** was based on

1. The X-chromosome only,
2. One autosome only, the longest chromosome,
3. Twenty-nine autosomes, or
4. Twenty-nine autosomes and X-chromosome.

For P2 (honey bees), all sixteen chromosomes were used to compute **G**.

The average correlations between **A** matrix inbreeding coefficients or **S** matrix inbreeding coefficients with the various **G** matrix inbreeding coefficients were calculated over 200 replicates to assess the effectiveness of the inbreeding calculation methods. Genomic relationships were calculated relative to the base population where the base allele frequencies were 0.5 for all loci. The correlations were calculated for females only in the last two generations for P1 (800 females) and in the last generation for P2 (2500 females).

## Results and Discussion

To simplify the discussion, let  $I_A$ ,  $I_S$ , and  $I_G$  represent the sets of inbreeding coefficients of females from the **A**, **S**, and **G** matrices, respectively. Then  $Cor(I_A, I_G)$  is the average correlation, over replicates, of the two sets of inbreeding coefficients,  $I_A$  and  $I_G$ , for example. The average correlations between genomic and pedigree-based inbreeding coefficients are given in Table 2.

**Table 2**  
Average correlations between **A** matrix based and **S** matrix based inbreeding coefficients and inbreeding coefficients from various genomic relationship matrices.

Scenario	Population	<b>G</b> based on	$Cor(I_A, I_G)$	$Cor(I_S, I_G)$
1	P1	X-chromosome	0.068	0.197
2	P1	One autosome	0.186	0.055
3	P1	29 autosomes	0.712	0.207
4	P1	29 autosomes and X	0.710	0.231
5	P2	16 chromosomes	0.584	0.679

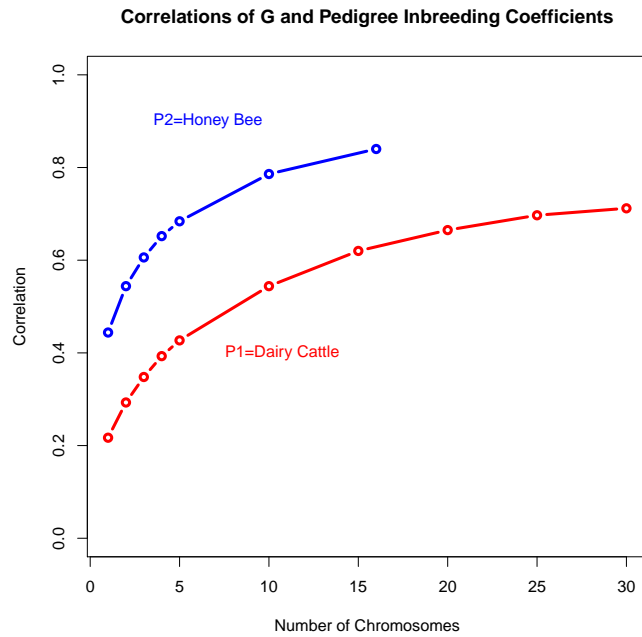
In scenario 1,  $Cor(I_S, I_G)$  was expected to be greater than  $Cor(I_A, I_G)$ , and this was the case. In scenario 2,  $Cor(I_A, I_G)$  was expected to be greater than  $Cor(I_S, I_G)$  because  $I_G$  was based on autosome inheritance, the same as  $I_A$ . For scenario 3,  $I_G$  were based on 29 autosomes and were thus, highly correlated with  $I_A$ . Similarly for scenario 4,  $I_A$  were expected to be more highly correlated with  $I_G$  than  $Cor(I_S, I_G)$ .

In scenario 5  $Cor(I_S, I_G)$  was expected to be greater than  $Cor(I_A, I_G)$ . This was true, but  $Cor(I_A, I_G)$  was also fairly high. In P2, the average value in  $I_A$  was 0.2, while the average value in  $I_S$  was 0.34. In P1 both of those averages were close to 0.1. Thus, inbreeding in  $I_A$  was underestimated relative to those in  $I_S$  in P2.

Inbreeding coefficients in **G** were calculated by adding one chromosome at a time. Chromosomes were added from longest to shortest, but recall that each chromosome had 1500 SNPs. For P1,  $Cor(I_A, I_G)$  are plotted in Figure 1 against number of chromosomes going into  $I_G$ . Adding chromosomes also added more SNPs into the calculation of  $I_G$ . More information makes

$Cor(I_A, I_G)$  go closer to unity. For P2,  $Cor(I_S, I_G)$  should be greater than  $Cor(I_A, I_G)$  because of the inheritance structure of the honey bee population. Thus,  $Cor(I_S, I_G)$  were plotted in Figure 1 for P2, as chromosomes were added to create  $I_G$ .

**Figure 1**



With one chromosome, the correlation between pedigree and genomic inbreeding was low, around 0.2 in P1, and 0.45 in P2. This was due to the fact that SNPs on the same chromosome are not segregating independently. This co-segregation or Mendelian sampling term is better captured by SNP information (Daetwyler et al., 2007) regardless of number of chromosomes. With a few chromosomes, deviation from Mendelian sampling due to the co-segregation of SNP cannot be appropriately accounted for with pedigree-based methods. However, as the number of chromosomes increased, the genomic Mendelian term became closer to the expectation based on pedigree information and there was an increase in  $Cor(I_A, I_G)$ . This could also be due to an increase in the number of SNP as each chromosome was added. According to Figure 1 and assuming similar genetic variance for each SNP, one may speculate that genetic evaluation using  $\mathbf{G}$  instead of  $\mathbf{A}$  is, on average, more accurate in species

with small number of chromosomes compared to species with larger number of chromosomes.  $Cor(I_A, I_S)$  for P1 and P2 were 0.32 and 0.84, respectively. This big difference might be due to the different population structures. In P1, few males produced large numbers of progeny with no outbreeding while in P2 a few queens (females) produced large numbers of progeny with the possibility of outbreeding.

In dairy cattle, X-chromosome is only a small part of the genome (1 pair versus 29 autosome pairs) and therefore, differences between  $I_G$  based on autosomes only and  $I_G$  based on all autosomes plus X-chromosome, may not be large (Visscher, 2009).  $I_A$  were multiplied by 29 and added to  $I_S$ , and the sum divided by 30. The correlation of the weighted mean inbreeding coefficients and  $I_G$  was 0.711, which was almost the same as  $Cor(I_A, I_G)$  alone (from Table 2). However, in applications where inheritance of a single chromosome or marker is of interest, proper calculation of IBD for X-chromosome is necessary. One example is estimation of the number of copies of a particular allele in a genotype of an animal using mixed model approach (Gengler et al., 2007). If the gene of interest was on the sex chromosome, then the use of  $\mathbf{S}$  would be better for estimating gene content for that gene.

Based on the simulation results, relationships among honey bees would be more accurately reflected if  $\mathbf{S}$  were used in mixed model equations, than if  $\mathbf{A}$  were used. With the direct calculation of the inverse of  $\mathbf{S}$ , the use of  $\mathbf{S}$  is now as easily implemented as is  $\mathbf{A}$ . Bienefeld et al. (2007) suggest that the genetic evaluation model should also contain maternal effects, which would have the  $\mathbf{S}$  structure of covariance matrix, as well as the covariance between direct and maternal effects.

## Conclusions

In situations where genes on the X chromosome are being studied, then additive relationships among animals should be calculated differently from the traditional  $\mathbf{A}$  matrix, pedigree based approach. This was demonstrated by the creation of matrix  $\mathbf{S}$ , and by showing that its inverse can be easily formed from knowing the pedigree and the gender of each animal. In honey bee populations,  $\mathbf{S}$  should always be used.

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