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# SDI FINAL EVALUATION FORM 1.1

**PART 1:**

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| Journal Name: | British Journal of Medicine and Medical Research |
| Manuscript Number: | Ms_BJMMR_32156 |
| Title of the Manuscript: | Screening for Fabry Disease among Dialysis Patients in Brazil: Findings from the First 18 months of a Nationwide Study |
| Type of Article: | Original Research Article |

**PART 2:**

| FINAL EVALUATOR'S comments on revised paper (if any) | Authors' response to final evaluator's comments |
|---|---|
| In their paper, the authors considered some mutations in the GLA gene as responsible for FD, even if their role in the disease is still unknown/controversial. The authors supported the causative role of mutation citing some databases without consulting the most important ones for FD like Fabry-database.org, and the databases that they used are not-well "consulted" (e.g. : S126G : they cited, among the databases, the NCBI VarClin. According this database, the pathological meaning of S126G is not clear). However, if they want to demonstrate that a patient in whom they found a controversial mutation is affected , they should perform the Lyso-Gb3 analysis, which was not carried out.<br>The definition of mutation as pathological or not is not a trivial issue, because it means that a patients will be treated or not with ERT, and this is an ethical issue for doubt mutations .<br>Moreover, since there is no validation, the algorith proposed by the authors is not scientifically robust.<br>In conclusion, the previous requests are still not satisfied | 1. We decided to withdraw the patients with the S126G mutation from the FD positive group. We relocate these patients into FD negative group.<br>The analysis, the corresponding table (Table 3) and figures (Figures 5, 6, 7, 8 and 9)were done again.<br><br>2. The algorithm is a proposal. Before this study we performed a content validity of the clinical questionnaire by clinical geneticists and nephrologists. The questionnaire was previously applied to 88 dialysis patients: five with FD (positive molecular test) and 83 without FD (negative molecular test); all five FD patients were considered suspected for FD, and the remaining were considered non-suspected by the algorithm (unpublished data).<br>We've modified the sentences where the algorithm was quoted in order to be adequate (yellow highlight).<br>In a near future we will be happy to validate the algorithm. We can consider this study as a pilot study. |