P–19; **EFFICIENCY OF THE NEW INNO-LIPA HPV GENOTYPING EXTRA COMPARED WITH LINEAR ARRAYS HPV FOR HPV GENOTYPING IN CERVICAL CELL SPECIMENS**

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Background: Different tests for human papillomavirus (HPV) screening are commercially available, detecting high-risk oncogenic HPV types with a pool of genotype-specific probes.

Objectives: The purpose of this study is to compare two commercial methods for HPV genotyping: Linear Arrays HPV genotyping test (Roche), capable of detecting and genotyping 37 different HPV types simultaneously, and the new INNO-LiPA HPV Genotyping Extra (Innogenetics), that detects 28 genotypes, including now HPV-26 (considered probable high-risk genotype) and HPV-82 (considered high-risk genotype), that were not included in the previous version. Both methods also include controls for cell adequacy.

Materials and Methods: A total of 100 HPV DNA-positive cervical samples by hybrid capture method were genotyped.

Results: Multiple genotypes were found more frequently with Linear Arrays (2.2) than INNO-LiPA (1.7). Comparison analysis was limited to HPV genotypes common to both assays. There were concordant results (absolute agreement between assays) in 65 samples and compatible results (correspondence for some but not all genotypes) were found in 33 samples. In 21 samples additional types by Linear Arrays were detected. In13 samples additional types by INNO-LiPA were detected (in one sample there was additional type detected by Linear Arrays and INNO-LiPA method). Only two samples were considered as discordant (did not show any similarity between the tests) and these were negative by INNO-LiPA and positive by Linear Array (both HPV-73). Analyzing kappa values we have found excellent concordance for 6 genotypes (26, 35, 45, 58, 68, and 70) and very good for other 8 genotypes (6, 16, 31, 33, 51, 52, 53 and 66), Concordance was considered good (0.6–0.8) for 5 genotypes (18, 39, 40, 54 and 56), moderate value (0.4–0.6) for HPV-59 and weak agreement (0.4–0.2) for HPV-11.

Conclusions: Both genotyping methods are highly comparable and suitable for clinical and epidemiological studies, as they are partially automated and detect all HPV genotypes of clinical interest.