Global DNA methylation alterations in diabetic nephropathy: a possible link to metabolic memory and aetiology of nephropathy

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Objectives: to evaluate whether global levels of DNA methylation status were associated with diabetic nephropathy.

Method: A case-control study of 142 patients with type 2 diabetes- 51 patients with nephropathy and 91 patients without nephropathy.

The 5-methyl cytosine content was assessed by reverse phase high pressure liquid chromatography (RP-HPLC) of peripheral blood leukocytes to determine individual global DNA methylation status.

Results: Global DNA methylation levels were significantly higher in patients with nephropathy compared with those in patients without nephropathy patients (4.91 ± 0.15 vs. 4.26 ± 0.15, respectively, p= 0.003).

There were significant differences in global levels of DNA methylation in relation to albuminuria (p = 0.0.027) and an interesting pattern of increasing global levels of DNA methylation in terms of albuminuria severity (figure 1).

In patients with diabetic nephropathy, we found no significant correlations between global DNA methylation levels and duration of diabetes (p= 0.87) (figure 1) and good and poor glycaemic control (p = 0.98).

Figure 1: Global DNA methylation levels in diabetes patients based on albuminuria

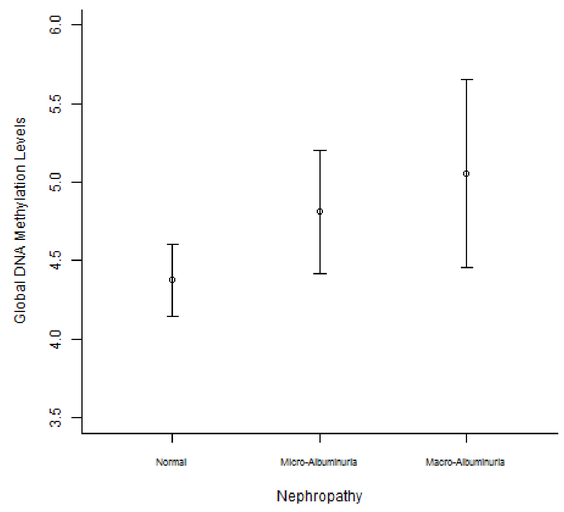
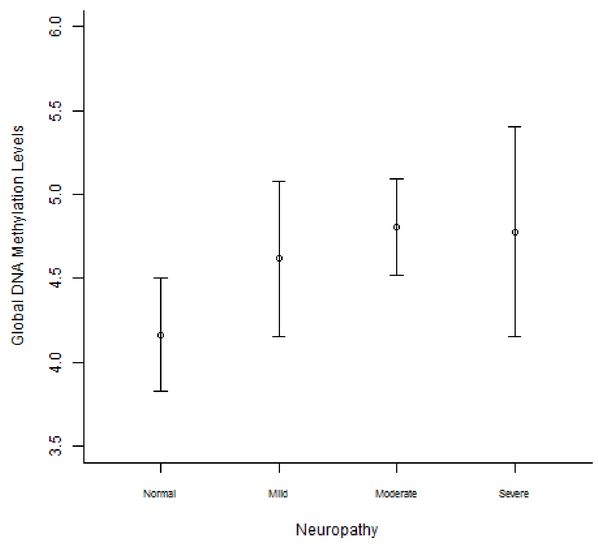


Figure 2: Global DNA methylation levels in diabetes patients with and without nephropathy based on duration of diabetes



Conclusions: These data may be helpful in further studies of the role of epigenetic in metabolic memory and aetiology of diabetes and its complications.