Dear Reviewer,

Please write the findings of the study briefly in the Introduction along with the rationale. Corrections are highlighted in blue.

1. Why did the author did not look at Variation analysis in other genes BMP1, CCDC134, CREB3L1, CRTAP, FKBP10, IFITM5, KDELR2, MBTPS2, MESD, P3H1, P4HB, PLOD2, PPIB, SEC24D, SERPINF1, SERPINH1, SP7, SPARC, TENT5A, TMEM38B and WNT1?

   We performed whole exome analysis. All these genes were analyzed for the presence of pathogenic variants.

2. Can the author perform a network analysis of the pathogenic variants in collagen gene with the other genes associated with the disease?

   The purpose of the study was primarily clinical, and if we had found several pathogenic variants in patients, we would have conducted a “network” analysis.

3. It would be great if authors could validate their results from data present in the publicly available data sets

   The question is not entirely clear. We checked all our results not only on our own population (RuSeq), but also on databases of 1000 genomes and others.

4. We have briefly added the results and rationale to the introduction.
   For example, we identified 6 genetic variants such as: pathogenic c.3505G>A (p. Gly1169Ser), c.769G>A (p.Gly257Arg), VUS c.4123G>A (p.Ala1375Thr), c.4114A>T (p.Asn1372Tyr) in the *COL1A1* and likely pathogenic c.2035G>A (p.Gly679Ser), c.739-2A>T in the *COL1A2* in 6 OI patients, 3 of them were 1 month of age, and two were aged up to 2 years. By this age, all patients had from 3 to 12 injuries and bone fractures, Table 2.