178 Blood pressure patterns in pregnant women with treated chronic hypertension according to the development of severe preeclampsia

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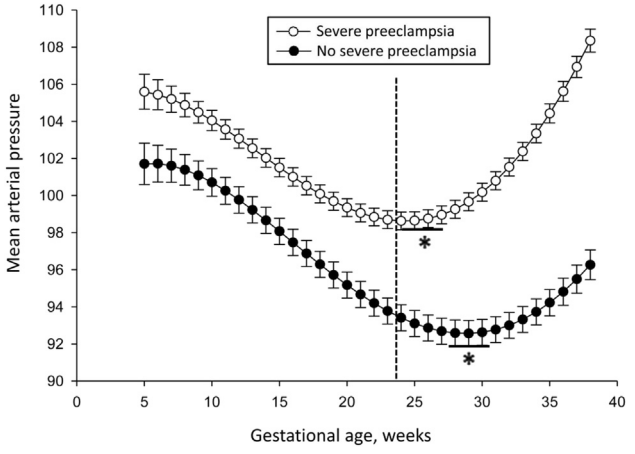
OBJECTIVE: To examine blood pressure patterns across pregnancy in women with treated chronic hypertension according to the development of severe preeclampsia (SPE).

STUDY DESIGN: This retrospective cohort study included women who required antihypertensive therapy during the first half of pregnancy. Management of these women includes titration of prenatal antihypertensive therapies in a coordinated fashion within a dedicated high-risk pregnancy clinic. Using a random effects model, predicted means of the mean arterial pressures (MAPs) were calculated from 5 to 40 weeks gestation for women with and without SPE with gestational age entered as a fourth order polynomial.

RESULTS: Between January 2002 and December 2014, a total of 433 women met the inclusion criteria. Of these women, 67% (291/433) developed severe preeclampsia. The mean MAP was significantly higher at entry into prenatal care in women who were ultimately diagnosed with SPE in comparison those who were not (105.6 vs 101.7, p=0.002). The rate of change in MAP was similar in both the preeclamptic and non-preeclamptic cohorts until 24 weeks at which point the rates diverged significantly (p= 0.029) and continued to differ significantly until delivery. As shown in the Figure, women who developed SPE reached a blood pressure nadir at a significantly earlier gestational age than those who did not develop severe disease (25.9±7.1 vs 29.0±7.6, p <0.001).

CONCLUSION: Blood pressure patterns differ significantly in pregnant women with treated chronic hypertension who do and do not develop severe preeclampsia. The blood pressure nadir occurs approximately 3 weeks earlier in those who are destined to develop severe preeclampsia.



179 Women with chronic hypertension treated during pregnancy - perinatal outcomes related to graduated 24-hour urinary protein excretion levels measured prior to 20 weeks

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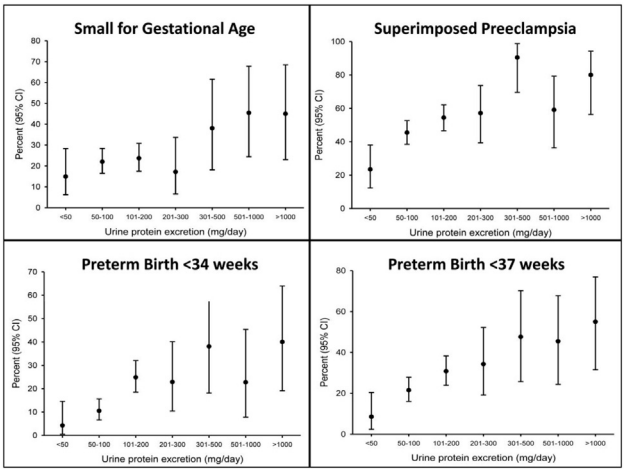
OBJECTIVE: To analyze the relationship between perinatal outcomes and stratified 24-hour urine protein excretion determined prior to 20 weeks in women with chronic hypertension (CHTN) treated during pregnancy.

STUDY DESIGN: This retrospective cohort study included pregnant women with CHTN for whom therapy was initiated and who completed urine protein quantification prior to 20 weeks. Management of these women is coordinated within a dedicated high-risk prenatal clinic. 24-hour urine protein excretion levels determined prior to 20 weeks were stratified as follows: <50 mg, 50-100 mg, 101-200 mg, 201-300 mg, 301-500 mg, 501-1000 mg, and >1000 mg. The frequencies of superimposed preeclampsia (SPE), preterm birth (PTB) and small-for-gestational age (SGA) infants <10th percentile were compared for each group according to these graded proteinuria levels.

RESULTS: Between January 2002 and December 2014, a total of 514 women met inclusion criteria and selected outcomes are shown in the Figure. The rates of SPE, PTB <34 weeks, PTB <37 weeks, and SGA were all significantly increased as 24-hour protein excretion levels increased (p-value for trend <0.001). The frequency of SGA infants was unrelated to co-existent rates of SPE when compared across strata of proteinuria levels (p=0.30). When outcomes of women with protein excretion levels <300mg/day were analyzed separately, there remained a significant association between increasing proteinuria strata and rates of SPE and PTB (Figure).

CONCLUSION: As the quantity of baseline proteinuria increased in pregnant women with treated CHTN, the frequencies of SPE, PTB, and SGA all significantly increased. This relationship remained significant for SPE and PTB at proteinuria levels heretofore considered to be within normal range (<300 mg/24 hours).



180 Do genetic and environmental influences on abnormal metabolic profile in pregnancy continue to second generation offspring?

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OBJECTIVE: Fetal programming contributes to metabolic and cardiovascular disease in offspring even during their adult life. Whether fetal programming increases the risks for disease in subsequent generations remain unknown. Our aim was to evaluate the effect of genetic and environmental inheritance on the metabolic profile in a transgenerational mouse model.

STUDY DESIGN: In order to study the effects of fetal programming on 2nd generation offspring we conducted three breeding schemes, all with wild type (WT) males. WT males were bred to heterozygous $eNOS^{+/-}$ females fed a high fat diet (HFD) manifesting metabolic-like syndrome (MLS) phenotype (Group 1), heterozygous $eNOS^{+/-}$ females fed a control diet (CD) manifesting hypertension (HTN) (Group 2), or WT female fed CD use as control (Group 3). WT male