decreasing incidence of grade 2 and grade 3 EC (AAPC, −2.61 and −2.63, respectively; P<0.001). Alternatively, the incidence of type II EC increased by 3.12% annually (P<0.001), leading to an increase of 63% since 2001. Serous carcinoma increased by 4.88% annually (P<0.001). 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<0.001).

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.2 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 hysterectomy prevalence. However, these trends suggest a potential impact of obesity on the rising rates of type II EC that should be explored further.

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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%.1−3 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%.4 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.

REFERENCES

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and counting without DNA amplification, microarrays, or sequencing.1

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 Citadel, 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
available for analysis. The median maternal age was 31 years (range, 18–51), maternal weight was 69 kg (range, 44–140), and gestational age at testing was 13.3 weeks (range, 10.0–38.1). A total of 21 (2.3%) women were carrying a twin pregnancy and 11 (1.2%) pregnancies were derived following in vitro fertilization. The Harmony test detected 34 of 35 cases of trisomy 21 and failed (for quality issues) in 1 case, whereas the Vanadis test failed all 15 cases. Harmony detected 11 of 15 cases of trisomy 18, classified 1 case as low-risk (FF=19.5%), and failed to detect trisomy 18 in 3 cases (all for quality issues), whereas the Vanadis test detected 14 of the 15 cases and classified 1 case as low-risk (FF=5.6%). Both tests detected all 3 cases of trisomy 13.

Overall, and after first attempt, Harmony failed in 29 (3.2%) cases, whereas the Vanadis test failed in 2 cases (0.2%; $P<0.05$) (Figure). Among the 29 failures with Harmony, 10 (34.5%) were secondary to a low FF. The 2 failures of the Vanadis test were caused by a high density of spot counts (exceeding 40,000) per image.

CONCLUSION: Our preliminary data demonstrated that the Vanadis assay provides high performance in screening for major trisomies in addition to a low failure rate. The performance of the test when the FF is below 4% needs further investigation.5

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REFERENCES

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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...