Maternal and Fetal Selenium Concentrations and Their Interrelationships in Dairy Cattle[1]

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ABSTRACT Paired dam-fetus serum, whole blood and liver samples were collected from 101 pregnant dairy cattle at slaughter to establish mean values for fetal tissue selenium concentration and to determine relationships between maternal and fetal selenium status. Samples were assayed for selenium concentration in serum, whole blood and liver and for whole blood glutathione peroxidase (GSH-Px) activity. Fetal age was estimated from fetal crown-to-rump length. Mean fetal liver (2.14 μg/g dry wt) and serum (21.4 ng/ml) selenium concentrations and whole blood GSH-Px activity (21.6 u/ml) differed ($P < 0.0001$, 0.0001 and 0.01, respectively) from corresponding maternal values (0.95 μg/g liver dry wt; 44.0 ng/ml; 16.7 u/ml, respectively), while no differences were found between whole blood or erythrocyte selenium concentrations. Fetal liver selenium concentration was greater than corresponding maternal liver selenium in 99% (96/97) of the dam-fetal pairs, suggesting efficient placental transfer and fetal concentrating ability. Maternal liver selenium concentration was most highly correlated to all fetal tissue selenium concentrations and used to develop prediction models. These data suggest that selenium efficiently passes the placenta, and based on published values of adequate adult liver selenium concentrations and maternal-fetal relationships, we suggest an adequate liver selenium concentration in the bovine fetus to be > 2.2 μg/g liver dry wt, and in whole blood, > 120 ng/ml. *J. Nutr.* 119: 1128–1137, 1989.

INDEXING KEY WORDS:

- *selenium* • *placental transfer* • *dairy cattle*
- *liver* • *glutathione peroxidase*

Since selenium (Se) was determined to be an essential nutrient (1), numerous selenium-deficiency syndromes afflicting a variety of domestic species have been described (2, 3), of which white muscle disease (nutritional myodegeneration) of young animals is the most common. Evidence suggests that selenium deficiency plays a role in numerous other economically important livestock diseases (2, 3). For example, all aspects of reproduction in cattle may be affected by selenium deficiency. Selenium-responsive problems include impaired fertility (4), abortion (5–7), retained placenta (8, 9) and neonatal weakness (10, 11).

Transfer of nutrients from dam to offspring occurs via two pathways, placental transfer and colostrum ingestion. Nutrient amounts transferred to the offspring will be dependent upon maternal nutrient status and efficiency of transplacental and mammary transport mechanisms. Selenium placental transfer has been documented (12–17), however, fetal selenium concentrations have been shown to be less (14, 15) and greater (13, 17) than corresponding maternal selenium concentrations.

Selenate transport across placental membrane vesicles has been described as an anion exchange pathway shared with sulphate, which is sodium independent and inhibited by other tetrahedral anions (18, 19). Additionally, selenoamino acids are actively transported from dam to fetus (14). Selenium transport into milk and colostrum occurs primarily through the secretory vesicle associated with casein in the mammary alveolar epithelial cell (20). Colostral selenium concentrations have been shown to be greater than those of milk (13, 21, 22), possibly as a result of the higher protein content of colostrum compared to milk.

Establishing the relationships between maternal and fetal selenium status would be beneficial so as to allow for the prediction of selenium-deficiency disease in the fetus, based on maternal selenium status. The present study was undertaken to determine mean tissue selenium concentrations of the bovine dam and fetus throughout gestation and to establish interrelationships between maternal and fetal selenium status to aid diagnostic evaluations of maternal and fetal susceptibility to selenium-deficiency disease.

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MATERIALS AND METHODS

Sample collection. Paired maternal-fetal serum, whole blood and liver samples from dairy cattle (n = 101) were collected on three separate occasions over a 6-mo period (May to September) at an abattoir located in southwestern Michigan. To minimize introducing biases into the data from sampling only culled animals, collection times were coordinated with times when animals from herds participating in the National Dairy Buyout Program, from Michigan and surrounding states, were received at the abattoir. Historical information pertaining to herd of origin, participation in the buyout program or levels of selenium and vitamin E supplementation was unavailable for evaluation.

Greater than 95% of the sampled cows were of the Holstein breed, with the remainder consisting of other dairy and mixed beef breeds. Therefore, all data were pooled and analyzed, allowing for potential biases in breed, age, herd and seasonal effects.

Duration of gestation in the bovine ranges from 273 to 296 d with breed variation (23). Gestation in the Holstein breed ranges from 278 to 282 d. Gestational age of sampled animals was estimated (± 0.5 mo) from measured fetal crown-to-rump length and compared to published bovine fetal growth curve data (24, 25).

Two samples of venous blood, one mixed with ethylenediamine tetraacetic acid (EDTA) for whole blood analysis, were collected from cows. Similarly, whole blood (EDTA) and serum were collected via cardiac puncture from all fetuses. A sample (approximately 10 g) was obtained from the left lobe of the liver from all cows and late gestation (> 4 mo) fetuses, while the entire liver was collected from all early gestation (< 4 mo) fetuses.

All blood and liver samples were kept on ice during the collection process and transport to the laboratory. Harvested serum and liver samples were kept frozen (−20°C) until analyzed. Whole blood samples were kept refrigerated (4°C) until assayed. Whole blood glutathione peroxidase (GSH-Px) assays were completed within 2 wk of collection.

Selenium analysis. Maternal and fetal serum, whole blood and liver selenium concentrations were determined fluorometrically (Aminco-Bowman Model J48961, Travenol Lab., Deerfield, IL) using the method described by Olson (26) as modified by Whetter and Ullrey (27). Liver samples were prepared by predigesting approximately 5 g of sample in 10 ml of 16 M nitric acid in 50-ml Erlenmeyer flasks for several hours or overnight. Organic matter was cleared by warming (40–50°C) on a hot plate in a fume hood. After clearing, the solution was heated (60–80°C) for 1 h in the hood and then allowed to cool. Double-distilled, deionized water was then added to each flask (total of 50 ml), and 3 ml of the solution was used for analysis. Liver dry weight was determined on a separate 2-g sample, oven heated (70°C) to a constant weight, and the result used to express the liver selenium concentration on a dry weight basis.

Erythrocyte selenium concentration was calculated from measured serum and whole blood selenium concentrations using the formula of Thompson et al. (28). Mean hematocrit values of 33% (personal communication from Harold Tvedten, Michigan State University) and 37% (29) were used to calculate all maternal and fetal erythrocyte selenium concentrations, respectively. Results are reported as ng selenium/ml of serum, erythrocytes or whole blood, and as μg selenium/g liver dry wt.

GSH-Px activity. Maternal and fetal whole blood GSH-Px activities were determined spectrophotometrically (Model 920, Gilford Instruments, Oberlin, OH) by a modification of the procedure described by Paglia and Valentine (30), using hydrogen peroxide (H_2O_2) as the substrate. A whole blood lysate sample was prepared by adding 50 μl of whole blood to 2.5 ml of double-distilled, deionized water. The reaction mixture was freshly prepared for each analysis and contained 100 mM potassium phosphate buffer (pH 7), 3 mM EDTA, 1 mM sodium azide, 0.1 mM NADPH, 1 U of glutathione reductase and 2 mM reduced glutathione (GSH). All chemicals were obtained from Sigma Chemical, St. Louis, MO. A 40-μl lysate sample was incubated with 0.95 ml of reaction mixture for 5 min at 37°C prior to initiating the reaction by adding 10 μl of 12 mM H_2O_2 (total volume of 1 ml). Rate of conversion of NADPH to NADP by enzymatic degradation of H_2O_2 was determined by the change in absorbance at 340 nm. A nonenzyme reference reaction was determined for each analysis by substituting 40 μl of double-distilled, deionized water for the lysate sample, and the rate was subtracted from the sample result. Results are reported as units (U) per ml of whole blood, where 1 U represents 1 μmol of glutathione oxidized per min at 37°C.

Statistical analysis. Means, Pearson correlation coefficients, analysis of variance (ANOVA) by general linear model and regression analyses were performed using Statistical Analysis System software (SAS Institute, Raleigh, NC) (31). All analyses were not completed for every sample due to either insufficient sample size or inability to match dam to fetal samples. Comparisons of maternal and fetal means were determined using a grouped t-test as a result of missing values. Differences between collection time or gestational age means were compared by Tukey's test, where ANOVA indicated differences between means. Results reported in text, tables and figures are means ± SEM, unless otherwise indicated.

RESULTS

Selenium concentrations. Maternal liver ($P < 0.05$) and serum ($P < 0.08$) and fetal serum ($P < 0.05$) selenium concentrations were influenced by collection time

TABLE 1

Mean bovine maternal and fetal tissue selenium (Se) concentrations and whole blood glutathione peroxidase (GSH-Px) activity[1]

Tissue	Maternal	Fetal	*P*-value
Liver Se, μg/g *dry wt*	0.95 ± 0.04 (101)	2.14 ± 0.13 (97)	0.0001
Serum Se, *ng/ml*	44.0 ± 2.3 (91)	21.4 ± 1.6 (97)	0.0001
Erythrocyte Se, *ng/ml*	322.7 ± 22.3 (63)	307.2 ± 14.9 (70)	0.82
Whole blood Se, *ng/ml*	136.6 ± 8.7 (63)	125.9 ± 5.7 (74)	0.37
Whole blood GSH-Px, *U/ml*[2]	16.7 ± 2.0 (64)	21.6 ± 2.1 (30)	0.01

[1]Values are means ± SEM; *n* is in parentheses.
[2]A unit (U) of enzyme activity is defined as μmol glutathione oxidized/(min·ml whole blood).

(data not shown), possibly as a result of herd or seasonal effects. Mean maternal and fetal tissue selenium concentrations and whole blood GSH-Px activity for all data are shown in **Table 1**. Mean fetal liver selenium concentration (2.14 ± 0.13 μg/g dry wt) was 2.3 times greater ($P < 0.0001$) than mean maternal liver selenium (0.95 ± 0.04 μg/g dry wt) with 99% (96/97) of the values for fetal liver selenium concentration being greater than their corresponding dam's liver selenium concentration. Mean maternal serum selenium concentration (44.0 ± 2.3 ng/ml) was twice that ($P < 0.0001$) of mean fetal serum selenium (21.4 ± 1.6 ng/ml). Mean fetal whole blood GSH-Px activity (21.6 ± 2.1 U/ml) was greater ($P < 0.01$) than mean maternal whole blood GSH-Px activity (16.7 ± 2.0 U/ml), although no difference was found between maternal and fetal erythrocyte (322.7 ± 8.7 and 307.2 ± 14.9, respectively) or whole blood (136.6 ± 8.7 and 125.9 ± 5.7, respectively) selenium concentrations.

Separation of whole blood selenium into fractions found in serum or erythrocytes (percent of whole blood basis) are presented in **Table 2**. Serum selenium comprised a greater ($P < 0.0001$) percentage of whole blood selenium in the dam (24.2%) than in the fetus (10.0%), with corresponding erythrocyte selenium fraction being 90.0% (fetal) and 75.8% (dam). There were no gestational age (by trimester) effects on the distribution of selenium between serum and erythrocyte fractions (**Table 2**). Mean serum selenium expressed as percent of whole blood selenium for trimester 1 was less than those for trimesters 2 or 3; however, there were insufficient values to determine statistical differences.

Mean fetal liver selenium concentration was consistently greater ($P < 0.05$–0.001) than mean maternal liver selenium concentration across gestation (**Fig. 1**, *top panel*), suggesting fetal concentrating ability and a possible selenium storage function for the fetal liver. Neither maternal nor fetal liver selenium concentrations were affected by gestational age. Maternal liver selenium tended to decrease after 8.5 mo, possibly as a result of selenium mobilization for colostrum or rapid fetal growth.

In contrast to liver selenium, mean maternal serum selenium concentration was consistently greater ($P < 0.05$–0.001) than mean fetal serum selenium until 8.5 mo, when maternal serum selenium declined rapidly (Fig. 1, *bottom panel*). Maternal serum selenium was influenced ($P < 0.01$) by gestational age, while no effect was observed for fetal serum selenium. This relationship between maternal and fetal serum selenium may potentially promote transport of selenium from the dam to fetus if the serum pool of selenium is responsible for selenium transport. The decline in maternal serum selenium at 8.5 mo may be related to losses to colostrum or rapid fetal growth, as suggested for maternal liver selenium.

TABLE 2

Mean bovine maternal and fetal serum and erythrocyte selenium as a percent of whole blood selenium concentration, by trimester[1]

Sample period	Serum selenium		*P*-value[2]	Erythrocyte selenium		*P*-value[2]
	maternal	fetal		maternal	fetal	
	%			%		
Trimester 1	10.1 ± 10.1[b] (2)	5.1 ± 0.9 (2)	0.9	89.9 ± 10.1 (2)	94.9 ± 0.9 (2)	0.9
Trimester 2	23.1 ± 1.6 (42)	9.2 ± 1.0 (48)	0.0001	76.9 ± 1.6 (42)	90.8 ± 1.0 (48)	0.0001
Trimester 3	28.0 ± 3.6 (19)	12.3 ± 2.3 (20)	0.0026	72.0 ± 3.6 (18)	87.7 ± 2.3 (20)	0.0025
Overall	24.2 ± 1.6 (63)	10.0 ± 0.9 (70)	0.0001	75.8 ± 1.6 (62)	90.0 ± 0.9 (70)	0.0001

[1]Values are means ± SEM; *n* is in parentheses.
[2]Grouped *t*-test comparison.

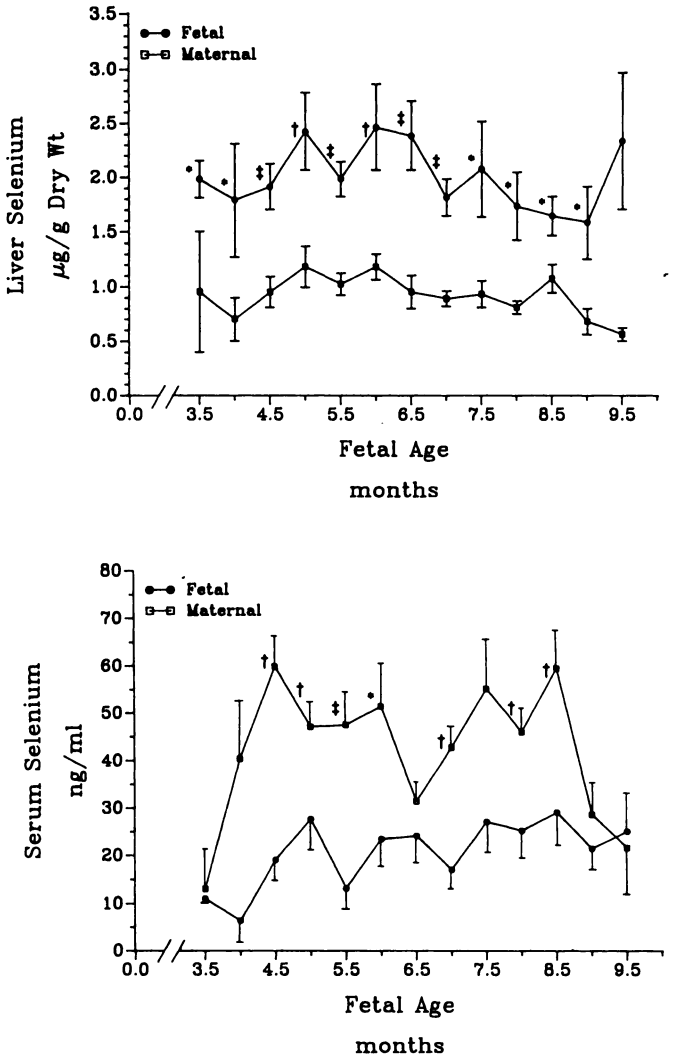

FIGURE 1 Variation in bovine maternal (□) and fetal (●) selenium concentrations in liver (***top panel***) and serum (***bottom panel***) during gestation. Each point represents a mean ± SEM for 1–13 animals. [ab]Maternal or fetal means with different superscript letters differ significantly ($P < 0.05$); all other means are not different. Maternal-fetal mean comparison: *$P < 0.05$, †0.01, ‡0.001.

Maternal and fetal mean erythrocyte (**Fig. 2**, *top panel*) and whole blood (Fig. 2, *middle panel* selenium concentrations and whole blood GSH-Px activity (Fig. 2, *bottom panel*) were variable across gestation, with minimal differences between dam and fetus. Maternal erythrocyte and whole blood selenium concentrations were affected ($P < 0.01$) by gestational age. Maternal erythrocyte and whole blood selenium concentrations each declined ($P < 0.05$) between 5.5 and 6.5 mo of gestation. However, this decrease was interpreted to be the result of a sampling bias. Fetal erythrocyte and whole blood selenium concentrations and maternal and fetal whole blood GSH-Px activities were not affected by gestational age.

Maternal-fetal interrelationships. Correlation coefficients were determined between estimators of selenium status in the dam and fetus and between esti-

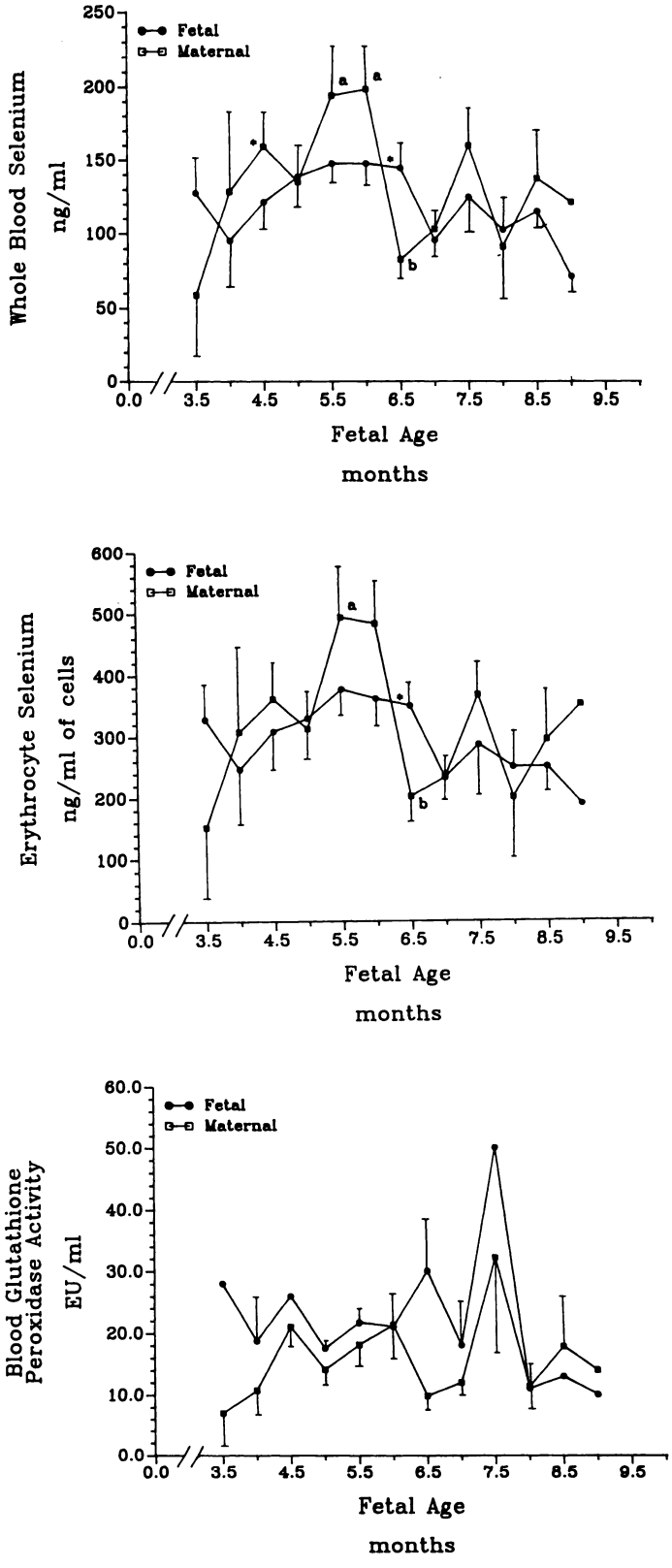

FIGURE 2 Variation in bovine maternal (□) and fetal (●) erythrocyte (***top panel***) and whole blood (***middle panel***) selenium concentrations and whole blood glutathione peroxidase activity (***bottom panel***) during gestation. Each point represents a mean ± SEM for 1–13 animals. [ab]Maternal or fetal means with different superscript letters differ significantly ($P < 0.05$); all other means are not different. Maternal-fetal mean comparison: *$P < 0.05$, †0.01, ‡0.001.

mators of fetal selenium status and fetal age (**Table 3**). In the dam, serum selenium concentration was correlated with liver ($r = 0.36$, $P < 0.0005$), erythrocyte ($r = 0.62$, $P < 0.0001$) and whole blood ($r = 0.75$, $P < 0.0001$) selenium concentrations and whole blood GSH-Px activity ($r = 0.62$, $P < 0.0001$). In the fetus, liver selenium concentration was correlated with erythrocyte ($r = 0.72$, $P < 0.0001$) and whole blood ($r = 0.68$, $P < 0.0001$) selenium concentrations and whole blood GSH-Px activity ($r = 0.88$, $P < 0.0001$), but not with serum selenium ($r = 0.09$, $P < 0.4$). Fetal erythrocyte ($P < 0.05$), liver ($P < 0.1$) and whole blood ($P < 0.16$) selenium concentrations tended to be negatively correlated to fetal crown-to-rump length, possibly a dilution effect related to rapid fetal growth; fetal serum selenium tended ($P < 0.07$) to be positively correlated. In the dam and fetus, whole blood GSH-Px activity was positively correlated to erythrocyte ($r = 0.63$, $P < 0.0001$ and $r = 0.83$, $P < 0.0001$, respectively) and whole blood ($r = 0.67$, $P < 0.0001$ and $r = 0.82$, $P < 0.0001$, respectively) selenium concentrations.

TABLE 3

Correlations between various estimators of selenium (Se) status and between estimators of selenium status and fetal crown-to-rump (C-R) length for the pregnant dairy cow and fetus[1]

Variables	Maternal	Fetal
Liver Se–Serum Se	0.358 (0.0005)	0.086 (0.41)
Liver Se–Erythrocyte Se	0.246 (0.05)	0.715 (0.0001)
Liver Se–Whole blood Se	0.277 (0.03)	0.684 (0.0001)
Liver Se–Whole blood GSH-Px[2]	0.178 (0.16)	0.883 (0.0001)
Liver Se–C-R length	—	−0.164 (0.11)
Serum Se–Erythrocyte Se	0.619 (0.0001)	0.196 (0.10)
Serum Se–Whole blood Se	0.747 (0.0001)	0.391 (0.0008)
Serum Se–Whole blood GSH-Px	0.619 (0.0001)	0.305 (0.11)
Serum Se–C-R length	—	0.187 (0.07)
Erythrocyte Se–Whole blood Se	0.984 (0.0001)	0.979 (0.0001)
Erythrocyte Se–Whole blood GSH-Px	0.629 (0.0001)	0.829 (0.0001)
Erythrocyte Se–C-R length	—	−0.236 (0.05)
Whole blood Se–Whole blood GSH-Px	0.672 (0.0001)	0.822 (0.0001)
Whole blood SE–C-R length	—	−0.166 (0.16)
Whole blood GSH-Px–C-R length	—	−0.129 (0.50)

[1]Values are Pearson correlation coefficients; *P*-values are in parentheses.

[2]Whole blood glutathione peroxidase activity.

Interrelationships between selenium status of the dam and fetus were assessed from correlation coefficients between maternal and fetal estimators of selenium status (**Table 4**). Compared to other maternal variables, maternal liver selenium concentration correlated best with fetal selenium variables (liver selenium: $r = 0.44$, $P < 0.0001$; serum selenium: $r = 0.20$, $P < 0.05$; erythrocyte selenium: $r = 0.65$, $P < 0.0001$; whole blood selenium: $r = 0.66$, $P < 0.0001$; and whole blood GSH-Px activity: $r = 0.41$, $P < 0.03$). There was a tendency ($P < 0.06$) for maternal liver selenium concentration to decline with increasing fetal crown-to-rump length, suggesting maternal liver selenium mobilization with fetal growth.

Prediction models. Based on the associations established between maternal and fetal selenium variables (Table 4), maternal liver selenium concentration best reflected fetal selenium status and whole blood GSH-Px activity. Prediction models were derived by regressing fetal tissue selenium concentration and whole blood GSH-Px activity on maternal liver selenium concentration (**Table 5**).

All fetal tissue selenium concentrations and whole blood GSH-Px activity were linearly related ($P < 0.05$) to maternal liver selenium concentration. However, response surface regression modeling (31) revealed a nonlinear parameter to be significant for all models except fetal liver. A quadratic parameter of maternal liver selenium concentration was found to be more significant, based on the coefficient's *t*-statistic, than the linear parameter for these models. A practical model derived from the data predicting fetal whole blood selenium concentration is shown in **Figure 3**.

Although the quadratic parameter from the statistical model did not significantly ($P = 0.3$) contribute to the prediction of fetal liver selenium, it was included in the prediction equation because its inclusion more accurately reflects the data (**Fig. 4**). A plateau in fetal liver selenium concentration occurs in the quadratic model between 2.4 to 2.8 μg/g dry wt, suggesting a saturation limit for selenium similar to that seen with other nutrients when supplied at adequate levels to meet the requirement, maintain dependent enzyme activity and prevent the incidence of clinical disease (32).

DISCUSSION

Observed values for maternal serum, erythrocyte, whole blood and liver selenium concentrations and whole blood GSH-Px activity range from deficient to

TABLE 4

***Correlations between bovine maternal and fetal tissue selenium (Se) concentrations, whole blood glutathione peroxidase (GSH-Px) activity and fetal crown-to-rump (C-R) length*[1]**

	Maternal variables				
Fetal variables	Liver Se	Serum Se	Erythrocyte Se	Whole blood Se	Whole blood GSH-Px
Liver Se	0.435 (0.0001)	0.110 (0.31)	0.260 (0.04)	0.236 (0.07)	0.026 (0.84)
Serum Se	0.203 (0.05)	0.167 (0.12)	−0.012 (0.93)	0.034 (0.80)	−0.016 (0.90)
Erythrocyte Se	0.648 (0.0001)	0.110 (0.40)	0.345 (0.008)	0.319 (0.01)	0.190 (0.15)
Whole blood Se	0.663 (0.0001)	0.149 (0.24)	0.326 (0.01)	0.307 (0.015)	0.103 (0.42)
Whole blood GSH-Px	0.407 (0.026)	0.169 (0.46)	0.142 (0.55)	0.155 (0.51)	−0.083 (0.72)
C-R length	−0.188 (0.06)	−0.083 (0.44)	−0.129 (0.31)	−0.109 (0.39)	0.065 (0.61)

[1]Values are Pearson correlation coefficients; *P*-values are in parentheses.

adequate (33). Of the maternal means, 13, 34 and 70% of the observed values for serum, liver and whole blood selenium concentrations, respectively, were in the adequate range, as judged by published values (33). This apparent discrepancy in maternal selenium status may result from acute changes in selenium supplementation, withdrawal or decreased feed intake, prior to and during transport to the abattoir.

Selenium status has been directly related to selenium intake, with rapid mobilization of reserves following dietary withdrawal (34–37). Liver and serum selenium concentrations have been shown to be sensitive indicators of acute changes in selenium intake (28), whereas whole blood selenium and GSH-Px activity are less responsive to changes in selenium intake (38), thereby reflecting chronic selenium status (37, 39, 40). Differences between tissue selenium mobilization rates may be related to the binding affinity of the particular tissue proteins for selenium.

We interpret our result of 13% of adequate serum selenium values to reflect the loose binding of selenium to plasma and erythrocyte proteins (41), allowing for rapid mobilization of the serum selenium pool during decreased selenium intake. In contrast, 70% of adequate whole blood selenium values reflects the rate of erythrocyte turnover (42) and tight binding of selenium to GSH-Px, which accounts for the majority of whole blood selenium (43). Therefore, whole blood selenium is less available for mobilization during deficiency, and adequate levels would be maintained. The 34% of ad-

TABLE 5

***Regression of bovine fetal selenium (Se) status on maternal liver selenium concentration (MLSE)*[1]**

Fetal dependent variable, *Y*	Regression equation x = MLSE in μg/g liver dry wt	R^2	*P*-value
	Linear model		
Liver Se, *μg/g dry wt*	$Y = 0.95 + 1.1x$	0.24	0.0001
Serum Se, *ng/ml*	$Y = 13.8 + 8.0x$	0.04	0.05
Erythrocyte Se, *ng/ml*	$Y = 96.8 + 217.4x$	0.42	0.0001
Whole blood Se, *ng/ml*	$Y = 41.4 + 86.9x$	0.44	0.0001
Whole blood GSH-Px,[2] *U/ml*	$Y = 10.0 + 13.9x$	0.17	0.026
	Quadratic model		
Liver Se, *μg/g dry wt*	$Y = 0.57 + 2.0x - 0.4x^2$	0.25	0.0001
Serum Se, *ng/ml*	$Y = 27.4 - 21.5x + 13.7x^2$	0.07	0.03
Erythrocyte Se, *ng/ml*	$Y = 191.5 + 11.2x + 97.7x^2$	0.44	0.0001
Whole blood Se, *ng/ml*	$Y = 83.9 - 6.1x + 44.3x^2$	0.46	0.0001
Whole blood GSH-Px,[2] *U/ml*	$Y = 47.2 - 83.0x + 54.2x^2$	0.41	0.0007

[1]Based on most significant correlations derived from the data (Table 4).
[2]Whole blood glutathione peroxidase activity. A unit (U) of enzyme activity is defined as μmol glutathione oxidized/(min·ml whole blood).

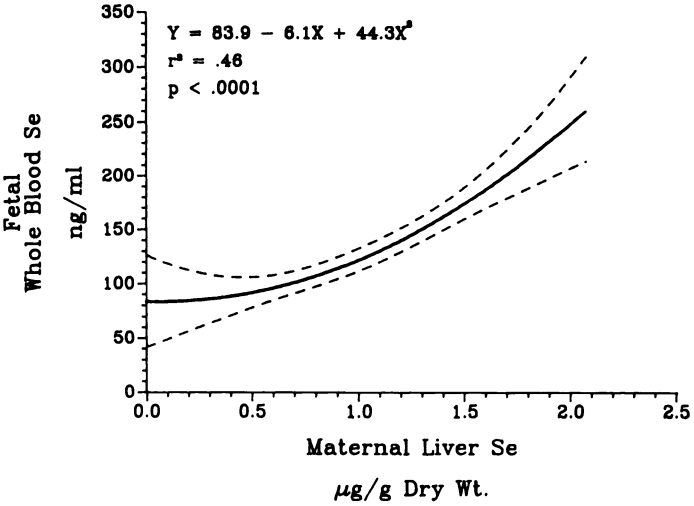

FIGURE 3 Regression of bovine fetal whole blood selenium (Se) concentration on maternal liver selenium concentration. Dashed line indicates 95% confidence intervals.

equate liver selenium is interpreted to be consistent with liver selenium being incorporated into GSH-Px and loosely bound to ligand proteins, allowing for some rapid mobilization.

Placental transfer of selenium has been documented in a variety of species (12–17, 44, 45), however, it appears that expected tissue concentrations for evaluation of selenium status in bovine fetuses have not been reported. Fetal liver selenium concentrations < 1.0 μg/g dry wt have been suggested to be deficient by association with histological lesions of white muscle disease in aborted fetuses of idiopathic etiology (5–7). Of 138 bovine abortion cases investigated, Yamini and Mullaney reported that, of the bovine fetuses aborted due to an undetermined etiology, 32% (24/74) had a liver selenium concentration < 1.0 μg/g dry wt, and nine of these fetuses had histological lesions of white muscle

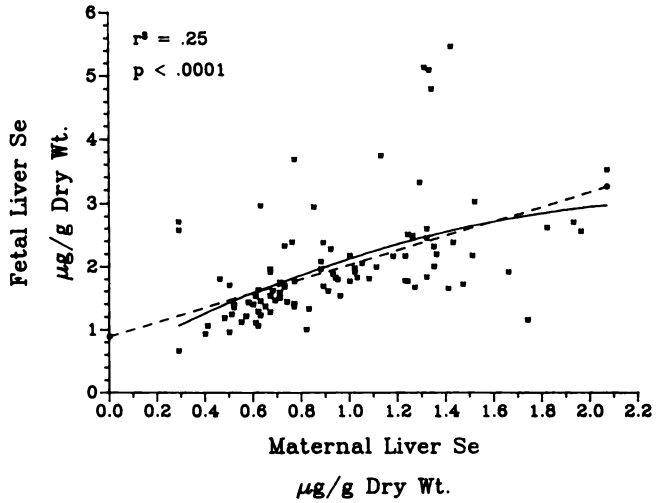

FIGURE 4 Relationship between bovine maternal and fetal liver selenium (Se) concentrations. (- -) Linear regression model, $Y = 0.95 + 1.1X$. (——) Quadratic regression model, $Y = 0.57 + 2.0X - 0.4X^2$.

disease (6). In comparison, 3% (3/97) of the fetuses from the current study had a liver selenium concentration < 1.0 μg/g dry wt, indicating a substantial difference between the selenium status of the aborted and sampled fetuses. This comparison would suggest a possible role of selenium deficiency in abortion syndrome.

Our data clearly demonstrate that the fetus has the ability to concentrate selenium in the liver in excess of concentrations found in the dam, even in the presence of low maternal selenium concentrations. Possibly the fetal liver has a higher affinity for selenium, clearing more selenium from the plasma, compared to the dam. This hypothesis is supported by data from Shariff et al. (44) describing plasma excretion of injected ^{75}Se in the fetus compared to the dam. Fetal plasma selenium clearance does not show a plasma selenium redistribution phase from the liver within the first 6 h of injection, as documented in the adult (46). Our data further supports this hypothesis of differential hepatic selenium metabolism from determined correlation coefficients. Maternal selenium measures were all highly correlated with maternal serum selenium, as opposed to all fetal selenium measures, which were correlated with fetal liver selenium concentration, with the exception of fetal serum selenium.

The fetus is totally dependent upon the dam for all nutrients. Therefore, a nutrient-concentrating ability would assist in providing that nutrient over a broad range of maternal nutrient states. Similar maternal-fetal relationships were found for macrominerals (47) and other microminerals (48) in the bovine. Our hypothesis of fetal selenium concentrating ability was further supported when the experimental population was divided into selenium-depleted (< 1.0 μg/g dry wt liver; < 100 ng/ml whole blood) and selenium-adequate (> 1.0 μg/g dry wt liver; > 100 ng/ml whole blood) dams and comparisons made between maternal and fetal liver and whole blood selenium concentrations. In selenium-depleted dams (0.67 μg/g dry wt liver; 59.0 ng/ml whole blood), corresponding fetal liver (1.66 μg/g dry wt) and whole blood (105.9 ng/ml) selenium concentrations averaged 248% and 180% of maternal values, respectively, whereas in selenium-adequate dams (1.35 μg/g dry wt liver; 167.1 ng/ml whole blood), corresponding fetal values (2.81 μg/g dry wt liver; 138.0 ng/ml whole blood) averaged 208% and 83% of maternal values, respectively. The in utero ability of the fetus to concentrate selenium in whole blood while in a selenium-depleted dam has been previously documented (13). These data suggest that the relationship between maternal and fetal liver and whole blood selenium measures appear to be curvilinear, rather than linear.

In contrast to fetal hepatic selenium being consistently higher than maternal hepatic selenium, fetal serum selenium was consistently lower than maternal serum selenium. Serum selenium concentrations from fetuses in the present study are in agreement with values reported for precolostrum-fed calves (16, 17, 45).

This maternal-fetal difference may potentially increase the concentration gradient between dam and fetus to facilitate placental transport. Shariff et al. (44) determined bidirectional placental transfer of selenium with an efficiency of exchange from dam to fetus of 2%, and for fetus to dam, 1%. Mean maternal (44 ng/ml) and fetal (21.4 ng/ml) serum selenium concentrations are consistent with this observation, suggesting the possibility that serum selenium is the fraction of maternal blood responsible for placental transfer. The maternal serum selenium pool is also hypothesized to supply selenium for colostrum, as suggested by the rapid decline in maternal serum selenium values the last month of gestation.

Similarities between maternal and fetal erythrocyte and whole blood selenium concentrations and whole blood GSH-Px activity, when standardized for hemoglobin content, imply an equivalent functional need for GSH-Px in the dam and fetus. Whole blood GSH-Px activity has been shown to be predominantly (> 98%) associated with erythrocytes in cattle (43), with measured activity correlated to erythrocyte and whole blood selenium concentrations (37, 42). Correlations between whole blood and erythrocyte selenium concentrations and whole blood GSH-Px activity from the present study are similar to reported values (49–51).

Direct measurement of fetal selenium status is impractical in most situations, except abortion cases. Therefore, the present data were evaluated to determine a potential model to predict fetal selenium status from maternal selenium status. Maternal liver selenium concentration was determined to be the best predictor of fetal selenium status. Two sets of equations, one linear and one curvilinear, were derived for predicting the various measures of fetal selenium status from maternal liver selenium concentration. In most cases, the curvilinear or quadratic equations accounted for only slightly more of the variation than the linear equations. Whole blood GSH-Px activity was an exception; the R^2 was 0.17 for the linear equation and 0.41 for the quadratic equation. Although either the linear or curvilinear equations appear to fit the data, we feel that the curvilinear equation best explains both the data and the underlying physiology. The graph of the equation (Fig. 4), which is relatively steep at a low maternal liver selenium concentration, flattens out as the dam's hepatic concentration increases. This pattern suggests that, as the dam's tissue selenium concentration improves and the fetal values reach some optimum level, there is a "need" for the fetus to create a fetal-maternal concentration gradient.

Based on our present data, we propose liver and whole blood selenium concentrations > 2.2 μg/g dry wt and > 120 ng/ml, respectively, to be considered as adequate selenium status in the bovine fetus. Using the derived prediction equations, a minimum range of maternal liver selenium concentration of 0.95–1.0 μg/g dry wt would be necessary to maintain adequate fetal liver and whole blood selenium concentrations. Fetal liver selenium concentration < 1.0 μg/g dry wt has been associated with histological myodegenerative lesions in undiagnosed abortion cases, which, based on these prediction models, suggests a corresponding maternal liver selenium concentration of 0.25 μg/g dry wt. This latter value is in agreement with reported liver selenium concentrations (< 0.3 μg/g dry wt) in selenium-deficient adult cattle. Investigations substantiating these relationships between fetal tissue selenium concentration and clinical disease are warranted.

Application of the derived models (Fig. 3, 4) to the general dairy cattle population should be done cautiously, in light of the significant effect of time of collection observed in these data. This collection-period effect was interpreted as a potential seasonal and herd effect. Herd effects may reflect short- and long-term selenium intake history of sampled animals, which previously has been documented to be a primary factor in selenium status variation (52). Attempts to minimize potential biases of an abattoir study were addressed by sampling concurrently with the Dairy Buyout Program. Sampling culled animals could potentially bias estimates downward due to age, disease and herd effects on selenium status. A controlled dose-response investigation would be suggested to better define the relationships established in the current study.

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