EXTENDED GENOTYPING OF HIGH RISK HPV AS A METHOD IN RISK ASSESSMENT OF CERVICAL CANCER

OBJECTIVE

Cervical cancer has a high incidence in South Africa. There is growing interest in methods of triaging HPV-positive women in terms of risk. Extended genotyping is one of the methods of assessment of an increased risk of developing cervical carcinoma. This study aims to assess in a private practice scenario the validity of utilising extended genotyping as a method of choice.

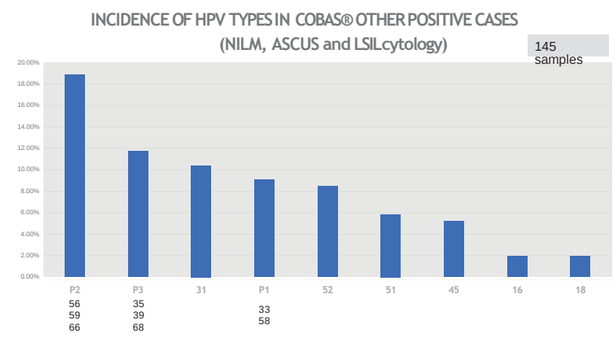
BACKGROUND

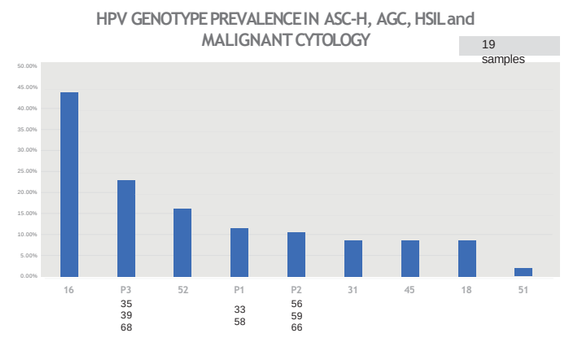
- HPV infection is a well-established cause of cervical cancer.
- HPV types 16 and 18 are responsible for approximately 70% of cervical cancers worldwide. [1]
- It is well known that HPV16 presents the highest risk of significant disease, but the relative risk of the other high risk genotypes that are routinely tested may vary with population and prevalence. [2]
- It has been proven that HPV testing is more sensitive than cytology for cervical screening. [3]
- Previous studies on extended genotyping have used CIN2+ and CIN3+ as the endpoint. There is limited data with carcinoma as an endpoint.
- Northern hemisphere research has shown HPV16 and HPV31 to carry the highest risk for CIN2+ disease in patients with normal Cytology. Intermediate risk includes 18/33/52/58. The lowest risk being associated with types 45/51/35/39/68/56/59/66.
- In a local prevalence study Denny et al showed HPV35 to be the most common hrHPVgenotype in Cape Town, South Africa. This was closely followed by 16 and 58. Within this cohort, 16 and/or 18 were associated with CIN2+ disease.[5]
- Van Aardt, Dreyer et al have shown various prevalence figures for extended genotyping in South African woman, with differences regarding HIV status. In

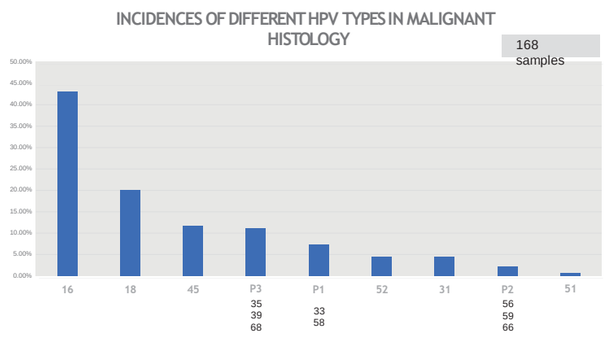
METHODS

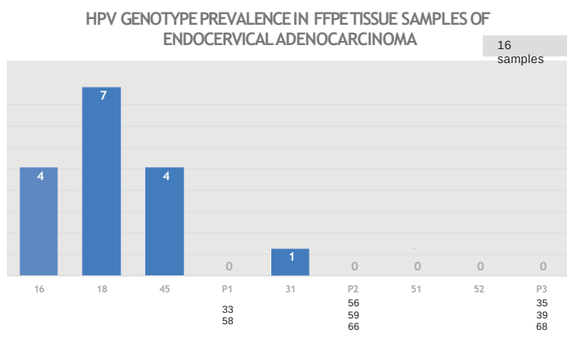
We undertook an investigation of HPV genotype prevalence within specific subsets of cervical cancer screening patients within South Africa. There were three patient cohort arms included in this study: (i) high-risk HPV positive (non-16/18) patients; (ii) high-grade cytology cases; and (iii) invasive cervical cancer.
All specimens were collected in BD SurePathvials and HPV genotyping analysis was conducted using the BD OnclarityHPV Assay. All biopsy specimens were analysed from formalin-fixed, paraffin embedded tissue (FFPE).

RESULTS









CONCLUSIONS

Emerging clinical evidence in the peer-reviewed literature has identified HPV extended genotyping as a potential triage method for high-risk HPV positive patients and atypical cytology cases. We have undertaken a systematic investigation of extended HPV genotyping as a triage tool applicable to the South African cervical cancer screening.
Incorporated in this study, is a unique data set using invasive carcinoma as the end point. In our series, the prevalence of subtypes in carcinoma differs from those in CIN2+ disease. In light of this, we propose a new management algorithm of co-testing. **(Fig 1)**

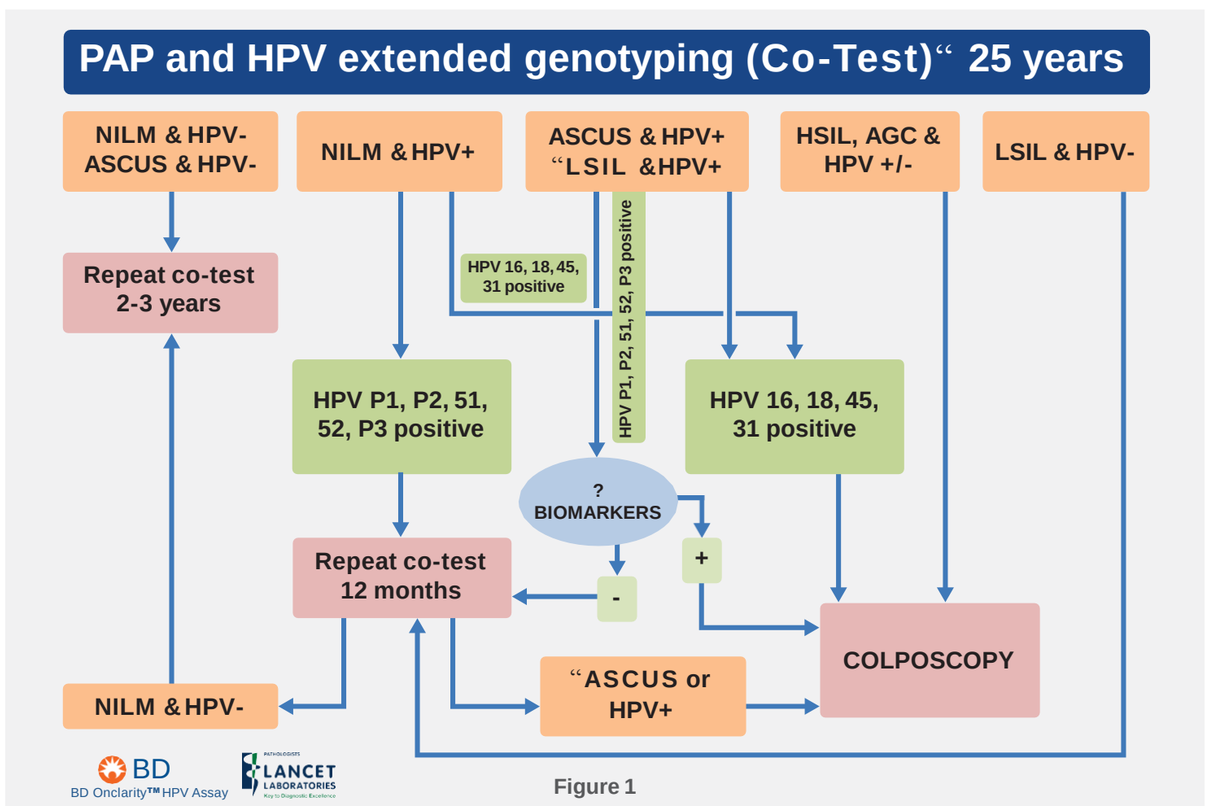


Figure 1

FURTHER RESEARCH DIRECTIVES

- The role of HIV/AIDS as a driver of progression to invasive carcinoma
- Biopsy follow-up of CIN2+ cytology and HPV 31
- The role of biomarkers in management

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