Discussion

To uncover potential biomarkers in the properties of an aged human hematopoietic system that may predispose to age-associated hematopoietic dysfunction, hematopoietic progenitor populations from healthy, hematologically normal young and elderly human bone marrow samples are evaluated.

Gene expression matrix was constructed, and computational analysis was done. The protocol is designed to study biologically significant genes. Microarray data analysis workflow includes quality control, data normalization, clustering, pathways enrichment, and PPI study. Clustering analysis identifies genes that are coexpressed. ese sets of coexpressed genes are used for pathway and process en- richment analysis. Gene ontology and pathway study reveal proteins that share common pathways and function. Further protein-protein interaction network is constructed to identify more number of proteins, which have physical interaction with coexpressed proteins. PPI network is subclustered to predict closely related proteins. Gene on- tology information of these proteins is used to identify function and disease associated with proteins. 12 proteins CASP3, CASP9, BAX, TP53, BAD, GSK3B, MTOR, BCL2L11, SIRT1, CASP8, AKT1, and CTNNB1 proteins are predicted that are involved in various types of cancers like lung cancer, breast cancer, ovarian cancer, colorectal cancer, and leukemia [60, 61, 62]. Some proteins like SOX2, STAT1, AKT1, and CTNNB1 proteins are associated with neuro- logical disease like abnormal brain development, mental retardation, schizophrenia, and mycobacterial and viral infections [63–66]. ese genes can be used as markers for neurological disease, for detection of abnormalities at the early stage of neuronal development [67]. Predicted pro- teins can also act as potential drug targets for the drug development process. Further work is required for wet lab verification of predicted genes that are expressed in neuro- logical disorders and express at the developmental stage. More research is required in the field of neurodevelopmental biology to identify neurological abnormalities at its budding stage. is paper also highlights the importance of microarray experiment in understanding the neurological diseases and methodology to study various outcomes of gene expression data, like coexpression analysis, pathway and process iden- tification, and protein-protein interaction network study.

Surprisingly, most researches concentrate on an individual genetic result or the results are de- rived from an alone cohort research through microarray analysis which is not uniform with each other (Derosa et al., 2012; Mortensen et al., 2015; Satake et al., 2010; Wen, Geng, Li, Guo, & Zheng, 2014). Our study performed bi-group comparison profile data sets from 3 category in which young, middle, and old aged samples within one data set and utilised bioinformatics methods to deeply analyse the data set and identified 453 significantly changed DEGs. The number of downregulated genes was significantly higher than the upregulated genes (326 versus 127).