ABSTRACT: Osteochondrosis (OC) is an important orthopedic developmental disorder in many horse populations. A review of the literature revealed widely variable heritability estimates for the disorder. We estimated the genetic variables (heritabilities and genetic correlations) of various manifestations of OC. Femoropatellar, tarsocrural, and metacarpophalangeal and metatarsophalangeal joints of 811 randomly selected yearlings from the Royal Warmblood Studbook of the Netherlands, descending from 32 representative stallions, were scored for OC at 28 predilection sites. At each site, OC was scored in 5 categories, distinguishing between flattened bone contours and fragments. At the animal level, the overall heritability of OC was 0.23, the heritability of flattened bone contours was 0.08, and the heritability of fragments was 0.22. At the joint level, heritability was greatest in the tarsocrural joints, intermediate in the metacarpophalangeal and metatarsophalangeal joints, and least in the femoropatellar joints. The heritability estimates for the contralateral joint homologs were very similar. The genetic correlation between the tarsocrural and femoropatellar joint was strong, whereas correlations between the metacarpophalangeal and metatarsophalangeal and other joints were moderate. The genetic correlation between flattened bone contours and fragments at the animal level was 0.80. Scoring OC on a 5-point categorical scale resulted in greater heritability on the observed scale than when analyzing OC as a binary trait. Our results suggest that selection against OC could best be performed by taking into account the OC status of all 4 joints, the femoropatellar, the tarsocrural, and the metacarpophalangeal and metatarsophalangeal joints, and discerning between flattened bone contours and fragments.

Key words: genetic correlation, heritability, horse, joint, osteochondral fragment, osteochondrosis

INTRODUCTION

Osteochondrosis (OC) is an important orthopedic developmental disorder in many horse populations. It is an endochondral ossification disturbance that occurs in young, growing individuals. Irregular ossification leads to the formation of thick cartilage plugs and areas of focal necrosis, eventually resulting in flattened bone contours and loose fragments (Jeffcott, 1997; van de Lest et al., 1999). The term manifestations is used to indicate both varieties of OC, flattened bone contours and fragments.

The etiology of OC is still not fully understood, but it is agreed that the disorder is multifactorial in origin (Jeffcott, 1991; Philipsson et al., 1993; Wittwer et al., 2006) and that genetic influences play an important role (Schougaard et al., 1990; Philipsson et al., 1993; van Weeren, 2006). Estimated heritabilities vary widely (Table 1), possibly because of differences in the materials and methods used among studies (Ricard, 2002). Because initial research into the genetic basis of OC indicates that it is complex (Wittwer et al., 2007), genetic progress can be made by using classical quantitative genetic approaches for selection. With radiographic data, the OC status of an individual can be measured in different joints and flattened bone contours can be distinguished from fragments. Phenotypic results (Van Grevenhof et al., 2009) have confirmed the strong simi-
The phenotypic relationships reflect underlying genetic relationships. It is necessary to estimate the genetic variables between joints and between manifestations to select and predict the selection response effectively. Radiographic data from 811 Dutch Warmblood yearlings were used to estimate the heritabilities of flattened bone contours and fragments, and to determine genetic correlations between these manifestations among joints.

**MATERIALS AND METHODS**

Animal care and Use Committee approval was not obtained for this study because the data were collected in a standard routine veterinary procedure for radiographing horses, additionally based on voluntary involvement of the owners of the yearlings.

### Table 1. Prevalence and heritabilities (h²) of osteochondrosis (OC) and fragments (OCD), by joint, for different horse populations

<table>
<thead>
<tr>
<th>Population¹</th>
<th>Number of sires (animals)</th>
<th>Radiographic finding²</th>
<th>Prevalence, %</th>
<th>h²SE</th>
<th>Method of analysis³</th>
<th>Author⁴</th>
</tr>
</thead>
<tbody>
<tr>
<td>Femoropatellar OC/OCD</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dutch WB stallions (n = 1,965)</td>
<td>OC</td>
<td>11.5</td>
<td>0.09</td>
<td>ATM (REML, DL)</td>
<td>I</td>
<td></td>
</tr>
<tr>
<td>French WB 103 sires (n = 733)</td>
<td>OC</td>
<td>1–7</td>
<td>0.00–0.17</td>
<td>LSM⁵</td>
<td>II</td>
<td></td>
</tr>
<tr>
<td>Italian WB 75 sires (n = 350)</td>
<td>OCD</td>
<td>16.6</td>
<td>0.097²⁰⁰</td>
<td>ATM (AIREML)</td>
<td>III</td>
<td></td>
</tr>
<tr>
<td>Tarsocrural OC/OCD</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dutch WB stallions (n = 1,965)</td>
<td>OC</td>
<td>16.0</td>
<td>0.11</td>
<td>ATM (REML, DL)</td>
<td>I</td>
<td></td>
</tr>
<tr>
<td>Dutch WB mares 30 sires (n = 590)</td>
<td>OC</td>
<td>13.7</td>
<td>0.01⁰⁰⁰</td>
<td>LSM⁵</td>
<td>IV</td>
<td></td>
</tr>
<tr>
<td>French WB 103 sires (n = 733)</td>
<td>OC</td>
<td>13.7</td>
<td>0.14⁰¹⁷</td>
<td>LAM (REML)</td>
<td>IV</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB 165 sires (n = 624)</td>
<td>OC</td>
<td>11–13</td>
<td>0.00–0.02</td>
<td>LSM⁵</td>
<td>II</td>
<td></td>
</tr>
<tr>
<td>SB Trotters 39 sires (n = 644)</td>
<td>OC</td>
<td>10.5</td>
<td>0.057⁰⁰⁵⁸</td>
<td>LAM (REML)</td>
<td>V</td>
<td></td>
</tr>
<tr>
<td>SB Trotters 24 sires (n = 793)</td>
<td>OC</td>
<td>14.3</td>
<td>0.52</td>
<td>LSM⁶</td>
<td>VI</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB (n = 3,725)</td>
<td>OCD</td>
<td>10.5</td>
<td>0.27¹⁰⁸</td>
<td>LSM⁶</td>
<td>VII</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB 569 sires (n = 5,231)</td>
<td>OC</td>
<td>9.6</td>
<td>0.37⁰⁰⁶</td>
<td>LAM (REML, DL)</td>
<td>VIII</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB 569 sires (n = 5,231)</td>
<td>OCD</td>
<td>9.2</td>
<td>0.28⁰⁰⁴⁴</td>
<td>LAM (REML, DL)</td>
<td>IX</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB 569 sires (n = 5,231)</td>
<td>OC</td>
<td>9.2</td>
<td>0.27³⁰⁴²</td>
<td>LAM (REML, DL)</td>
<td>IX</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB 569 sires (n = 5,231)</td>
<td>OCD</td>
<td>9.2</td>
<td>0.17⁰⁰⁵⁷</td>
<td>STM (GS)</td>
<td>IX</td>
<td></td>
</tr>
<tr>
<td>Danish Trotters 9 sires (n = 325)</td>
<td>OCD</td>
<td>12.0</td>
<td>0.26¹⁰⁴</td>
<td>STM⁶</td>
<td>X</td>
<td></td>
</tr>
<tr>
<td>Metacarpophalangeal/ metatarsophalangeal OC/OCD</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>French WB 103 sires (n = 733)</td>
<td>OC</td>
<td>8.11</td>
<td>0.04–0.21</td>
<td>LSM⁵</td>
<td>II</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB 165 sires (n = 624)</td>
<td>OC</td>
<td>18.3</td>
<td>0.12⁰⁰⁹⁰</td>
<td>LAM (REML)</td>
<td>V</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB (n = 3,725)</td>
<td>OCD</td>
<td>20.8</td>
<td>0.19³⁰⁴⁵</td>
<td>LAM (REML, DL)</td>
<td>VIII</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB 569 sires (n = 5,231)</td>
<td>OCD</td>
<td>23.5</td>
<td>0.17³⁰⁰⁸</td>
<td>LAM (REML, DL)</td>
<td>IX</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB 569 sires (n = 5,231)</td>
<td>OCD</td>
<td>23.5</td>
<td>0.16⁰³⁰³</td>
<td>LAM (REML, DL)</td>
<td>IX</td>
<td></td>
</tr>
<tr>
<td>Hanoverian WB 569 sires (n = 5,231)</td>
<td>OCD</td>
<td>23.5</td>
<td>0.12³⁰⁴⁹</td>
<td>STM (GS)</td>
<td>IX</td>
<td></td>
</tr>
<tr>
<td>SB Trotters 39 sires (n = 644)</td>
<td>OCD</td>
<td>11.8</td>
<td>0.21</td>
<td>STM (REML)</td>
<td>VI</td>
<td></td>
</tr>
<tr>
<td>SB Trotters 24 sires (n = 793)</td>
<td>OCD</td>
<td>21.5</td>
<td>0.17³⁰⁶⁶</td>
<td>LSM⁶</td>
<td>VII</td>
<td></td>
</tr>
<tr>
<td>All</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Italian WB 75 sires (n = 350)</td>
<td>TC, FP, MCP/MTP, OCD</td>
<td>16.6</td>
<td>0.14²⁰⁰²⁵</td>
<td>LAM (REML, DL)</td>
<td>III</td>
<td></td>
</tr>
</tbody>
</table>

¹WB = Warmblood; SB = Standardbred.
²TC = tarsocrural; FP = femoropatellar; MCP/MTP = metacarpophalangeal and metatarsophalangeal.
³ATM = animal threshold model; LSM = linear sire model; LAM = linear animal model; STM = sire threshold model; DL = Dempster-Lerner transformation (Dempster and Lerner, 1950); AIREML, average information REML; GS, Gibbs sampling.
⁴I = der Kinderen (2005); II = Ricard (2002); III = Pieramati et al. (2003); IV = KWPN (1994); V = Schober et al. (2003); VI = Grendahl and Dolvik (1993); VII = Philipsson et al. (1993); VIII = Stock et al. (2005); IX = Stock and Distl (2006); X = Schougaard et al. (1990).
⁵Discrete and bivariate measures.
⁶χ² heterogeneity test, DL.

**Animals**

Data were collected on 811 yearlings from the population of the Royal Warmblood studbook of the Netherlands (KWPN) population during 2005 (n = 593) and 2006 (n = 218). Animals descended from 32 breeding sires and 801 dams. The breeding sires were representative of the population of approved breeding sires and included both older and younger sires and both show-jumping- and dressage-bred sires with at least 25 registered offspring in the 2005 and 2006 breeding seasons. For approval as a breeding sire within the KWPN studbook, a negative OC status is prerequisite. Until 1994, OC status was assessed using radiographs of the tarsocrural (TC) joint (hock joint) only. After that time, the femoropatellar (FP) joint (stifle joint) was included in the assessment as well. Of the 32 breeding sires, 7 had been evaluated before 1994. Thus, the OC status of the FP joint was unknown for those 7 sires.

The number of animals per sire varied from 22 to 28. The animals had a mean (±SD) age of 12 (±2.6) mo
and a minimum age of 9 mo and included 47.3% males. The proportion of Thoroughbred genes in the pedigree ranged from 0 to 58%. The animals had a mean withers height of 149 (±5.7) cm, and a mean chest circumference of 165 (±9.3) cm. The animals had been reared by their breeders; therefore, the feeding, housing, and exercise levels varied among the animals.

**Radiography**

Animals were scored for OC based on radiographs from 8 joints: contralateral homologs of the FP, TC, metacarpophalangeal (MCP), and metatarsophalangeal (MTP) joints (fetlock joints). A total of 28 predilection sites were scored in each animal: 5 sites in the FP joint, 7 sites in the TC joint, and 1 site each in the MCP and MTP joints. In the MCP and MTP joints, we included only the proximodorsal part of the sagittal ridge of the third metacarpal and metatarsal bone in the MCP and MTP joints. Radiographs and predilection sites were described in detail by Van Grevenhof et al. (2009). At each site, OC was scored on a categorical scale from A through E, which was adapted from the original scale from Dik et al. (1999). An A score indicates a normal joint contour, B score indicates smooth, flattened bone contours, C score indicates irregular, flattened bone contours, and D and E scores indicate fragments (see Dik et al., 1999, for a detailed explanation; see also Table 1 in Van Grevenhof et al., 2009). The term manifestations is used to indicate both varieties of OC, flattened bone contours and fragments. The mean percentage of score A in the population was 30% (Van Grevenhof et al., 2009). The radiographs were taken by 15 preselected equine veterinary practices, 2 of which were responsible for 61% of all radiographs. An experienced radiologist evaluated all radiographs.

**Genetic Analysis**

To enable quantitative genetic analysis, the A through E categorical scores were transformed into quantitative values on a continuous scale, as described in detail by Van Grevenhof et al. (2009). For the transformation, we assumed a normally distributed liability underlying the categorical scores. Each categorical score was transformed into a mean liability value for that score (Falconer, 1965). This procedure resulted in 3 quantitative traits, 2 for each joint and 1 for the entire animal: the ALL trait, representing the overall OC value, including both flattened bone contours and fragments; the FLAT trait, representing only flattened bone contours; and the FRAG trait, representing only fragments. Therefore, the ALL trait summarized the overall OC status of either a joint or the entire animal, assuming that flattened bone contours and fragments were manifestations of the same disorder, which was unknown a priori. The FLAT and FRAG traits summarized the OC status separately for flattened bone contours and fragments, for either a joint or the entire animal. Hence, each animal had ALL, FLAT, and FRAG values for each of its joints, as well as an overall value for ALL, FLAT, and FRAG. Values for ALL, FLAT, and FRAG were calculated for each joint by summing the values of all sites within that joint, and the traits were calculated for each animal by summing all values in the entire animal. The value for the entire animal was obtained by summing the ALL, FLAT, and FRAG values for each of its 8 joints.

The prevalence of OC for each separate predilection site was low, varying from 0 to 23% (Van Grevenhof et al., 2009), which reduced the precision of genetic analysis for individual predilection sites. To enable a meaningful genetic analysis, we reduced the number of traits by combining strongly similar traits into a single trait. For this purpose, we used results of a cluster analysis. Inputs in that analysis were the FLAT and FRAG values for each of the 8 joints, giving a total of 16 traits for each animal. The cluster analysis of Van Grevenhof et al. (2009) showed strong similarities between the right and left homologs. Intermediate similarities were present between the MCP and MTP joints. Fewer similarities were found between flattened bone contours and fragments. The least similarity was found between different joints, except for the combination of the MCP and MTP joints (Van Grevenhof et al., 2009). Therefore, we combined contralateral homologs and the MCP and MTP joints into a single trait, but treated flattened bone contours and fragments, and the other joints, as separate traits. This resulted in the following 12 traits for the genetic analysis: ALL, FLAT, and FRAG for the animal, and ALL, FLAT, and FRAG separately for the FP joint, TC joint, and the combined MCP and MTP joints.

**Estimation of Genetic Variables**

For the estimation of genetic variables, pedigree information on 5 generations was used. The pedigree data contained 7,799 horses. Genetic variables were estimated univariately (heritabilities) and bivariately (genetic correlations) using REML with ASREML software (Gilmour et al., 2006). The following linear animal model was used:

\[
Y_{ijklm} = \mu + \text{sex}_i + \text{EVP}_j + \text{age}_k + \text{year}_l + \text{animal}_m + e_{ijklm},
\]

where \(Y_{ijklm}\) is the continuous OC value for ALL, FLAT, or FRAG of the animal or joint; \(\mu\) is the mean; \(\text{sex}_i\) is the fixed class effect of sex (\(i = \text{male or female}\)); \(\text{EVP}_j\) is the fixed class effect of the equine veterinary practice responsible for taking radiographs (\(j = 1, 2, 3, \ldots, 15\)); \(\text{age}_k\) is the fixed class effect of age in months (\(k = 9, 10, 11, \ldots, 22\)); \(\text{year}_l\) is the fixed class effect of the year of scoring (\(l = 2005 \text{ or } 2006\)); \(\text{animal}_m\) is the random additive genetic effect of the mth animal (\(m = 1, 2, 3, \ldots, 811\)); and \(e_{ijklm}\) is the residual. All fixed effects in
the genetic model had a significance level of $P \leq 0.10$. The month of scoring did not affect the OC score ($P > 0.2$).

To investigate the benefit of converting OC scores to a continuous liability scale, heritability was additionally estimated for OC expressed on both a binary scale and a scale of 1 to 5. On the binary scale, an individual had an OC score of zero only when all predilection sites were scored as A; otherwise, an individual had an OC score of 1. Therefore, a zero indicated the complete absence of OC. On the scale of 1 to 5, OC scores A through E were expressed as values 1 through 5, respectively.

**RESULTS**

**Heritabilities**

At the animal level, the estimated heritability was $0.23 \pm 0.09$ (SE) for ALL, $0.08 \pm 0.06$ for FLAT, and $0.22 \pm 0.09$ for FRAG (Table 2). At the joint level, the heritability was greatest in the TC joints (0.36), intermediate in the MCP and MTP joints (0.14), and least in the FP joints (0.05; Table 2). The heritabilities of the separate contralateral homologs were very similar (data not shown), but were approximately 16% less than estimates from the combined scores. The combination of information from both limbs reduced the impact of measurement errors, decreased the estimate of environmental variance, and led to greater heritabilities.

Sires were compared by means of the EBV by using continuous OC scores. The mean EBV of the sires were standardized by the phenotypic SD of OC values at the animal level. The standardized means of the sires (Figure 1) showed large variation between sires, varying from $-0.47$ to $0.33$, which indicates the possibility of using quantitative genetic approaches for selection based on radiographic OC status.

The use of a binary scale for measuring OC resulted in reduced heritabilities (decreased to between 68 and 72% of the original values, excluding the FP joint) at both the joint and animal level compared with OC on the continuous scale (Table 2; note that heritabilities for the binary trait are expressed on the observed scale, not on the underlying liability scale). However, in the FP joint, the heritability showed only a limited decrease to 95% ($h^2 = 0.05$). In contrast, heritability estimated using a scale of 1 to 5 for OC showed very similar estimates compared with OC on the continuous scale (98 to 112% of the original estimates, excluding the MCP and MTP joints). However, in the MCP and MTP joints, the heritability decreased to 80% of the original value ($h^2 = 0.14$).

**Genetic Correlations**

Genetic correlations between ALL, FLAT, and FRAG were strong at the animal level (Table 3), although the genetic correlations of FLAT and FRAG with ALL contained a component of autocorrelation. The correlation between FLAT and FRAG at the animal level was $0.80$, with large associated SE. Genetic correlations of ALL between the FP and TC joints were intermediate ($0.59$), but correlations with the MCP and MTP joints were low ($0.09$ and $0.26$) (Table 4). Residual correlations are presented, because the selection response is also dependent on the residual correlation. Residual correlations ranged between $0.01$ and $0.69$ (SE = $0.04$ to $0.09$).

Genetic correlations between FLAT and FRAG within the same joints varied widely (data not shown). The
SE of those estimates were very large, indicating reduced accuracy of estimates, which are therefore not shown.

DISCUSSION

Methodology

In most studies, OC is scored as a binary trait, whereas the multifactorial origin of the disorder implies an underlying continuous character (Jeffcott, 1991; Philipsson et al., 1993; Wittwer et al., 2006). Indeed, our results show that defining OC as a binary trait may be one reason for the variable heritability found in previous studies. Scoring OC in 5 categories increased heritability on the observed scale compared with scoring OC as a binary trait. Therefore, OC should be scored minimally in more than 2 categories. For scoring on a categorical scale, the actual number of categories needed remains to be defined and may vary per joint. In most joints, a scale of 1 to 5 had results similar to OC scored on a continuous scale, but using the scale still decreased the estimated heritability in the MCP and MTP joints. Thus, detailed scoring of OC increased heritability, but the transformation to a liability scale had little impact.

The wide variability in estimated heritabilities reported in the literature is caused by differences in definitions and breeds used, varying ages at assessment, and sometimes the use of small sample sizes or progeny groups, or the use of preselected data (Ricard, 2002). Data in this study originated from a balanced, randomly drawn sample of offspring from a representative sample of the Dutch Warmblood (KWPN) breeding sire population. This design minimized the risk of selection in the data. Furthermore, we studied yearlings that had passed the age at which the radiographic OC status was still unstable because of the dynamic character of the disorder at a young age (Dik et al., 1999), but before selection on OC took place. This reduced the risk of biased estimates of the genetic variables caused by selection. The detailed scoring in our study, together with the virtual absence of preselection, enabled estimates of heritability for FLAT and FRAG separately per joint.

Heritabilities

In this study, the heritability of OC at the animal level indicates substantial genetic variation of the disorder, which agrees with the large variation in the standardized means of the progeny groups per sire. Heritabilities for the TC joint (0.36) and ALL (0.23) were greater in our study compared with previous studies (0.00 to 0.27), except for those of Stock et al. (2005) and Grøndahl and Dolvik (1993) for the TC joint. Although there will always be differences between populations, we determined these greater values to be reliable.
because of the balanced and well-controlled character of the sampled population and the many factors that may have affected the accuracy of the estimation of heritability for OC in some of the previous studies in which the same population was used (Ricard, 2002). The heritability estimates in the current study confirmed previous findings (Van Grevenhof et al., 2009), including the strong relationship between the contralateral homologs at the joint level and the differences between joints. The genetic correlation between flattened bone contours and fragments was strong (0.80), with a large associated SE, but the heritability of both traits was substantially different.

**Which Joints Should Be Taken into Account**

The heritability of the TC joint indicates that OC can be scored accurately in this joint and that genetic variation is evident. In contrast, the heritability of the FP joint is less. Improvement in the scoring of OC in the FP joint may increase the heritability estimate for that joint. The decrease in accuracy seen for the FP joint could indicate a large impact of measurement errors on the environmental variance. This results in a reduced heritability estimate for the FP joint. More measurement errors are expected for the FP joint than for the other joints, also because sedation was shown to be a significant influence in diagnosing OC in the FP joint (Van Grevenhof et al., 2009). Therefore, reduction of OC in the FP joint is relevant because the prevalence of OC in this joint is high (Van Grevenhof et al., 2009). Although the apparent differences in the TC and FP joint heritabilities suggest that selection on the FP joint may be of little use, there is another factor to be considered, namely, the difference in the clinical relevance of OC in each joint. Osteochondrosis in the FP joint is the most important cause of lameness in the stifle, and surgical treatment results are reported as being fair to good (Stick, 2006). Conversely, OC in the TC joint rarely leads to lameness and has an excellent prognosis for return to athletic activity after surgery (Auer and Stick, 2006). Therefore, the importance of selection on the FP joint should not be underestimated.

Effective breeding against OC in the FP and TC joints requires recording of both traits because the TC joint showed strong heritability and the FP joint is clinically important. A correlated response of the FP joint when selecting for the TC joint would be uncertain, given the large SE associated with the genetic correlation estimate.

In this study, we included only the proximodorsal part of the sagittal ridge of the third metacarpal and metatarsal bone in the MCP and MTP joints. In contrast to many other sites in the MCP and MTP joints, osteochondral abnormalities at this site belong to the OC complex (Hurtig and Pool, 1996). The heritability of OC in the MCP and MTP joints was moderate (0.14), and the genetic correlations between the MCP-MTP and FP joints (0.26), and between the MCP- MTP and TC joints (0.09) were less, and not significant. Therefore, there would be only a small correlated response in the MCP and MTP joints when selection is performed on the FP and TC joints. Separate recording of OC lesions by joint and location in the joint is required to breed efficiently against OC in the MCP-MTP, TC, and FP joints, which is in agreement with the results of Stock and Distl (2006) regarding the TC and MCP-MTP joints.

**Physiology**

A previous physiological study (Dik et al., 1999) showed that, during the process of development and repair, osteochondrotic lesions were rarely found directly after birth in the FP joint, but that they generally developed during early growth, between the third and eighth month of age. This could indicate a major environmental effect rather than a large genetic component. In contrast, lesions in the TC joint were generally shown to exist from birth and to recover during early growth, between the second and fifth month of age. This could indicate an underlying genetic background rather than large environmental effects during growth. These physiological results correspond to the low heritability found for the FP joint and the moderate heritability found for the TC joint in the present study.

---

**Table 4. Genetic correlations and residual correlations of the linear osteochondrosis values between both flattened bone contours and fragments (ALL) and specific joints, using a continuous scale**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Animal</th>
<th>FP</th>
<th>TC</th>
<th>MCP/MTP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Animal</td>
<td>0.77 (0.23)</td>
<td>0.86 (0.10)</td>
<td>0.58 (0.22)</td>
<td></td>
</tr>
<tr>
<td>FP</td>
<td>0.65 (0.04)</td>
<td>0.59 (0.37)</td>
<td>0.26 (0.49)</td>
<td></td>
</tr>
<tr>
<td>TC</td>
<td>0.50 (0.07)</td>
<td>0.011 (0.08)</td>
<td>0.09 (0.31)</td>
<td></td>
</tr>
<tr>
<td>MCP/MTP</td>
<td>0.69 (0.04)</td>
<td>0.13 (0.06)</td>
<td>0.09 (0.09)</td>
<td></td>
</tr>
</tbody>
</table>

1Above diagonal.
2Below diagonal.
3Values in parentheses are SE.
4Joints: FP = femoropatellar joint; TC = tarsocrural joint; MCP/MTP = metacarpophalangeal and metatarsophalangeal joints. ALL was used in the calculation of the genetic correlations between these joints.
**Flattened Bone Contours and Fragments**

The genetic correlation between FLAT and FRAG was high (0.80) at the animal level, although FLAT did not differ significantly from FRAG. Both FLAT and FRAG were heritable \( \left( h^2 = 0.08 \right. \) and 0.22) at the animal level. Therefore, selection against FRAG \( \left( h^2 = 0.22 \right. \) will also decrease FLAT in a correlated response, but the selection response in FLAT will be less compared with selection on both FLAT and FRAG. Therefore, both FLAT and FRAG should be considered separately in selection against OC.

It can be concluded at the joint level that heritability was greatest in the TC joint, intermediate in the MCP and MTP joints, and least in the FP joints. Flattened bone contours had substantially reducedheritabilities compared with fragments, but the genetic correlation between those manifestations was high. The heritability estimates confirmed a strong relationship between the contralateral homologs at the joint level, as well as differences between joints. Therefore, OC should be scored minimally in more than 2 categories and in all 4 joints, and should take into account both flattened bone contours and fragments.

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**LITERATURE CITED**


der Kinderen, L. 2005. Heritability of osteochondrosis in Dutch Warmblood stallions from the second stallion inspection. MS Thesis. Wageningen University, Wageningen, the Netherlands.


