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# Putative trans-regulator network of the krüppel-like factor 14 (*KLF14*): Potentials sources of information to personalized medicine in type 2 diabetes mellitus and related traits

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**Introduction:** The aim of this study is to identify potentials sources of information to personalized medicine in T2DM and related traits.

**Methods:** Putative transcription factors within 10-20 kb upstream and 10 kb downstream of *KLF14* gene were searched with data extraction from SABiosciences of the QIAGEN company. The STRING v9.1 software was used to identify the known and predicted protein-protein interaction in the *KLF14* protein network.

**Results:** Upstream of *KLF14* gene, there are 62 transcriptions factors (with three of them encode by AHR, HOXA3 and HOXA9 genes located on the same chromosome) that came to bind within 10-20 Kb upstream and 10 Kb downstream of KLF14 gene for his transcription. This transcription is repressed by Sin3A protein which leads to the HDAC1 and HDAC2 enzymatic proteins important for transcription repression, Mad and MeCP2 (DNA binding proteins) and the Ikaros and SMRT (co-repressor). The resulting mRNA is translated in *KLF14* protein. This protein act on ten genes identified to have GWST association driven by rs4731702 (C/T) polymorphism of *KLF14* gene and established protein-protein interactions with 32 proteins implicated in metabolic diseases and others biological processes. Of are the presence UBC and TCF7L2. The physical interactions which exist between *KLF14* and UBC could regulate the amount of *KLF14* protein available by its degradation.

**Conclusion:** These findings provide a variety drug development targets according to the genetic risk in the form of signal pathways that can reduce the progression of multiple metabolic phenotypes or the risk of their complications by personalization of medicine.

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