BACKGROUND

Psychiatric illnesses such as bipolar disorder (BD), schizophrenia (SZ) and schizoaffective disorder (SZA) are severe, disabling disorders associated with decreased quality of life (QOL) and functioning (1–3). Stigmatization, co-morbidities, adverse effects of medications, care models with deficits in personal and social recovery needs and chronic symptoms due to treatment resistance are factors that can lead to severe reductions in quality of life and functioning (4, 5). In this study, we aim to characterize patients with good and poor outcomes according to QOL and functioning scores across diagnoses. Using cluster analysis, we sought to identify longitudinal trajectories and investigate whether levels of QOL and functioning are associated with the individual burden of schizophrenia polygenic risk scores (SZ-PRS). Determining clusters of patients at higher risk of poorer outcomes is critical to provide early and effective interventions.

RESULTS

The dimension which explained the most variance was used for cluster analysis. Computed by FAMD, the strongest loadings on the first dimension were observed for self-satisfaction, life enjoyment, and ability to cope with daily tasks, energy, and quality of life. Three clusters of longitudinal trajectories were observed on the first dimension: cluster A (39.4%) consisted of participants with the highest average scores for functioning and QOL, cluster B (33.8%) including participants with the lowest average scores for functioning and QOL, and cluster C (26.8%) consisting of participants who had great improvement in functioning and QOL scores over the course of the longitudinal study (see Figure 2).

Genotyping and polygenic scoring

The Infinium Psycharray from Illumina was used to genotype patients. For imputation the 1000 Genomes Phase 3 reference panel was used. SZ-PRS were calculated for all individuals using PLINK. The results are preliminary and have to be interpreted with caution. Nevertheless, the approach of longitudinal clustering to identify cross-diagnostic subgroups based on a common phenotype seems to be promising. Phenotypic data provide insight to target sufferers of severe mental illness with worse outcomes. Levels of functioning and QOL seem to be associated with SZ-PRS. There was no significant association between cluster membership and SZ-PRS in the single models. Non-significant trends: Cluster B members show higher polygenic burden versus Cluster A. Cluster C members have less polygenic burden than Cluster A. Overall, SZ-PRS at certain thresholds can be predicted by the clusters (see Figure 4).

CONCLUSION

The authors declare no conflict of interest.

ACKNOWLEDGEMENTS

We thank all of the patients for participating in this study. This research was funded by the Deutsche Forschungsgemeinschaft (DFG). Schulze: DFG SCHU 1603/5-1, DFG 1603/7-1; Theis: DFG TH 900/9-1.