Correspondence on 'Machine learning algorithms reveal unique gene expression profiles in muscle biopsies from patients with different types of myositis'

I read the paper by Pinal-Fernandez *et al* in your journal with great interest.[1] They reported that machine algorithms can be trained on transcriptomic data to classify muscle biopsies from patients with various idiopathic inflammatory myopathies (IIM). I think this classification model can be applied to personalised medicine by targeting the specific molecules. Here, I would ask the questions and comments to clarify the further usefulness of this study and development of IIM management in the future.

First, how many patients with IIM had interstitial lung disease (ILD) and was there any discrepancy of gene expression with or without ILD in patients with specific myositis-specific autoantibodies (MSA)? ILD is a life-threatening major complication of IIM[2] and elucidating the underlying pathogenesis is an urgent problem; however, obtaining enough biopsy specimen from lung is highly invasive and may cause serious complication such as pneumothorax. Most of ILD are known to emerge concurrent with IIM, indicating underlying mechanism can be common, thus it would be significant to show some relevance with ILD from this study.

Second, how did you determine the site of muscle biopsy? Also, patients with antimelanoma differentiation-associated gene-5 antibody are known to amyopathic, but did all cases have any muscular symptoms? I am concerned about bias of biopsy site that can affect the results of gene expressions because degrees of inflammation in muscle are usually not uniform.[3]

Third, classification of IIM is changing during the recent decades along with the progress in the identification of MSA and MSA-dependent clinical characteristics.[4–7] This study applied the classification based on clinical manifestations and MSA[7] including dermatomyositis, antisynthetase syndrome (AS), immune-mediated necrotising myopathy and inclusion body myositis. However, patients with AS are relatively homogeneous, but the distribution and timing of myositis, ILD, and rashes differ among patients with individual AS.[8] From the view point of this study, gene profile and pathogenesis can be different among the same category. Considering the points above, classification based on gene expression of IIM can be optimal that reflecting distinct individual pathogenesis, which may provide the personalised management for IIM. Therefore, this study is noteworthy and I hope that the results of this study will be confirmed by other validated cohort and contribute to the further development of management of IIM.

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