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Smoking and sports participation

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It has long been recognized that both smoking and sports participation tend to cluster in families. In this chapter, we first describe the current status of smoking and sports participation as cardiovascular risk factors. After an outline of the principles of the quantitative genetic approaches to the analysis of individual differences in behaviour, we will review the literature on genetic and environmental determinants of smoking and sports participation. In the second half of this chapter, results from the Dutch Twin/Family Study of Health-Related Behavior are presented.

SMOKING AND PHYSICAL INACTIVITY AS CHD RISK FACTORS

Cardiovascular disease, the main cause of death in our western society, is to a considerable extent a product of our lifestyle. The parallel decline in mortality of coronary heart disease (CHD) and of the levels of its risk factors since the mid-1960s seems to support this statement. It is not clear, however, to what extent the decline in mortality can be attributed to a favourable change in risk factors[1,2]. Moreover, the decline in incidence of CHD is much smaller than the decline in mortality. This suggests that the decline in mortality is due to improved survival of new cases rather than to a substantial decline in incidence. The exact balance between the contributions to the decline in CHD mortality of reduced incidence, improved case/fatality rate as the result of improved medical care, and the effects of primary and secondary prevention on risk factors will remain a matter of dispute in the near future.

Setting aside the result of this dispute, it is agreed that behavioural factors, like diet, smoking and physical activity, do affect CHD risk. The status of smoking as a risk factor for CHD is well established and unequivocal. Smokers have at least twice the risk of CHD of non-smokers. The effect depends upon current dose and cumulative consumption. The risk is similar for males and females. On the other hand, the effects of smoking seem to fade away relatively fast after cessation. The largest risk decrement, of about

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50%, is in the first year with a gradual return to the level of non-smokers in 5–10 years[3]. In younger people, the decline in risk after cessation seems to occur even more rapidly[4].

There is general agreement now that a sedentary lifestyle is associated with increased CHD incidence. The results of about 50 epidemiological studies were reviewed by Powell et al.[5] and quantified by meta-analysis later on by Berlin and Colditz[6]. Both reviews observed a median risk ratio of about 2 across all studies, which means that CHD occurred about twice as often in inactive persons compared with the highly active. The better-quality studies were more likely to report a favourable association. Two thirds of the studies allowed the assessment of a dose–response relationship. The chance of developing CHD appeared to increase linearly with decreasing physical activity level. Some studies allowed an adjustment of the relationship between physical activity and CHD risk for the confounding effect of traditional risk factors [e.g. Reference 7]. These adjustments had only moderate effects on the risk ratios of physical activity, supporting its role as an independent CHD risk factor. Strictly speaking, this association does not necessarily represent a causal one, as selection factors may form an alternative explanation. Nevertheless, based on the well-accepted criteria for causality in epidemiological research (consistency and strength of the association, dose–response relationship and biological plausibility), we tend to conclude with Powell et al.[5] that, 'the accumulated data do point to a causal relationship between inactivity and CHD risk'.

A good reason to focus our attention on the factors that influence these behavioural risk factors is that the potential gain in health on the population level is enormous. Though the CHD risk associated with smoking and inactivity is about equal in magnitude to the classical risk factors, hypertension and elevated cholesterol levels, the 'population-attributable risk' is much larger. The percentage of people at risk because of smoking and inactivity is much higher than for hypertension and cholesterol. For instance, only about 10% of the population have systolic blood pressure levels above 150 mmHg (roughly doubling their risk as compared with persons with pressures lower than 130 mmHg) whereas the Campbell's Survey of 22 000 Canadians indicated that only 11% of the population older than 10 years of age performed physical activity with an intensity and frequency high enough to maintain or improve their physical fitness[8]. This leaves 89% of the population 'at risk' because of their inactivity.

Because the habits of smoking and physical activity are established early in life and tend to track into adulthood, the determinants of these habits in younger age groups deserve special attention. Adolescence is a transitional period with respect to physical activity level: it typically declines. In the Campbell's Survey, the only exception to the positive time trend was observed in a younger age group. Young men and women (age 20–24) decreased their activity by 10% between 1981 and 1988. Adolescent smoking is irregular and develops gradually to a more steady smoking pattern in adults. The majority of adolescents experimenting with smoking do not progress to regular smoking. For preventive purposes, it is important to gain insight into the factors determining the large variation in smoking across lifetime.

BEHAVIOUR GENETIC APPROACHES

The genetics of complex behavioural traits can be studied with twin, family, or adoption designs. Evidence for the influence of genetic factors on smoking behaviour and sports participation comes mainly from the first two types of studies, i.e. with twin and nuclear families.

Traditionally, heritability estimates (abbreviated to h^2) based on twin data have been obtained by doubling the difference between MZ and DZ twin correlations: $h^2 = 2(r_{MZ} - r_{DZ})$, where h^2 represents the part of the total or phenotypic variance that is accounted for by genetic factors and where r_{MZ} and r_{DZ} are the correlations between MZ and DZ twins, respectively[9]. When $r_{MZ} < 2r_{DZ}$, this additional resemblance indicates the importance of a common environment shared by twin siblings. This common environment may be created by influences from family or peers. The contribution of common or shared environment (abbreviated to c^2) to phenotypic variance may be estimated by the formula $c^2 = 2r_{DZ} - r_{MZ}$. However, this intuitively simple method of comparing twin correlations does not test any explicit model for individual differences. It only works with twins and does not generalize to more complex data sets, and it does not consider non-genetic transmission from parents to children[10]. If parents of twins are included in the design, it becomes possible to assess the presence of assortative mating, that is a correlation between spouses for the trait under study, the effects of parental influences (cultural inheritance) on offspring, and the effect of residual shared environment among the offspring that cannot be attributed to parental influences[11–13]. In nuclear family designs, correlations between phenotypic data of siblings and/or parents and offspring provide an estimate of the degree of familial clustering for a certain characteristic. However, these data do not permit a distinction between shared genes and shared family environment. Separation of genetic from environmental influences is possible if, in addition to the phenotype, family members are also measured on environmental variables that affect the phenotype[14]. However, if this so-called environmental index is itself influenced by genetic factors, heritability will tend to be underestimated while common environmental influences will be overestimated[15].

For many traits, heritability estimates obtained from twin data are often higher than estimates obtained from other family groupings. This may reflect the possible bias in heritabilities obtained from family data if an environmental index is used, the presence of genetic non-additivity, the presence of a special (MZ) twin environment, age-dependent trends in the magnitude of the genetic effects, or a correlation between genetic effects across time that is less than unity.

In adoption studies, the resemblance between foster parents and offspring and/or between siblings who are not biologically related yields estimates of the importance of common environmental influences shared by family members. The resemblance between biological parents and their adopted offspring gives an estimate of genetic influences, but, for smoking and sports participation, no studies of biological parents and their adopted children are currently available.

GENETIC AND ENVIRONMENTAL DETERMINANTS OF SMOKING BEHAVIOUR

Most studies on the genetic aspects of smoking have focused on adult and elderly twins. Hughes[16] reviewed adoption, family and twin studies on smoking. The family studies showed that adolescent smoking was associated with parental and sibling smoking. One study of nuclear families and adoptees[17] indicated that these resemblances were influenced by genetic factors. In this study, the correlation for number of cigarettes smoked per day of parents and offspring was significant whereas the correlations of adoptees with their adoptive parents were zero. The twin studies showed consistently that the concordance rates for smoking were higher in MZ twins than in DZ twins. Reported heritability estimates ranged from 0.28 to 0.84 (mean 0.53). Hughes concluded that genetic factors have a small influence on both the acquisition and the maintenance of smoking. In a study of 5044 adult male twins from the Finnish Twin Registry[18], also reviewed by Hughes, factor scores for cigarette smoking were used for analyses. The factors for smoking consisted of years smoking, cigarettes smoked per day, current smoker and ever smoker. A problem with this factor analytical method is that different aspects of smoking behaviour, which may show different patterns of inheritance, are summarized into one score. The heritability of this factor was estimated for five age groups. With increasing age, concordance rates declined for both MZ and DZ twins. The heritability remained fairly stable (from 0.55 in twins aged 18–29 years to 0.42 in the age group 50–59 years), except for those older than 60 years in which h^2 was 0.12. Overall, the estimate of heritability was 0.45 for cigarette smoking.

Other studies employing very large samples of twins have suggested substantial genetic influences on several aspects of smoking behaviour. In a study of 4380 adult male twin pairs (American World War II veterans), Carmelli et al.[19] reported a heritability (h^2) of 53% for quantity smoked. After adjustment for alcohol and coffee use, occupation and socioeconomic status, by means of regression analysis, the estimate of the heritability was reduced to 35%. Alcohol use and number of cigarettes ever smoked per day were significantly correlated ($r = 0.22$). A multivariate genetic path model approach would have been more informative to estimate the separate and the shared genetic and environmental effects that underlie this correlation. A follow-up 16 years later of this same population showed that never smoking, current smoking and quitting were moderately influenced by genetic factors[20]. Within the group of current smokers, concordance rates were higher in MZ twins than in DZ twins for both light and heavy smoking, suggesting genetic effects on the dependence of smoking.

Indications that independent genetic factors influence different aspects of smoking come from several other studies. Heath et al.[21] showed, in a study of adult Australian twins, that factors which determine smoking onset were not identical to factors that influence the age at which smoking starts. Shared environmental and genetic influences were both important in determining whether or not smoking would occur, while, for age of onset of smoking, only genetic factors contributed to the variance. In a cohort aged 31 years

and older, the genetic effect on smoking persistence was independent of the genetic effect on smoking initiation[22]. For smoking persistence, 53% of the variance was explained by genetic factors. In a study of the Virginia Twin Registry, Meyer et al.[23] found that starting to smoke and quantity smoked were inherited independently. As in the Australian sample, additive genetic and shared environmental factors both contributed to the variance in starting to smoke ($h^2 = 48\%$ and $c^2 = 33\%$). For quantity smoked, only genetic influences were significant ($h^2 = 69\%$). In 3 cross-sectional samples of adult twins, Heath et al.[24] investigated self-reported data on smoking initiation. With different birth cohorts, they tested whether the decline in the percentages of smokers had led to a change in the relative contributions of genes and environment to the risk of becoming a smoker. There was no evidence for cohort differences in the genetic and environmental effects, despite the marked decline over time in the proportion of males who ever smoked. There were sex differences and cross-cultural differences in the estimates of the genetic and environmental contributions to the risk of becoming a smoker. Among American males, 60% of the variance was explained by genetic factors and 23% by shared environment. For females, these estimates were 51% and 28%, respectively. Among Australian twins, the genetic contribution was larger in females ($h^2 = 67\%$) than in males ($h^2 = 33\%$). Shared environmental effects explained 15% in females and 39% in males. These estimates came from models in which the correlation between shared environmental effects in opposite sex twins was 0.33 in the Americans and 0.49 in Australians.

Gurling et al.[25] reviewed the behavioural genetic approaches used in the studies on substance use. They pointed to the need to investigate both environmental and genetic influences and to account for cultural transmission and assortative mating within the genetic models of substance use. Only a few studies take assortment for smoking behaviour into account. Assortment may result in either more genetic or environmental resemblances between relatives or both. Therefore, heritability estimates in twin and family studies for smoking behaviour that do not take assortative mating into account, may be biased. In a study of changes which take place in smoking behaviour of married couples over time, Price et al.[26] fitted different probability models. They showed that spouses with identical smoking habits at the time they first began dating each other, tended to be more stable in their smoking behaviour than spouses who had initially dissimilar smoking habits. A study from the Colorado Adoption Project examined spouse similarity for biological, adoptive and non-adoptive parents[27]. Assortative mating coefficients were calculated for 55 pairs of biological parents, 116 adoptive and 76 non-adoptive parents. The results indicated moderate to large assortment for current smoking (0.69 in biological parents, 0.32 in adoptive parents and 0.39 in non-adoptive parents). The biological parents were considerably younger than either the adoptive or the non-adoptive parents. The assortative mating coefficients were significantly different among the three types of parents, but Ho gives no explanation for these differences. For ever-smoked assortative mating coefficients were smaller (0.23, 0.28 and 0.21, respectively). Pérusse et al.[28] assessed, as a part of the Canada Fitness Survey, the degree of familial resemblance for smoking. They observed a spouse

correlation of 0.61 for smoking status. Parent–offspring and sibling correlations were 0.40 and 0.57, respectively. The spouse and sibling correlations were higher than the parent–offspring correlations. This suggests that familial resemblance for smoking may result primarily from environmental factors common to members of the same generation.

Several studies have focused on the environmental factors that predict the experimentation with and the subsequent onset of smoking in adolescents. Chassin and Presson[29] found among 3015 adolescents that the initial experience with smoking was dependent on the presence of parents and older siblings who smoked and on deviance-prone personality characteristics. Two other studies showed that peer group influence is the most important factor that predicts the experimentation with cigarettes[30,31]. Mittelmark et al.[31] also found evidence for the influence of smoking siblings on experimentation with smoking. Evidence that prior experimentation is associated with the subsequent onset of smoking comes from two studies[32,33]. On the other hand, Pederson and Lefcoe[30] followed 2245 subjects for 8 years from young adolescence to late adolescence/early adulthood and found that early experimentation was not a strong predictor of increased involvement with smoking in adolescence.

Several studies found that the risk of taking up regular smoking is associated with smoking siblings, peer influences, spending time with opposite-sex friends and having a boy/girl friend[29,33,34]. The influence of peer smoking increased over the adolescence years and girls were more vulnerable to external influences than boys[29]. An association between smoking of parents and adolescent smoking was also found[33,35]. Another study showed an influence of maternal smoking for girls only[34]. In the study by McNeill et al.[32], family smoking was not a significant predictor for the subsequent onset of smoking in adolescence. Bauman, Foshee, Linzer and Koch[36] found that ever smoking of parents was more strongly correlated with adolescent smoking than was current parental smoking. Ever smoking of parents was as strongly related as peer smoking with adolescent smoking. Other factors that increase the risk of taking up regular smoking are attitudes and beliefs about smoking and behavioural intentions to smoke[29,30,32,33], being dismissive of the hazards of smoking[31,34], lower social class[35], low self-esteem[33] and having been drunk[32].

These studies did not take the possible genetic influences into account. For example, studies which show a relationship between parental smoking and children's smoking assume that parental smoking is a component of the environmental influences in children. However, parents and offspring not only share, to some extent, their environment but also share on average 50% of their genes. Within the genetic models, it is possible to account for the genetic relatedness between parents and offspring and to separate environmental factors that are shared between parents and children from environmental factors that are shared in siblings only. In this way, the contribution of parental smoking to the environmental influences of their children can be estimated.

DETERMINANTS OF PHYSICAL ACTIVITY

There is not much research on the determinants of adolescent participation in physical activities. Lewko and Greendorfer[37] reviewed the family influences and sex differences in children's socialization into sports. They stated that the family rather than the school and peers are most influential on children's sports socialization, that parents are more influential than siblings and that the father is most relevant in the sports socialization process, regardless of the sex of the child. In an update of this review[38], these statements were adjusted. The peer group, rather than the family, was now considered the most influential social system. Whether parents or siblings were more influential remains unanswered, but some evidence was provided to support the father's role as the most influential for socialization into sports. In a study of the correlates of sports participation among adolescent girls, Snyder and Spreitzer[39] found that socialization into sports begins in childhood with encouragement by parents and continues into adolescence with encouragement from significant other individuals (peers, teachers and coaches).

Gregson and Colley[40] examined the association between parental sports involvement and sports participation in adolescent males and females. The results indicated a more important role of parents in sports socialization for females than for males. For females, there were significant correlations between sports participation and father's participation ($r = 0.22$), mother's participation ($r = 0.20$) and mother's achievement ($r = 0.21$). Maternal and paternal sports participation were also correlated. No significant correlations were found between parental sports involvement and sports participation in males. The difference in the socialization of males and females into sports is also supported by the finding that the school is more influential for males than for females[37,38]. Familial aggregation in physical activity was observed in 30 children, aged 5–9 years, and their parents[41]. Children of active and less active parents exhibited physical activity patterns similar to their parents.

The above-cited studies showed evidence for parental influences in sports participation and physical activity of their children. However, the question of whether these familial influences are mediated by cultural inheritance or by genetic relatedness was not addressed.

The degree of familial resemblance for activity level was assessed in 16 477 subjects, aged 10 years and older, from the Canada Fitness Survey[28]. Pairs of spouses, siblings and parent–offspring were formed to compute familial correlations in energy expenditure, time on activity and activity level. Evidence for familial resemblance was observed for all these variables. Familial correlations were higher within generations (spouses and siblings) than across generations (parent–offspring). The correlations within generations were similar for spouses and for siblings. This suggests that familial resemblance may result primarily from environmental factors common to members of the same generation. A second study by Perusse et al.[42], in a large family cohort (1610 subjects from 375 families), assessed environmental and genetic effects on overall level of habitual physical activity (including all types and intensities of activities) and on exercise/sports participation (activites requiring at least five times the resting oxygen consumption).

Different kinds of familial correlations were computed, including foster parent with adopted child and twin correlations. With a path analytical model, transmission from one generation to the other was separated into genetic and cultural components of inheritance. Level of habitual physical activity was significantly influenced by genetic factors (29%). For exercise participation, transmission was accounted for by cultural factors (12%). However, non-transmissible environmental factors (i.e. factors shared in one generation not shared with the other generation) accounted for most of the variance of both of these physical activity indicators. In this study, habitual activity levels were corrected for age, sex, body mass index, socioeconomic status and physical fitness as assessed by PWC 150. Fitness levels have a rather strong genetic component[43] so correcting for this variable may lead to underestimation of the influence of genetic factors on physical activity. This might explain why 'participation in sports', a potentially preferred choice for genetically fit persons, shows no genetic contribution.

Evidence that genetic factors influence physical activity comes from a study on adult male twins in the Finnish Twin Registry. Kaprio et al.[18] factor analysed physical activity variables (amount, intensity, duration and number of years of physical activity) assessed by questionnaires. The factor score obtained for physical activity was used to compute correlations in MZ and DZ twins, resulting in a heritability estimate of 0.62. A genetic contribution to activity levels was also observed in two studies on twins under 10 years of age[44,45]. In a study by Fagard et al.[46] of 48 male twins aged 18–31 years, an index of sports activity, including present and previous involvement in sports, showed identical intrapair differences in monozygotic and dizygotic twin pairs, whereas most indices of maximal aerobic power showed a strong contribution of genetic factors.

THE DUTCH TWIN/FAMILY STUDY OF HEALTH-RELATED BEHAVIOR

The Dutch Twin/Family Study of Health-Related Behavior is a large-scale study on the genetic and environmental determinants of alcohol consumption, smoking and physical activity. Data are collected by mailed questionnaire. Almost 1600 adolescent twins and their parents participated in the first wave of data collection. Over the next four years, we will measure this population another twice and add siblings of the twins to the design. The first results for smoking and sports participation are presented here.

Subjects

All city councils in the Netherlands (699) were asked by letter for addresses of twins aged 13–22 years. A positive response was received from 252 city councils, representing all parts of the Netherlands, which supplied 3859 addresses; 177 addresses were available from other sources. Of these, 2375 families of twins indicated their willingness to participate in the twin project.

These families received mailed questionnaires on health and lifestyle. A total of 1610 families (68%) returned questionnaires. Data from 17 families were not used because the twins were either too young or too old or because one or both twins had not completed the questionnaire. This leaves a total of 1593 families. Of these, 1339 families included both parents and twins.

The questionnaires consisted of items on zygosity, health, alcohol and tobacco use, sports participation and personality. Age of the twins was between 13 and 22 years, mean age was 18 years (SD = 2.3). Mean age of the fathers and mothers was 48 years (SD = 5.7) and 46 years (SD = 5.2), respectively. Zygosity of the twins was determined by questionnaire, consisting of items about physical similarity (similarity of face, eye colour, hair colour, skin colour) and frequency of confusion of the twins by family and strangers. In a group of 131 same-sex adolescent twin pairs who participated in a study on cardiovascular risk factors[47], agreement between zygosity based on this questionnaire and zygosity based on bloodgroup polymorphisms and DNA fingerprinting was 95%. The twins were divided into five groups by sex and zygosity; MZ males, MZ females, DZ males, DZ females and DZ opposite sex twins. Both twins and parents were asked, 'Do you participate in sports?' and, 'Did you ever smoke?' In addition we also asked the parents whether they were currently smoking. The questions could be answered with 'yes' or 'no', resulting in dichotomous variables.

Statistical analyses

To perform quantitative genetic analyses with dichotomous data, it is assumed that the underlying distribution of the variable is continuous and normal[9]. The variance of this distribution is caused by multiple genetic and environmental factors. A threshold divides the distribution into two categories, for example 'never smoked' and 'ever smoked'. Due to the sum of different genetic and environmental influences, an individual can exceed the threshold and express the trait, e.g. starts to smoke. The correlation between two dichotomous variables (e.g. smoking in twin 1 with smoking in twin 2) is called the tetrachoric correlation. PRELIS, a preprocessor for LISREL, was used to estimate the tetrachoric correlation by maximum likelihood, under the assumption that the two variables have a bivariate normal distribution[48].

By comparing the MZ and DZ correlations, the relative contributions of genetic and environmental influences to individual differences were estimated, using the method of path analysis[49]. A path diagram of the twin model is given in Figure 15.1. In the full model, the total phenotypic variance is explained by an additive genetic factor, a unique (individual-specific) environmental factor, and a shared environmental factor. If a variable is related to age, as was the case with smoking and sports participation, then differences between twin pairs in age will contribute to estimated shared environment variance. Therefore age was included in the model as a separate factor, explaining part of the total variance. The expected correlations between the phenotypes of the twins can be derived by tracing all connecting

routes in the path diagram. With LISREL7, a linear structural equation modelling package, the path coefficients of this path analytical model were estimated and the expected correlations were fitted to the observed correlations, using the weighted least squares (WLS) approach[50]. WLS requires, as a weight matrix, an asymptotic covariance matrix of the sample correlations, which was estimated by PRELIS. Different genetic models were fitted by constraining the genetic factor or the shared environmental factor to zero. The goodness of fit of the models was assessed by likelihood-ratio χ^2 tests. The acceptabilty of a model, not only depends on how well it fits the data, the model also needs to be consistent; it needs to be simple and the parameters of the model need to be significant[49].

Within the twin model, two kinds of sex differences in the genetic architecture of a trait can be tested[51]:

1. The same genes or environmental factors contribute to trait variation in males and females, but the magnitude of their effects is different,
2. Genes or shared environmental influences expressed in one sex are not expressed in the other sex.

By comparing the heritability based on data from male MZ and DZ twins with heritability estimated from data of female MZ and DZ twins, the first hypothesis was examined. By including opposite-sex DZ twins in the design, a group traditionally excluded from most twin studies, it was possible to test the second hypothesis and to estimate the genetic or the environmental correlation between these effects shared by male twins and these effects shared by female twins. With twin data only, it is not possible to test simultaneously for imperfect correlations in both gene effects and shared environmental effects, since there are no opposite-sex MZ twins[52].

Including the parents of twins in the design makes it possible to account for sources of variation that are confounded in twins[53]. The correlation between spouses was modelled as based on phenotypic assortment. Cultural transmission was modelled as the influence of the parental phenotype on the shared environment of the children. In this way, the variance of the shared environmental factor in twins was partitioned in cultural transmission and environmental effects that are shared by twins only. The genetic relatedness between parents and offspring was modelled as a path (with value 0.5) from the genotype of the parent to the genotype of the child. The effects of cultural transmission and phenotypic assortment induce a correlation between the genetic and environmental factors. It is assumed that these effects are going on for some generations and have reached a state of equilibrium[11,12]. Estimation of the parameters in this model involves a set of non-linear constraints[13]. Because of these constraints, it is not (yet) possible to use the LISREL computer program for these analyses. We used Mx, a structural equation modelling package specifically designed for modelling genetically informative data[54].

Smoking behaviour

There were 1582 twin pairs with complete data for smoking, and 1324 families in which both parents and children completed the questions. Table

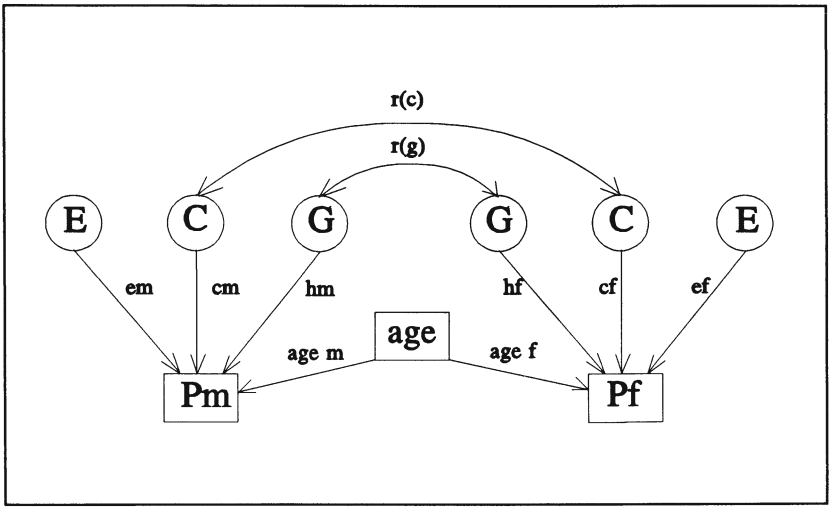

Figure 15.1 Path diagram for DZ opposite-sex twins. Squares represent observed variables and circles represent latent variables. Pm = phenotype male; Pf = phenotype female. E stands for the environmental factors that are not shared between twins, C stands for shared environmental influences, G for additive genetic influences; e, c, h and age represent the path coefficients of these respective factors; m and f stand for male and female. The proportion of variance due to genetic and environmental influences is equal to the squared path coefficients. The correlation between the genetic factors is represented by r(g); r(g) = 1 for MZ twins and r(g) = 0.5(1 + γ) (γ = correlation between the genotypes of the parents) for DZ twins. The correlation between the shared environmental factors is represented by r(c). Sex differences can be expressed by different path coefficients for males and females or by an imperfect correlation between either the shared environmental factors or the genetic factors

15.1 gives the number of twins in each sex by zygosity group, and the prevalence, concordance and tetrachoric correlation for smoking. There were no sex differences in smoking status, 26% of male twins and 23% of female twins had ever smoked ($\chi^2 = 2.66$, df = 1, $p = 0.10$). In the parental generation, there were significant sex differences for ever smoked (fathers 84%, mothers 66%, $\chi^2 = 106.7$, df = 1, $p < 0.01$) and for smoking at present (fathers 38%, mothers 29%, $\chi^2 = 20.8$, df = 1, $p < 0.01$).

The polyserial correlation between smoking and age of the twins was 0.33 in both sexes. Heterogeneity tests of the twin correlations showed that MZ male and female tetrachoric correlations were not significantly different (the constrained estimate was 0.91), and that DZ same-sex correlations also did not differ (constrained estimated = 0.75), but that the DZ opposite-sex correlation was lower than the DZ same-sex correlation (χ^2 for difference = 6.16 with 1 df). Model fitting with the twin data showed that the best fitting model included both genetic and shared environmental influences and, in addition, allowed the correlation between the shared environments of boys and girls to take its own value. Under this model, 9% of the total variance was accounted for by individual specific factors, 11% by age, 30% by additive genetic factors, and 50% by environmental influences shared by siblings growing up in the same family. The estimated correlation between

Table 15.1 Percentage, concordances and tetrachoric correlations for smoking behaviour in twins

	n *(pairs)*	*% Smoking*	*Concordance (%)*			*Tetrachoric correlation*	
			Both	*One*	*Neither*	r	*SE*
MZM	245	23	17.1	12.6	70.2	0.87	0.042
DZM	236	26	16.1	19.5	64.4	0.73	0.067
MZF	329	22	17.6	9.5	72.9	0.92	0.026
DZF	301	23	14.0	16.2	69.8	0.77	0.056
DOS	454	29 male 26 female	14.1	26.0	59.5	0.54	0.064

MZM = monozygotic male twins; DZM = dizygotic male twins; MZF = monozygotic female twins; DZF = dizygotic female twins; DOS = dizygotic opposite-sex twins; r = tetrachoric correlation; SE = standard error of the correlation

Table 15.2 Spouse correlations and parent–offspring correlations for ever smoking in children with currently smoking and ever smoking in parents

	n	*Currently smoking*		*Ever smoked*	
		r	*SE*	r	*SE*
Father–mother	1324	0.43	0.040	0.18	0.052
Father–son	1222	0.19	0.048	0.24	0.060
Mother–son	1222	0.14	0.050	0.05	0.051
Father–daughter	1426	0.17	0.046	0.21	0.055
Mother–daughter	1426	0.23	0.046	0.20	0.047

r = tetrachoric correlation; SE = standard error of the correlation

boys and girls for these shared environmental influences was 0.55 (SE = 0.13).

Table 15.2 presents the correlations between spouses for smoking at present and at any time, and the correlations between these variables in parents and smoking status of their sons and daughters. The association between spouses for 'ever smoked' was significant, but rather low (0.18), and quite high (0.43) for 'smoking now'. Correlations between parents and offspring were also low (between 0.05 and 0.24) and did not depend on either the sex of the parent or the offspring. Correlations between 'smoking now' in the parents and smoking in children were not systematically higher than correlations between 'ever smoking' in parents and smoking in children. Genetic model fitting to smoking data of twins and parents gave estimates for cultural transmission parameters from parents to offspring that did not differ significantly from zero (Table 15.3). Resemblance between parents and offspring could be accounted for completely by their genetic relatedness, both when considering smoking behaviour in children with 'smoking now' in their parents and smoking in children with 'ever smoked' in their parents. However, the first model showed a better fit to the data than the second one, probably due to the low correlation between mothers and sons for 'ever smoking'. From both analyses, we obtain similar heritability estimates, resembling the estimate obtained from the analysis of the twin data. From the analysis with 'smoking now' in the parents, the estimates for h^2 and c^2 were 30% and 62%, and from the analysis with 'ever smoking' in parents, these estimates were 32% and 61%, respectively.

Table 15.3 Model fitting results of the phenotypic assortment/cultural transmission model for ever smoked in twins with currently smoking and ever smoking in parents

	Currently smoking		*Ever smoked*	
	Full model	*Cult. trans.* = 0	*Full model*	*Cult. trans.* = 0
h	0.70	0.54	0.64	0.57
c	0.74	0.79	0.75	0.78
e	0.26	0.28	0.26	0.27
Spouse correlation	0.45	0.45	0.21	0.20
Cultural transmission	−0.12	—	−0.06	—
G × C correlation	−0.11	—	−0.04	—
r(Cm, Cf)	0.56	0.55	0.66	0.64
χ^2	23.50	25.87	45.02	45.67
df	25	26	25	26
p	0.55	0.53	0.01	0.02

h represents the influence of the genotype on the phenotype, c the influence of shared environment, and e the influence of unique environment. The square of the path coefficients gives the proportion of variance due to each component; total variance = $h^2 + c^2 + e^2 + 2hsc = 1$, where s = genotype–environment covariance (G × C). The spouse correlation is an estimate of the correlation between the phenotypes of husband and wife. The cultural transmission parameter represents the influence of the parental phenotype on the shared environment of the children. This transmission induces a correlation (G × C) between genotype and environment. r(Cm, Cf) represents the correlation between shared environmental influences of males and females

Sports participation

The complete data for sports participation were available from 1587 twin pairs and 1294 parents. In Table 15.4, the percentages for sports participation are shown. Boys reported more often participating in sports than did girls (74% vs 70%, $p = 0.006$). In the parents, there were no significant sex differences, 50% of the fathers and 53% of the mothers reporting sports participation.

The tetrachoric correlations in Table 15.4 showed that resemblances in sports participation were higher in MZ twins than in DZ twins, suggesting that genetic factors contribute to individual differences in sports participation. The correlations did not differ for MZ males and MZ females (constrained estimate = 0.87) or for DZ males and DZ females (constrained estimate = 0.68). The correlation in the opposite-sex twins was significantly lower than the correlations in the same-sex DZ twins ($p \sim 0.000$). This suggests different factors influencing the behaviour of males and females. There was a small ($r = -0.16$) biserial correlation between age of the twins and sport participation, indicating that participation in sports declined with age.

Different genetic models were fitted to these observed twin correlations. A model in which the resemblances in twins were explained by both genetic and shared environmental factors gave the best fit ($p = 0.531$). The contributions of the genetic and environmental factors did not differ for males and females. The low correlation in the opposite-sex group was explained by the absence of correlation for shared environmental influences in this group. In this model, 48% of the total variance was explained by

Table 15.4 Percentages, concordances and tetrachoric correlations for sports participation in twins

	n *(pairs)*	*% sport*	*Concordance (%)*			*Tetrachoric correlations*	
			Both	*One*	*Neither*	r	*SE*
MZM	249	76	69.9	11.6	18.5	0.89	0.036
DZM	241	76	64.7	22.8	12.4	0.60	0.086
MZF	329	67	59.0	16.1	24.9	0.85	0.037
DZF	303	70	59.7	21.1	19.1	0.72	0.058
DOS	456	70 male 72 female	54.4	32.7	12.9	0.35	0.074

MZM = monozygotic male twins; DZM = dizygotic male twins; MZF = monozygotic female twins; DZF = dizygotic female twins; DOS = dizygotic opposite-sex twins; r = tetrachoric correlation; SE = standard error of the correlation

Table 15.5 Spouse and parent–offspring correlations for sports participation

		Tetrachoric correlation	
	n	r	*SE*
Father–mother	1294	0.49	0.035
Father–son	1190	0.37	0.049
Mother–son	1190	0.32	0.047
Father–daughter	1398	0.29	0.051
Mother–daughter	1398	0.30	0.048

SE = standard error of the correlation

genetic factors, 38% was explained by shared environmental factors and 12% was explained by unique environmental factors. Only 2% of the total variance was explained by age of the twins.

Table 15.5 lists the spouse and parent–offspring correlations for sports participation. A high spouse correlation ($r = 0.49$) was observed. The correlations between parents and offspring did not depend on the sex of the parent or the sex of the children. Overall, the estimation of the parent–offspring correlation was 0.32 (SE = 0.03). A model which accounts for assortment in the parental generation and cultural transmission from the parents to their offspring, was fitted to the data of 1294 families. The results are given in Table 15.6. In the full model phenotypic assortment, cultural transmission and the correlation between the shared environment of boys and girls were estimated. As in the twin model, the correlation in the opposite-sex twins between the shared environment in boys and girls did not differ significantly from zero. The estimation of the cultural transmission was also not significant, indicating that the correlation between parents and offspring was due to their genetic relatedness. For the best-fitting model, the estimation of the heritability was 45%; shared environment explained 44% of the total variance. These estimations were comparable to the estimations from the twin model.

Table 15.6 Model fitting results of the phenotypic assortment/cultural transmission model for sports participation

	Full model	r*(Cm, Cf) = 0*	*Cult. trans. = 0*
h	0.69	0.71	0.67
c	0.66	0.65	0.67
e	0.33	0.32	0.33
Spouse correlation	0.49	0.49	0.49
Cultural transmission	−0.02	−0.04	—
G × C correlation	−0.02	−0.04	—
r(Cm, Cf)	0.13	—	—
χ^2	26.93	27.36	27.50
df	25	26	27
p	0.360	0.391	0.437

For explanation, see Table 15.3

DISCUSSION

For both smoking and sports participation, we found evidence for genetic influences in adolescents. Although the genetic effects in our study were substantial, shared and unique environmental influences together were more important. For smoking, the shared environmental influences contributed more to the total variance than the genetic factors, whereas, for sports participation, their contribution was about equal. For other cardiovascular risk factors, a smaller influence of shared environmental factors is usually found. Most studies of lipid and lipoprotein levels, for example, show no or only a very small influence of common environmental factors shared by family members[55].

The most important sources for sibling resemblance in smoking and sports participation were environmental factors shared between siblings but not between parents and offspring. Parent–child correlations were even lower than spouse correlations for currently smoking and sports participation. Pérusse et al.[28] observed the same patterns of familial resemblances for smoking and activity levels. This pattern of higher resemblance within generations (spouses and siblings) than across generations (parent–offspring) suggests that familial resemblance results from environmental influence common to members of the same generation. Biometric analyses of our data confirm this indication. The results strongly suggest that parental smoking behaviour does not directly influence smoking behaviour of their children. This is in agreement with other studies of adolescent smoking behaviour[32,34]in which parental smoking was only a weak predictor of the taking up of smoking in their children. The parent–offspring correlations for sports participation, too, were not explained by cultural inheritance, in line with other studies. Lewko and Greendorfer[38] found that for sports participation peers and school wield more influence than parents. Pérusse et al.[42] showed that non-transmissible environmental factors were most important for physical activity. Intensive family-based health promotion programmes with healthy families did not increase children's or parents' physical activity[56]. The absence of cultural transmission for smoking and sports participation might also have been the result of the model that we used to analyse parent–

offspring resemblances. This model assumes that the genetic correlation between parents and offspring is 0.5. When genes are expressed at different ages, a lower correlation between parents and offspring is found. Unfortunately, this age-dependent expression of genes can only be tested in a longitudinal design.

In opposite-sex twins, an imperfect correlation between environmental effects shared by males and environmental effects shared by females was found. This sex difference is in agreement with results from other studies. Swan et al.[34] found, for example, that sports participation decreased the risk of taking up smoking in girls, but not in boys, whereas organized social activities increased risk in girls but not in boys. Lewko and Greendorfer[37] noted that sports activities are valued more highly in boys than in girls. In line with several other studies, our results showed that males are more physically active than females[56,57]. Another explanation for the lower correlation in the opposite-sex twins might be that genetic factors are not correlated for males and females. However, as far as we know, there is no biological relevance to assume different genes in males and females for smoking and sports participation.

Several studies have shown that smoking and physical activity are related. Kaprio et al.[18] showed in adult males a small negative correlation ($r = -0.16$) between physical activity and smoking. In a longitudinal study on 6000 adolescents, girls were less likely to take up smoking if they were involved in sports or games[34]. For boys, sporting activities did not seem to affect their risk of uptake. Marti and Vartianen[58] showed that the clustering of behavioural CHD risk factors starts early in adolescence. They found, for boys and girls aged 15, an inverse relationship between physical activity and daily smoking, an association independent of the socioeconomic family background. Results from our study also showed that participation in sports somewhat reduced the risk of taking up smoking for both males and females. In a crosstabulation of sports participation and smoking, 21% who participated in sports, compared with 33% of those who did not, had ever smoked. Thus, smoking and physical activity tend to be weakly correlated.

How do genetic factors influence complex behaviours, such as smoking and sports participation? The possible mechanisms involved in the regulation of tobacco use are: the sensitivity of an individual to the pharmacological and toxicological effects of nicotine, the ability to develop tolerance to the effects and the severity of the withdrawal symptoms[59]. In a review of animal studies[59], Collins found evidence that sensitivity and tolerance development are under genetic control. Inbred strains of mice showed differences in a dose required to elicit a standard effect. There were also differences in the direction of the effect. In some strains, nicotine elicited a stimulation effect, whereas in others a depression/relaxation effect was shown. These differences in sensitivity to nicotine were partially due to differences in the number of the receptors that bind nicotine. Strain differences were also evident for tolerance development. Strains most sensitive to an acute dose of nicotine also developed tolerance more readily. Translating these results to humans, people with a certain genetic make-up might be unique in experiencing a stimulating or relaxing effect of nicotine, and become regular smokers. For

sports participation, there is evidence that genes influence correlated aspects. For example, aerobic power[46], endurance performance[60] and motor development and performance[61], are all under genetic control. Genetically fit persons might be selectively attracted to participate in sports.

In our study of adolescent twins and their parents, we found, for smoking, a much larger influence of shared environment and a lower influence of genetic factors than commonly observed in studies of adult twins. For sports participation, evidence was found for both genetic and shared environmental influences. Parents did not contribute to the environmental effects in twins. The results have important implications for prevention. Successful prevention should concentrate on environmental factors outside the family. For example, physical education programmes at school may be more successful than family-based intervention programmes. Besides, prevention needs to be targeted at boys and girls separately, at least partly.

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