Epidemiology and social psychiatry

FC28

A multi-attribute utility instrument suitable for use in individuals with psychosis – the AQoL-4D: Findings from the Second Australian National Survey of Psychosis

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Introduction Multi-attribute utility instruments (MAUIs) are generic health-related quality of life (HRQoL) measures that enable valuation of health states relative to death (0.0) and full health (1.0). The usefulness of MAUIs in people with psychosis has been questioned, with the EQ-5D considered "insensitive", the 15D "problematic" and the SF-6D "unsuitable".
Objectives Confirm the Assessment of Quality of Life (AQoL)-4D MAUI is useful and meaningful in people with psychosis.
Aims Assess utility values across demographic, general and disease-specific health categorisations for a large nationally-representative sample with psychosis ($n = 1825$).
Methods Participants underwent a comprehensive 32 module interview encompassing psychopathology to service use. Utility values were calculated by applying a standard algorithm to responses to each of 12 items of the AQoL-4D.
Results Utility values were assessed for 1793 participants (98.2%). No ceiling effect was observed and only 6.6% of participants scored in the top decile of HRQoL [0.9–10.0]. In contrast, 10.8% scored in the lowest decile [−0.04–0.10], a floor effect observed in 0.4%. The mean utility value was 0.49 (95% CI: 0.48–0.51), significantly lower than the Australian population norm of 0.81 (95% CI: 0.81–0.82). Greatest impacts on HRQoL were for diminishing global independent functioning as measured by the MSIF (ES_{MSIF}: 0.68–2.24), self-rated current mental health (ES_{MH}: 0.15–1.65) and physical health status (ES_{PH}: 0.11–1.21). Strong effects also observed for course of disorder (ES_{CoD}: 0.08–1.13), current suicidal ideation (ES_{CSI1}: 0.76–1.08), and labor force participation (ES_{LFP}: 0.11–0.97).
Conclusions The AQoL-4D had good lower end sensitivity in a large sample of people with a psychotic illness, and demonstrated responsiveness across subjective, objective and symptom measures.
Disclosure of interest The authors have not supplied their declaration of competing interest.

http://dx.doi.org/10.1016/j.eurpsy.2016.01.032

FC29

Loneliness is adversely associated with lifestyle and physical and mental health

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Introduction Loneliness is a common emotional distress experience and there is increasing evidence of associations with unhealthy lifestyle and adverse health-related factors. Little is known about age and sex as potential effect modifiers, and about the prevalence of loneliness.
Objective/aims To assess the associations of loneliness with behavioral, physical and mental health factors, taking sex and age into account and to examine the prevalence of loneliness in individuals aged 15+ years.
Methods Data from 20,007 participants of the cross-sectional population-based Swiss Health Survey 2012 were analyzed. The association of loneliness with lifestyle and health-related factors were assessed with logistic regression analyses. Wald tests were used to test for age and sex differences.
Results Loneliness was reported by 64.1% of individuals, and was associated with smoking (OR 1.13, 95% CI 1.05–1.23), physical inactivity (1.20, 1.10–1.31), non-adherence to the 5-a-day recommendation for fruit and vegetable consumption (1.21, 1.07–1.37), and more visits to a physician within the last year (1.29, 1.17–1.42). Loneliness was also associated with high cholesterol levels (1.31, 1.18–1.45), diabetes (1.40, 1.16–1.67), self-reported chronic diseases (1.41, 1.30–1.54), impaired self-perceived health (1.94, 1.74–2.16), moderate and high psychological distress (3.74, 3.37–4.16), and depression (2.78, 2.22–3.48). Age modulated the associations in BMI, smoking, visiting a physician within the past year, and self-perceived health. Sex did generally not modulate the associations.
Conclusion Loneliness is associated with unhealthy lifestyle, and poorer physical and mental health. Associations were modulated by age, but not sex. Further longitudinal studies are needed to elucidate the causal relationships of these associations.
Disclosure of interest The authors have not supplied their declaration of competing interest.

http://dx.doi.org/10.1016/j.eurpsy.2016.01.033

Genetics and molecular neurobiology

FC30

Potential blood gene expression markers for postpartum psychosis

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Background Postpartum psychosis (PP) is the most severe psychiatric disorder associated with childbirth. Previous evidence has shown gene expression alterations in immune profile in women

https://doi.org/10.1016/j.eurpsy.2016.01.034 Published online by Cambridge University Press

with PP when compared with healthy postpartum women. However, no study has ever evaluated women at risk who do not develop the disorder.
We conducted an exploratory analysis of a gene expression profile that could distinguish women with PP episode (PPE) from women at risk who do not develop PP (NPPE) after delivery.
Methods The sample was characterised by 24 women at risk of PP of which $n = 12$ with PPE and $n = 12$ with NPPE and 21 healthy women in the same postpartum period. Following Microarray analysis, we assessed gene expression signature across the 3 groups using ANOVA. We then studied Pathway analysis of genes differently expressed in PPE and PPE exploring canonical pathways and upstream regulators using Ingenuity Pathway Analysis software.
Results Following an exploratory gene expression analysis we identified 719 genes that are differently expressed across PPE and NPPE. The PPE presented upregulation of several genes involved in the inflammatory pathway and increased gene expression levels of *GRIA4*, *AKT3*, *SP4* and *NRG1* genes, which have been previously described in psychotic disorders. Moreover, 5 differently expressed canonical pathways were identified including ones relevant to development, mitochondrial formation and immune system.
Conclusion These preliminary results reveal the presence of an immuno-neuro-endocrine dysregulation in postpartum psychosis, with an upregulation of the immune system specific to those women at risk who actually develop postpartum psychosis episodes.
Disclosure of interest The author has not supplied his declaration of competing interest.

http://dx.doi.org/10.1016/j.eurpsy.2016.01.034

FC31

A meta-analysis of gene (5-HTT) × environment interactions in eating pathology using secondary data analyses

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Background Gene × environment (G × E) interactions in eating pathology have been increasingly investigated, however studies have been limited by sample size due to the difficulty of obtaining genetic data.
Objective To synthesize existing G × E research in the eating disorders (ED) field and provide a clear picture of the current state of knowledge with analyses of larger samples.
Method Complete data from seven studies investigating community ($n = 1750$, 64.5% female) and clinical ($n = 426$, 100% female) populations, identified via systematic review, were included. Data were combined to perform five analyses: 5-HTTLPR × Traumatic Life Events (0–17 events) to predict ED status ($n = 909$), 5-HTTLPR × Sexual and Physical Abuse ($n = 1097$) to predict bulimic symptoms, 5-HTLPR × Depression to predict bulimic symptoms ($n = 1256$), and 5-HTTLPR × Impulsivity to predict disordered eating ($n = 1149$).
Results The low function (s) allele of 5-HTTLPR interacted with number of traumatic life events ($P < .01$) and sexual and physical abuse ($P < .05$) to predict increased likelihood of an ED in females but not males (Fig. 1). No other G × E interactions were significant, possibly due to the medium to low compatibility between datasets (Fig. 1).
Conclusion Early promising results suggest that increased knowledge of G × E interactions could be achieved if studies increased uniformity of measuring ED and environmental variables, allowing for continued collaboration to overcome the restrictions of obtaining genetic samples.

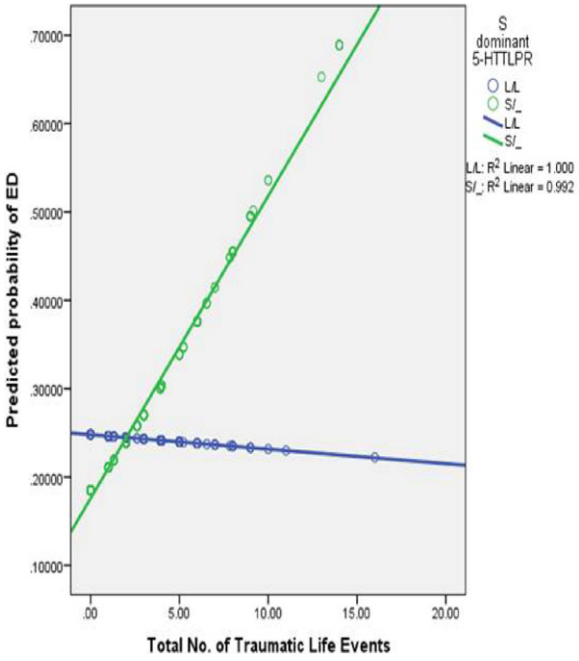

Fig. 1 The interaction between 5-HTTLPR (s-allele present versus s-allele absent) and number of traumatic life events to predict likelihood of an eating disorder in females.

Disclosure of interest The authors have not supplied their declaration of competing interest.

http://dx.doi.org/10.1016/j.eurpsy.2016.01.035