Although these authors (1) specified that their purpose was to determine the feasibility of this type of study, I have some biologic and behavioral inquiries concerning the results. For instance, there was no talk about the error associated with obtaining DNA. Even though cheek cells are very specific and can be easily identified by a trained researcher, I am not convinced that contaminated or faulty DNA should not be accounted for. The article mentioned that 26 percent of the interviewees returned buccal swabs but that only 18 percent were successfully genotyped. What happened to the missing 8 percent of the samples?

In addition, there was no mention in this article (1) about what could have been done to improve response and return rates. Did the time of day that these people were interviewed play a role in their willingness to take part in the study? Would adding a question as to why people did not want to be involved in this study have led to important information for improving rates in future studies? In modern genetic and/or behavioral studies, it is common to use questionnaires with a large number of items for acquiring as much about the subject as possible. Would a more in-depth questionnaire have resulted in lower DNA return rates? Overall, I am convinced of the feasibility of using random digit dialing to obtain DNA, but I would like to see how these results compare to a follow-up study in which more confounding factors are explored.

REFERENCE


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THE AUTHORS REPLY

We thank Mr. Peters (1) for his comments on our paper (2). It would be good to have had more information on why people chose not to participate in our study. We have some data on that issue but found that people were generally not that expansive in their reasons; for example, they indicated “not interested,” “don’t want to,” “don’t want to give name or address,” or “too busy.” Many of the “no’s” happened before the respondents learned about the genetic theme of the project.

We examined day-of-the-week and time-of-day effects on agreeing to receive the kit and found no reliable differences. Interviewer experience (measured by number of interviews conducted) did not influence acceptance rates. However, there were individual differences among experienced interviewers in terms of acceptances. Of those who conducted 100 or more interviews (eight interviewers), three had response rates of less than 48 percent and five had response rates of more than 62 percent. Perhaps overall response rates could have been improved by selecting only the most skilled interviewers. Although a longer interview would have produced more data per subject, completion rates, especially for telephone interviews, drop considerably with longer interviews.

The ease of taking a buccal swab and the painless nature of the technique maximize participation from those who might not want to be bothered or are afraid of needles (3). Our method of collecting samples by sending a kit of cotton swabs in the mail with a return envelope did produce some problems when the swabs were not returned quickly. Some of the swabs returned after an extended delay had developed visible microbial growths. Swabs such as these were some of the “problem” samples that did not yield successful genotypes, but, interestingly, there was not a strong correlation between length of delay in returning the swab by the volunteer and difficulty in generating a genotype. The greatest difficulty came in genotyping samples that yielded very small quantities of DNA. Even in a more controlled situation in the laboratory where volunteers could be watched, swabs yielded a wide range of DNA, from 0 µg to more than 50 µg. The average recovery from swabs was 16 µg. One method that might be used to produce 2–3 times more DNA and still be painless is a mouth rinse. Several comments from investigators at meetings suggest that 30–50 µg of DNA on average can be recovered by asking the volunteer to rinse with 10 ml of an over-the-counter mouthwash and expectorate into a tube that is then sent to the laboratory. Our preliminary tests did not reveal any significant difference between swabbing and rinsing, but it appears that most other laboratories have greater success with the rinse.

The discrepancy between the return rate of swabs in our study (2) (26 percent) and those successfully genotyped (18 percent) may have been due to low concentration of DNA to start and poor quality of that DNA. By poor quality, we suggest that the DNA might have degraded, which diminished the number of intact targets to be amplified in a polymerase chain reaction. Work in progress in our laboratory is examining the relative intactness of DNA collected from swabs and blood. Finally, the genotype of the variable number of tandem repeats in the dopamine transporter gene (SLC6A3) is notoriously difficult to amplify, but this difficulty is not something that is reported in the literature.

REFERENCES


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