The Eysenck Personality Questionnaire: an examination of the factorial similarity of P, E, N, and L across 34 countries

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Abstract

The factorial similarity of Psychoticism (P), Extraversion (E), Neuroticism (N), and Social Desirability (L), as measured by the Eysenck Personality Questionnaire, was assessed using gender- specific data collected from 34 countries. As in an earlier study using data from 24 countries (Eysenck et al., 1985), the Kaiser-Hunka-Bianchini (KHB) procedure was utilised as a measure of factorial similarity. However, given the recent evidence concerning the flawed interpretation of the original KHB coefficients, two other coefficients were used to make an assessment of factorial similarity: a congruence coefficient computed from the KHB maximally congruent orthogonalised factors, and a congruence coefficient computed from the oblique factor patterns of the U.K. target and foreign country matrices. The results of these procedures (using the U.K. factor matrices as targets, toward which each country's factor pattern is rotated) indicated that: (1) the Eysenck factors are strongly replicable across all 34 countries (2) the modified KHB similarity procedure is sound, given the nature of these particular comparisons (3) in comparison to the oblique pattern matrix congruences, those computed over the KHB maximally congruent matrices were found to be optimal both in terms of size and variation. It was concluded that contrary to pessimistic observations made elsewhere, concerning the validity of the factor comparisons based upon 'original' KHB coefficients, the analyses in this paper conclusively demonstrate a significant degree of factorial similarity with the U.K. data, across the 34 comparison countries. © 1998 Elsevier Science Ltd. All rights reserved.

Key words: EPQ; Factor Similarity; Cross-Cultural; Psychometrics

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1. Introduction

In a series of studies, implemented over the preceding 20 years, the Eysencks (Eysenck and Eysenck, 1983) have both encouraged and assisted in collecting data for cross-cultural comparisons between different countries and cultures, using the Eysenck Personality Questionnaire (Eysenck and Eysenck, 1975) as the primary measuring instrument. The essential comparison strategy has been to initially compare the factorial structure of the EPQ within each country, to that found within a representative U.K. dataset. The purpose of this comparison is to establish the universality of the psychometric scales of Psychoticism (P), Extraversion (E), Neuroticism (N), and Social Desirability (L). The first three psychometric scales (P, E, and N) are predicated upon a biologically based theory of personality, from which such a deductive prediction of universality can be made. That is, the questionnaire scales are not simply arbitrary sets of items that happen to measure attributes of behaviours, but rather are based upon a theory of personality which seeks causal explanation at the level of brain physiology and biochemistry (Eysenck and Eysenck, 1985; Eysenck, 1990). The deduction made by the Eysencks, on the basis of their theory, was that the psychometric measurement of the personality constructs of P, E, and N would prove to be universal across all countries and cultures. Although the factor of Social Desirability (L) has not been theoretically specified to the same extent as the P, E, N triad, it was considered nevertheless to be conceptually strong to the extent that it would also demonstrate almost the same degree of measurement similarity across cultures.

The methodological procedure used by the Eysencks for their comparison work has revolved around the use of exploratory factor analysis as the primary technique for determining the underlying dimensionality of the data in each country. Specifically, four principal component factors are extracted from each sample of males and females within a particular country. These components are then obliquely rotated via promax or direct oblimin to a maximal simple structure configuration. Finally, each matrix of rotated factor pattern loadings is compared to the respective rotated factor pattern of the U.K. males and females using the Kaiser et al. (KHB: 1971) procedure. Eysenck et al. (1985), in response to criticisms by Poortinga (1984) concerning the likelihood of obtaining high KHB coefficients by chance, recently reported the results of such comparisons using data from 24 countries. These results indicated that the occurrence of extremely high KHB coefficients (near 1.0) was confined solely to homologous factor pairs, that is, between P_{uk}–P_c, E_{uk}–E_c, N_{uk}–N_c, and L_{uk}–L_c (where the subscripts 'uk' and 'c' denote the U.K. and 'other' country respectively). Mean non-homologous factor comparisons were valued at about 0.16 overall.

Bijnen et al. (1986) subsequently demonstrated that, when using a 40-variable $\times$ 8 factor matrix of artificial data, then permuting item loadings within each factor vector to create 16 'randomised' factor structures, they were able to demonstrate KHB coefficients as large as 0.98 between the original target factors and one or more permuted variable factors within the randomised matrices. They concluded that such evidence seriously weakened the evidence put forward by the Eysencks, on the basis of cross-cultural factor comparison. Barrett (1986) attempted to demonstrate that the KHB coefficients were meaningful, using a procedure of analysis that relied upon monte-carlo simulation methods and incremental degradation of real EPQ factor patterns. The main conclusion reached in this paper was that the KHB procedure was sound, although the use of Kaiser's 'mean solution cosine' was seen as a mandatory constraint on any future use of the technique. That is, unless this coefficient was high (above about 0.90), it was considered wise to carefully assess the

factor comparisons at the individual item level (in order to determine the items that may be causing excessive disparity between the two factor patterns).

However, further statistical work by Bijnen and Poortinga (1988) conclusively demonstrated that the KHB similarity coefficients were actually not similarity coefficients, but rather were cosines indexing the amount of angular transformation required to bring a pattern matrix into maximum agreement with a target matrix, irrespective of whether or not the resulting maximally congruent matrices were similar to one another. In other words, the coefficients put forward by Kaiser et al. were not measures of factor similarity at all, but rather, simply a measure of the angular transformations required to minimise the vector disparities between two orthogonal factor patterns. The KHB procedure failed to take into account that the two sets of factor vectors could be completely disparate, yet might only require a small transformation to bring them into maximum possible congruence, yielding very high transformation cosines (near 1.0). Hence, the observations by Bijnen et al. (1986), and Barrett (1986) that KHB coefficients could achieve near unity, using either random or virtually random data. Ten Berge (1996) elaborated further on the use of the KHB procedure, noting that only where the product of the transpose of the target matrix with a comparison matrix is symmetric (where the numbers of factors are equal in both matrices being compared) and positive semidefinite, can the KHB congruential fit procedure be considered valid. However, the use of the KHB 'similarity' coefficients is still incorrect, as demonstrated in a simple computational example by ten Berge. Finally, ten Berge concludes that given his own mathematical arguments, Bijnen et al.'s (1986), and Bijnen and Poortinga's (1988) analytical studies, all of which demonstrate the same flaw, the KHB method is to be considered invalid as a method of factor comparison. Notably, Bijnen and Poortinga (1988) conclude.

> "In our opinion, the conclusion is inescapable that the high level of factor congruences established in cross-cultural research with the EPQ to a substantial extent are attributable to statistical deficiencies in the KHB procedure" (p. 198).

Since only the KHB coefficients have been used by the Eysencks, it is clear that another attempt at determining the measure of factorial agreement between the U.K. and all other country data is required. The demonstration that the KHB coefficients have no relevance to factorial similarity has serious implications both for the empirical work implemented to date and for a theory that purports to claim the universality of P, E, and N. Further, it is not clear that the Kaiser et al. methodology is flawed to the extent that it is unusable or invalid, as ten Berge has argued. Rather, we show below that the methodology can be modified slightly to enable its use as a conventional orthogonal target rotation procedure. In addition, we also compare the KHB orthogonal procrustes procedure with that of direct oblique pattern matrix comparison using hyperplane maximised direct oblimin rotation as the sole rotation algorithm.

2. Method

2.1. The datasets

Table 1 below presents the list of all data used in the study, along with the number of participants within each sample analysed. Each dataset represented the maximum number of participants

Table 1
The sample sizes of the datasets used, comparing each of the countries with the respective male and female U.K. datasets

Country	Males	Females
Australia	336	318
Brazil	636	579
Bulgaria	506	516
Canada	432	780
Catalania	412	393
Czechoslovakia	416	1496
Egypt	596	1196
Finland	501	448
France	983	466
Germany	747	374
Hong Kong	268	461
India	972	959
Israel	688	362
Italy	403	378
Japan	717	808
Korea	661	539
Lebanon	634	605
Lithuania	555	849
Mexico	474	514
Netherlands	401	475
Nigeria	825	455
Norway	377	425
Poland	532	661
Portugal	1109	1269
Puerto Rico	535	558
Romania	465	549
Sicily	374	401
Singapore	493	501
Spain	434	595
Sri Lanka	507	523
U.S.A.	508	873
U.S.S.R.	538	529
Uganda	918	555
Zimbabwe	473	365

available—combining multiple samples from the same country where possible. Although much of the data originally published was based upon a 101 item EPQ, many of the later datasets used a 90 item EPQ. Further, more U.K. data had been collected on the 90 item EPQ thus permitting the potential increase in sample size of a U.K. reference sample. Therefore, all datasets were reconstructed, where necessary, to conform to the 90 item EPQ as published in 1975 (all 101 item datasets contained the 90 items of the published EPQ).

2.2. The factor comparison procedures

Given the flawed interpretation of the original KHB coefficients, a decision had to be made whether to discard the KHB procedure altogether or perhaps modify its use by regarding it as primarily an orthogonal procrustes procedure, assessing agreement between factors using a conventional congruence coefficient. Since the only flaw in the KHB seemed to be one of incorrect interpretation of an inappropriate submatrix, it was decided to remain with the use of the KHB procedure, but to constrain its functionality as an orthogonal procrustes procedure, using the congruence coefficient as the measure of agreement between factor vectors in the maximally congruent factor patterns. The slightly modified KHB procedure as used for the analyses reported below assumes two factor pattern matrices are input, each with associated factor correlation matrix:

Given:

N = number of variables

k = number of factors

$\mathbf{A_1}$ = the $N \times k$ oblique/orthogonal factor pattern **target** matrix

$\mathbf{L_{11}}$ = the $k \times k$ factor correlation matrix for $\mathbf{A_1}$ (identity matrix if $\mathbf{A_1}$ is orthogonal)

$\mathbf{F_1}$ = an $N \times k$ orthogonal factor pattern **target** matrix

$\mathbf{T_1}$ = a transformation matrix that transforms the factors of $\mathbf{F_1}$ into $\mathbf{A_1}$

$\mathbf{A_2}$ = the $N \times k$ oblique/orthogonal factor pattern **'to be compared'** matrix

$\mathbf{L_{22}}$ = the $k \times k$ factor correlation matrix for $\mathbf{A_2}$ (identity matrix if $\mathbf{A_2}$ is orthogonal)

$\mathbf{F_2}$ = an $N \times k$ orthogonal factor pattern **'to be compared'** matrix

$\mathbf{T_2}$ = a transformation matrix that transforms the factors of $\mathbf{F_2}$ into $\mathbf{A_2}$

Generate (if not orthogonal matrix input) $\mathbf{T_1}$ and $\mathbf{T_2}$ matrices by factoring the respective $\mathbf{L_{11}}$ and $\mathbf{L_{22}}$ matrices so that:

$$\mathbf{L_{11}} = \mathbf{T_1'T_1} \tag{1}$$

$$\mathbf{L_{22}} = \mathbf{T_2'T_2} \tag{2}$$

$$\mathbf{F_1} = \mathbf{A_1T_1'} \tag{3}$$

$$\mathbf{F_2} = \mathbf{A_2T_2'} \tag{4}$$

$$\mathbf{H_1^2} = \mathbf{diag}\,(\mathbf{F_1F_1'}) \tag{5}$$

$$\mathbf{H_2^2} = \mathbf{diag}\,(\mathbf{F_2F_2'}) \tag{6}$$

$$\mathbf{C} = (\mathbf{H_1^{-1}F_1})'(\mathbf{H_2^{-1}F_2}) \tag{7}$$

$$\mathbf{G} = \mathbf{CC'} = \mathbf{WM^2W'} \tag{8}$$

where $\mathbf{W}$ = the matrix of unit-length eigenvectors (loadings) of $\mathbf{G}$, and $\mathbf{M^2}$ is the diagonal matrix of the eigenvalues of $\mathbf{G}$

$$\mathbf{K'} = \mathbf{C'WM^{-1}W'} \tag{9}$$

$\mathbf{K}$ is the matrix that transforms $\mathbf{H_2^{-1}F_2}$ into maximum congruity with $\mathbf{H_1^{-1}F_1}$. It is at this point that we now assess the similarity between the two matrices $\mathbf{H_1^{-1}F_1}$ and $\mathbf{H_2^{-1}F_2}$, using the congruence

coefficient of Tucker (1951) to assess the similarity between the column vectors (factors) across each matrix. Whereas the original KHB coefficients were interpreted from the elements of the matrix:

$$\mathbf{L_{12} = T_1' K T_2} \tag{10}$$

we now instead compute the congruence between the vectors of matrices $\mathbf{(H_1^{-1}F_1)H_1^{-1}}$ and $\mathbf{(H_2^{-1}F_2)KH_2^{-1}}$, which are re-expressed in the original factor space (postmultiplying by the respective normalising matrices $\mathbf{H^{-1}}$).

There is, however, a problem in using this modification with oblique factor pattern matrices that have no transformation matrix (as in the case of direct oblimin rotation). Although the $\mathbf{A_1}$ and $\mathbf{A_2}$ factor loading matrices are transformed into an orthogonalised form as $\mathbf{F_1}$ and $\mathbf{F_2}$, these latter two matrices are essentially uninterpretable as they do not conform to simple structure constraints but rather are an arbitrary orthogonalised transformation of the original oblique loading matrices. Whilst the interpretation of the congruence coefficients remains unaffected by such a transformation, the identification of which vector corresponds to which 'named' factor is virtually impossible. Therefore, the only use of such a technique is in contrasting the overall size of coefficients with those say from a direct oblique factor pattern matching procedure using congruence coefficients. The solution to this problem is to constrain the target matrix to an orthogonal simple structure matrix, with an identity matrix (of k factor dimensionality) as the factor correlation matrix. This permits the input of an artificial (0, 1) target loading matrix, or, as was done here, the Varimax simple structure rotated solution of the U.K. male and female reference sample datasets. Since there is no transformation required of the orthogonal target matrix, the comparison oblique matrix is orthogonalised and fitted to this specified target matrix. Identification and interpretation of factor congruences is now unambiguous.

The final parameter extracted from the KHB procedure was what Kaiser et al. called the 'mean solution cosine'. This is computed as:

$$\mu = \left(\frac{1}{N}\right) * \mathbf{trace\,(H_1^{-1}F_1KF_2'H_2^{-1})} \tag{11}$$

This coefficient is the mean cosine of all variable pair cosines computed between the corresponding target and comparison matrix variables (e.g. variable 1's loadings across factor vectors are compared using the values in the target and comparison matrix). However, it is important to note that the trace elements of $\mathbf{H_2^{-1}F_1KF_2'H_2^{-1}}$ are in fact congruence coefficients as defined by Tucker (1951), calculated across factor vectors, using the formula of:

$$r_c = \frac{\sum_{i=1}^{k} a_{it}a_{ic}}{\sqrt{\left(\sum_{i=1}^{k} a_{it}^2\right)\left(\sum_{i=1}^{k} a_{ic}^2\right)}} \tag{12}$$

where a_{it} is the loading of variable i on a particular factor in the target matrix t.
where a_{ic} is the loading of variable i on a particular factor in the comparison matrix c.

These may only be considered as cosines (equivalent to Pearson product moment correlations)

when the row vectors in the target and comparison matrices are transformed to have a mean value of zero (the loadings are expressed as deviation values from the mean value of each row vector; there is no need for the SDs of each transformed vector to be 1.0 unless the investigator wishes to express and view the transformed loadings on the same unit scale). Since this form of row transformation is not implemented in the KHB procedure (or here), we will in future refer to this index as the **mean solution congruence**. Its meaning is that as attributed to any congruence coefficient that varies between ± 1.0.

Since all rotations of the EPQ data have involved oblique transformations, it was also decided to measure the congruence between the oblique rotated factor vectors provided by the U.K. and comparison country oblique factor patterns. Whereas the KHB is a targeted fit procedure, the direct oblimin solutions are entirely unconstrained in that they simply conform to the simple structure oblimin criteria and those imposed by the hyperplane count maximisation at each value of δ. It is of substantive interest to compare the effectiveness or otherwise of targeted rotation, especially in the light of the recent suggestions by McCrae et al. (1996) concerning the use of orthogonal procrustes rotations in personality research, and the results indicating that orthogonal transformations recover underlying structure more accurately than those using oblique axis rotations (Gerbing and Hamilton, 1996).

2.3. The analysis sequence

For each country, the unscored data were split into male and female datasets, then submitted to principal component analysis. Four component factors were always extracted and rotated to simple structure using direct oblimin rotation with the δ parameter swept from -10.5–0.5 in steps of 0.5. For the KHB comparison, each rotated factor pattern matrix was compared to the respective male or female U.K. target varimax rotated factor pattern matrix. For the oblique congruence comparisons, the same matrices were compared to the respective male or female U.K. target direct oblimin rotated factor pattern matrix. For comparative purposes, the original KHB 'transformation' indices (from eqn 10, above) were collated, along with the modified KHB congruences, and the oblique pattern matrix congruences.

3. Results

As a preliminary check on the sufficiency of a male and female Varimax rotated U.K. factor pattern to serve as a target matrix, a KHB factor comparison analysis was initially implemented between a Varimax and direct oblimin rotated factor pattern for both the male and female U.K. datasets. That is, the male Varimax solution would be compared to the male direct oblimin solution; likewise for the females. Given the processes involved in the KHB procedure, the Varimax solution should serve as one of any number of orthogonal transformations of the data. However, it was also considered of interest to compare the Varimax orthogonal solution to a direct oblimin oblique solution, using factor congruences calculated directly from the untransformed factor patterns. The results of these tests indicated that the minimum modified KHB congruence (computed using the maximally congruent target and comparison matrix) between same factor pairs of P–P, E–E, N–N, and L–L in both male and female data, was 1.00. The direct pattern matrix

comparison yielded a minimum coefficient size of 0.99 in only one out of the 8 comparisons (the rest all being 1.00), indicating that there is really no substantive obliquity within the U.K. EPQ factor patterns at all. Mean solution congruences were 1.00 in both cases.

Tables 2, 4, and 6 below present the mean absolute-value coefficients computed from the comparison of each country's male data to the U.K. male reference sample dataset. Each table shows the full set of comparisons between all four factors in the target U.K. matrix and those from the comparison matrix. The main diagonal of each matrix corresponds to the mean homologous factor comparisons P_{uk}–P_c, E_{uk}–E_c, N_{uk}–N_c, and L_{uk}–L_c (where the subscripts 'uk' and 'c' denote the U.K. and comparison country respectively). Tables 3, 5 and 7 present the corresponding indices for the females.

Table 2
KHB transformation matrix coefficients for MALE datasets, averaged over 34 countries

	P	E	N	L
P	**0.95**	0.06	0.17	0.15
E	0.05	**0.99**	0.04	0.03
N	0.19	0.06	**0.96**	0.07
L	0.10	0.05	0.05	**0.98**

Table 3
KHB transformation matrix coefficients for FEMALE datasets, averaged over 34 countries

	P	E	N	L
P	**0.97**	0.07	0.13	0.13
E	0.07	**0.99**	0.05	0.04
N	0.13	0.06	**0.98**	0.06
L	0.11	0.07	0.06	**0.98**

Table 4
Modified CHB congruence matrix coefficients for MALE datasets, averaged over 34 countries

	P	E	N	L
P	**0.86**	0.04	0.14	0.27
E	0.04	**0.92**	0.11	0.14
N	0.15	0.12	**0.92**	0.15
L	0.27	0.15	0.15	**0.88**

Table 5
Modified KHB congruence matrix coefficients for FEMALE datasets, averaged over 34 countries

	P	E	N	L
P	**0.83**	0.04	0.10	0.27
E	0.04	**0.91**	0.17	0.12
N	0.10	0.17	**0.92**	0.13
L	0.27	0.12	0.13	**0.87**

Table 6
Oblique factor pattern congruence matrix coefficients for MALE datasets, averaged over 34 countries

	P	E	N	L
P	**0.78**	0.05	0.13	0.16
E	0.05	**0.92**	0.11	0.07
N	0.19	0.09	**0.90**	0.11
L	0.11	0.04	0.09	**0.87**

Table 7
Oblique factor pattern congruence matrix coefficients for FEMALE datasets, averaged over 34 countries

	P	E	N	L
P	**0.74**	0.04	0.12	0.14
E	0.07	**0.92**	0.14	0.05
N	0.13	0.11	**0.92**	0.11
L	0.13	0.05	0.09	**0.86**

As can be seen from Tables 2 and 3, the original KHB homologous transformation coefficients are very high, virtually identical with those reported over 24 countries in Eysenck et al. (1985). The non-homologous coefficients are likewise very low and consistent with the values reported in the earlier paper. Figures 1 and 2 show a median-based box-plot for the coefficients reported in Tables 2 and 3.

The shaded area in each boxplot encompasses the interquartile range (middle 50% of observations) with the whiskers encompassing the minimum and maximum values of each factor vector comparison coefficient dataset. The boxplots show clearly that there is little variability in the sizes of the respective coefficients, around the median values, across factor vector pairs.

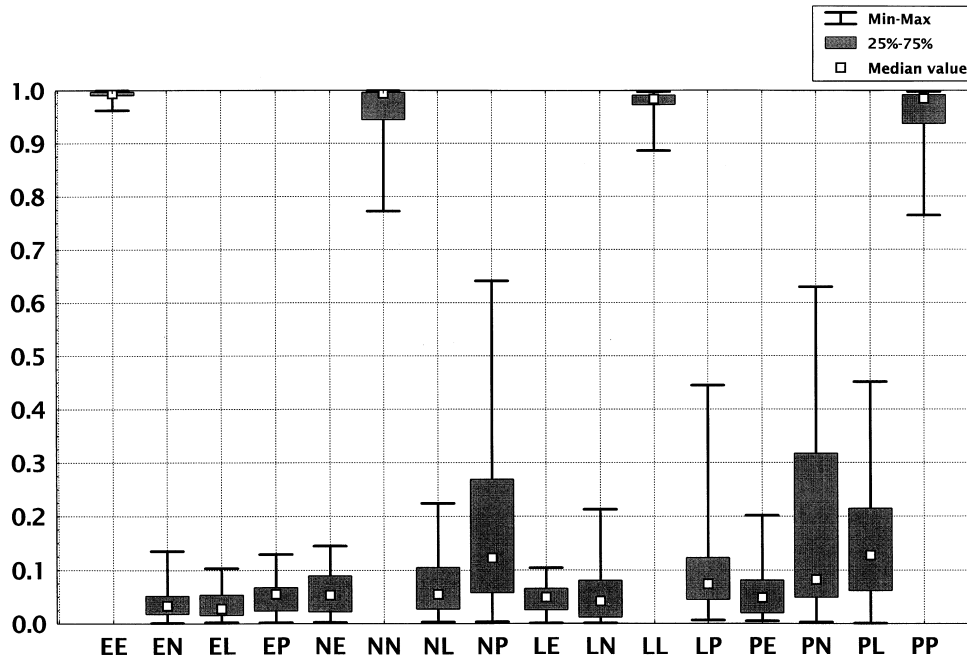With regard to the modified mean KHB 'congruence' coefficients reported in Tables 4 and 5,

Fig. 1. Median and interquartile range box and whisker plot for MALE datasets, displaying the distributional form of the KHB transformation coefficients computed across the 34 countries. The 16 possible factor comparison pairs are plotted on the *x*-axis, with the absolute valued coefficient size on the ordinate axis. The homologous factors pairs are EE, NN, LL, PP.

these values remain above 0.90 for the E and N factors, but drop to around 0.86 for P and L. Once again, non-homologous coefficients are very low in comparison to the homologous coefficients. All mean non-homologous coefficients are less than 0.28 in size. Figures 3 and 4 show a median-based box-plot for the coefficients reported in Tables 4 and 5. The boxplots are even more impressive that those shown in Figs 1 and 2. The variability in non-homologous coefficients is now overall much lower than that for the transformation coefficients, whilst homologous coefficient sizes remain high and easily discriminable—either using mean or median values, and taking into account the variability in coefficient size across the 34 country comparisons.

Finally, the results for the oblique factor pattern congruence calculations are presented for male and female datasets in Tables 6 and 7, with the corresponding boxplots for the coefficients presented in Figs 5 and 6.

These data and figures demonstrate that although there is little difference between these mean values for the E, N, and L homologous factor pairs, the values for P are significantly lower than those reported in Tables 4 and 5 above, based upon orthogonal, targeted rotation congruences. Further, the boxplots show that the variability present in the values for the oblique congruences is significantly higher than that shown on Figs 3 and 4. For both the male and female datasets, there is overlap between the largest non-homologous comparison coefficient and the smallest homologous factor comparison coefficient.

With regard to the properties of the mean solution congruence, that is, computed as part of
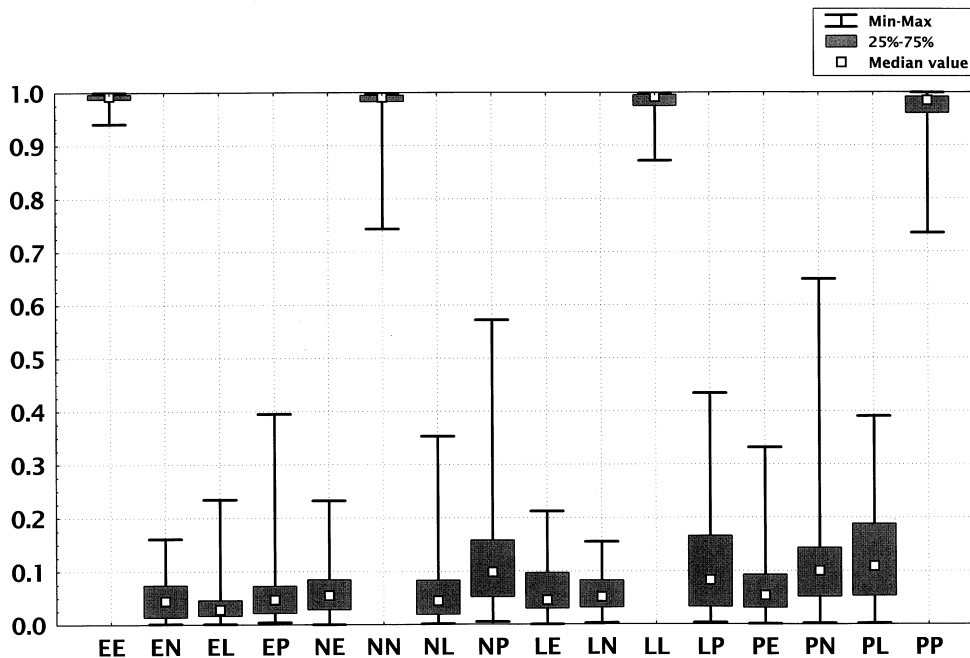
Fig. 2. Median and interquartile range box and whisker plot for FEMALE datasets, displaying the distributional form of the KHB transformation coefficients computed across the 34 countries. The 16 possible factor comparison pairs are plotted on the *x*-axis, with the absolute valued coefficient size on the ordinate axis. The homologous factors pairs are EE, NN, LL, PP.

each target-country comparison, the mean value for male and female matrices respectively is: 0.89 (range 0.76–0.95) and 0.88 (range 0.75–0.94). The median values are 0.89 for both males and females. It is useful to compare the mean and minimum values observed here with those computed over 2000 random data matrices, as reported in Barrett (1986). In this latter Monte-Carlo study, the mean solution congruence was 0.17, with a maximum value of 0.31. These figures are substantially lower than those reported above. Looking at the relationship between the size of the mean solution congruence and that of the average homologous factor congruences (the average of the P_{uk}–P_c, E_{uk}–E_c, N_{uk}–N_c, and L_{uk}–L_c comparisons), computed across each of the 34 comparisons, we observe a correlation of 0.999 for males and 0.998 for the females. This would appear to confirm the one-to-one mapping of the mean solution congruence to the average size of homologous congruence similarity coefficient computed via the modified KHB procedure. Contrary to Bijnen and Poortinga's (1988) arguments concerning its lack of use as an index of overall solution similarity, we find a direct mapping between it and the congruence coefficients computed from the maximally congruent orthogonalised KHB factor pattern matrices.

4. Discussion

From the results reported above, it is clear that the original KHB transformation coefficients were misleadingly high when used as indexes of factorial similarity. However, the modified KHB
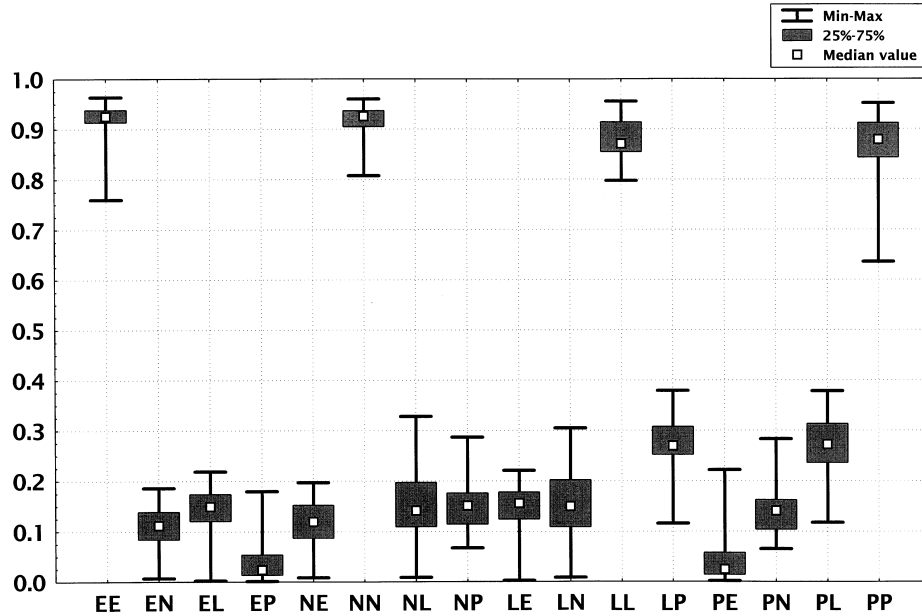
Fig. 3. Median and interquartile range box and whisker plot for MALE datasets, displaying the distributional form of the modified KHB congruence coefficients computed across the 34 countries. The 16 possible factor comparison pairs are plotted on the *x*-axis, with the absolute valued coefficient size on the ordinate axis. The homologous factors pairs are EE, NN, LL, PP.
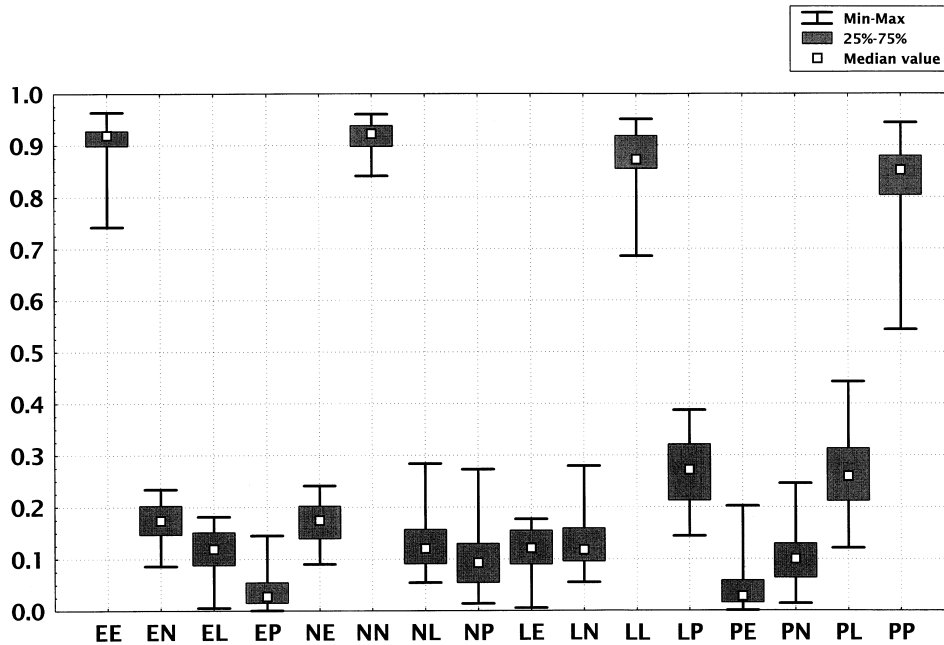

Fig. 4. Median and interquartile range box and whisker plot for FEMALE datasets, displaying the distributional form of the modified KHB congruence coefficients computed across the 34 countries. The 16 possible factor comparison pairs are plotted on the *x*-axis, with the absolute valued coefficient size on the ordinate axis. The homologous factors pairs are EE, NN, LL, PP.
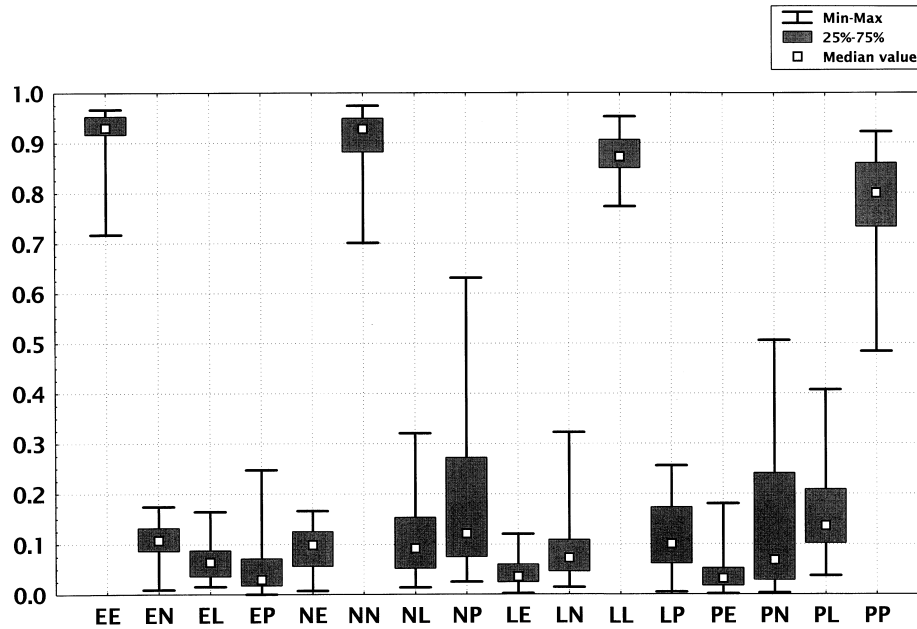
Fig. 5. Median and interquartile range box and whisker plot for MALE datasets, displaying the distributional form of the oblique factor pattern congruence coefficients computed across the 34 countries. The 16 possible factor comparison pairs are plotted on the *x*-axis, with the absolute valued coefficient size on the ordinate axis. The homologous factors pairs are EE, NN, LL, PP.
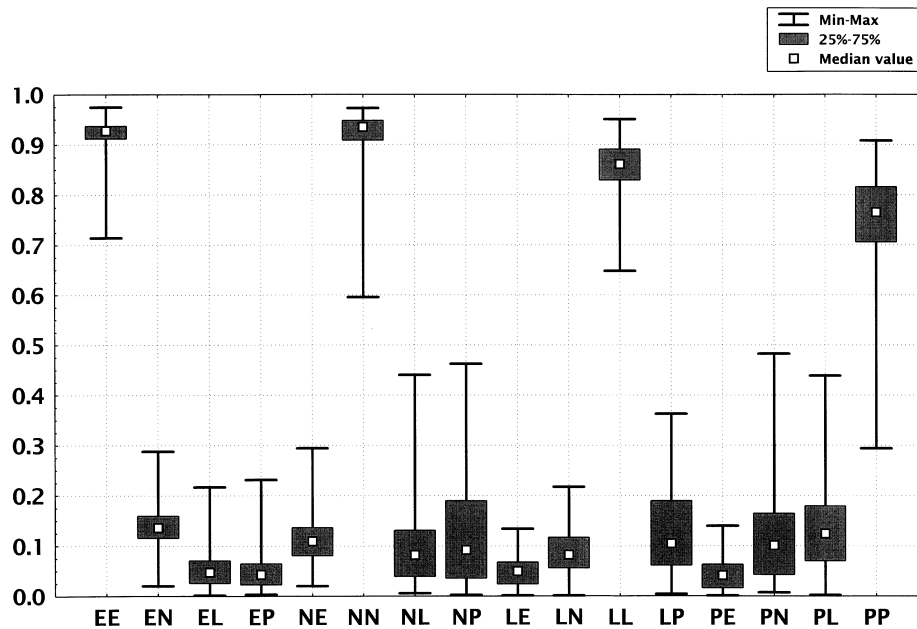

Fig. 6. Median and interquartile range box and whisker plot for FEMALE datasets, displaying the distributional form of the oblique factor pattern congruence coefficients computed across the 34 countries. The 16 possible factor comparison pairs are plotted on the *x*-axis, with the absolute valued coefficient size on the ordinate axis. The homologous factors pairs are EE, NN, LL, PP.

coefficients proposed within this paper do appear to be sensible alternatives that permit the assessment of similarity between a target and comparison factor matrix. Within the datasets used here, the variability of such coefficients is smaller than that for the oblique factor congruences reported in Tables 6 and 7. Although there is little difference between the oblique factor mean homologous congruence coefficients and the corresponding modified KHB congruence coefficients, the difference is considered substantive with regard to the P factor vector (0.78–0.86 and 0.74–0.83, respectively, for male and female comparisons). On this basis, it is considered that the modified KHB method is the optimal matching procedure for the EPQ factor structure and for all such datasets where an orthogonal target matrix is considered a relevant target, and where the number of factors being compared is equal in both comparison datasets. For the example given by ten Berge (1996) that demonstrates KHB transformation coefficients of 1.0, with obviously disparate factor patterns, the modified KHB congruence coefficients have values of 0.008 and 0.316.

Additionally, the use of the mean solution congruence is also considered a useful indicator of overall 'fit', although given its one-to-one mapping onto the mean homologous factor vector congruences, it is probably now of less importance than Kaiser et al. (1971) and Barrett (1986) attributed to it. Perhaps of more significance is the ability to isolate which variable vectors lack agreement in any solution, using the information provided by the variable vector congruences. This certainly assists an investigator in identifying disparity in agreement between global vectors.

Although much of this paper has concentrated on optimising a measure of factorial agreement, it must not be forgotten that the ultimate purpose of this paper was to demonstrate that the EPQ factors are universal across cultures. Of course, a problem immediately arises as to how one defines 'universal'. Previous definitions, based either upon the KHB transformation coefficients or conventional congruence coefficients, have generally indicated that coefficients above 0.8 are considered a minimum, with Eysenck and Eysenck (1983) proposing 0.95 as indicative of similarity and 0.98 and above as indicating essential identity. However, this bound-setting of coefficient values is rather arbitrary unless some rationale exists to minimally justify the bounds. As with all measures of agreement, there are no clear rules for when a coefficient is to be judged 'high' or 'higher'. Specifying bounds based upon a consensus position is not the way to proceed, as is becoming apparent in the debate concerning the '$P < 0.05$' level in classical significance testing (Cohen, 1994; Schmidt, 1996). Rather, it seems better to advance the hypothesis of universality based upon consideration of the behaviour of the similarity coefficients when contrasted with those from random data matrices. This is exactly the way the significant eigenvalue parallel analysis criterion (Horn, 1965) is justified. From Barrett (1986) it is known that the minimum mean solution congruence of the EPQ comparisons (observed above) is at least twice the size of the largest observed value from the 2000 random data matrix comparisons. Further, it is now known that there is a one-to-one mapping of the mean solution congruence to the average size of congruence coefficient homologous factor comparisons. Finally, the vast majority of all homologous factor comparisons are above the value of 0.85, with no overlap between the distributions of the homologous and non-homologous coefficients. Although it may be argued that coefficients of this size do not demonstrate identity between factor pattern vectors, they do nevertheless demonstrate an extraordinary degree of consistency and similarity. Even though specific items may be 'lost' in various cultures, the results above indicate that the 'core' factor remains identifiable and mathematically discriminable. It is this clear result that demonstrates the universality of P, E, N,

and L. Of course, the next step in this sequence of analyses is to now examine the item loss across cultures, and the hypothesis that a core set of items define P, E, N, and L uniquely across all cultures.

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