

Personal Standard for Personalized Medicine

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Opinion

As more works has been done on urinary biomarker discovery from animal models, more interesting candidates were found from every diseases studied. Even though it is still hard for people especially editors and reviewers to understand and to accept the facts that there are early markers in urine in every diseases we studied. Facts are facts. The results are gradually being published [1-4], even some are still in preprint forms [5-8].

But a question that I was asked many times when I was giving talks stays in my head. "How can you solve the problem of individual differences you showed on the SDS-PAGE." "Without solving that problem, how can you use your result in clinical setting?" People want to know how to translate the finding into how many units of each candidate markers in each ml of human urine.

In animal model studies, we often compared with the time zero when the disease was not started yet. Since human urinary proteins are so variable, I doubt myself if we can ever find a common pattern for all the people. I often think the ranking of those candidate markers in the whole profile of urinary proteome may be more robust than the absolute concentration, because it solved the urine volume problem. But from SDS-PAGE Figure 1, I am still worried if there is a common standard suitable to all the human beings.

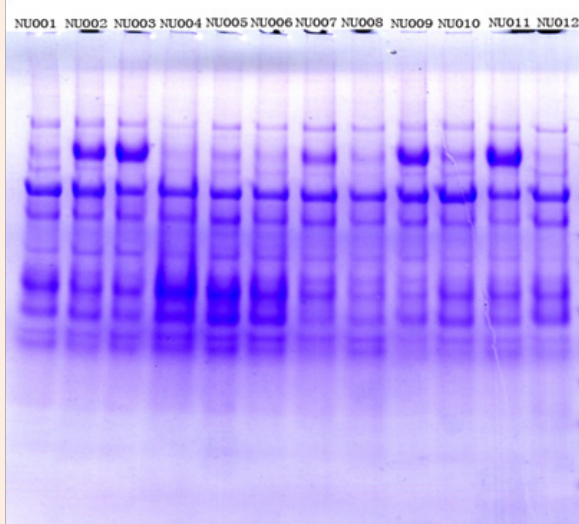


Figure 1: SDS-PAGE.

What if we never be able to find a single standard for all the people? Could we still use the results produced in those animal model experiments? The worst of all is that all individuals are so different; we cannot even find a common standard for any two people. But even if so, can we apply the strategy used in animal

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experiment to each human being? Maybe we can simply collect urine sample from a person when he/she is healthy and analyze its urine proteome, and save the data as the healthy control of only that particular individual. In this case, everybody has its own healthy control. When we do the next urinary proteome analysis, we can then compare with that person's control data to look for all changed proteins. Then the profile of changed proteins is compared with all the experiments the whole world has done to look for similarities. If we found the pattern of changes is similar to the pattern of particular condition, the person is more likely to have that particular condition. Is that the ultimate personalized medicine? It may looks too luxury for now. But if early diagnosis or early clues detected, with effective treatment, the cost of medical care in the late stage will be greatly reduced. It pays off to have a personal standard. Maybe the worst will now happen; maybe there are only a few types of people in the world. Millions of us may share a common standard. Overall we are not that complete different, we are all human beings.

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Conflict of Interest

The author is the chief architect of Authors Journal and chief editor of MOJPB.

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