Towards Optimally Replacing the Current Version of MELD

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I was delighted to read that Ge et al. (2022) [1] published a review in the Journal of Hepatology that included a summary of leading liver allocation models and computational methodologies, also MELD-Plus, a model which was developed as a collaboration between Massachusetts General Hospital and IBM Research in 2017 [2]. The authors also highlighted MELD 3.0, which was proposed to replace the current version of MELD, the MELD-Na score [3]. The methodology of developing MELD 3.0 involved evaluating and using additional variables that were not included in the MELD-Na model. The performance of MELD 3.0 seems promising, especially because it correctly reclassified a net of 8.8% of decedents to a higher MELD tier, resulting in a simulated model with fewer wait list deaths compared to MELD-Na. Although MELD 3.0 seems promising as a potential top candidate to replace MELD-Na, I would like to raise a few points for further consideration.

The development of MELD 3.0 included the evaluation of additional variables on top of MELD-Na’s, including measurable variables such as albumin and height; however, the evaluation did not include components of other leading models, such as lactate (MELD-lactate) [4], blood urea nitrogen (MELD-GRAIL-Na) [5–6], and MELD-Plus’s white blood cells, and total cholesterol [2]. The rationale behind excluding these variables should be discussed.

Note that the limitation specified in Table 1 [1], that MELD-Plus can only be calculated after a cirrhosis-related hospital admission is found to be incorrect. It is true that MELD-Plus was developed based on analyzing electronic health records of cirrhosis-related admissions; however, there is no limitation to using the model at any given time point, while considering the most recent value of each variable [e.g., 7–8]. MELD-Plus indeed has not been studied in patients exclusively registered on the liver transplant wait list [3]. Note, however, that all patients of the MELD-Plus study had cirrhosis at the time of their admission and an average MELD score of 14.2 (6.1), only slightly lower compared to the value calculated in the MELD 3.0 cohort [3]. Additionally the patents of the MELD-Plus study were associated with high prevalence of liver-related comorbidities, including ascites (37.9%), hepatic encephalopathy (28.6%), hepatocellular carcinoma (4.3%), and hepatorenal syndrome (3.2%), as well as chronic conditions not directly related to the liver, such as diabetes (57.0%), hypertension (58.9%), and heart failure (36.7%). A cohort with such a high burden of comorbid conditions may be comparable with a one that exclusively contains candidates for liver transplant.
Note also that MELD-Plus has a version with 7 variables that has comparable performance to the 9-variable full version and does not rely on admission length of stay [2, 9]. Furthermore, while MELD 3.0 was indeed found to be more discriminating compared to MELD-Na (by approximately 0.8%), MELD-Plus was consistently found to be more discriminating compared to MELD-Na in two independent large databases by 11.4% and 16.9% in the Mass General Brigham and IBM Explorys repositories, respectively [2]. I therefore encourage all members of the scientific community to assess further well-validated and well-calibrated [10] leading risk models of the liver, as well as their individual components, as we work toward optimally replacing the current version of MELD.

References

Author names in bold designate shared co-first authorship.


https://doi.org/10.1002/hep.30932.


https://doi.org/10.1002/hep.30321.


9. MELD-Plus source code, GitHub; https://github.com/kartoun/meld-plus