P-211 - EVALUATION OF CFTR MUTATIONS ANALYSIS AFTER 16 YEARS OF CYSTIC FIBROSIS NEWBORN SCREENING PROGRAM

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BACKGROUND: Cystic fibrosis (CF) newborn screening (NBS) program has been conducted in Buenos Aires city through an IRT/IRT protocol from December 2002 to December 2016, and an IRT/PAP protocol since January 2017, both followed by confirmation with sweat test (ST) and/or genetic analysis. OBJECTIVE: Describe biochemical results and molecular characterization of CFTR gene in CF patients identified by NBS, and compare different molecular approaches. METHODS: A retrospective observational study was conducted by analyzing data from 929 samples received from the NBS program. Inclusion criteria: first IRT (DELFIA) measurement ≥60ng/mL and/or meconium ileus. Molecular analysis was performed by screening between 20 and 50 mutations, depending on the kit available at that moment. RESULTS: Inclusion criteria was met by 799 individuals. Among them, 59 CF patients were identified, 49 bearing two mutations and 10 only one. The most frequent mutations among the 118 CF alleles were F508del (72.9%) and G542X (3.4%). The median value of first IRT measurement was 190 ng/mL, and 180.5 ng/mL (n=43) for the second. PAP measurements were available in 9 patients, and were over the cut-off value. Sweat test, available in 39 patients, was positive in 34, and intermediate in 5. Regarding carrier detection, the median value of first IRT in 34 individuals bearing one mutation was 97.5 ng/mL, and 83 ng/mL (n=19) for the second. PAP measurements (n=6) were over the cut-off value. Sweat test, available in 24 individuals, was negative in 18, and intermediate in 6. Three molecular approaches were evaluated: analysis of F508del, analysis of F508del and other 6 frequent CF mutations, and analysis of 50 mutations by a commercial kit. Each strategy would detect 73%, 80% and 99% out of 118 affected alleles, and would identify at least one mutation in 91%, 95% and 100% of the CF patients, respectively. CONCLUSION: Molecular analysis proved to be specially useful in diagnosing CF patients without ST measures or with intermediate results, since it can be performed on blood spot samples. The analysis of 50 mutations currently utilized would have detected at least one mutation in all the patients identified during 16 years of NSB in Buenos Aires city.