

First-Trimester Prediction of Macrosomia

Leona C.Y. Poon^a George Karagiannis^{a, b} Violeta Stratieva^{a, b}
Argyro Syngelaki^{a, b} Kypros H. Nicolaides^{a, b}

^aHarris Birthright Research Centre for Fetal Medicine, King's College Hospital, and ^bFetal Medicine Unit, University College Hospital, London, UK

Key Words

Macrosomia · Screening · Free β -human chorionic gonadotrophin · Pregnancy-associated plasma protein-A · Nuchal translucency

Abstract

Objective: To determine if combinations of maternal characteristics and measurements of parameters used in screening for aneuploidies at 11–13 weeks provide significant prediction of macrosomia. **Method:** Maternal characteristics, fetal nuchal translucency (NT), free β -human chorionic gonadotrophin (β -hCG) and pregnancy-associated plasma protein-A (PAPP-A) were recorded at 11⁺⁰–13⁺⁶ weeks in 36,743 singleton pregnancies. Regression analysis was used to determine if in predicting macrosomia significant contributions are provided by maternal factors, fetal NT, free β -hCG and PAPP-A. **Results:** The risk for macrosomia increased with maternal weight and height and was higher in parous women with previous delivery of a macrosomic baby and in those with diabetes mellitus; the risk was lower in women of African and South Asian racial origins, in cigarette smokers and in those with chronic hypertension. In the macrosomic group compared to the unaffected group there were higher Δ -NT (0.167 vs. 0.116 mm), free β -hCG (1.010 vs. 0.964 MoM) and PAPP-A (1.103 vs. 1.003 MoM). Prediction of macrosomia provided by maternal factors was significantly improved by fetal

NT, free β -hCG and PAPP-A (34.4 vs. 33.1% at a false-positive rate of 10%). **Conclusion:** Prediction of macrosomia is provided in the first trimester of pregnancy by a combination of maternal characteristics and measurements of parameters used in screening for aneuploidies.

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Introduction

Fetal macrosomia, commonly defined as a birth weight above the 90th centile for gestational age (GA), is associated with increased risks for the mother, including cesarean section and trauma to the birth canal, and for the baby, including shoulder dystocia and consequent brachial plexus or facial nerve injuries, fractures of the humerus or clavicle and birth asphyxia [1–6].

Birth weight is affected by GA at delivery and several maternal characteristics, including racial origin, age, body mass index, parity and cigarette smoking, and medical conditions, such as pre-pregnancy diabetes mellitus [7–10]. There is also some evidence that birth weight is related to placental function in early pregnancy, reflected in the maternal serum concentration of the pregnancy-associated plasma protein-A (PAPP-A) at 11–13 weeks of gestation. Several studies reported that in pregnancies delivering small for gestational age (SGA) neonates se-

rum PAPP-A at 11–13 weeks was decreased and that in those delivering macrosomic neonates PAPP-A was increased [11–18]. One study reported that neonatal macrosomia was more common in 389 fetuses with nuchal translucency (NT) thickness above the 95th centile than in 386 fetuses with NT within the normal range [19].

The aims of this study in a population of more than 30,000 singleton pregnancies attending for routine care at 11–13 weeks was to firstly determine if combinations of maternal characteristics, fetal NT, serum concentrations of PAPP-A and free β -human chorionic gonadotrophin (β -hCG) are significant predictors of macrosomia and secondly to estimate the performance of first-trimester combined screening in the prediction of macrosomia.

Materials and Methods

The study reports the development of an algorithm for neonatal macrosomia using data from an ongoing prospective screening study for adverse obstetric outcomes in women attending for their routine first hospital visit in pregnancy. In this visit, which is held at 11⁺⁰–13⁺⁶ weeks of gestation, we recorded maternal characteristics and performed a transabdominal ultrasound scan to confirm GA from the measurement of the fetal crown-rump length, to diagnose any major fetal abnormalities, and to measure fetal NT [20]. Automated machines that provide reproducible results within 40 min were used to measure PAPP-A and free β -hCG (DELFIAXpress system, PerkinElmer Life and Analytical Sciences, Waltham, Mass., USA) as part of screening for chromosomal abnormalities [21]. Data on pregnancy outcome were collected from the hospital maternity records or their general medical practitioners. Written informed consent was obtained from the women agreeing to participate in the study, which was approved by the King's College Hospital Ethics Committee.

Maternal characteristics recorded were age, racial origin (Caucasian, African, South Asian, East Asian and mixed), cigarette smoking during pregnancy (yes or no), parity (nulliparous if there were no previous pregnancies beyond 23 completed weeks or parous), previous delivery of a macrosomic baby (yes or no), method of conception (spontaneous or assisted) and medical history of chronic hypertension and pre-pregnancy diabetes mellitus (yes or no). The maternal weight in kilograms (kg) and height in centimetres (cm) were measured.

Statistical Analysis

The measured NT was expressed as a difference from the expected normal mean for gestation (δ -value). Similarly, the measured concentrations of maternal serum free β -hCG and PAPP-A were converted to multiples of the expected normal median (MoM) corrected for fetal crown-rump length, maternal weight, smoking status, racial origin, parity and method of conception [21]. The birth weights were expressed as centiles corrected for GA derived from the same dataset as in the current study [22]. The

neonate was considered to be macrosomic if the birth weight was more than the 90th centile for GA. The Mann-Whitney U test was used to compare the δ -NT, MoM β -hCG and MoM PAPP-A between the macrosomic and the unaffected groups. Multivariate logistic regression analysis was used to determine the factors amongst the maternal characteristics with significant contributions in predicting macrosomia and the extent to which such prediction is improved by the addition of fetal NT, free β -hCG and PAPP-A. The performance of screening was estimated by receiver operating characteristic (ROC) curves. The performance of different methods of screening was compared by the areas under the ROC curves (AUROC) [23].

The statistical software package SPSS 15.0 (SPSS Inc., Chicago, Ill., USA) and MedCalc (MedCalc Software, Mariakerke, Belgium) were used for the data analyses.

Results

During the study period (March 2006 to September 2009) first-trimester combined screening for chromosomal defects was carried out in 36,743 singleton pregnancies. We excluded 3,141 cases because they had missing outcome data ($n = 2,005$), the pregnancies resulted in miscarriage before 24 weeks of gestation, they were terminated for fetal abnormalities or maternal psychosocial indications or they resulted in the birth of babies with major defects ($n = 1,136$). Statistical analysis was performed in the remaining 33,602 pregnancies.

Maternal Characteristics

In 3,353 (10%) of the neonates the birth weight was above the 90th centile corrected for GA. The maternal characteristics of the study population are shown in table 1.

Multiple regression analysis demonstrated that in the prediction of macrosomia there were significant contributions from maternal racial origin, weight, height, previous delivery of macrosomic neonates, smoking and history of chronic hypertension and diabetes mellitus (table 2).

The AUROC of macrosomia in screening by maternal factors was 0.715 and the detection rates at false-positive rates of 5 and 10% were 22.4 and 33.1%, respectively (fig. 1; table 3).

Fetal NT, Maternal Serum Free β -hCG and PAPP-A

There was a significant linear association between Δ -NT and birth weight centile (Δ -NT = 0.106424 + 0.001076 \times birth weight centile; $r = 0.071$, $p < 0.0001$). There was a significant linear association between \log_{10} MoM β -hCG and birth weight centile (\log_{10} MoM β -hCG = $-0.026587 + 0.000487 \times$ birth weight centile; $r =$

Table 1. Maternal characteristics in the unaffected group and in those delivering macrosomic neonates

Variables	Unaffected (n = 30,249)	Macrosomia (n = 3,353)
Maternal age, years, median (IQR)	32.2 (27.8–35.9)	33.2 (29.2–36.7) ^c
Weight, kg, median (IQR)	65.0 (59.0–74.0)	73.0 (64.0–84.0) ^c
Height, cm, median (IQR)	164.0 (160.0–168.0)	167.0 (162.6–170.2) ^c
Racial origin, n (%)		
White	21,498 (71.1)	2,651 (79.1) ^c
Black	5,837 (19.3)	507 (15.1) ^c
South Asian	1,394 (4.6)	78 (2.3) ^c
East Asian	620 (2.0)	43 (1.3) ^b
Mixed	900 (3.0)	74 (2.2) ^a
Parity, n (%)		
Nulliparous	14,989 (49.5)	1,171 (34.9) ^c
Parous, no previous macrosomic baby	14,002 (46.3)	1,572 (46.9)
Parous, previous macrosomic baby	1,258 (4.2)	610 (18.2) ^c
Cigarette smoker, n (%)	2,578 (8.5)	160 (4.8) ^c
Conception, n (%)		
Spontaneous	29,117 (96.3)	3,214 (95.9)
Assisted conception	1,132 (3.7)	139 (4.1)
Chronic hypertension, n (%)	349 (1.2)	35 (1.0)
Pre-pregnancy diabetes, n (%)	170 (0.6)	88 (2.6) ^c

Comparisons between the macrosomic and the unaffected groups were by χ^2 or Fisher's exact test for categorical variables and by Mann-Whitney U test for continuous variables: ^a $p < 0.05$, ^b $p < 0.001$, ^c $p < 0.0001$.

0.052, $p < 0.0001$). There was a significant quadratic association between $\log_{10}\text{MoM PAPP-A}$ and birth weight centile ($\log_{10}\text{MoM PAPP-A} = -0.083243 + 0.002241 \times \text{birth weight centile} - 1.075818 \times \text{birth weight centile}^2$; $r = 0.140$, $p < 0.0001$).

Fetal $\Delta\text{-NT}$, maternal serum MoM $\beta\text{-hCG}$ and MoM PAPP-A were significantly higher in the macrosomic than in the unaffected group ($p < 0.0001$) (fig. 2; table 4). Pearson's correlation between $\Delta\text{-NT}$, $\log_{10}\text{MoM } \beta\text{-hCG}$ and $\log_{10}\text{MoM PAPP-A}$ in the unaffected and macrosomic groups are shown in table 5.

Multiple regression analysis demonstrated that in the prediction of macrosomia there were significant contributions from $\Delta\text{-NT}$, $\log_{10}\text{MoM } \beta\text{-hCG}$ and $\log_{10}\text{MoM PAPP-A}$ in addition to maternal factors (table 2).

The relations between the risk for macrosomia with serum PAPP-A and the effects of maternal factors for women of Caucasian and African racial origin are illustrated in figure 3.

In screening for macrosomia the addition of fetal NT, $\beta\text{-hCG}$ and PAPP-A to maternal factors improved the prediction provided by maternal factors alone (AUROC 0.727 vs. 0.715, $p < 0.001$; fig. 1; table 3).

Discussion

This study has demonstrated that the birth of macrosomic neonates is related to certain maternal characteristics and the results of first-trimester markers used in screening for fetal aneuploidies. The combined model could detect about 34% of women who delivered macrosomic neonates at a false-positive rate of 10%.

The findings that the risk for macrosomia increases with maternal weight and height and is higher in parous women with previous delivery of a macrosomic infant and in those with a medical history of diabetes mellitus and that the risk is lower in women of African and South Asian racial origins, in cigarette smokers and in those with a medical history of chronic hypertension are compatible with previous reports [1, 5, 24–38]. Parous women are 2–3 times more likely than nulliparous women to have macrosomic neonates [24, 25]. Furthermore, population-based studies have reported that parous women with previous delivery of a macrosomic neonate are 7–15 times more likely to deliver another macrosomic neonate in a subsequent pregnancy [26–28]. Racial differences in the rate of macrosomia have been observed, with the re-

Table 2. Logistic regression analysis for the prediction of macrosomia by maternal factors, fetal NT, free β -hCG and PAPP-A

Independent variable	Maternal factors only			Maternal factors, NT, β -hCG, PAPP-A		
	adjusted OR	95% CI	p	adjusted OR	95% CI	p
Weight	1.092	1.074–1.110	<0.0001	1.091	1.073–1.110	<0.0001
(Weight) ²	1.000	1.000–1.000	<0.0001	1.000	1.000–1.000	<0.0001
Height	1.030	1.025–1.036	<0.0001	1.030	1.024–1.036	<0.0001
Parity						
Nulliparous	1			1		
Parous, no previous macrosomic baby	1.439	1.327–1.560	<0.0001	1.435	1.323–1.557	<0.0001
Parous, previous macrosomic baby	4.937	4.382–5.562	<0.0001	4.901	4.346–5.526	<0.0001
Smoking	0.482	0.407–0.572	<0.0001	0.477	0.402–0.566	<0.0001
Racial origin						
Caucasian	1			1		
African	0.516	0.464–0.574	<0.0001	0.510	0.458–0.568	<0.0001
South Asian	0.695	0.547–0.884	0.003	0.707	0.555–0.899	0.005
Mixed	0.687	0.535–0.882	0.003	0.656	0.510–0.844	0.001
Chronic hypertension	0.555	0.384–0.801	0.002	0.568	0.392–0.821	0.003
Pre-pregnancy diabetes	3.194	2.405–4.242	<0.0001	3.534	2.655–4.703	<0.0001
Δ -NT	–	–	–	1.509	1.338–1.703	<0.0001
(Δ -NT) ²	–	–	–	0.924	0.878–0.971	0.002
\log_{10} MoM PAPP-A	–	–	–	2.798	2.319–3.376	<0.0001
(\log_{10} MoM PAPP-A) ²	–	–	–	0.464	0.283–0.761	0.002
(\log_{10} MoM PAPP-A) ³	–	–	–	0.398	0.258–0.612	<0.0001
\log_{10} MoM β -hCG	–	–	–	1.205	1.040–1.396	0.013
	$R^2 = 0.121$			$R^2 = 0.132$		

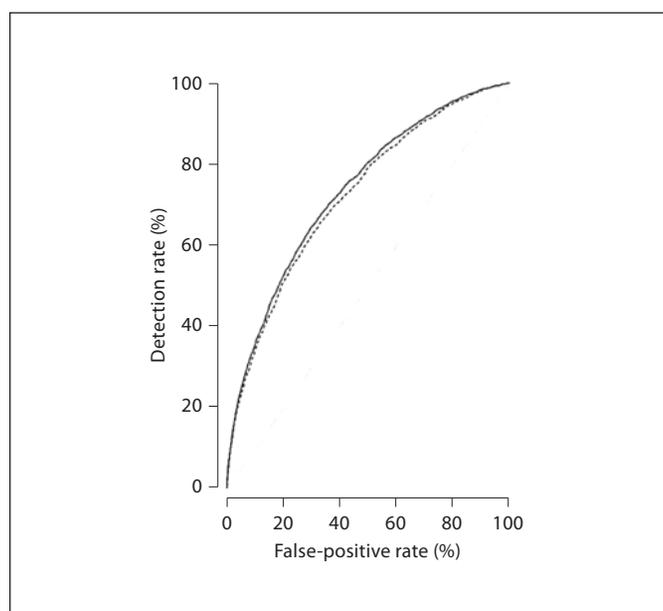


Fig. 1. ROC curves of maternal factors only (-----) and a combination of maternal factors, fetal NT, maternal serum β -hCG and PAPP-A (—) in the prediction of macrosomia.

Table 3. Performance of screening for macrosomia by maternal factors only, maternal factors with fetal NT thickness, free β -hCG and PAPP-A

Screening test	AUROC (95% CI)	
Maternal factors	0.715 (0.710–0.719)	
Maternal factors plus		
Fetal NT	0.718 (0.713–0.723)	
Serum β -hCG	0.716 (0.712–0.721)	
Serum PAPP-A	0.723 (0.718–0.728)	
NT, β -hCG, PAPP-A	0.727 (0.722–0.732)	
	Detection rate with 95% CI for fixed false-positive rate	
	5%	10%
Maternal factors	22.4 (21.0–23.8)	33.1 (31.5–35.7)
Maternal factors plus		
Fetal NT	22.6 (21.2–24.1)	33.6 (32.0–35.2)
Serum β -hCG	22.6 (21.2–24.1)	33.5 (31.9–35.1)
Serum PAPP-A	23.4 (22.0–24.9)	34.2 (32.6–35.9)
NT, β -hCG, PAPP-A	23.5 (22.1–25.0)	34.4 (32.8–36.0)

Fig. 2. Box-whisker plots of maternal serum PAPP-A, β -hCG and fetal NT in the macrosomic and unaffected groups.

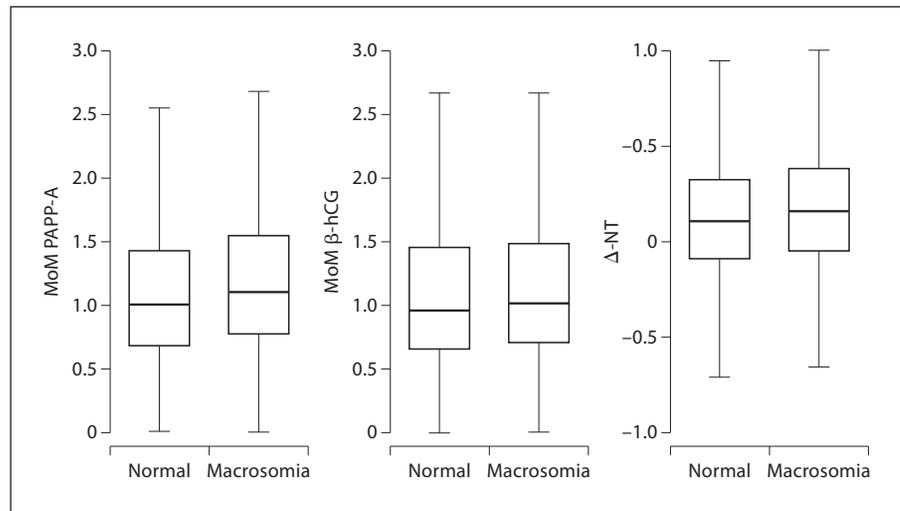


Table 4. Measurement of fetal NT thickness, free β -hCG and PAPP-A in the unaffected group and in those delivering macrosomic neonates

Variables	Unaffected (n = 30,249)	Macrosomia (n = 3,353)	p
Δ -NT, median (IQR)	0.116 (-0.084 to 0.331)	0.167 (-0.036 to 0.387)	<0.0001
MoM β -hCG, median (IQR)	0.964 (0.654 to 1.463)	1.010 (0.710 to 1.493)	<0.0001
MoM PAPP-A, median (IQR)	1.004 (0.685 to 1.430)	1.103 (0.769 to 1.539)	<0.0001

Comparisons between the macrosomic and the unaffected groups were by Mann-Whitney U test.

ported risk being lower in African than in Caucasian women [24, 29, 30]. However, the results on South Asian women are contradictory, with the risk of macrosomia being reduced or increased [29, 30].

The association between maternal obesity and macrosomia is well documented [24, 29, 31, 32]. A similar trend is found for maternal height, which has also been shown to be an independent determinant of high birth weight [33, 34]. The mechanisms by which maternal overweight induces fetal macrosomia remain to be determined, but its effect on fetal weight appears independent of that of diabetes or glucose intolerance [39]. Thus, there appears to be additional metabolic factors related to maternal overweight that influence fetal growth [40–42]. Insulin resistance increases with maternal weight and this may cause metabolic disturbances that result in an increased flux of nutrients across the placenta, causing fetal hyperinsulinemia and accelerated fetal growth [43–46]. Diabetes in pregnancy is associated with a significant risk of

fetal macrosomia, even when good metabolic control is achieved [35]. The mother develops an insulin-resistant state induced by hormones produced by the placenta [47], which in turn results in hyperinsulinemia leading to asymmetrical macrosomia with a high proportion of fat relative to length [48]. The restricting effects of chronic hypertension and smoking in pregnancy are well known and they both reduce the risk of neonatal macrosomia [29, 36–38].

Maternal serum free β -hCG and PAPP-A increase with birth weight centile. The association between low PAPP-A and birth of SGA neonates has been well documented in several studies [11–18]. These and two previous studies have demonstrated that at the other end of the spectrum high serum PAPP-A is associated with macrosomia [12, 18]. A possible mechanism for this association is related to the proteolytic properties of PAPP-A which cleaves insulin-like growth factor (IGF)-binding proteins, thereby increasing the bioavailability of IGF which

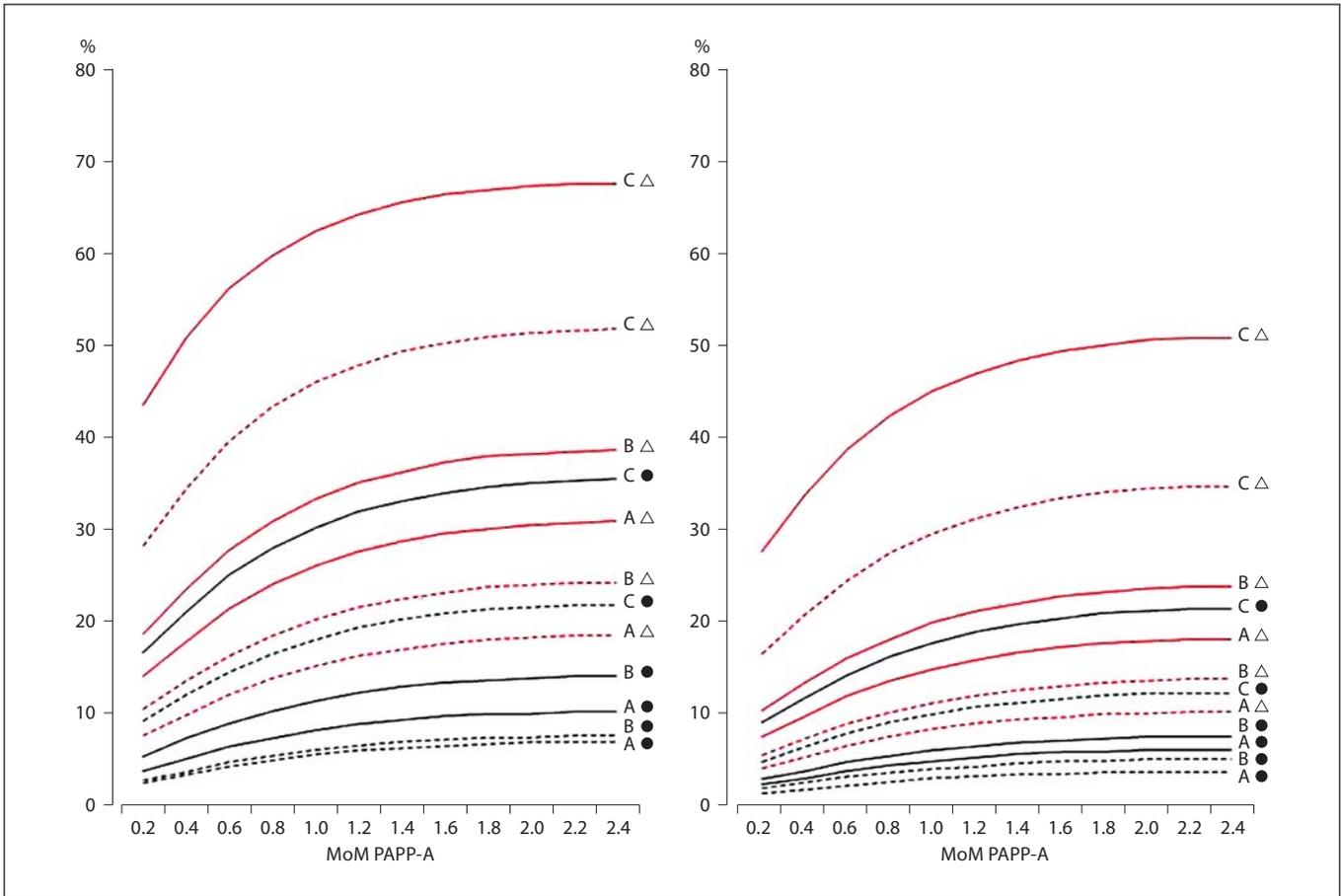


Fig. 3. Risks of macrosomia (>90th centile corrected for GA at delivery) for women of Caucasian (left) and African (right) racial origin. Δ = History of diabetes mellitus, \bullet = non-diabetic. A = Nulliparous, B = parous with no previous macrosomic neonate, C = parous with previous macrosomic neonate; interrupted lines = body mass index (BMI) ≤ 25 , solid lines = BMI >25 .

Table 5. Pearson's correlation between Δ -NT, \log_{10} MoM β -hCG and \log_{10} MoM PAPP-A in the unaffected group and in those delivering macrosomic neonates

	Δ -NT		\log_{10} MoM β -hCG		\log_{10} MoM PAPP-A	
	unaffected	macrosomia	unaffected	macrosomia	unaffected	macrosomia
Δ -NT						
Pearson's correlation	1	1	-0.030	-0.003	0.009	0.025
p	-	-	<0.0001	0.871	0.111	0.143
\log_{10} MoM β -hCG						
Pearson's correlation	-0.030	-0.003	1	1	0.213	0.192
p	<0.0001	0.871	-	-	<0.0001	<0.0001
\log_{10} MoM PAPP-A						
Pearson's correlation	0.009	0.025	0.213	0.192	1	1
p	0.111	0.143	<0.0001	<0.0001	-	-

is thought to play a key role in the control of placental growth and transfer of nutrients to the fetus [49–51]. Studies examining free β -hCG have reported that there is no significant association between low first-trimester serum levels and subsequent birth of SGA neonates [17, 22]. Our study has shown that although the relation between birth weight centile and serum free β -hCG is weaker than that with PAPP-A, the relation is statistically significant and the first-trimester serum levels are increased in pregnancies delivering macrosomic neonates.

This study has also demonstrated that birth weight increases with increasing fetal NT and that a large fetal NT is associated with an increased risk of delivering macrosomic neonates. Kelekci et al. [19] reported that the incidence of developing gestational diabetes and delivering macrosomic neonates in 389 pregnancies with increased fetal NT was significantly higher than in 386 pregnancies with normal fetal NT, and it was concluded that increased fetal NT was predictive of gestational diabetes. It was also suggested that maternal hyperglycemia causes enhanced capillary permeability which results in an increase in fetal NT. However, Leipold et al. [52] reported that the fetal NT was not significantly different in 135 women who developed gestational diabetes compared to 329 women with normal glucose tolerance. Similarly, Spencer et al. [53] examined 79 pregnancies with pre-pregnancy insulin-dependent diabetes mellitus and reported that the fetal NT was not significantly different from non-diabetic pregnancies. Bartha et al. [54] examined 65 women with pre-pregnancy insulin-dependent diabetes mellitus and reported that fetal NT thickness

was not related to years of diabetes, dose of insulin, glycosylated hemoglobin concentration or capillary glucose profiles.

The 11- to 13-week approach to combining factors from the maternal history with sonographic and serum biochemical measurements for effective early screening for aneuploidies and other fetal abnormalities is now well accepted [55, 56]. There is increasing evidence that the same approach of combining maternal characteristics with the results of biophysical and biochemical tests can be used for early identification of pregnancies at high risk for subsequent development of preeclampsia, fetal death and fetal growth restriction [22, 57, 58]. This study expands on this concept in the prediction of macrosomia. Although the performance of early screening for macrosomia is poor compared to that of screening for aneuploidies and preeclampsia, our findings can form the basis of future research to improve screening by the addition of potentially new markers. Similarly, the extent to which knowledge of the individual patient-specific risk for macrosomia by first-trimester combined screening can improve antenatal surveillance and prevention of macrosomia itself or the intrapartum complications related to macrosomia remains to be determined by future studies.

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