

d. Diagnostics

00246 POOL-TESTING APPROACH FOR MOLECULAR DIAGNOSTIC AND SURVEILLANCE OF SARS-

COV-2 SPREAD

B.M. Pennati¹, E. Lecini¹, P. Caligiuri², R. Cerruti², G. De Rosa², M. Ferraris², B. Galano², G. Guarona², N. Nigro², S. Varesano², M. Lo Casto², V. Ricucci², A. Orsi¹, G. Icardi¹, B. Bruzzone¹ ¹Department Of Health Sciences, University Of Genoa - Genoa (Italie), ²Hygiene Unit, Ospedale Policlinico San Martino Irccs - Genoa (Italie)

Background The recent health emergency caused by SARS-CoV-2 spread has involved diagnostic laboratories worldwide. During the first months of coronavirus disease (COVID-19) pandemic many oro-pharyngeal swabs had to be processed in a short time, soon revealing issues related to rapidity of having results and availability of reagents for molecular tests. In this study we investigated the possibility of sample pool-testing for molecular diagnostics of SARS-CoV-2 infection.

Methods Samples collected in the first two weeks of June 2020 from hospitalized patients in Genoa, capital of Liguria region, north-west Italy, were tested for SARS-CoV-2 at the regional reference laboratory of Ospedale Policlinico San Martino IRCCS, Hygiene Unit. For this study, 14 positive and 60 negative samples were selected. Samples were previously individually tested for SARS-COV-2 in real time RT-PCR. Positive samples were divided into 5 pools, based on the real time RT-PCR Ct values (<25, 25-30, 30-33, 33-36, >36). Transport media of each positive sample was combined with transport media of 4 negative samples; pools created with positive samples with Ct value <33 were repeated in triple whereas those with positive samples with Ct value >33 in quintuple. Each sample and pool was extracted with STARMag 96x4 Viral DNA/RNA 200L Kit and amplified with Allplex SARS-COV-2 Assay (Seegene).

Results Differences between Ct values of the pools and Ct values of the individually tested samples ranged from 0 to 4 cycles. This trend was also confirmed in Ct values findings for the single targets (E, N, RdRP and S genes) taken separately within the pools and singularly. There were no significant differences in Ct values increase between pools with Ct value <33 and those with Ct value >33. Only in three cases, it was not possible to obtain results, probably due to issues during sample preparation (Figure 1).

Conclusions The tested pooling method was proven effective and could be used for reducing time and costs in SARS-CoV-2 molecular diagnostics, thus providing an useful tool for the virus spreading surveillance.

Conflict of interest All Authors declare no conflict of interest.

