Methodology This is a retrospective cohort study of patients undergoing RVT and RRT from 2003 to 2021. Clinical and pathological data was extracted from DGCD and validated through electronic medical journals. All analyses were performed with SPSS.

Results A total of 206 patients were included, of which 78 underwent RRT and 128 underwent RVT. There were no significant differences in age, smoking status, ASA score, FIGO 2009 stage, histology, invasion or tumor size. Median BMI in the VRT and RRT group was 23.0 (range 17.7–48.7) and 24.3 (range 18.0–48.4), respectively (p=0.032). The rate of microscopic free-margins in the VRT and RRT group was 99.2% and 97.4%, respectively (p=0.558). The rate of lymph node metastases was 2.3% and 1.3%, respectively (p=1.000). Hazard ratio for recurrence in the RRT group was 0.59 (CI95% 0.12–2.86, p=0.509), 0.77 (0.14–4.15, p=0.763) when adjusting for BMI, FIGO 2009 and LVSI, and 0.84 (0.16–4.50, p=834) when additionally excluding patients with lymph node metastasis at surgery (n=4). The rate of cancer-specific mortality in the VRT and the RRT was 2.3% (n=3) and 2.5% (n=2), respectively.

Abstract 2022-RA-878-ESGO Figure 1

Conclusion RRT seems oncologically safe for radical trachelectomy compared with RVT.

THE VAGINAL MICROBIOTA COMPOSITION IS ASSOCIATED WITH SEVERITY OF CERVICAL DYSPLASIA

Introduction/Background Certain compositions of vaginal microbiota, and specific bacterial species, seem to be associated with HPV infection and the subsequent development of cervical dysplasia and cancer. In order to better understand the association between vaginal microbiota, HPV-infection and dysplasia, we performed shotgun metagenomic sequencing to taxonomically and functionally characterize the composition of the vaginal microbiota of women with and without cervical dysplasia. The HPV status for all study persons was also analysed.

Methodology Women with histologically verified cervical dysplasia (n = 161; low grade dysplasia (LSIL) n=73, high-grade dysplasia (HSIL) n= 88) were recruited at Uppsala University hospital, Sweden. Women with two normal consecutive cervical screening tests were included as controls (n = 175) Samples were sequenced using shotgun metagenomics, ALDEx2 was used for differential abundance analysis of metagenomic data, Kraken and Optivag databases for taxonomic data, and metabphlan3 and Humann3 for functional data. All samples were analysed for HPV using Luminex.

Results A total of 336 women were recruited between 2017–2020. The vaginal microbiota diversity increased with increasing severity of the dysplasia (alpha-diversity measures, Shannon diversity median values: normal =0.771, LSIL= 1.027, HSIL=1.150, and inverse Simpson diversity: normal=1.486, LSIL=1.837, HSIL =2.216). There was a significant difference in diversity when comparing normal to HSIL group (Shannon p < .0001, Inverse Simpson: p < .0001), Figure 1. The relative abundance of Lactobacilli species decreased with increased severity of dysplasia, especially L crispatus, L iners and G vaginalis were more common among LSIL and the vaginal microbiota of the high grade dysplasia were characterized by mainly non-lactobacilli species, for example Fecalibacterium prausnitzii, Eubacterium rectale, Bacteroides uniformis, Blautia obeum and Ruminococcus bromii.

Conclusion The vaginal microbiota diversity increased with increasing severity of dysplasia. Further, LSIL and HSIL were characterized by different vaginal microbiota compositions.