Conclusion: Using target proteome profiling technique, we demonstrated PON1 as a potential biomarker of D2T RA. However, these results have to be validated on a larger cohort.

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Results: A total of 2670 DEGs and 371 TSPJ targets were obtained, including 52 overlapping genes. 41 genes had protein interactions that are used to build the PPI network. The results of the KEGG enrichment analysis included VEGF and HIF-1 signaling pathway. Seven negative correlation genes and 16 positive correlation genes were obtained by correlation analysis of DEGs in VEGF and HIF-1 signaling pathways. SRC proto-oncogene, nonreceptor tyrosine kinase (SRC), and the signal transducer and the activator of transcription 3 (STAT 3) had a higher value of degree in PPI and showed a significant correlation in the pathways; they were regarded as key targets. Compared with the CIA model group, TSPJ significantly decreased the AI and histology scores. Moreover, the expression of VEGF-A, HIF-1α, IL-17A in serum or spleens significantly reduced in a dose-dependent.

Conclusion: Present study show that SRC and STAT 3 may be the key targets of TSPJ acting on the VEGF and HIF-1 signaling pathways, thus inhibiting angiogenesis and improving RA.

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References:

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