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Major Depression and Life satisfaction: A population-based twin study

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Abstract

Background—The extent to which positive and negative indicators of mental health share etiological influences has been studied to a limited degree only. This study examines the genetic and environmental influences on association between liability to lifetime DSM-IV Major Depressive Disorder (MDD) and dispositional life satisfaction (LS).

Methods—Two-wave questionnaire data on LS (assessed 6 years apart) and lifetime MDD obtained by structured clinical interviews in a population-based sample of adult twins were analysed using structural equation modelling in Mx.

Results—The prevalence of lifetime MDD was estimated to be 11.1% and 15.8% in males and females, respectively. Individuals fulfilling the criteria for MDD reported significantly lower levels of LS. The co-variation in MDD and dispositional LS was found to be accounted for by genetic and unique environmental influences only. The phenotypic correlation was estimated to be 0.36, of which genetic influences accounted for 74% and environmental factors the remaining 26%. The correlation between genetic factors for MDD and LS was estimated to be –0.55 and the correlation between unique environmental factors to be –0.22. Heritability was estimated to 0.34 and 0.72 for MDD and LS, respectively.

Limitations—The sample consists of twins only and there are limitations associated with the twin design.

Conclusions—Whereas genetic influences on vulnerability to lifetime MDD are considerably shared with liability to (low) LS, environmental influences are more distinct. Thus, environmental factors associated with risk of MDD do not strongly impact on dispositional LS, and conversely, environmental factors influencing dispositional LS do not strongly buffer against MDD.

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Keywords

depression; internalizing disorders; well-being; life satisfaction; twin study

INTRODUCTION

Internalizing disorders have consistently been shown to be influenced by genetic as well as environmental factors. A number of biometric studies also suggest that co-occurrence between different internalizing disorders, such as anxiety and depression, is likely to be due to common genetic factors that predispose individuals to clusters of internalizing psychiatric disorders (Kendler et al., 2003, Krueger and Markon, 2006, Krueger, 1999) with distinct environmental stressors leading to the various forms of psychopathology to manifest (Kendler and Karkowski-Shuman, 1997).

Different aspects of positive mental health have also been shown to share a genetic core (Bartels and Boomsma, 2009, Caprara et al., 2009, Keyes et al., 2010). Partly overlapping sets of genes has been shown to influence emotional, social, and psychological well-being (Keyes et al., 2010) as well as self-esteem, life satisfaction (LS), and optimism (Caprara et al., 2009). Using an extended twin-sibling design, Bartels and Boomsma (2009) also recently showed that four common well-being indicators (quality of life in general, quality of life at present, LS, subjective happiness) load on similar sets of genes, suggesting that these different well-being measures are not different at the genetic level. The collective findings have lead some researchers to propose a general and genetically influenced, “positive orientation” (Caprara et al., 2009, p. 278), or “co-vitality factor” (Weiss *et al.* 2002, p. 1147), similar to the “comorbidity factors” accounting for association between different internalizing disorders.

A related question concerns the commonality and specificity underlying association between well-being and internalizing psychopathology. Outside of the genetic arena, numerous studies have dealt with the association between distinct positive and negative emotions and the issue of whether positive and negative emotions are relatively independent (the dual continua, bivariate view) or operate inversely (the one-dimensional, bipolar view). Most studies report moderate correlations and support a partly independent model (Bradburn, 1969, Knutson et al., 1998) indicating that research on indicators of positive mental health is adding a distinctive dimension to psychiatric research.

To date, few have used formal diagnostic data to examine the relationship between common mental disorders and positive emotional states. One study using diagnostic data showed that 85% of subjects with double/chronic depression, 63% with a current major depressive disorder (MDD) and 56% of subjects with dysthymia had satisfaction scores in the severely impaired range, consistent with a monotonic gradient between the severity of depression and satisfaction impairments (Rapaport et al., 2005). A number of studies have also shown dissatisfaction to be strongly associated with poor health and health behaviour, poor social functioning, personality problems, current and future depression (Koivumaa-Honkanen et al., 2004a) and to predict mortality, suicide, and work disability due to psychiatric or somatic causes (Koivumaa-Honkanen et al., 2003, Koivumaa-Honkanen et al., 2004b). In addition, subjective life satisfaction has been shown to constitute an important component of functional outcome in both unipolar and bipolar mood disorders and to be impaired in patients with affective disorders even after recovery (Goldberg and Harrow, 2005). Few have explored genetic and environmental influences on the associations between mood disorders and well-being indicators, however, despite their important implications. Further insight into the etiological underpinnings of well-being and psychopathology may allow us

to develop more targeted models of psychotherapy and care and articulate better strategies for health promotion and resource allocation.

To our knowledge, only three previous studies have examined genetic and environmental influences on associations between well-being and internalizing problems in adults. Vinberg and colleagues examined quality of life in first-degree relatives of probands with affective disorder, finding quality of life to be impaired in twins with an affected co-twin, and suggesting a common familial vulnerability with affective disorders (Vinberg et al., 2007). Nes and colleagues (Nes et al., 2008) explored etiological factors explaining associations between LS and self-report symptoms of anxiety and depression, using a single-item LS measure and a short-form of the Hopkins Symptom Checklist (Tambs and Moum, 1993). More recently, Kendler and colleagues (2011) explored the generality and specificity of etiological factors for co-occurrence between internalizing psychopathology (IP) and (low) well-being (Kendler et al., 2011a). The authors used a latent common IP factor based on three different diagnoses (MDD, generalized anxiety disorder, panic attacks) measured by the Composite International Diagnostic Interview Short Form, and a latent well-being construct comprising emotional, psychological, and social well-being (MWB). The three studies yield qualitatively similar findings. The two larger studies (Kendler et al., 2011b, Nes et al., 2008) show a substantial, but far from complete overlap in genetic factors for current internalizing symptoms and well-being (40-60%), but less sharing of environmental influences. For example, the environmental overlap was estimated to be 5% using cross-sectional data and 29% when exploring the stable components of IP and MBW using longitudinal data (Kendler et al., 2011b). This indicates that the environmental influences are largely specific. However, environmental influences with long-lasting impact on liability to IP have more impact on MBW than environmental influences with mainly transient effects on IP.

The findings from the biometric studies clearly extend our knowledge on the associations between well-being and psychopathology. There are, however, some limitations associated with the approaches used. Firstly, the study by Nes and colleagues relied on self-report measures of psychological distress and not formal DSM-IV psychiatric disorders. The only study that have used formal diagnostic data (Kendler et al., 2011b) therefore need replication. Secondly, Kendler and colleagues (2011) used an aggregate MWB measure containing both negative and positive affect items. Measures of IP and MBW are therefore likely to at least partially overlap, consequently generating problems of tautology and measurement redundancy. When indicators reflect broad and general phenomena (e.g. global well-being, common internalizing syndromes) this problem may be particularly present. Insights into the etiological mechanisms for association between more narrowly defined, clinically relevant indicators may also be more important to clinicians than knowledge on broader aggregate measures (i.e. comorbidity and co-vitality factors). Thirdly, when well-being and psychopathology are measured concurrently, state-dependent perception and memory are likely to constitute a common source of variance (i.e. well-being levels mainly mirror current levels of depression) (Atkinson et al., 1997).

The present study explores the genetic and environmental substrate for covariation between liability to lifetime DSM-IV MDD and a latent disposition to LS in a population-based sample of adult Norwegian twins. Both well-being and psychopathology are measured by specific, commonly used indicators rather than composite measures, and well-being is measured by a cognitive evaluation rather than emotional content. To reduce problems associated with mood-mediated state-dependent recall both LS and MDD are operationalized as stable liabilities, and most importantly – are not measured concurrently. In addition to reporting etiological influences on the covariation, we also present heritability estimates for MDD and stable LS. The latter has, to our knowledge, not previously been

reported. The sample is fairly age homogenous (range 12 years), thus reducing potential problems due to different etiological risk and protective factors across age. We have also examined sex-specific effects, as a number of previous studies have reported sex-specific etiological influences on well-being and internalizing problems (Kendler et al., 2006, Nes et al., 2006, Nes et al., 2010).

METHOD

Sample

Subjects were recruited from the Norwegian Institute of Public Health Twin Panel which includes the entire cohort of twins ($N = 15,370$) born in Norway between 1967 and 1979 (Harris et al., 2002, Harris et al., 2006, Tambs et al., 2009a). The twins were originally identified through the Medical Birth Registry of Norway (MBRN), which receives mandatory notification of all live births from 16 week gestation. Two questionnaire studies (Q_1 and Q_2) were conducted in 1992 (twins born 1967-1975) and in 1998 (twins born 1967-1979) and an interview study assessing Axis I and II disorders was conducted between 1999-2004. The present study is based on data from all three assessments (Q_1 , Q_2 , interview study).

Altogether, 5,864 and 8,045 twins participated in the Q_1 and Q_2 surveys, giving an individual response rate of 74% and 63%, respectively, and about 80% of the twins participating at Q_1 also participated at Q_2 . Eligible participants for the interview study were defined as the 3,153 complete twin pairs who participated in the Q_2 study and agreed to participate in the interview. Of eligible twins, a total of 2,794 (44%) twins were interviewed. Non-participants included persons unwilling or unable to participate (0.8%), twin pairs in which only one twin agreed to participate (16.2%), and persons who did not respond after one reminder (38.2%).

Approval was received from The Norwegian Data Inspectorate and the Regional Ethical committee, and written informed consent was obtained from all participants after complete description of the study. The interviews were mainly conducted face-to-face. For practical reasons 231 participants (8.3%) were interviewed by telephone. The interviewers were mostly psychology students in their final part of training or experienced psychiatric nurses. All received a standardized training program by professionals with extensive experience with the instruments, and were supervised during the data collection period.

The mean age of the participants at the Q_1 and Q_2 surveys was 21.7 (range 18-25) and 25.6 (range 18-31) years, respectively. The mean age of the interview participants was 28.2 years (range 19-36) and 63% were female. Interview participants did not differ from non-participants on a check list of symptoms of anxiety and depression, or other health indicators included in the Q_2 questionnaire (Tambs et al., 2009b). Further detail can be found in (Orstavik et al., 2007).

Zygosity assignment was initially based on discriminant function analyses using questionnaire items, shown to categorize correctly more than 97% (Magnus et al., 1983). Twenty-four micro-satellite markers were then genotyped on a sub-sample of 676 like-sexed pairs in the sample. Seventeen out of the 676 pairs with DNA information were found to be misclassified by the questionnaire data and zygosity corrected. This corresponds to a misclassification ratio for the total sample of 1.38%, a rate unlikely to substantially bias the results.

Measures

Lifetime major depressive disorder (MDD) was assessed using the Norwegian version of the computerized Munich Composite International Diagnostic Interview (CIDI) (Wittchen and Pfister, 1997). The CIDI is a comprehensive structured diagnostic interview for assessment of DSM-IV axis I and ICD-10 diagnoses, developed by the World Health Organization and used worldwide in major psychiatric surveys. The instrument has been shown to have good test-retest and inter-rater reliability (Wittchen et al., 1998). MDD was used as a dichotomous variable in all analyses.

LS was measured by the following single-item Q₁ and Q₂ “When you think about your life at present, would you say that you are mostly satisfied with your life, or mostly dissatisfied?”. The participants responded on a scale ranging from 0 = “extremely dissatisfied” to 5 = “very satisfied”. Responses to single-item LS judgements have been shown to be quite valid and reliable (Lucas and Donnellan, 2012, Scherpenzeel, 1995). The correlation between our single LS item and the Satisfaction With Life Scale (SWLS) (Diener et al., 1985) has been estimated to be 0.73. Factor analyses of the 5 SWLS items and our LS item using Maximum Likelihood (ML) and Principal Component Analyses in Mplus (Muthen and Muthen, 2007) yielded one factor (eigenvalue = 4.06) and our LS item loaded 0.81 (ML) and 0.83 (PCA) on this factor. Based on these and previous results (Schimmack et al., 2010, Schimmack and Oishi, 2005), the reliability of our single-item measure is likely to be 60-65%. Previous research has shown that retest correlations for LS mostly reflect stable dispositions (Lucas and Donnellan, 2007, Schimmack et al., 2010, Schimmack and Oishi, 2005). We therefore constructed a latent LS factor based on the data from the Q₁ and Q₂ assessments.

Analyses

The goal of our statistical genetic analyses was to estimate the importance of genetic and environmental factors to individual differences in i) dispositional LS and ii) vulnerability to lifetime MDD, and their importance for iii) association between LS and MDD.

Knowledge about the differential degree to which pairs of monozygotic (MZ) and dizygotic (DZ) co-twins are correlated for genetic and environmental effects enables estimation of genetic and environmental sources of variation. In classical univariate twin studies, individual differences in liability are assumed to arise from three broad causes of variation – additive genetic (A), common environmental (C), and unique environmental (E) factors. Twin resemblance may arise from A and C. Because MZ twins share all their genes and DZ twins share on average 50% of their segregating genes, A contributes twice as much to the MZ as to the DZ correlation. C contributes equally to the correlation in MZ and DZ twins (i.e. MZ and DZ twins are assumed to share all their C factors). E reflects environmental experiences that contribute to differences in liability as well as measurement error (i.e. unreliability). Thus, E constitutes the residual variance after the effects of A and C have been removed.

Multivariate models extend the basic univariate model by decomposing the variance of each phenotype (LS, MDD) and the correlation between them, into genetic and environmental sources. The degree to which different phenotypes share genetic and environmental influences will thus be reflected in the correlations (r_a , r_c , r_e) between the latent factors (Figure 1). Furthermore, the proportions of genetic and environmental contributions to the phenotypic correlations may be estimated. These estimates can be quite different from the genetic or environmental correlations. For example, the genetic contribution to two given traits may be minor. Yet, the genetic correlation could be very strong, indicating that to the

extent that they influence the phenotypes, the same genes are essentially affecting both traits.

Model fitting analyses were conducted using the raw maximum likelihood (ML) method in Mx (Neale et al., 1999). Previous research has shown that LS retest correlations are mostly due to stable dispositions that commonly explain about 50% of the time-specific variance. Assuming that 50% of the time-specific LS variance reflects a stable LS disposition (Lucas and Donnellan, 2007, Schimmack et al., 2010, Schimmack and Oishi, 2005) and a reliability estimate of about 0.60, the shared variance between the assessments will mostly (i.e. 80%) represent a stable disposition. We therefore specified an expanded liability-threshold model integrating a common pathway model (LS) and a correlated factor model (Figure 1).

Data from all five zygosity groups enables exploration of two different sex-effects: i) scalar sex-specific genetic effects which indicate sex differences in the magnitude of the genetic and environmental influences and ii) non-scalar sex-specific effects which indicate sex-specific genes. Although non-scalar sex differences may exist for LS and MDD, models simultaneously addressing phenotypic covariation and sex specific genes have inherent limitations (Neale et al., 2006a), and exploration of sex-specific genes was considered beyond the scope of this study.

The fit of the full model was compared to nested submodels. When using ML analysis of raw data, no overall measure of fit is obtained. However, as the difference in $-2 \log$ likelihood between the models are distributed as χ^2 , the relative fit of the submodels against the saturated model can be compared using the χ^2 difference test ($\Delta\chi^2_{df}$). Model fit was finally based on the principle of both parsimony and fit, using the Akaike Information Criterion (AIC), calculated as the χ^2 difference minus twice the difference in degrees of freedom ($\Delta\chi^2 - 2\Delta df$) (Akaike, 1987). The lower the AIC value, the better is the balance between explanatory power and parsimony.

RESULTS

Our final sample included Q₁ data from 2222 complete twin pairs, Q₂ data from 3298 pairs, and interview data from 1385 pairs. Follow-up data on LS (both Q₁ and Q₂) were available from 1680 complete pairs, 1353 pairs participated at both Q₂ and the interview study, and 772 pairs participated at all time points.

The lifetime prevalence of MDD was estimated to be 14.1% ($n = 394$) and similar to previously reported estimates from large-scale surveys (Kessler et al., 2003, Kessler et al., 2011). The prevalence was significantly higher in females (15.8%, $n = 281$) than in males (11.1%, $n = 113$) ($\chi^2 = 12.06$, $df = 1$, $p < 0.0001$). Mean satisfaction scores (range 0 to 5) were estimated to be 3.45 ($SD = 0.99$) and 3.52 ($SD = 1.00$) for the Q₁ and Q₂ assessments, respectively, and did not differ across sex. Compared with respondents who did not fulfil the criteria for lifetime MDD, respondents fulfilling the criteria had significantly lower ($p < 0.001$) LS scores in both the Q₁ ($M = 3.33$, $SD = 1.06$ vs. $M = 3.59$, $SD = 0.93$) and Q₂ assessment ($M = 3.19$, $SD = 1.07$ vs. $M = 3.64$, $SD = 0.94$).

The phenotypic correlations between MDD, LS₁ and LS₂ for the total sample and males and females separately are shown in Table 1. These phenotypic correlations are based on the single LS item and thus considerably influenced by measurement error. Correcting the LS retest correlation for unreliability, assuming reliability of 0.60-0.65, gives a correlation estimate of 0.60 (0.36/0.60).

Polychoric cross-twin and cross-trait correlations for all five zygosity groups are shown in Table 2. The cross-twin within-trait correlations for both liabilities were higher in MZ than

in DZ twins, indicating genetic effects (column 1 to 3). The cross-twin cross-trait correlations (column 4 to 6) were also higher for MZ than DZ twins, suggesting genetic influences on the association between LS and MDD. The two cross-trait correlations between MD and LS for DZmales differed somewhat from the remaining zygosity groups. The correlations were based on a fairly small number (116 DZmales pairs), however, and the CIs were substantial (MDD-LS₁: $r = 0.11$, CI = $-0.15, 0.35$; MDD-LS₂: $r = 0.13$, CI = $-0.12, 0.36$).

Table 3 displays the results of the model-fitting procedure. The full model (Model 1) included all specified pathways from all latent variables for MDD and LS, and allowed the path coefficients to differ between the sexes. In models II and III, we set to zero all shared environmental and all genetic parameters. Model II resulted in an improvement of fit (AIC = -3.758) over model I, whereas model III, which included no genetic effects, resulted in a substantial deterioration in fit (AIC = 52.910) and was therefore rejected. In the next set of models (Models IV-VI), we constrained the parameters to equality across the sexes (no scalar sex effects). The ACE model (model IV) produced further improvement in fit (AIC = -4.955). However, the AE model (Model V) showed the lowest AIC values (-14.956) and the overall best fit of all the models tested.

The parameter estimates and the genetic and environmental correlations for the full and the best-fitting models are shown in Table 4. In the best-fitting model, the r_a (95% CI) was estimated to be -0.55 ($-0.81, -0.31$) and the r_e to be -0.22 ($-0.49, -0.04$). This indicates that both genes and unique environmental experiences contribute to the covariation between MDD and LS, although the environmental influences are more specific than are the genetic influences. From the best-fitting model, the phenotypic correlation (r_p) between the latent LS factor and MDD is estimated to be -0.36 of which genetic factors account for 73.9% and unique environmental factors the remaining 26.1%. This indicates that the association between lifetime MDD and stable LS is largely due to genetic influences.

Figure 1 shows the path coefficients for the best-fitting model. The parameter estimates for the LS and MDD can be calculated from the path coefficients: For the stable propensity to LS, a^2 was 0.72 (0.85^2) and e^2 was 0.28 (0.53^2) and for MDD a^2 was 0.34 (0.58^2) and e^2 was 0.66 (0.81^2). Figure 2 shows the variance for MDD and LS decomposed at each specific time-point. Genes account for 41% of the variance in LS₁ ($A_{\text{common}} = 15\%$, $A_{\text{latent}} = 12\%$, $A_{\text{specific}} = 14\%$) and for 32% of the variance in LS₂ ($A_{\text{common}} = 15\%$, $A_{\text{latent}} = 12\%$, $A_{\text{specific}} = 5\%$). The heritability of MDD, estimated to be 0.34 , is accounted for by genetic factors shared with LS ($A_{\text{common}} = 19\%$) and genes specific to MDD only ($A_{\text{specific}} = 15\%$). Environmental influences specific to each phenotype and measurement error largely accounted for the remaining variance. Common environmental influences explained 0.02% of the variance in LS₁ and LS₂ and 13.0% in MDD.

DISCUSSION

This study examined the genetic and environmental influences on the association between lifetime MDD and dispositional LS. Consistent with previous studies, our results show that MDD and disposition to LS are moderately inversely related ($r_p = -0.36$), indicating that the two phenotypes belong to separable, but correlated dimensions. In accordance with the results from the three previous studies, exploring related phenotypes (Kendler et al., 2011b, Nes et al., 2008, Vinberg et al., 2007), our findings show a substantial, but far from complete overlap in genetic risk factors ($r_a = -0.55$). Thus, a disposition to life satisfaction does not merely constitute the “other end” of the genetic liability to depression. Although some genetic factors for (low) LS convey risk for MDD, high levels of enduring life

satisfaction also reflect other independent genetic influences associated with healthy psychological functioning.

Environmental influences explain only a small part (26%) of the association between MDD and LS and the environmental influences are considerably more distinct ($r_e = -0.22$) to each separate phenotype than are the genetic influences. These estimates are quite consistent with previously reported estimates (Kendler et al., 2011b) and indicate that environmental exposures associated with vulnerability to MDD do not strongly impact on dispositional LS, and conversely, environmental exposures to dispositional LS do not strongly protect against MDD.

The heritability estimate for liability to lifetime MDD was estimated to be 0.34, similar to results from previous studies (Sullivan et al., 2000). Heritability for dispositional LS was estimated to be 0.72. Although we are not aware of previous studies reporting heritability for dispositional LS, two previous studies report fairly similar heritability estimates (0.75 – 0.81) for stable levels of subjective well-being (SWB) (Lykken and Tellegen, 1996, Nes et al., 2006). The collective findings thus suggest that liability to internalizing psychiatric disorders and dispositional well-being, and the covariance between them are influenced by both genes and environmental factors of which some are shared. The commonality of the genetic influences is, however, considerably greater than the commonality of the environmental influences.

Common genetic factors underpinning the two phenotypes may, at least partly, reflect personality. The personality trait of neuroticism (N) has been found to strongly predict comorbidity among the internalizing disorders (Bienvenu et al., 2001, Hettema et al., 2006), and biometric studies consistently indicate considerable overlap between the genetic factors for N and for liability to internalizing disorders (Hettema et al., 2004, Hettema et al., 2006). For example, Kendler et al. (2006) showed N to strongly predict risk for lifetime major depression (MD), and reported the association between the two phenotypes to be largely due to common genes. In a more recent study, (Kendler and Myers, 2010) examined the relationship between lifetime MD and the five-factor model of personality, finding N and conscientiousness (C) to have moderately strong both phenotypic and genetic correlations with liability to MD, and openness, extraversion (E) and agreeableness, to have somewhat smaller correlations. However, a substantial proportion of the relationship between C and MD was found to result from shared variance with N. Numerous studies have also shown N and E to be strongly related to a range of well-being measures (Lucas and Diener, 2008). Furthermore, Weiss and colleagues (2008) recently found no support for unique genetic effects on SWB, finding the genetic sources of SWB to be entirely shared with genetic influences on N and E, and to a lesser extent C (Weiss et al., 2008).

Considerable work has been invested in detecting variants in specific genes involved in the etiology of personality traits and psychiatric disorders. A frequently studied functional polymorphism in the promoter region of the serotonin transporter gene (*5-HTTLPR*) has been implicated in neuroticism and neuroticism-related traits and disorders (Lesch et al., 1996). Although many studies have failed to replicate this finding, two meta-analyses have supported significant associations between *5-HTTLPR* and anxiety-related traits (Munafo et al., 2003, Sen et al., 2004). A recent molecular genetic report also suggests that the *5-HTTLPR* is a promising candidate for better understanding of individual heterogeneity in LS (De Neve, 2011). Whereas the ‘short’ *5-HTTLPR* genotype has been suggested to be a risk allele for anxiety-related phenotypes, the ‘long’ genotype was identified as having a sizeable positive association with self-reported LS in this recent study. This report presents the first evidence relating the *5-HTTLPR* to life satisfaction. The results were based on a somewhat crude LS measure and further studies are clearly needed to evaluate the importance of De

Neve's finding. As MDD and LS are multi-factorial phenotypes resulting from a wide range of genetic and environmental risk factors, future studies also need to apply other molecular genetic approaches to refine our understanding of the specific biological and environmental processes underlying the relationship between well-being and psychopathology.

Whilst MDD, less severe depressive conditions, and poor subjective well-being constitute a major burden to the individual and to the society at large, satisfaction and positive emotions are linked to a range of salubrious outcomes. Positive emotions are associated with improved health and longevity (Danner et al., 2001, Lyubomirsky et al., 2005) and have been shown to contribute to the building of enduring personal resources (e.g. social connections and coping strategies), to facilitate behavioural flexibility and creativity, and to physiologically down-regulate lingering negative emotions (Fredrickson, 2001, Fredrickson and Levenson, 1998, Fredrickson and Losada, 2005). These findings underscore the importance of well-being as a health policy issue and raise questions about the potential of positivity and satisfaction interventions for prevention of mental disorders. In this study, we find that the overlap in environmental sources of MDD and LS is quite small. The majority of environmental events impacting on dispositional LS do not affect vulnerability to MDD (e.g. reducing risk). Some of these specific environmental influences may reflect measurement error rather than environmental influences per se, but there is no straightforward way of distinguishing between the two.

Our findings do not refute reports indicating that interventions targeting satisfaction and positive emotions reduce negative affect in a clinical treatment setting. Experimental and clinical research clearly indicate that positive emotional experiences and intervention tools such as mindfulness-based cognitive therapy may accumulate to alleviate distress and improve well-being (Grossman et al., 2004, Hofmann et al., 2010), and meditation techniques have been shown to simultaneously increase satisfaction and reduce symptoms of depression (Fredrickson et al., 2008). Outside of the laboratory or clinical setting, however, people are active agents in selecting and shaping their surrounding environments (i.e. stable dispositions, personality, gene environment correlation). Individuals at risk for major depression tend to select themselves into high-risk environments (Kendler et al., 1999), whereas individuals with a propensity to high life satisfaction probably select themselves into environments that amplify or strengthen their genetically based dispositions toward satisfaction and well-being. Such genetic effects on exposure to environmental risk and protection do not disqualify intervention attempts, but certainly has implications for effective public health work.

Limitations

These results should be interpreted in the context of some potentially significant methodological limitations.

LS was measured by a single global item. It is generally argued that such measures have low reliability, leading to inflated estimates of situation-specific variance. We used responses from two time points, however, analysing a latent stable disposition to LS, thus reducing the impact of situation-specific variance.

The magnitude of the heritability estimates for MDD and LS are not entirely comparable due to the latent LS measure being based on two separate assessments and thereby not influenced by time-specific measurement error. The contribution from genes and environmental factors to the phenotypic correlation between liability to MDD and dispositional LS are not likely to change with additional assessments of MDD, however. These correlations are also fairly similar to previously obtained estimates for related

measures (Kendler et al., 2011b, Nes et al., 2008). Correction for unreliability, however, would decrease the time-specific E-influences on LS considerably.

We found no evidence for sex differences in the magnitude of the genetic and environmental effects (quantitative sex-specific effects) despite some studies indicate sex-specific effects on LS, SWB, and MDD (Kendler et al., 2006, Nes et al., 2006, Nes et al., 2010). Non-scalar sex differences (qualitative sex-specific effects) may exist but models simultaneously addressing phenotypic covariation and sex specific genes have inherent limitations (Neale et al., 2006b), and the issue of sex-specific genes is beyond the scope of this study. If non-scalar sex-specific effects have been ignored, the low correlation between unlike sexed co-twins have somewhat inflated the heritability estimates. However, the genetic correlation between the genetic latent factors has probably not been much affected by such a possible mis-specification of the model.

Although we include a large number of twins, substantial attrition was observed from the MBRN through the three waves of contact. Results from an attrition study (Tambs et al., 2009b) showed that cooperation was strongly predicted by female sex, monozygosity and educational status, but not by symptoms of psychiatric disorders. A series of analyses did not show any evidence of changes in the genetic and environmental covariance structure due to recruitment bias for a broad range of mental health indicators in the second questionnaire. Although we cannot be certain that our sample was representative with respect to psychopathology, these findings suggest that substantial bias is unlikely.

Lastly, the results were obtained from a sample of young adult Norwegian twins and may not fully extrapolate to other cultural, ethnic and age groups. Also, we cannot rule out that that a current depressive episode might have influenced the answers on LS at Q₁ and Q₂.

Conclusion

Further insight into the genetic and environmental sources of positive and negative emotional states, and how they operate conjointly, may allow us to build more powerful models of psychotherapy and care and facilitate more appropriate allocation of health care resources. This study indicates that genetic influences on vulnerability to lifetime MDD are partially shared with, and partially independent of a disposition to (low) LS, whereas the environmental sources are more distinct. Thus, the environmental exposures that confer risk of MDD do not seem to strongly impact on dispositional LS, and conversely, environmental influences of importance to dispositional LS do not strongly protect against MDD.

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Figure 1.

Path diagram of the best-fitting model.

Note. Capital letters A and E in circles denote the latent variables for additive genetic and environmental effects. The subscripts, 1 and 2, refer to time points 1 and 2.

Figure 2.

Proportion of the variance accounted for by genetic and environmental factors at each assessment.

Note. A = additive genetic influences, E = environmental effects, LS = life satisfaction, MDD = Lifetime Major Depressive Disorder, Q1 = First assessment, Q2 = Second assessment.

Table 1

Phenotypic correlations

	Phenotypic correlations		
	LS ₁ - MDD	LS ₂ - MDD	LS ₁ - LS ₂
All	-0.16 (-0.23, -0.10)	-0.24 (-0.31, -0.19)	0.36 (0.33, 0.39)
Females	-0.16 (-0.24, -0.06)	-0.29 (-0.36, -0.22)	0.35 (0.31, 0.38)
Males	-0.14 (-0.27, -0.01)	-0.15 (-0.26, -0.04)	0.38 (0.34, 0.43)

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Table 2

Twin correlations for MDD and LS at time points 1 and 2 by zygosity.

	Cross-twin Within-trait			Cross-twin Cross-trait		
	MDD	LS ₁	LS ₂	MDD-LS ₁	MDD-LS ₂	LS ₁ -LS ₂
MZ _m	0.49	0.43	0.37	-0.28	-0.19	0.28
MZ _f	0.33	0.38	0.31	-0.12	-0.20	0.21
DZ _m	0.33	0.25	0.13	0.11	0.13	0.19
DZ _f	0.26	0.20	0.20	-0.02	-0.16	0.12
DZ _u	-0.09	0.10	0.10	-0.14	-0.04	0.13

Note. The subscripts 1 and 2 refer to time points 1 and 2, the subscripts f, m and u refer to females males, and unlike sexed, respectively. MZ = monozygotic, DZ = dizygotic.

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Table 3

Results from model-fitting

Sex effect	Model	-2LL	$\Delta \chi^2$	Δdf	p	AIC
Yes	1. ACE	36734.93				
	2. AE	36749.17	14.24	9	0.11	-3.76
	3. CE	36805.84	70.91	9	0.00	52.91
No	4. ACE	36755.98	21.05	13	0.07	-4.96
	5. AE	36755.97	21.04	18	0.28	-14.96
	6. CE	36812.75	77.82	18	0.00	41.82

Note. Note. The best-fitting model is shown in bold.

Table 4

Parameter estimates for MDD and latent life satisfaction in the full and best-fitting models.

Model	MDD				LS			
	a^2_m	c^2_m	e^2_m	a^2_f	c^2_f	e^2_f	a^2_m	e^2_f
Full	0.15	0.32	0.53	0.31	0.00	0.69	0.73	0.63
Best-fitting	0.34	0.00	0.66	0.34	0.00	0.66	0.73	0.28

Note. Parameters (small letters): a = additive genetic effect, c = shared environmental effects, e = non-shared environmental effects. The subscripts f and m to females and males, respectively.