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Quantitative genetics and the evolution of ontogeny.

III. Ontogenetic changes in correlation structure among live-body traits in randombred mice

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SUMMARY

Ontogenetic series of phenotypic, additive genetic, maternal and environmental correlation matrices are presented and interpreted in the light of recent models for the ontogenetic origin and variation in correlation between traits. A total of 432 mice from 108 full-sib families raised in a cross-fostering design were used to estimate the various components of phenotypic correlation for five live-body traits at eight ages. The level of genetic and phenotypic correlation decreased with age, while levels of maternal and environmental correlation remained more or less constant. Genetic correlations probably decreased due to compensatory growth. Phenotypic correlations decreased primarily due to the relative decrease in importance of highly correlated maternal effects and consequent increase in poorly correlated environmental effects as portions of phenotypic variation. The effect of compensatory growth on genetic correlation was also responsible for a portion of the decline in phenotypic correlation. Phenotypic correlation patterns remained constant over the ages studied here. It also seems likely the genetic, maternal and environmental correlation patterns do not change with age for the characters analysed.

1. INTRODUCTION

Attention has recently been directed to the ontogeny of variance and covariance components in an attempt to elucidate the genetic and developmental basis of morphological integration as it affects the evolutionary process (Atchley & Rutledge, 1980; Cheverud *et al.* 1983*a*, *b*; Riska, Atchley & Rutledge, 1984; Atchley, 1984; Leamy & Cheverud, 1984; Atchley *et al.* 1984, 1985*a*, *b*; Fong, 1985). This body of research is a specific attempt to quantify the effects of development and developmental constraints on evolution, currently a subject of much debate (Bonner, 1982; Gould, 1980; Alberch & Alberch, 1981; Oster & Alberch, 1982; Goodwin, Holder & Wylie, 1983). The effects of developmental constraints on evolution by natural selection are measured by the genetic variance/covariance

matrix (Cheverud, 1984*a*), which plays a crucial role in determining the direction and rate of evolution in quantitative genetic evolutionary theory (Lande, 1979). Thus, investigation of ontogenetic changes in genetic variance and covariance patterns and how they are affected by patterns of growth will help elucidate the role of development in evolution.

Studies of changes in character variance with growth on a logarithmic scale have shown that variance increases with age during the exponential phase of growth until about three weeks in mice, and then undergoes a dramatic decline before levelling off at a relatively low value (Atchley, 1984; Riska *et al.* 1984; Monteiro & Falconer, 1966). This change in variance with age is attributed to compensatory growth, or the convergence of individual growth trajectories due to negative correlations between growth rate and size at the beginning of each growth period (Riska *et al.* 1984; Atchley, 1984). Although the magnitude of character variance has been shown to decrease during later growth periods, heritabilities – the proportion of that variance due to additive genetic effects – are only slightly affected. They tend to remain constant or increase slightly with age (Cheverud *et al.* 1983*b*), because both phenotypic and additive genetic variances show the same pattern of ontogenetic change due to compensatory growth (Riska *et al.* 1984; Atchley, 1984). In contrast to heritability, the proportion of phenotypic variance due to maternal effects decline significantly with age, leading to a proportionate increase in the importance of residual environmental effects (Cheverud *et al.* 1983*b*).

Given the existence of compensatory growth, Atchley (1984; Atchley *et al.* 1985*b*) predicts that correlations among a set of characters will tend to decrease with increasing age after a period of early 'correlating' growth. However, very little data are available to test this hypothesis. Furthermore, ontogenetic changes in the level of genetic correlation among characters will have important consequences for the level of morphological integration displayed by evolution in response to age-specific selection pressures (Lande, 1982).

Our longitudinal database provides one of the few opportunities for multivariate quantitative genetic analyses of growth. We present phenotypic, additive genetic, maternal and environmental correlations among a set of live-body characters measured at eight ages in order to test the hypothesis that correlations will decrease with increasing age, as suggested by Atchley (1984). The exponential growth period ends at approximately 31 days for the mice analysed here (Cheverud *et al.* 1983*b*), after which compensatory growth occurs (Riska *et al.* 1984). Thus we expect a decrease in the level of correlation among characters after 31 days of age. We will also test for alterations in the pattern of correlation with age. If traits differ in their pattern or timing of growth, this should be reflected in a changing pattern of correlation with age, as in the brain–body size correlations described by Riska & Atchley (1985) and Atchley *et al.* (1984). Such changes would be of importance in determining the varied effects of selection at divers ages. Inspection of the growth curves (Cheverud *et al.* 1983*b*) reveals no major heterogeneity in pattern or timing of growth for the traits analysed here, so we expect a relative constancy of correlation pattern across ages.

2. MATERIALS AND METHODS

Male and female mice from the randombred ICR strain were randomly mated, and longitudinal growth data were collected on 108 full-sib families of four pups each (432 mice) from a balanced cross-fostering design, allowing the separate estimation of additive genetic and maternal effects. Details of the experimental design as applied to this sample are given in Cheverud *et al.* (1983*b*), Cheverud (1984*b*), and Leamy & Cheverud (1984), and will therefore only by summarized here.

Two replicate sets of experiments were performed in the same laboratory nine months apart. Replicate A included 60 full-sib families nested within 30 cross-fostering pairs (240 mice) which were measured at 17, 24, 31, 45, 52, 59 and 66 days. Mice in replicate B, with 48 full-sib families nested within 24 cross-fostering pairs (192 mice), were measured at 17, 24, 31, 38, 45 and 52 days. Thus a total of 432 mice was used for estimates at 17, 24, 31, 45 and 52 days. Smaller samples of 240 mice were available at 59 and 66 days, while the 38-day sample contained a total of 192 mice. Five traits were measured at each age in both replicates: weight (WT), head length (HL), trunk length (TRL), trunk circumference (TRC) and tail length (TL). The replicates are combined here when possible. No significant difference in heritability was detected between replicates, although replicate A's heritabilities were typically slightly larger than replicate B's (Cheverud *et al.* 1983*b*). Since all estimates are within cross-fostered pairs of families, between-replicate variation does not affect the estimates.

Genetic, maternal and environmental variances and covariances were estimated from multivariate analysis of variance nested within cross-fostered family pairs using the GLM procedure in SAS-79 (Helwig & Council, 1979). The linear model specified was

$$Y_{ijkln} = \mu + \mathrm{S_i} + \mathrm{P_j} + \mathrm{d_{k(j)}} + \mathrm{n_{l(j)}} + \mathrm{dn_{kl(j)}} + \mathrm{e_{kln(j)}} \qquad (1)$$

where Y_{ijkln} is the trait value of the nth pup of sex i nursed by the lth nurse born the kth dam nested within the jth cross-fostered family pair. Effects due to dam (d), nurse (n), dam-by-nurse interaction (dn), and the residual (e) were assumed to be random effects, with zero means and variances V_d, V_n, V_{dn} and V_e respectively. Heritabilities (h^2), proportions of variance due to maternal effects (m^2), and proportions of variation due to residual environment (e^2) are reported in Cheverud *et al.* (1983*b*).

Genetic covariances were estimated by twice the dam component, maternal covariances by the nurse component, and environmental covariances by a sum of dam-by-nurse interaction and residual components. Phenotypic covariances are the sum of the three separate covariances listed above. Correlations were estimated by the ratio of covariance to the square root of the product of the variances for the two traits being considered.

The overall level of correlation was measured by the index of integration as defined by Cheverud *et al.* (1983*a*). The index I' was specifically chosen because some of the matrices estimated were negative semi-definite. This index is

a standardized standard deviation of the eigenvalues obtained by spectral decomposition of the correlation matrix. Thus,

$$I' = (\sum_{i=1}^{n}(\lambda_i - 1)^2/(n^2 - n))^{\frac{1}{2}}, \quad (2)$$

where λ_i is the i^{th} eigenvalue and n is the total number of variables represented in the correlation matrix. The index is standardized relative to the variance of eigenvalues when all of the variation in a trait set is explained by a single eigenvector. Thus it will usually, but not always, vary from zero to one, with a value of one indicating a very high level of integration. Wagner (1985) has indicated that the variance of eigenvalues is a sensitive measure of the level of integration displayed in a correlation matrix. Regrettably, there is as yet no significance test for this index of integration (I').

Correlation patterns will be compared using matrix correlations. Statistical significance of matrix correlations is tested using quadratic assignment procedures (QAP), a nonparametric test which takes into account the lack of independence of correlation estimates drawn from a single matrix (Dow, 1985; Mantel, 1967; Hubert & Schultz, 1976; Costanzo, Hubert & Golledge, 1983). A modified version of the test procedure presented by Costanzo *et al.* (1983) was used (Dow, 1985). The first two principal components of the matrices will also be compared in order to measure the structural similarity of matrices. This will be done using vector correlations (Blackith & Reyment, 1971). Simulation analysis indicates that vector correlations greater than 0·80 occur at a frequency of 6% when two randomly generated five-element vectors are compared. Thus vectors closer together than 36° are significantly similar ($\cos(36°) = 0{\cdot}80$).

3. RESULTS

The phenotypic, additive genetic, maternal and environmental correlation matrices for each of the eight ages are presented in Appendix 1. While all of the phenotypic and environmental correlation matrices are positive definite, only two genetic matrices (ages 45 and 52) – and none of the maternal matrices – are positive definite. Indices of integration (I') for each matrix are presented in Table 1. The level of integration is highest for the maternal correlations, averaging nearly 1·00 over the eight ages. This indicates that the effects of maternal environment on offspring phenotypes are conjoint. Maternal performance for weight, head length, trunk length, trunk circumference and tail length are all one and the same character. Genetic integration is also quite high, averaging 0·88 over the eight ages, indicating the overwhelming prevalence of positive pleiotropy for genes affecting these characters. Environmental integration is quite low, averaging 0·32 over the eight ages, indicating that these characters are more or less independently affected by environmental variation. Phenotypic integration, being a weighted average of its components, is intermediate, averaging 0·62 over the eight ages.

The maternal and environmental indices of integration display no patterned variation with age. The level of these correlations remains more or less constant

over the growth period. The level of genetic integration shows some tendency to decrease with age, although this is obscured by the 38- and especially 66-day correlation matrices. These two genetic correlation matrices are perhaps the least accurately estimated ones. Thus their relatively high integration levels may be due to statistical rather than biological factors. The 38-day matrix may display a

Table 1. *Indices of integration (I') for phenotypic (P), genetic (G), maternal (M) and environmental (E) correlation matrices at 17, 24, 31, 38, 45, 52, 59 and 66 days*

	Correlation type			
Age	P	G	M	E
17	0·71	0·92	0·93	0·22
24	0·78	0·95	0·97	0·45
31	0·73	0·93	0·98	0·37
38	0·56	1·08	1·10	0·15
45	0·52	0·61	0·87	0·31
52	0·56	0·80	1·11	0·24
59	0·55	0·79	0·98	0·42
66	0·52	0·98	1·02	0·39

relatively high level of integration because of the relatively small sample size (192 mice) used to estimate it. As sample size decreases, the level of correlation estimated becomes more extreme. Therefore, there is a higher probability of negative semi-definite matrices (Hill & Thompson, 1978) and a greater dispersion of eigenvalues (Hayes & Hill, 1981) for matrices estimated from smaller sample sizes. This may explain the large genetic index of integration at 38 days. The genetic index of integration is especially high at 66 days, primarily due to one very large correlation (between head length and trunk circumference), which is clearly overestimated. If trunk circumference, which is not significantly heritable at 66 days, is removed from the correlation matrix, the overall level of genetic correlation at 66 days is similar to the level at 45, 52 and 59 days. The average genetic index of integration over the first three ages (17, 24 and 31 days) is 0·93, after which the average (over 45, 52 and 59 days) drops to 0·73. Thus there appears to be some reduction in the level of genetic correlation after 31 (or 38) days, as expected due to independent convergent growth.

The phenotypic indices of integration also decrease with age from an average over the first three ages (17, 24 and 31 days) of 0·73 to an average of 0·54 over the last five ages (38, 45, 52, 59 and 66 days). This drop in the level of correlation is quite sharp, all of the decrease occurring between 31 and 38 days. Since the phenotypic correlations are the weighted average of genetic, maternal and environmental correlations, one would expect some decrease in phenotypic correlation due to the observed decrease in genetic correlation with age. However, proportions of variance due to maternal effects decrease sharply with age, especially between 31 and 45 days of age, resulting in a consequent increase in proportions due to environmental variance (Cheverud *et al.* 1983*b*). Since maternal correlations are high and environmental correlations are low throughout ontogeny, this shift in the relative importance of the variance components will also result in an overall decrease in

phenotypic correlation with age. Consideration of the relative importance of the various factors indicates that approximately 70% of the reduction in phenotypic integration is due to the decrease in maternal effects (and consequent increase in environmental effects), and only 30% is due to the reduction in genetic correlation.

Table 2. *First and second principal components and eigenvalues* (λ) *of the 45-day phenotypic* (*P*), *genetic* (*G*), *maternal* (*M*) *and environmental* (*E*) *correlation matrices*

	Component							
Trait	P1	P2	G1	G2	M1	M2	E1	E2
WT	0·513	0·060	0·489	0·186	0·479	−0·055	0·538	−0·075
HL	0·386	−0·654	0·431	−0·469	0·468	−0·195	0·298	0·730
TRL	0·475	0·117	0·501	−0·063	0·482	−0·238	0·432	−0·547
TRC	0·377	0·712	0·338	0·812	0·337	0·933	0·497	−0·190
TL	0·470	−0·219	0·458	−0·285	0·455	−0·180	0·433	0·354
λ	3·040	0·770	3·374	0·854	4·430	0·574	2·202	0·974
% variance	61	15	68	17	89	11	44	19

Matrix correlations among the age-specific phenotypic correlation matrices are all high, varying from 0·66 to 0·95, and all significantly greater than zero, as indicated by the QAP procedure. Thus there is no significant change in the pattern of phenotypic correlation during ontogeny. The ranges of correlation between characters within each age are not very large, being only 0·16 at 31 days. There is very little evidence for significant similarity within genetic, environmental and maternal sets of correlation matrices across ages, less than 10% of the matrix correlations being significant at the 5% level. This may be largely due to the small range of correlation estimates relative to the standard errors of the correlations. Given the relatively indistinct pattern discerned in the phenotypic correlation matrices, sample sizes may have been insufficient for the detection of age-related variation in genetic, maternal and environmental correlation patterns. Also, since the maternal correlations typically approximate to 1·00, there may be no maternal correlation pattern to detect.

The patterns of correlation were also analysed using principal components. The first two phenotypic principal components at 45 days are presented in Table 2 as an example, since results were similar at each age. The first eigenvector is only 7° (vector correlation (r_v) = 0·99) from an isometric vector (in which all loadings are 0·45). First eigenvectors at other ages are even closer to isometry. This indicates that all traits increase at approximately the same rate as overall size over the range of sizes represented at any single age. Size is defined here as the first principal component score. All of the first eigenvectors of age-specific phenotypic matrices are within 5° of one another ($r_v > 0{\cdot}9962$) and, on average, account for 68% of the variance. The second eigenvector explains only 12% of the variance, on average, and contrasts trunk circumference with head length and tail length. It relates to variation on a long–slender vs. short–stout shape axis. The second phenotypic principal components at each age are all within 38° of one another, with an average angular displacement of 23° ($r_v = 0{\cdot}92$).

The first two principal components of the genetic, maternal and environmental correlation matrices at 45 days are presented in Table 2. The genetic correlation matrix for 45 days was one of only two positive definite genetic matrices estimated here (see above) and one of the few in all of the quantitative genetic literature. The first genetic principal component explains 67 % of the variance and represents size and size-related shape variation. It is only 7° from an isometric vector and 4° from the comparable phenotypic first principal component. All of the genetic first principal components are within 8° of the isometric vector and within 10° of each other, indicating a strong similarity in the overall level of genetic correlation at the various ages. Averaged over the eight ages, the first genetic principal component explains 88 % of the genetic variance for these characters. The second genetic principal component explains 17 % of the variance and contrasts trunk circumference with head and tail lengths. It is only 18° from the corresponding phenotypic second component. This similarity of phenotypic and genetic principal component results is reflected in the statistically significant matrix correlation between genetic and phenotypic matrices at 45 days ($r = 0{\cdot}82$). This is by far the highest correlation between comparable phenotypic and genetic correlation matrices, but the 45-day genetic correlation matrix is probably the most accurately estimated one due to the relatively high sample size and high geometric mean heritability at this age (Hayes & Hill, 1981).

The first two maternal principal components from the 45-day matrix are very similar to their phenotypic (angular displacement (AD) = 5° for PC1 and 36° for PC2) and genetic counterparts, although the maternal first principal component explains 89 % (average over eight ages equals 98 %) of the variance and the second explains only 11 %. The first component represents size and size-related shape variation and is only 7° from the isometric vector, while the second principal component contrasts trunk circumference with head length, tail length and trunk length. Matrix correlations of maternal with phenotypic and genetic matrices are 0·63 and 0·85 respectively, both being significantly greater than zero. This indicates an overall similarity of patterns among maternal, phenotypic and genetic correlations.

The first environmental principal component is 9° from the corresponding phenotypic vector and 11° from the isometric vector, but explains only 44 % of the variance. The second environmental principal component is different from the ones presented for the previous matrices, being 41° from the corresponding phenotypic vector. It contrasts trunk length with head and tail lengths and accounts for 19 % of the variance. The matrix correlations of environmental with phenotypic, genetic and maternal matrices are 0·50, 0·02 and −0·29, respectively. None of these matrix correlations is significantly different from zero at the 0·05 level.

4. DISCUSSION

Genetic and phenotypic correlations among live-body traits in the mice used here tend to decrease with age, holding fairly constant from 17 to 31 days and then dropping sharply to a lower level which is maintained from 45 (or 38) to 66 days. The decrease in genetic correlation occurs, but is not of great magnitude (only 20 % reduction). The level of genetic integration is quite high regardless of age. The

reduction in correlation may be due to a combination of lower correlations among these traits for late growth (31–66 days) than for early growth (17–31 days) and the effects of compensatory growth. Compensatory growth could lower the genetic correlations if early growth in one trait is negatively correlated with late growth in the other trait. Since Riska *et al.* (1984) show that compensatory growth leads to negative correlations between early and late growth in weight in a large study (690 families, which included sibs of the animals presented here), it seems likely that compensatory growth would also result in negative cross-trait correlations. Each of the individual traits reported here may show signs of compensatory growth in that the genetic correlations among within-trait series of age-specific values decrease with increasing time between measurements (Leamy & Cheverud, 1984). Thus compensatory growth may be one mechanism responsible for the reduction of genetic correlation with age for the entire trait system analysed here. Phenotypic integration may also decrease due to compensatory growth, or relatively low correlations for late growth. However, most of its reduction is due to the relative decrease in highly correlated maternal effects and the consequent increase in lowly correlated environmental effects as a proportion of phenotypic variaton (Cheverud *et al.* 1983*b*).

The maternal correlations are very high, virtually representing a matrix in which all elements have a value of one. This indicates that maternal performance for live-body traits is a single, unified character. The high maternal correlations between age-specific trait values reported by Leamy & Cheverud (1984) and Riska *et al.* (1984) for these mice and by Cheverud *et al.* (1983*a*) for rats indicate that this unified maternal performance trait also has the same effect at each age, as well as for each trait at a given age. This suggests that a single unified character exists for maternal performance as it affects offspring growth. Environmental correlations are low, indicating a relative independence of environmental effects on these live-body traits. Neither maternal nor environmental correlations change in any regular way with age.

The pattern of phenotypic correlation showed no age-related change. The age-specific matrices varied in the overall level of correlation but not in the pattern of that correlation. While there is little statistical similarity of pattern across ages for genetic correlations, this is probably due to a combination of the small range of correlation values exhibited and the relatively high standard errors (S.E. $\approx 0{\cdot}16$; Klein, DeFries & Finkbeiner, 1973) for these correlations. Constancy of phenotypic correlation pattern across ages, combined with the strong similarity of the best estimated genetic correlation matrices and their phenotypic counterparts, suggests that genetic correlation patterns may also remain relatively constant over the ages considered. The same arguments would then also apply to the maternal and environmental correlation matrices. At least for ages with the most accurately estimated correlation matrices, patterns of phenotypic, genetic and maternal correlation are similar.

The principal-components analysis uncovered an isometric first component for all of the matrices considered. This indicates an independence of size and shape variation for these characters in the ICR strain. This first component explained most of the total variance in phenotypic, genetic and, especially, maternal

correlation matrices and about half of the variation contained in the environmental correlation matrices. The second principal component typically contrasted trunk circumference with body lengths, especially head and tail lengths, and thus represents variation on a short–stout to long–slender shape axis.

These results contrast those of Atchley *et al.* (1984) and Riska & Atchley (1985) for brain–body weight correlations. This brain–body weight correlation decreases dramatically with increased age, primarily due to a combination of the relatively early cessation of brain growth and convergent growth's subsequent effects on body weight (Atchley *et al.* 1984). If brain weight, with its unusual growth dynamics, had been included in this study, we would observe its correlations with the other characters decreasing with age at a much higher rate than for any other trait, resulting in contrasting correlation patterns at early and late ages. The timing and pattern of growth exhibited by weight, head length, trunk length, trunk circumference and tail length are relatively homogeneous, resulting in a relative constancy of correlation pattern across ages.

Genetic correlations are, in part, a measure of the effects of developmental constraints on heritable variation (Cheverud, 1984*a*). Our analysis indicates that the evolution of juvenile characters will be more strongly constrained than that of adult characters, as juvenile characters are more tightly interwoven with one another. This age-related decline in the level of integration may be attributed to lower correlations among characters during later growth due to the supersession of a common mitogen system for all organs early in growth by more organ-specific growth controls at later ages (Atchley *et al.* 1984, 1985*b*) or to compensatory growth. However, the overall pattern of constraint does not change with ontogenetic development for the characters studied here.

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Appendix 1. *Phenotypic (P), genetic, (G), maternal (M), and environmental (E) correlations among weight (WT), head length (HL), trunk length (TRL), trunk circumference (TRC) and tail length (TL) at 17, 24, 31, 38, 45, 52, 59 and 66 days of age*

Age 17

		G						M				
		WT	HL	TRL	TRC	TL		WT	HL	TRL	TRC	TL
	WT	1·00	1·02	0·93	0·99	0·87		1·00	0·91	0·99	1·02	0·82
	HL	0·71	1·00	1·18	0·96	0·91		0·05	1·00	0·97	0·94	0·86
P	TRL	0·82	0·70	1·00	0·62	0·85	E	0·36	0·05	1·00	1·03	0·86
	TRC	0·75	0·57	0·64	1·00	0·73		0·20	0·07	0·20	1·00	0·88
	TL	0·78	0·70	0·73	0·62	1·00		0·24	0·16	0·40	0·12	1·00

Age 24

		G						M				
	WT	1·00	0·85	1·03	1·05	1·03		1·00	1·01	1·01	1·09	0·93
	HL	0·79	1·00	0·89	0·85	0·99		0·56	1·00	0·97	1·04	0·91
P	TRL	0·89	0·80	1·00	0·98	0·92	E	0·64	0·53	1·00	0·99	0·91
	TRC	0·76	0·69	0·77	1·00	0·84		0·30	0·29	0·29	1·00	0·85
	TL	0·82	0·78	0·83	0·68	1·00		0·55	0·45	0·40	0·27	1·00

Age 31

		G						M				
	WT	1·00	0·80	1·00	0·83	0·86		1·00	0·90	1·01	1·04	0·88
	HL	0·72	1·00	0·82	1·02	0·67		0·45	1·00	0·95	1·03	0·91
P	TRL	0·82	0·70	1·00	1·21	1·00	E	0·43	0·31	1·00	1·09	0·94
	TRC	0·74	0·66	0·73	1·00	1·01		0·45	0·13	0·14	1·00	0·98
	TL	0·78	0·70	0·77	0·67	1·00		0·56	0·46	0·32	0·19	1·00

Age 38

		G						M				
	WT	1·00	1·08	0·74	1·12	0·78		1·00	1·01	0·98	1·20	1·11
	HL	0·61	1·00	0·98	1·09	1·58		−0·06	1·00	0·89	1·27	0·91
P	TRL	0·73	0·48	1·00	1·43	0·94	E	0·39	−0·03	1·00	1·44	1·06
	TRC	0·55	0·41	0·49	1·00	0·74		0·11	0·06	−0·09	1·00	1·00
	TL	0·68	0·54	0·66	0·37	1·00		−0·05	−0·13	0·06	0·10	1·00

Age 45

		G						M				
	WT	1·00	0·65	0·78	0·62	0·61		1·00	1·02	1·08	0·69	0·92
	HL	0·51	1·00	0·67	0·22	0·65		0·23	1·00	1·03	0·59	0·93
P	TRL	0·70	0·41	1·00	0·49	0·78	E	0·42	0·09	1·00	0·58	1·01
	TRC	0·54	0·26	0·46	1·00	0·35		0·43	0·19	0·40	1·00	0·59
	TL	0·66	0·50	0·59	0·38	1·00		0·42	0·23	0·16	0·32	1·00

Age 52

		G						M				
	WT	1·00	0·79	0·84	0·90	0·62		1·00	1·06	1·12	0·98	1·03
	HL	0·61	1·00	0·93	0·82	0·86		0·12	1·00	1·38	1·21	0·99
P	TRL	0·73	0·55	1·00	0·79	0·84	E	−0·37	0·02	1·00	0·91	1·03
	TRC	0·58	0·42	0·47	1·00	0·53		0·40	0·16	0·31	1·00	1·28
	TL	0·58	0·58	0·61	0·38	1·00		0·28	0·05	0·30	0·15	1·00

Age 59

		G						M				
	WT	1·00	0·91	0·99	0·68	0·48		1·00	1·23	0·96	1·29	0·74
	HL	0·52	1·00	1·03	0·73	0·78		0·06	1·00	1·14	0·26	0·67
P	TRL	0·77	0·51	1·00	0·82	0·44	E	0·67	0·16	1·00	1·18	0·81
	TRC	0·64	0·39	0·49	1·00	0·86		0·57	0·25	0·35	1·00	1·05
	TL	0·60	0·48	0·54	0·43	1·00		0·67	0·01	0·56	0·14	1·00

Age 66

		G						M				
	WT	1·00	0·76	0·62	0·06	0·54		1·00	1·08	0·75	1·28	0·64
	HL	0·50	1·00	0·74	2·51	0·74		0·09	1·00	1·18	1·42	1·02
P	TRL	0·69	0·53	1·00	0·87	0·41	E	0·71	0·17	1·00	1·08	0·65
	TRC	0·65	0·28	0·54	1·00	0·10		0·50	−0·05	0·35	1·00	0·77
	TL	0·54	0·51	0·45	0·35	1·00		0·52	0·01	0·42	0·37	1·00

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