decreasing incidence of grade 2 and grade 3 EC (AAPC, −2.61 and −2.63, respectively; P<0.01). Alternatively, the incidence of type II EC increased by 3.12% annually (P<0.01), leading to an increase of 63% since 2001. Serous carcinoma increased by 4.88% annually (P<0.01). Clear cell and carcinosarcoma also increased significantly (AAPC, 1.02 and 1.51, respectively; P<0.05). For illustrative purposes, we calculated the percentage increase in the incidence of cancer types over the last 17 years in comparison with the year 2001 (Figure). Overall, the proportion of women with obesity also increased significantly from 19.5% to 27.5% during this period (AAPC, 1.5; P<0.01).

CONCLUSION: Utilizing 17 years of data from a national cancer registry, we demonstrated that the incidence of high-risk type II EC has increased, whereas the incidence of low-risk grade I EC has remained stable. In another survey study, we showed the rising incidence of obesity. These findings suggest that the traditional type I/II approach to classifying EC may be oversimplified, particularly as it relates to obesity. Recent studies utilizing The Cancer Genome Atlas classification for EC demonstrated an association between a mean body mass index (BMI) of ≥30 and each of the 4 clusters except for DNA polymerase epsilon gene ultramutated tumors. Furthermore, up-regulation of several genes known to play a role in EC pathogenesis were associated with BMI, suggesting that obesity may create a unique, proinflammatory microenvironment that affects tumor biology at a molecular level. Limitations of the current study include possible information reporting bias, lack of central pathology review, and limited ability to correlate data between multiple databases. Incidence rates are also not corrected for information reporting bias, lack of central pathology review, and limited ability to correlate data between multiple databases. Incidence rates are also not corrected for hysterectomy prevalence. However, these trends suggest a potential impact of obesity on the rising rates of type II EC that should be explored further.

Courtney M. Eakin, MD
Department of Obstetrics and Gynecology
University of California, Los Angeles
Los Angeles, CA
Cheng-I Liao, MD
Department of Obstetrics and Gynecology

Cell-free DNA analysis for noninvasive examination of trisomy: comparing 2 targeted methods

INTRODUCTION: Cell-free DNA (cfDNA) tests for major fetal trisomies are highly effective among high- and low-risk women, with a detection rate of 99.7% for trisomy 21 and a false positive rate of 0.04%. In many countries, cost and complexity are the main obstacles to the implementation of cfDNA tests as first-line aneuploidy screening tests. The Vanadis assay was recently introduced as a cost-effective method with reduced complexity. It provided a high detection rate combined with a low failure rate because samples can be analyzed readily with a fetal fraction (FF) limit of <2%. This is achieved by using novel molecular probe technology that specifically label target chromosomes combined with a new readout format using a nanofilter to enrich single molecules for imaging
and counting without DNA amplification, microarrays, or sequencing. However, there are very limited data on the Vanadis test and no studies comparing it with a well-established, targeted cfDNA method in screening for major trisomies.

**STUDY DESIGN:** We therefore conducted a prospective, single-center study in which 936 women underwent both a Vanadis test (Laboratoire Hospitalier Universitaire de Bruxelles, University Hospital Brugmann, Bruxelles, Belgium) and a Harmony Prenatal Test (Labocita, CHR Citadelle, Liège, Belgium). Participants received the results of the Harmony test but were blinded to the results of the Vanadis test. Aneuploidy status was confirmed for all women included in the final analysis by outcome at birth or following invasive diagnostic procedures. For both methods, we evaluated the performance in screening for trisomy 21, 18, and 13 and by total failure rate. Written informed consent was obtained for this ethics committee-approved study (CE2015/27).

**RESULTS:** From September 2018 through March 2019, 936 women were enrolled and the results for 900 women were evaluated. A flowchart of the study data is included.

---


540 American Journal of Obstetrics & Gynecology SEPTEMBER 2022
Factors associated with SARS-CoV-2 transplacental transmission

OBJECTIVE: Transplacental transmission of SARS-CoV-2 is a rare event, although severe cases have been described.1 We know that the transmission may occur through Hofbauer cells in a minority of cases.2 Therefore, other factors, such as placental expression of viral receptors, viral load, degree of inflammation, or some clinical features, might be involved in the transmission. We investigated these factors, and we hypothesized that these factors might play a relevant role.

STUDY DESIGN: We observed a series of 6 cases of SARS-CoV-2 transplacental transmissions; as we suspected that the first ascertained case of transplacental transmission3 was linked to fetal distress, all these cases received fetal monitoring. These 6 cases presented placental positive real-time polymerase chain reaction (RT-PCR). Moreover, we recruited 4 other women affected by COVID-19 during the third trimester of pregnancy with positive placental RT-PCR but without transplacental transmission: these 6 and 4 cases constitute the group of 10 pregnancies complicated by COVID-19 and placental infection (C+P+; ie, the 6 transplacental transmissions were in this group). In the same period, we also recruited 10 women with COVID-19 during the third trimester of pregnancy and negative placental RT-PCR (C+P−; ie, pregnancies complicated by COVID-19 but without placental infection) and 11 healthy pregnant women without any SARS-CoV-2 infection (controls). Clinical management of all studied patients is described in the Supplemental Methods.

We performed a translational cohort study analyzing biological data (enzyme-linked immunosorbent assay [ELISA] for viral receptors, RT-PCR with viral load