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Shared versus distinct genetic contributions of mental wellbeing with depression and anxiety symptoms in healthy twins

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ABSTRACT

Mental wellbeing and mental illness symptoms are typically conceptualized as opposite ends of a continuum, despite only sharing about a quarter in common variance. We investigated the normative variation in measures of wellbeing and of depression and anxiety in 1486 twins who did not meet clinical criteria for an overt diagnosis. We quantified the shared versus distinct genetic and environmental variance between wellbeing and depression and anxiety symptoms. The majority of participants (93%) reported levels of depression and anxiety symptoms within the healthy range, yet only 23% reported a wellbeing score within the "flourishing" range: the remainder were within the ranges of "moderate" (67%) or "languishing" (10%). In twin models, measures of wellbeing and of depression and anxiety shared 50.09% of variance due to genetic factors and 18.27% due to environmental factors; the rest of the variance was due to unique variation impacting wellbeing or depression and anxiety symptoms. These findings suggest that an absence of clinically-significant symptoms of depression and anxiety does not necessarily indicate that an individual is flourishing. Both unique and shared genetic and environmental factors may determine why some individuals flourish in the absence of symptoms while others do not.

1. Background

Mental wellbeing and illness have traditionally been conceptualized as opposite ends of a continuum, such that the absence of mental illness is thought to indicate the presence of mental health. Such a model would imply that knowledge of one state would necessitate an understanding of the other. Yet, with the advent of the positive psychology movement, the construct of 'mental health' has been reframed in light of advanced theoretical notions of wellbeing which now include both satisfaction with life as well as positive psychological attributes such as optimism, autonomy and life mastery (Gatt et al., 2014; Keyes, 2005; Seligman and Csikszentmihalyi, 2000; Williams et al., 2009). In such models, individuals who score high on dimensions of wellbeing are said to be 'flourishing'. That is, they display high levels of both hedonic or 'subjective' wellbeing (defined by positive affect and feelings of life satisfaction), and eudaimonic or 'psychological' wellbeing (defined by a sense of life purpose, meaning and fulfilment) (Deci and Ryan, 2008), and not just the absence of illness symptoms.

Evidence from recent studies support the contention that states of mental wellbeing and mental illness symptoms are independent yet related, sharing only a small proportion of common variance (Kendler et al., 2011a, 2011b; Keyes, 2005). In Keyes (2005) study, a confirmatory factor analysis supported a two-factor dual-continua model of mental wellbeing and illness over a single factor continuum. In addition, only a quarter of the phenotypic variance between the latent factors of mental wellbeing and mental illness was shown to be shared, indicating that the two conditions were defined by separate correlated axes. Prevalence studies in the United States (US) suggest that lifetime risk for developing affective disorder ranges anywhere up to 32% (Brown and Ryan, 2003), with the remainder of the population thought to be healthy and disorder-free at any single point in time. Yet, of the total population sample in Keyes (2005) study who reported no mental illness in the previous 12 months (77%), only 21% were actually

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flourishing and functioning optimally, suggesting that even in normative samples, an absence of illness symptoms does not necessarily imply a thriving mental state. Although much higher rates of flourishing have been reported in other studies – for example, 44% in a sample of 1043 American yoga practitioners (Ross et al., 2013), and 49% in a sample of 5689 college students in the United States (Keyes et al., 2011) – this difference in flourishing rates is more likely due to the health characteristics of the specific samples (by virtue of age or health practise) rather than actual variations in flourishing rates in the general population.

Twin studies have similarly reported some evidence of shared variance between mental illness and mental wellbeing, as well as its genetic and environmental derivatives in monozygotic (MZ) and dizygotic (DZ) twin pairs. In a general population cohort, the shared genetic and environmental variance of 1386 MZ and DZ twins were compared in terms of mental wellbeing and "internalizing disorders" (previous-year prevalence of clinical levels of Major Depressive, Generalized Anxiety or Panic Disorder) and they were found to share 50% genetic variance and 5% unique environment variance (Kendler et al., 2011b). The contribution of additive genetics to the phenotypic correlation ranged from 69% at baseline to 86% across ten years (Kendler et al., 2011b), suggesting that genetics ultimately played a larger role than environment in the shared associations between wellbeing and internalizing disorders of depression and anxiety. Unique environment (e.g., birth order, differential parenting styles, peer groups, or individual personality differences) showed considerably less overlap such that most of the environmental influences on wellbeing were independent from mental illness. However, as unique environment also includes measurement error, this environmental overlap between the variables could also be confounded by this variation. Common environment (e.g., shared household rearing, parenting style and socioeconomic class) on the other hand did not contribute to these shared relationships. Together, these findings suggest that unique genetic and environmental influences specifically contribute to wellbeing and mental illness symptoms. They also suggest that the same environmental factors contribute very little to the relationship between wellbeing and mental illness such that the environments that foster wellbeing are largely unrelated to those that impact mental illness, and vice versa. Similar genetic and environmental relationships have also been reported in nonclinical twin cohorts such as the Norwegian twin study of 6326 young adults aged between 18 and 31 years (Nes et al., 2008). This study examined the genetic and environmental overlap for symptoms of depression, anxiety and wellbeing defined by a life satisfaction scale in men and women. They found the genetic and environmental relationship to be strongest between symptoms of depression and anxiety (genetic correlation, rG: 0.92 (CI, confidence intervals: 0.83–1.00) in males and females; environmental correlation (rE): 0.52 (0.42–0.61) in males, 0.60 (0.54–0.65) in females), followed by life satisfaction and depression (rG: −0.79 (−0.90 to −0.68) in males and females; rE: −0.48 (−0.56 to −0.40) in males, −0.59 (−0.64 to −0.54) in females), with the weakest relationship between life satisfaction and anxiety (rG: −0.64 (−0.78 to −0.50) in males and females; rE: −0.29 (−0.39 to −0.19) in males, −0.34 (−0.40 to −0.26) in females). However, the age range covered in this study spanned what is traditionally a period of substantial transition and development, so whether it is generalizable to a broader adult age range is unclear. Moreover, the single-item measure of "life satisfaction" is not a comprehensive assessment of mental wellbeing in that it does not measure eudaimonic aspects of wellbeing.

In this study, we examine the relationship between mental wellbeing and the normative range of anxiety and depression symptoms in healthy adult twins. We aim to derive the cross-frequency distribution of wellbeing and depression and anxiety symptoms in a healthy normative adult population, and the genetic and environmental derivatives of the shared and unique variance of wellbeing and depression and anxiety symptoms using twin modeling. The twin modeling thus allows us to examine the genetic and environmental interplay between wellbeing and depression and anxiety symptoms; that is, the degree to which genetic and environmental factors contribute in common and/or independently to both health outcomes.

2. Methods and materials

2.1. Participants

The sample comprised healthy same-sex MZ and DZ twin pairs from the TWIN-E study (the Twin study in Wellbeing using Integrative Neuroscience of Emotion) conducted at the University of Sydney, Australia (see Gatt et al., 2012, for complete study protocol). The study received approval from the Human Research Ethics Committees of the University of Sydney (03–2009/11430) and Flinders University (FCREC#08/09). All participants provided written informed consent prior to participation and after receiving a complete written description of the study.

Twins were recruited from the Australian Twin Registry. Eligible participants were healthy adult same-sex twin pairs (aged 18-62 years), with English as primary language, and of pure European ancestry. Zygosity was determined using the twins' responses to a 12-item questionnaire developed for the study (Gatt et al., 2012), using items from measures previously validated as having 95% convergence with DNA results (Eisen et al., 1989; Jackson et al., 2001; Magnus et al., 1983). For further details, see Burton et al. (2015). Ethnicity of the cohort was determined from self-report measures of the participant's parents' and grandparents' ancestry. Exclusion criteria included current or lifetime psychiatric illness, history of stroke or neurological disorder, genetic disorder, brain injury (causing loss of consciousness for more than 10 min), chronic and serious medical conditions (e.g., cancer, heart disease), blood-borne illnesses, substance abuse, or vision impairments not corrected by glasses/lenses.

A total of 2370 twins were recruited from the Australian Twin Registry for the study. 108 participants were excluded as ineligible, including 21 on the basis of past or current mental illness. This resulted in a total sample of 2262 twins, of which 1669 successfully completed Phase I baseline testing of the web-based questionnaires. 1486 participants (743 twin pairs) were included in the current analysis following the exclusion of 92 incomplete pairs (82 pairs had one twin who did not complete the web questionnaire, and another 10 pairs had indeterminate zygosity). Of the 1486 participants, 39.6% (n=588) were male. The mean age was 39.79 years (SD =12.74; range =18 to 62 years) and mean education was 14.35 years (SD =3.00). 60.3% of the total sample were monozygotic twin pairs (MZ; n=896 or 448 twin pairs), of which 45.1% were male (n=404; 202 twin pairs) and 54.9% female (n=492; 246 twin pairs). The remaining 39.7% of the sample were dizygotic twins (DZ; n=590 or 295 twin pairs), of which 31.2% were male (n=184; 92 twin pairs) and 68.8% female (n=406; 203 twin pairs).

2.2. Measures

The protocol and measures for the TWIN-E study have been previously published (Gatt et al., 2014, 2012). This study uses data derived from the first phase of the study for which participants completed the WebQ, an online test battery of self-report questionnaires (Gatt et al., 2012). Here we used total scores derived from the Depression, Anxiety and Stress Scale (DASS-42) scale

(Lovibond and Lovibond, 1995) as we were interested in measuring general risk for anxiety and depression symptoms and their relationship with mental wellbeing rather than the differential risk associated with specific symptomatology. Moreover, confirmatory factor analyses of the DASS-42 subscales confirmed a common latent factor model as the optimal model for the data, supporting the use of total DASS score as a representative indicator of general anxiety and depression symptoms (Burton et al., 2015).

Mental wellbeing was measured using total scores on the 26-item COMPAS-W scale of wellbeing (Gatt et al., 2014). The COMPAS-W scale is a composite index of subjective (hedonic) and psychological (eudaimonic) wellbeing and also provides scores for its subcomponents of Composure, Own-worth, Mastery, Positivity, Achievement and Satisfaction. This measure was derived for a previous phase of this study by factor analyzing previously validated measures of personality traits: NEO Five-Factor Inventory (Costa and McCrae, 1992); emotion regulation: Emotion Regulation Questionnaire (Gross and John, 2003); perceived control: Internal Control Index (Duttweiler, 1984); and quality of life: World Health Organisation Quality of Life scale (The WHOQOL Group, 1998) and Satisfaction with Life Scale (Diener et al., 1985). A confirmatory factor analysis of the final model was tested in twin 1 and confirmed in twin 2. Cronbach's Alpha confirmed the internal reliability of the total scale and subscales, and validity was ascertained by comparing correlations with independent measures of mental health: DASS-42; Modified Differential Emotions Scale (Fredrickson et al., 2003); and the Somatic and Psychological Health Report (Hickie et al., 2001); in addition to the scales the items were derived from. Tertile categorical groupings for "flourishing", "moderate mental health" and "languishing" groups were created and the validity confirmed using nonlinear canonical correlation analysis (Gatt et al., 2014).

2.3. Analyses

Initially we checked for relationships between sex, age, mental wellbeing and DASS scores. We split the sample by twin, and checked for sex differences using *t*-tests. There were no significant differences in wellbeing scores (Twin 1: $p=0.69$; Twin 2: $p=0.56$) between males (T1: $M=0.16$, $SE=0.06$; T2: $M=0.10$, $SE=0.06$) and females (T1: $M=0.13$, $SE=0.05$; T2: $M=0.14$, $SE=0.05$). There were no significant differences in DASS scores (T1: $p=0.41$; T2: $p=0.72$) between males (T1: $M=-0.04$, $SE=0.06$; T2: $M=0.02$, $SE=0.05$) and females (T1: $M=0.02$, $SE=0.04$; T2: $M=0.00$, $SE=0.04$). We used Pearson's correlation coefficient to check for relationships between DASS score, wellbeing and age. There were significant correlations between age and wellbeing (T1: $r=0.16$, $p=0.00$; T2: $r=0.12$, $p=0.00$), and age and DASS score (T1: $r=-0.15$, $p=0.00$; T2: $r=-0.15$, $p=0.00$). For completeness, we covaried for both age and sex effects in all analyses.

2.4. Distribution of wellbeing and depression and anxiety scores

To examine differences in the distribution of mental wellbeing and depression and anxiety scores, we used a chi-square test of independence of the categorical scores in SPSS Version 21.

For the 26-item COMPAS-W mental wellbeing score, participants were categorized into either "Languishing" (a score lower than -1), "Moderate Mental Health" (-1 to 1), or "Flourishing" (>1) based on their standardized scores. For the DASS-42 total score, raw score values were categorized using Crawford and Henry's (2003) conversion of total scores into "Normal" (score of 1–26), "Mild" (27–35), "Moderate" (36–60), "Severe" (61–79) and "Extremely Severe" (80+). However, due to small numbers in the Moderate to Extremely Severe categories, we collapsed participants into the one category of "Moderate-Severe".

2.5. Twin genetic modeling: total and partitioned variance

Bivariate genetic modeling was performed using Open Mx version 1.4 on R version 3.0.2 (Boker et al., 2011; R: A language and Environment for Statistical Computing, 2013). The purpose of bivariate modeling is to examine the shared and unique additive genetic (A), common environment (C) and unique environment (E) variance between two traits or phenotypes; in this instance, between the standardized z scores for total COMPAS-W wellbeing scores and total DASS-42 scores, with age, sex and education included as covariates. It also provides information on total phenotypic variance shared.

Comparative model fit is evaluated using Akaike's information criterion (AIC), with a lower AIC value indicating a better-fitting model (Keyes et al., 2010a). Assumption tests verified that means and variances could be constrained across twins 1 and 2, and across MZ and DZ twin pairs. A correlated-factors ACE model was fit to the data, with the A and C paths sequentially eliminated to determine the most parsimonious model. The significance of the genetic and environmental correlations were then tested by setting them to 0 and comparing the fit to the best model. A significant difference between models indicated a significant change in fit.

After fitting the correlated-factors model, we used calculations provided by Loehlin (1996) to determine cross-path estimates and decompose the amount of shared and unique variance between symptoms of anxiety and depression, and mental wellbeing. Calculations are included in the Supplementary results. To calculate the phenotypic correlation, we summed the correlation due to additive genetics and the correlation due to environmental effects. The additive genetic correlation was determined by multiplying the square roots of the heritability estimates by the genetic correlation (i.e., $\sqrt{h^2}$ for DASS symptoms x rG x $\sqrt{h^2}$ for wellbeing). The environmental correlation was calculated in the same way. Thus, the proportion of the phenotypic correlation due to genetics was the additive genetic correlation divided by the phenotypic correlation.

3. Results

3.1. Distribution of wellbeing and depression and anxiety scores

The majority of participants (93%, n=694) fell into the "normal" range for total depression and anxiety scores, versus 3.8% (n=28) for "mild" and 2.8% (n=21) for "moderate-severe" depression and anxiety DASS scores (for twin 1; similar distributions identified for twin 2). For mental wellbeing, 22% (n=162) of total twin 1 participants reported scores within the "flourishing" category, versus 64% (n=478) for "moderate" wellbeing and 14% (n=103) for "languishing".

A chi-square test for independence indicated that there was a significant relationship between DASS symptoms and the mental wellbeing category (Fisher's Exact test $=78.13$, $p<0.0001$). Fig. 1 presents the composition of each DASS group category according to wellbeing scores. Notably, of those participants coded as "normal" on the DASS, only 23% were considered as "flourishing" on the wellbeing scale; the remainder were either of "moderate" wellbeing (67%) or "languishing" (10%).

3.2. Twin genetic modeling: total and partitioned variance

Fit statistics of the bivariate models of total wellbeing and total DASS scores tested are presented in Table 1. Dropping C from the model did not result in deterioration in fit, and improved the AIC value. Dropping A, however, did cause a significant decline in fit.

Thus, the best model was the AE model (see Fig. 2). Setting the A and E correlations to 0 resulted in a significant deterioration in fit, indicating that the genetic and environmental correlations between depression and anxiety and wellbeing were significant.

The additive genetic variance (heritability) for total DASS anxiety and depression symptoms and wellbeing was 37.88% (95% Confidence Interval: 30–45%) and 49.92% (CI: 44–56%) respectively, with unique environment contributing the remaining 62.12% (CI: 55–70%) and 50.08% (CI: 44–56%) to total DASS and mental wellbeing scores (respectively). Of the total genetic variance for wellbeing, the amount *shared* with anxiety and depression scores was 50.09%, and the amount unique to symptoms of wellbeing was 49.91%. Therefore, about half the genetic influences on wellbeing were shared with symptoms of depression and anxiety, and half were independent.

Environmental influences showed much less overlap. Of the total environmental variance for wellbeing, only about 18.27% was shared with environmental influences on anxiety and depression, with the remaining 81.73% unique to wellbeing.

The phenotypic correlation between wellbeing and anxiety and depression was −0.55, indicating that slightly more than a quarter of the total variance in scores (0.55^2; 29.94%) was shared. Of the −0.55 phenotypic correlation, −0.31 (56.34%) was a result of genetic effects, with the remaining accounted for by common forms of unique environment. Thus, scores on the DASS scale explain about 30% of the variance in scores on the wellbeing scale (or vice versa), with half of this due to genetic factors and half to environment.

We also conducted a multivariate twin model of wellbeing with the three DASS subscales (instead of total DASS scores) and confirmed a similar pattern to the bivariate model (see Supplementary Results and Supplementary Fig. 2 for further details).

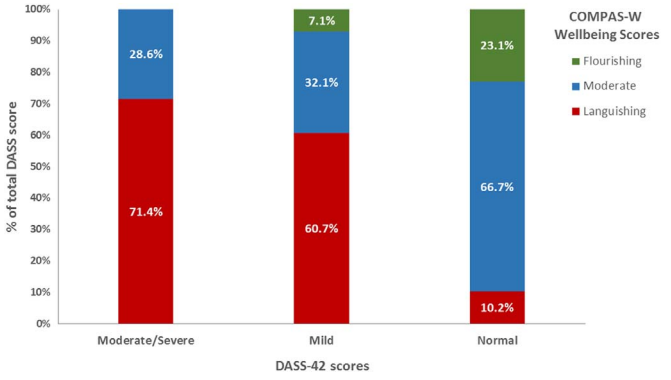

Fig. 1. Frequency (%) of COMPAS-W wellbeing categories as a proportion of total DASS-42 depression and anxiety scores. N = 743, twin 1 (similar distributions were found for twin 2).

4. Discussion

The goal of this study was to examine the relationship between wellbeing and anxiety and depression symptoms in 1486 healthy adult twins from the TWIN-E study. The two aims of the study were to examine the cross-frequency of wellbeing and depression and anxiety symptoms in a normative sample, and to understand the role of shared and unique genetics and environment between these symptoms.

First, in terms of frequencies, we found that the majority of the sample (93%) was classified as "normal" according to the DASS-42 Depression, Anxiety and Stress Scale; however of these participants, only 23% were also reported to be "flourishing" on the COMPAS-W wellbeing scale. Similarly, of the total number of participants who were languishing, more than two-thirds (10% of a total 14%) were "normal" in terms of DASS symptoms. These figures replicate Keyes (2005) results for which 22% of the participants who were free of mental illness were flourishing, and 10% of the total 17% of languishing participants had no mental illness as reflected in the DASS score. These findings highlight the gap between "absence of mental illness" and "optimum mental health". Within our healthy population, the majority of participants had scores within the "normal" range of depression and anxiety symptoms, yet less than a quarter (22%) was flourishing and a comparable rate (14%) was languishing. Therefore, while all participants were technically "healthy" (i.e., displaying an absence of mental illness), they varied considerably in levels of "wellness".

The second aim of this study was to understand the role of common genetics and environment that may underpin wellbeing

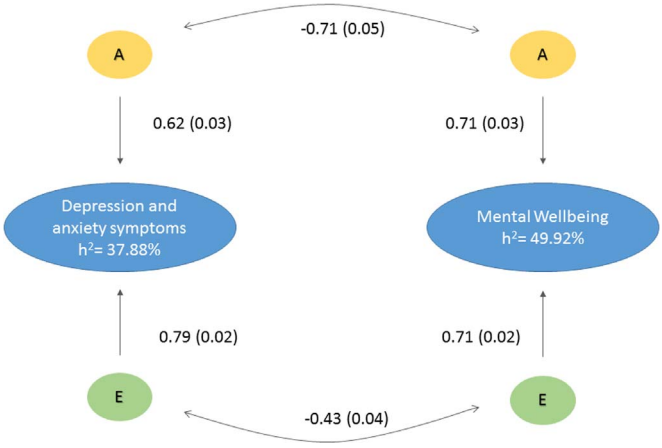

Fig. 2. *Correlated-factors AE model for symptoms of depression and anxiety and wellbeing.* Figure displays results for twin 1, and includes additive genetic (A) and unique environmental (E) influences on the latent phenotypes depression and anxiety symptoms, and mental wellbeing. All path estimates are standardized, with standard errors in brackets. Single-headed arrows indicate the impact of the genetic and environmental factors on the latent phenotypes; double-headed arrows represent the genetic and environmental correlations between latent factors.

Table 1
Model fit statistics for bivariate genetic modeling of DASS-42 and COMPAS-W Wellbeing total scores.

Model	−2LL	df	AIC	diff LL	diff df	p	Compared to model
1. Corr Factors ACE	7917.461	2955	2007.461				
2. Corr Factors AE	**7917.461**	**2958**	**2001.461**	**0.00**	**3**	**1.00**	**CF ACE**
3. Corr Factors CE	7945.427	2958	2029.427	27.97	3	0.00	CF ACE
4. Corr Factors E	8111.245	2961	2189.245	193.78	6	0.00	CF AE
5. CF AE – no A corr	8008.297	2959	2090.297	90.84	1	0.00	CF AE
6. CF AE – no E corr	8030.88	2959	2112.88	113.42	1	0.00	CF AE

Note. Bolding indicates the best model. CF: correlated factors model; A: additive genetics; C: common environment; E: unique environment.

and depression and anxiety symptoms. The phenotypic correlation between DASS and wellbeing (−0.55) is consistent with previous studies (Kendler et al., 2011a, 2011b; Nes et al., 2008) confirming that while there is a strong negative relationship between the constructs – such that decreases in one are associated with increases in the other - there is also a clear distinction between them. Genetic factors contributed to about half of the phenotypic correlation between depression and anxiety symptoms and wellbeing (i.e., 56.34%). This estimate is within the ranges of 22–60% reported by Nes et al. (2008), but lower than Kendler's reported genetic contributions of 69–86% in their studies of internalizing psychopathology and mental wellbeing. However, these differences are likely accounted for by differences in measurement period and cohort inclusion criteria. Thus, while Kendler's study defined symptoms according to their incidence in the previous year, and amongst the general population, this study examined symptoms specific to the previous week and excluded participants with psychiatric history which may have diluted the strength of the genetic relationship that caseness might contribute.

In the optimal twin model, half the total variance in wellbeing scores was a result of genetic factors and the other half a result of unique environment. Of the total variance in wellbeing scores, genetics (heritability) accounted for 50% of the variability (of which 25% was shared with depression and anxiety symptoms and 25% was unique to wellbeing), and unique environment accounted for 50% of the variability (with 9% shared with depression and anxiety symptoms and 41% unique to wellbeing), replicating the results of Kendler et al. (2011b). The large proportion of unique environment attributable to variance in mental wellbeing independent of depression and anxiety symptoms suggests that it is impacted by various life experiences and possibly interventions that may not necessarily have a direct impact on depression and anxiety symptoms. An interesting point is that, although the amount of environmental variance shared between wellbeing and depression and anxiety was low, the unique environmental correlation was moderate (−0.43). This suggests that the twin with higher scores on depression and anxiety tends to be the same twin with lower scores on wellbeing, and that the environmental factors that reduce (or increase) symptoms of depression and anxiety may also potentially increase (or decrease) mental wellbeing.

Two-thirds of the total variance in wellbeing scores was completely distinct from anxiety and depression symptoms. This indicates that the majority of genetic and environment factors influencing wellbeing do not also impact anxiety and depression symptoms. Theoretically, the results support Keyes' (2002, 2005) complete state model of mental health which suggests that mental wellbeing and illness are two separate but correlated dimensions. The clear distinction between depression and anxiety symptoms and wellbeing was apparent in our results, at both the phenotypic level and at the genetic-environmental level. Although this distinction has since been supported by a number of studies in different ways (Kendler et al., 2011a, 2011b; Nes et al., 2008), research and policy around mental illness and wellbeing still seem to operate in parallel. For instance, the most recent national survey of mental health and wellbeing in Australia included only a single measure of mental illness and no measure of wellbeing (ABS, 2008), and in the Measure of Australia's Progress 2013 update, the Australian Bureau of Statistics (ABS) concluded that “mental health and wellbeing in Australia has progressed since 2001 because the levels of psychological distress (our progress indicator for mental health and wellbeing) have decreased” (ABS, 2014). Future studies need to measure an individual's complete health; that is both symptoms of ill health but also symptoms of wellbeing. Inclusion of measures of wellbeing such as the COMPAS-W scale are important additions in population-level indices of health to get a complete picture of the state of mental health in the general population, and to inform preventative educational programs and interventions. This is particularly the case in light of recent findings demonstrating that positive mental health has a protective benefit against risk for future mental illness (Keyes et al., 2010b), suicidal ideation (Keyes et al., 2011) and premature mortality (Keyes and Simoes, 2012). On the flipside, lower rates of wellbeing have been shown to predict future risk for mental illness (Grant et al., 2013; Keyes et al., 2010b; Lamers et al., 2015). Together, these findings bear on the need for the inclusion of positive mental health or wellbeing measures in mental health research and surveillance.

Clinical research into mental illness also needs to include wellbeing as a treatment outcome measure following intervention. The aim of recovery from mental illness is not merely the reduction of symptoms to non-clinical levels, but also an increase in mental wellbeing such as an increase in positivity, mastery and a sense of own-worth. Further, it would help identify aspects of clinical treatment that separately foster an increase in wellbeing over and above a reduction in risk symptoms which may be more broadly applicable to the general population.

Several potential limitations are worth discussing. In this study, questionnaires and cognitive testing were completed online to maximise efficiency in data collection and ease of access to participants who may reside in distant or remote locations. As such, eligibility criteria included having internet and computer access to complete the questionnaires. Alternative modes of data acquisition such as phone interviews and/or in-laboratory testing could have been adopted but at the significant expense of sample power and testing feasibility.

Another potential limitation worth considering is the nature of the twin models adopted. In the current study, we used total scores (both wellbeing and DASS scores) as the tested variables in the model. We decided to use these total scores as the factor analytical structure of each scale from the individual items has already been validated using confirmatory factor analysis in the same sample of participants (Burton et al., 2015; Gatt et al., 2014). An alternative approach would be to instead use the individual items from both scales in the current twin model which may arguably reduce measurement error and take into account the non-normal distribution of the DASS scores. However, modeling such a large number of items and parameters could also reduce the parsimony of the model and stability in parameter estimation. Therefore, in the current study, total scores were the preferred option.

In the current study, we treated the wellbeing and depression and anxiety scores as separate yet related constructs, as suggested by Keyes (2002, 2005) model of mental health. These constructs could equally be represented as measures of the same dimension, should the measurement instruments actually reflect this. But they currently do not. For instance, the DASS scale measures symptoms of mental illness over the past week, with “did not apply to me at all” at one end of the continuum, to “applied to me very much, or most of the time” on the other. This is clearly a unipolar measure of the presence or absence of depression and anxiety symptoms, and not the presence of depression and anxiety symptoms and the absence of wellbeing. The difficulty arises when it is interpreted as a bipolar measure, as in the case of the ABS using reductions in levels of psychological distress as a de facto indicator of health. Whether or not wellbeing and depression and anxiety are independent or related constructs, the point of this study is to emphasise that we need measures of both aspects to get a true reflection of health. As it stands, we are only measuring and treating the dimension of illness.

In conclusion, this study supports the notion that depression and anxiety symptoms and wellbeing, though overlapping, are two distinct constructs. Support for this theory was demonstrated

upon examination of both cross-frequencies for wellbeing and depression and anxiety symptoms, and twin bivariate models of their shared and unique genetic and environmental variances. We therefore conclude that measures of both mental wellbeing and illness symptoms should be considered in future discovery or clinical research examining underlying mechanisms and treatment efficacy.

Financial disclosure statement

The Brain Resource Ltd. (BR) was the industry partner on the ARC-linkage grant which funded this study, but had no further role in design or implementation of the project. JMG has previously received fees from BR for consultancies unrelated to this study, was a postdoctoral fellow on the ARC-linkage grant which funded this project, and is a stockholder in Freedomsway Corp. Pte Ltd. LMW has previously held stock options in BR and has received fees from BR for consultancies unrelated to this study. KMR, KLOB, AH, PRS and CRC have no conflicts of interest to report.

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Appendix A. Supporting information

Supplementary data associated with this article can be found in the online version at doi:10.1016/j.psychres.2016.07.016.

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