weight than DZ twins (MZ within-pair correlation = 0.61; DZ = 0.70). By one year of age, however, the MZ twins had become increasingly similar ($rmz = 0.87$), while the DZ twins moved further apart in weight ($rdz = 0.55$). The same pattern was evident for length in even more pronounced form; at birth, the MZ correlation was 0.58 and the DZ correlation was 0.77. By two years of age, however, the MZ correlation reached 0.89, while the DZ correlation regressed to 0.58. The results are discussed in terms of (*a*) prenatal influences that differentially affect birth size within MZ pairs and DZ pairs, and (*b*) the rapid convergence of each twin on his genetic growth curve during the first year of life.

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DETECTION OF GENETIC VARIANCE IN BLOOD PRESSURE: THE NATIONAL HEART AND LUNG INSTITUTE TWIN STUDY

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The National Heart and Lung Institute Twin Study has examined 514 white adult male twin sets aged 42-56 at five centers in the United States. Blood pressure measurements for cotwins were obtained on the same day at the same center but by different physicians according to a standardized protocol. The distributions of diastolic and systolic blood pressures in the twins were comparable to those observed in other populations. Significant differences between centers were observed but no differences by zygosity were demonstrable after adjustment was made for center differences.

The data were analyzed by a method of Christian et al. which eliminates possible biases in estimated genetic variances that could result from different total variances in MZ and DZ twins. Results of the test for the presence of genetic variance indicate that both systolic and diastolic blood pressure are to a considerable extent genetically controlled with an estimated heritability of 0.8 for systolic and 0.6 for diastolic pressure. Although these findings are at variance with some previous reports, it is thought that much of the discrepancy results from application of different analytic techniques, not in the data themselves. The application of these findings to our understanding of hypertension epidemiology and community hypertensive control programs are discussed.

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GENETICS OF PLASMA CHOLESTEROL AND TRIGLYCERIDES

A Study of Adult Male Twins

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White male twins born from 1917 to 1927 (514 sets, 250 MZ and 264 DZ) were studied in 5 U.S. Centers as a part of the National Heart and Lung Institute Twin Study. Fasting plasma triglycerides and cholesterol, as well as cholesterol in very-low-density and high-density lipoproteins (HDL), were measured. Analysis of variance of the five lipids revealed no significant differences between the means of MZ and DZ twins and only HDL cholesterol was significantly variable among the 5 centers.

A new method was used to choose an estimate of genetic variance. This method includes an estimate of genetic variance for

use when the total variances of MZ and DZ twins are unequal. DZ twins had greater total variance for triglycerides. When genetic variance was estimated by subtracting the within-MZ-sets mean square from the within-DZ-sets mean square, all of the lipids had significant estimates of genetic variance; however, when genetic variance was estimated by a method designed to correct bias due to unequal total variances of MZ and DZ twins, only triglycerides had significant genetic variance. The heritability of plasma triglycerides was calculated to be 0.6.

Differential within-twin-pair environmental effects on MZ and DZ twins have been postulated to cause differences in total variance. If this is true, previous reports of twins showing significant estimates of genetic variance for plasma cholesterol may be due to environmental bias.

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A TWIN STUDY ON THE HERITABILITY OF LIPOPROTEIN FRACTIONS

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The first investigation to be undertaken by the newly-established Toronto Twin Register is concerned with the heritability of serum lipid concentrations and of specific lipoprotein fractions. Volunteer adult subjects (ages range from 18 to 65), after a 12-hour fast, provide two 15-ml samples of blood for analysis by Auto Analyser II, by agarose electrophoresis and by direct gas chromatography. Provisional diagnosis of zygosity is based on subjects' own opinions, supported by dermatoglyphic analysis and, in any difficult case, substantiated by an enzymatic series.

Analysis of the AA-II and electrophoresis data on the first 2×42 subjects shows a significant positive correlation within MZ pairs for each of the 10 lipid measurements considered, while the estimate of correlation within DZ pairs is lower in every case. Heritability appears to be higher for cholesterol than for triglyceride fractions. The electrophoretic band for the sinking pre-beta lipoprotein fraction has behaved like a simple genetic marker.

Another aspect of the analysis is the study of lipid differences between MZ cotwins in relation to corresponding intrapair differences in body weight and medical history: male pairs, but not female pairs, show a measurable statistical dependence of cholesterol and triglyceride levels on " excess " body weight.

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PLASMA PROTEIN VARIABILITY IN MZ TWINS

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Protein synthesis is under direct genetic control, with environmental influences limited to regulation and to some " high variability " fractions (viz., immunoglobulins). Thus the superimposable genome of MZ twins obviously leads to superimposable protein composition. This can certainly be utilized for zygosity diagnosis.

A previous study had shown that only MZ twins are easily exchanged by trained police dogs. This is certainly due to the superimposability of the biochemical basis of body scent.

A different approach has now been tried, based on plasma protein fractionating procedures.

A pilot study (in the course of publication elsewhere) has shown that disc Poly Acrilamide Gel Electrophoresis (PAGE) results, as expected, in widely different patterns only in DZ twin pairs.

Plasma specimens from a sample of 60 MZ twin pairs were analysed by PAGE. The substantial superimposability of MZ cotwin pattern was confirmed. An analysis of the different fractions indicates the extent of environmental variability.

This and other similar methods seem to deserve application in twin zygosity diagnosis and in clinical genetics in general.

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