Tipo	Periódico
Título	Molecular Signatures of High-Grade Cervical Lesions
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Programa/Curso (s)	Programa de Pós-Graduação Stricto Sensu em Ciências da Saúde
DOI	10.3389/fonc.2018.00099
Assunto (palavras chaves)	human papilloma virus screening, metabolomics, mass spectrometry, cervical cancer, cervical cytologic specimens, translational research, pre-neoplastic phenotype, molecular signatures
Idioma	Inglês
Fonte	Título do periódico: Frontiers In Oncology ISSN: 2234-943X Volume/Número/Paginação/Ano: v. 8, p. eCollection2018, 2018
Data da publicação	12 April 2018
Formato da produção	Digital https://doi.org/10.3389/fonc.2018.00099
Resumo	Cervical cancer is the fourth most common neoplasia in women and the infection with human papilloma virus (HPV) is its necessary cause. Screening methods, currently based on cytology and HPV DNA tests, display low specificity/sensitivity, reducing the efficacy of cervical cancer screening programs. Herein, molecular signatures of cervical cytologic specimens revealed by liquid chromatography-mass spectrometry (LC-MS), were tested in their ability to provide a metabolomic screening for cervical cancer. These molecules were tested whether they could clinically differentiate insignificant HPV infections from precancerous lesions. For that, high-grade squamous intraepithelial lesions (HSIL)-related metabolites were compared to those of no cervical lesions in women with and without HPV infection. Samples were collected from women diagnosed with normal cervix (*N* = 40) and from those detected with HSIL from cytology and colposcopy (*N* = 40). Liquid-based cytology diagnosis, DNA HPV-detection test, and LC-MS analysis were carried out for all the samples. The same sample, in a customized collection medium, could be used for all the diagnostic techniques employed here. The metabolomic profile of cervical cancer provided by LC-MS was found to indicate unique molecular signatures for HSIL, being two ceramides and a sphingosine metabolite. These molecules occurred independently of women's HPV status and could be related to the pre-neoplastic phenotype. Statistical models based on such findings could correctly discriminate and classify HSIL and no cervical lesion women. The results showcase the potential of LC-MS

	as an emerging technology for clinical use in cervical cancer screening, although further validation with a larger sample set is still necessary.
Fomento	