Caldrer S et al. work on functional assay is interesting. However, there are few queries and suggestions

We thank the reviewer for the useful comments and suggestions that were included in the final version of the ms.

Major

1. There is no clarity on how the CFTR mutation was identified in the proband. Was the entire CFTR gene sequenced? If so, were there other mutations that were identified?

   Denaturing Gradient Gel Electrophoresis (DGGE) and Reverse Dot Blot (kit INNOLiPA CFTR Deletions +6) were performed (detection rate 98%) without detecting any other mutation.(Page 10)

2. Were the pedigree details taken from the patient? If yes what was the status of other family members with respect to both the disease and the mutation?

   We have added this information (page 10)

3. The authors had written under Genetic examination that mutations associated with pancreatitis in SPINK1 and PRSS1 genes provided negative results. What were the mutations that were screened? Was the entire gene sequenced?

   Sequencing of entire coding regions of both genes was performed,as detailed (Page 12)

4. What is the final conclusion? Do the authors suggest to perform all the functional tests henceforth in all the patients to confirm/exclude CFTR related pancreatitis. What should be the algorithm? Suggest the authors to include the same. What according to the authors is the combination that is sensitive to identify the same.

   We can not suggest to apply all the innovative tests described in all patients, our intention was to compare different methods available defined as standardized procedures and new tests and evaluate whether the results could overlap, as was the case. Individual case might be evaluated using one or possibly at least two of these tests according to the availability of equipment/expertise and collaborations with specialized centres. These considerations have been added (page 14).

Minor

Although ICM is expanded as Intestinal current measurement in Introduction, kindly expand it under CFTR FUNCTIONAL ASSAYS for the reader.

Done

Please notice that we have corrected the IVS8 polymorphism from T7/T7 to T7/T9 (Title, page 5).