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NMR-based metabolomic analysis of blood plasma as a pancreatic cancer diagnostic tool

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Current diagnosis of pancreatic cancer (PC) is insufficient and mostly late due to asymptotic course and unspecific symptoms. Thus, the mortality rate is very high, only 5% of PC patients survive 5 years. However, the poor prognosis can be improved by early diagnosis. In this context, the relationship between PC and diabetes mellitus should be investigated, as diabetes or impaired glucose tolerance had been observed in 80% of PC patients.¹ Pancreatogenic diabetes (T3cDM) is a specific type of diabetes mellitus characterized with increased risk of PC development. Unfortunately, T3cDM is often misdiagnosed for the most prevalent type 2 diabetes mellitus (T2DM) because of similar development. T3cDM patients are associated with an up to 7-fold increased risk of PC development.¹ The crucial role of early PC diagnosis is the differentiation of T3cDM-T2DM among recent onset diabetes mellitus (RODM) patients. NMR-based metabolomics may help to solve this complicated problem of current clinical diagnosis.^{2,3}

In this work, ¹H NMR metabolomic analysis of blood plasma was used as an alternative diagnostic tool of PC. The concentration profile of 58 metabolites was used to discriminate PC patients from long-term T2DM patients and healthy controls. Based on successful discrimination, a specific biomarker panel of eight metabolites was proposed. Furthermore, a prediction model for the identification of risk individuals for PC development in RODM group was developed and the patients with increased risk of PC development were identified. Similar metabolic features with PC were observed in six of 59 RODM patients, and therefore their health conditions were re-examined. Our findings correlate with pathological changes or hereditary predisposition. Recent results also indicate subtle metabolic changes among individual PC clinical stages that could be used for their differentiation in future.



References

1. Pannala, R.; Basu, A.; Petersen, G. M.; Chari, S. T. *Lancet Oncol.* **2009**, *10*, 88-95.
2. Michálková, L.; Horník, Š.; Sýkora, J.; Habartová, L.; Setnička, V. *Analyst* **2018**, *143*, 5974-5978.
3. Michálková, L.; Horník, Š.; Sýkora, J.; Habartová, L.; Setnička, V.; Bunganič, B. *J. Proteome Res.* **2021**, *20*, 1744-1753.

