

Heritability Estimation for Speech-Sound Traits with Developmental Trajectories

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Received: 12 February 2010 / Accepted: 22 June 2010 / Published online: 10 July 2010
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Abstract Numerous studies have examined genetic influences on developmental problems such as speech sound disorders (SSD), language impairment (LI), and reading disability. Disorders such as SSD are often analyzed using their component endophenotypes. Most studies, however, have involved comparisons of twin pairs or siblings of similar age, or have adjusted for age ignoring effects that are peculiar to age-related trajectories for phenotypic change. Such developmental changes in these skills have limited the usefulness of data from parents or siblings who differ substantially in age from the probands.

Edited by Stacey Cherny.

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Employing parent–offspring correlation in heritability estimation permits a more precise estimate of the additive component of genetic variance, but different generations have to be measured for the same trait. We report on a smoothing procedure which fits a series of lines that approximate a curve matching the developmental trajectory. This procedure adjusts for changes in measures with age, so that the adjusted values are on a similar scale for children, adolescents, and adults. We apply this method to four measures of phonological memory and articulation in order to estimate their heritability. Repetition of multisyllabic real words (MSW) showed the best heritability estimate of 45% in this sample. We conclude that differences in measurement scales across the age span can be reconciled through non-linear modeling of the developmental process.

Keywords Speech · Language · Longitudinal ·
Developmental genetics · Spline fitting

Introduction

Genetic analyses of developmental traits present considerable challenges as speech, language, reading, and other cognitive abilities change considerably with advancing age. These skills show rapid growth in early childhood and continue to develop through school age, adolescence and sometimes even into early adulthood. However, rates of development typically slow in later childhood and adolescence, and the difference between skill levels at different ages decreases over time, suggesting non-linear growth trajectories. Such developmental trajectories reflect aspects of developing brain structure (Castellanos et al. 2002; Posthuma et al. 2000). To the extent that the measure in a child is predictive of the measure later in life, it is

reasonable to postulate that both childhood and adult values reflect some common ability that may be heritable. Therefore, prior to estimating the heritability of such an ability, the values for children in early childhood, children at school age and adolescents/adults need to be age-adjusted. Often, however, a simple transformation of the data will not suffice. This problem is particularly relevant for the longitudinal study of complex genetic traits, where the change in the phenotype is mediated through age-related timed mechanisms, offset by environmental influences. For example, the number of words recalled has been shown to follow a developmental trajectory, in that it has a nonlinear relationship with age (Hanten et al. 2007).

Examples of disorders with a developmental trajectory are speech sound disorders (SSD). SSD include both errors of articulation or phonetic structure (due to structural or motor constraints on the production of speech sounds) and phonological errors (due to cognitive-linguistic constraints on the underlying representations and retrieval of speech sounds and sound combinations). Children are diagnosed with SSD in early childhood, usually between 3 and 6 years of age. Prevalence estimates suggest rates are as high as 15.6% in 3 year old children (Campbell et al. 2003; Shriberg et al. 1999b) falling to 3.8% of children at 6 years (Shriberg et al. 1999a) and 3.6% at 8 years (Wren et al. 2009). The precipitous decline in rates of SSD during early childhood may be due to remediation or maturation, but most likely a combination of both influences. Thus, as children with SSD age, they present with less severe speech difficulties and perform better on phonology tasks because their skills have improved over time. However, many of these children have persistent speech errors, and/or have reading, academic, and other difficulties in domains associated with the underlying etiology. Studies that have followed children with early childhood SSD to school age have found later academic difficulties in 50–75% of their samples (Aram and Hall 1990; Bishop et al. 2003; Cantwell and Baker 1987; King et al. 1982; Young et al. 2004). Our follow-up of young children with SSD revealed that 18% of participants with an isolated SSD had reading problems in mid-elementary school, compared with 75% of those with combined SSD and language impairment (LI) (Lewis et al. 2000b).

Although individuals with co-morbid conditions may have more severe impairments in one or both domains, recent studies have demonstrated that even in individuals with isolated SSD, speech processing difficulties may persist in adulthood. One of the few studies of adult outcomes of childhood speech-language impairments showed that participants with histories of SSD alone scored lower than controls in real word decoding, indicating that individuals with histories of SSD alone can have significant long-term deficits (Young et al. 2002). Parents of a proband-child with a history of childhood SSD differ from parents in families

without a history of SSD on phonology measures (Lewis et al. 2006). However, these adults no longer present with overt speech errors and may score significantly better than their children simply because the age-mediated overt speech errors resolve either through intervention or maturation while deficits in written language persist. Hence, the scores on measures of speech production and phonological processing of both older siblings and parents of probands with SSD require special care when adjusting for age differences. Owing to the shape of developmental trajectories of component cognitive skills (or endophenotypes) related to SSD, heritability estimates for endophenotypes incorporating parental data have typically been considered inestimable if tests done at approximately the same ages are not available. However, any age adjustment that results in a significant parent–offspring correlation, whether environmentally or genetically caused, implies that there is something common to an individual’s measures at two different time points.

In summary, children with SSDs, LI, and/or reading disorders (RD) cannot be compared with relatives of widely varying ages to estimate trait heritability without adjustment for the age differences. Many methods of estimating familial correlations assume a linear or simple polynomial relationship between the trait and its covariates, with underlying bivariate normality of residuals between relationship types. Familial correlations, and thus heritability estimates, that make these assumptions will be inaccurate if this assumption is not met. The method to be described uses a more flexible, non-polynomial relationship and does not assume multivariate normality of the residuals to estimate heritability.

In the present analysis, we had two objectives. First, we sought to identify endophenotypes that could be used to gain further insight into SSD in adulthood. Second, we aimed to develop an age-appropriate model for such phenotypes. We have adapted a smoothing procedure (Cleveland 1979) which fits a series of lines that approximate a curve matching the developmental trajectory. This procedure flexibly adjusts for changes in measures with age, so that the adjusted values have a common referent (i.e., age-expected performance) in examining persons of widely different ages. We then applied this method to measures of articulation and phonological encoding in order to estimate their heritability in a sample of pedigrees ascertained through a proband with SSD.

Subjects and measures

Family ascertainment

The proband children were identified at 4–6 years of age from the clinical caseloads of speech/language pathologists working at community speech and hearing centers, schools, or in private practice in the greater Cleveland area.

All probands were screened to ensure that they met the following criteria: (1) moderate to severe expressive SSD as defined by a score of 1 SD or greater below the mean on the Goldman–Fristoe Test of Articulation Sounds-in-Words subtest (Goldman and Fristoe 1986) and by commission of at least three phonological error types as identified by the Khan–Lewis Phonological Analysis (Khan and Lewis 1986); (2) normal hearing acuity as defined by passing a pure tone audiometric screening test at 25 dBHL ISO for 500, 1000, 2000, and 4000 Hz bilaterally and <6 episodes of otitis media prior to 3 years as reported by the parent; (3) normal peripheral speech mechanism as documented by the Total Structure Score on the Oral and Speech Motor Control Protocol (Robbins and Klee 1987); (4) absence of a history of neurological disorders or developmental delays other than speech and language as reported by the parent; and (5) normal intelligence defined as a Performance IQ ≥ 80 on the Wechsler Preschool and Primary Scale of Intelligence-Revised (Wechsler 1989).

All of the available siblings and parents of the probands were invited to participate in the testing. All consenting children (probands and siblings) and parents in each family were assessed as described previously (Stein et al. 2004). Siblings and parents were evaluated at the same time as the proband.

In this study, we were particularly interested in quantitative traits derived from measures for which age normative data were not available, and are important predictors of SSD and reading difficulty in both children and adults. These particular measures fall into two domains: phonological memory and articulation. Poor phonological skills in pre-school put children at risk for developing difficulties in spelling, reading, and language at school age (Lewis et al. 2000a; Lewis and Freebairn 1998) that persist into adulthood (Lewis et al. 2007). In addition, adults with a history of SSD perform more poorly than adults without a history of SSD on measures of articulation (Felsenfeld et al. 1992). Two measures of phonological memory were included: the Multisyllabic Word Repetition Test (Catts and Kamhi 1986), and the Repetition of Nonsense Words Test (Catts 1986a). Participants were asked to repeat 20 multisyllabic real and 15 nonsense words in response to audiotaped presentations of the words. Responses were audiotaped and transcribed, and the percentage of words correctly repeated was recorded. These measures were administered to probands, siblings, and parents individually and audiotape recorded for later phonetic transcription and analysis. Two measures of articulation were also obtained. For the Speech Error Phrases (ERRORW (Catts, 1987, Speech error phrase repetition task. Personal communication)) task, participants were asked to repeat difficult to articulate phrases such as ‘mixed biscuits’ or ‘blue plaid pants’; the score was the percentage of phrases repeated correctly. The other measure

obtained from the audiotaped conversational speech sample was the Percent of Consonants Correct (Shriberg et al. 1997a), which indexes speech competence. The relevance of these measures to SSD has been described previously (Catts 1986b; Lewis and Freebairn 1992; Shriberg et al. 1997b).

Statistical analysis

Because there is not a suitable parametric regression model for trajectory data, a robust locally weighted nonlinear regression model was used to efficiently adjust for effects of covariates that confound the quantitative trait for each individual subject (Cleveland 1979). This method is ideal for modeling complex processes. Based on a smoothing technique, the procedure is expressed as: $y_i = g(x_i) + \varepsilon_i$, where g is a smoothing function, the ε_i 's are random errors with mean 0 and constant scale. Letting \hat{y}_i be the estimate of $g(x_i)$, we can express \hat{y}_i as the fitted value of the polynomial regression at x_i ,

$$\hat{y}_i = \sum_{j=0}^d \hat{\beta}_j(x_i)x_i^j,$$

where d is the degree of the polynomial regression and β_j is the weighted least squares estimate obtained by minimizing the expression

$$\sum_{k=1}^n w_k(x_i)(y_k - \beta_0 - \beta_1 x_k - \dots - \beta_d x_k^d)^2.$$

This allows the neighborhood points of (x_i, y_i) to be given more weight to infer \hat{y}_i . To provide an robust estimate of β_i , the weight $w_k(x_i)$ is chosen to be the product of $w_k(u)$ and $\delta_k(v)$. $w_k(u)$ is the tricube function defined by

$$w_k(u) = \begin{cases} (1 - u^3)^3 & |u| < 1, \\ 0 & |u| \geq 1 \end{cases}$$

where $u = \frac{|x_i - x_k|}{\max|x_i - x_k|}$. From this definition, $w_k(u)$ is increased when the points are close to x_i , which allows close points to play a more important role in determining \hat{y}_i . $\delta_k(v)$ is the bisquare function defined by

$$\delta_k(v) = \begin{cases} (1 - v^2)^2 & |v| < 1, \\ 0 & |v| \geq 1 \end{cases}$$

where $v = \frac{|y_i - \hat{y}_i|}{6 \cdot \text{median}|y_i - \hat{y}_i|}$. Incorporating $\delta_k(v)$ into the equation guarantees a robust estimate as extreme values (outliers) have less of an impact on the parameter estimates. The spline fitting function weights more for points locally (those tend to have similar variance, e.g., those with older age). It also has a more robust performance than simple linear regression when there is heteroscedasticity. All the nonparametric regression analyses in this paper were done using S-Plus Release 6.2 (1988).

In the second step, we use the residuals obtained from this nonlinear spline as adjusted variables for each individual. Heritability, which is the proportion of trait variance attributable to genetic effects, can be estimated using parent–offspring, sibling, and spousal correlations (Stein et al. 2003) as follows. We assume there is random mating, no parent–offspring environmental correlation, no epistatic components of variance in the siblings, that $Cov(\text{parent, offspring}) = \frac{1}{2}\sigma_g^2$ and $Cov(\text{siblings}) = \frac{1}{2}\sigma_b^2 + \sigma_c^2$, and $Cov(\text{spouse}) = \sigma_c^2$, where σ_c^2 is a common environmental variance, the same for sibs and spouses, and σ_g^2 is the genetic variance. Denoting parent–offspring correlation by $r(\text{po})$, sibling correlation by $r(\text{sibs})$, and spousal correlation by $r(\text{spouse})$, we estimate heritability and its variance by $h^2 = 2(w_1r(\text{po}) + w_2r(\text{diff}))$ and $\sigma_{h^2}^2 = 4\left(w_1^2\sigma_{r(\text{po})}^2 + w_2^2\sigma_{r(\text{diff})}^2 + w_1w_2Cov(r(\text{po}), r(\text{diff}))\right)$, where $r(\text{diff}) = r(\text{sibs}) - r(\text{spouse})$, and the weights w_1 and w_2 are inversely proportional to the variances of these components:

$$w_1 = \frac{\frac{1}{\sigma_{r(\text{po})}^2}}{\frac{1}{\sigma_{r(\text{po})}^2} + \frac{1}{\sigma_{r(\text{diff})}^2}} \text{ and } w_2 = \frac{\frac{1}{\sigma_{r(\text{diff})}^2}}{\frac{1}{\sigma_{r(\text{po})}^2} + \frac{1}{\sigma_{r(\text{diff})}^2}}.$$

This method of estimating heritability allows for non-zero spousal correlations, thereby accounting for shared environment and reducing the chances that heritability estimates are upwardly biased due to shared environmental effects. Familial correlations for the residuals and their standard errors were estimated using FCOR from the program package S.A.G.E. version 4.5. (2004).

Results

The total sample consisted of 1,291 individuals from 257 families, comprising 1,442 parent–offspring pairs, 288 spousal pairs, 711 sibpairs, and 94 half sibling pairs. First, we examined the untransformed mean and standard deviations for each trait. As we expected, these trait values were distributed very differently owing to the developmental trajectory effects (Table 1).

To model these trajectories, a robust locally weighted regression model (LOWESS spline) was applied to adjust for covariates, age and sex, as these have been shown in

previous studies to influence the distribution of these traits. Figure 1 shows the pattern of our data and fitted LOWESS curves. These plots illustrate how trait values increase rapidly during younger ages, then hit a plateau, such that adolescents and adults do not differ much from each other, but differ dramatically from children. Furthermore, these results demonstrate that a simple linear or quadratic adjustment for age would not sufficiently account for this trajectory. Means and standard deviations for the fitted values are shown in Table 2. There are two key observations from these results. First, the standard deviations are much smaller after fitting the splines, particularly in the parents. Thus, the spline fitting model stabilized the variances in the data for the older individuals (the parents), which is important for heritability estimates using parent–offspring correlations. Second, there is a much bigger difference in the means between parents and offspring, which is what we would expect after accounting for the developmental trajectory.

We obtained the residuals from this nonlinear fit and then calculated familial correlations and their asymptotic standard errors by using the FCOR program in S.A.G.E. Release 4.5. For comparison purposes, we also estimated familial correlations from the raw data with no age adjustment, and also from residuals obtained from linear regression models with adjustment for age and age² (simple age adjustment). Familial correlations obtained using no adjustment and simple age adjustment are provided in Table 3, and correlations obtained after spline fitting are listed in Table 4. First, a comparison of Tables 3 and 4 reveal the effect of not properly adjusting for age effects. For the data where there was no age adjustment, the parent–offspring and sibling correlations for NSW and PCC are much lower than the estimates obtained after spline fitting. This shows that some age adjustment is necessary, since parents are a different age than the children, and the siblings are also of different ages, and performance on these tests improves with age. When comparing the simple age adjustment to the spline fitted values, the spousal correlations and sibling correlations for NSW and PCC are much higher with the simple age adjustment. This is because a simple age adjustment treats all incremental differences in age equally. However, as seen in Fig. 1, a

Table 1 Means (and standard deviations) for traits by relative type

	Parents only	Offspring only	Whole sample
MSW (% correct)	90.8 (13.4)	47.6 (31.7)	58.1 (33.8)
ERRORW (% correct)	93.0 (11.8)	53.5 (37.2)	62.8 (37.0)
NSW (% correct)	65.6 (20.8)	42.3 (29.0)	48.1 (29.1)
PCC (% correct)	97.9 (2.4)	89.9 (8.9)	91.2 (9.5)

Table 2 Means (and standard deviations) for traits after spline fitting, by relative type

	Parents only	Offspring only	Whole sample
MSW (% correct)	92.4 (1.7)	47.2 (22.7)	53.3 (26.1)
ERRORW (% correct)	94.5 (0.9)	51.0 (29.8)	61.3 (31.9)
NSW (% correct)	67.1 (0.3)	40.6 (15.4)	47.1 (17.5)
PCC (% correct)	98.1 (0.1)	90.8 (5.8)	92 (5.9)

Table 3 Relative pair correlations obtained after no age adjustment and after age adjustment using a regression model

Trait	No age adjustment			Simple age adjustment ^a		
	<i>r</i> (Spouse)	<i>r</i> (PO)	<i>r</i> (Sibs)	<i>r</i> (Spouse)	<i>r</i> (PO)	<i>r</i> (Sibs)
MSW	0.2833	0.2868	0.1363	0.1795	0.1521	0.1232
ERRORW	0.0652	0.062	−0.0001	0.2772	−0.1034	−0.0318
NSW	0.0898	0.160	0.1624	0.1235	0.0995	0.1702
PCC	0.0434	0.0798	0.0749	0.4549	−0.1314	0.0613

^a Adjusted for age and age²

Table 4 Relative pair correlations and resulting heritability after applying spline technique

Trait	Relative pair correlations			Heritability	
	<i>r</i> (Spouse)	<i>r</i> (PO)	<i>r</i> (Sibs)	Estimate	Standard error
MSW	0.1228	0.2553	0.1880	0.453296	0.09805
ERRORW	0.0110	0.0803	0.0355	0.143483	0.10387
NSW	0.0852	0.1407	0.2320	0.283647	0.113062
PCC	0.0465	0.2257	0.2253	0.438847	0.119591

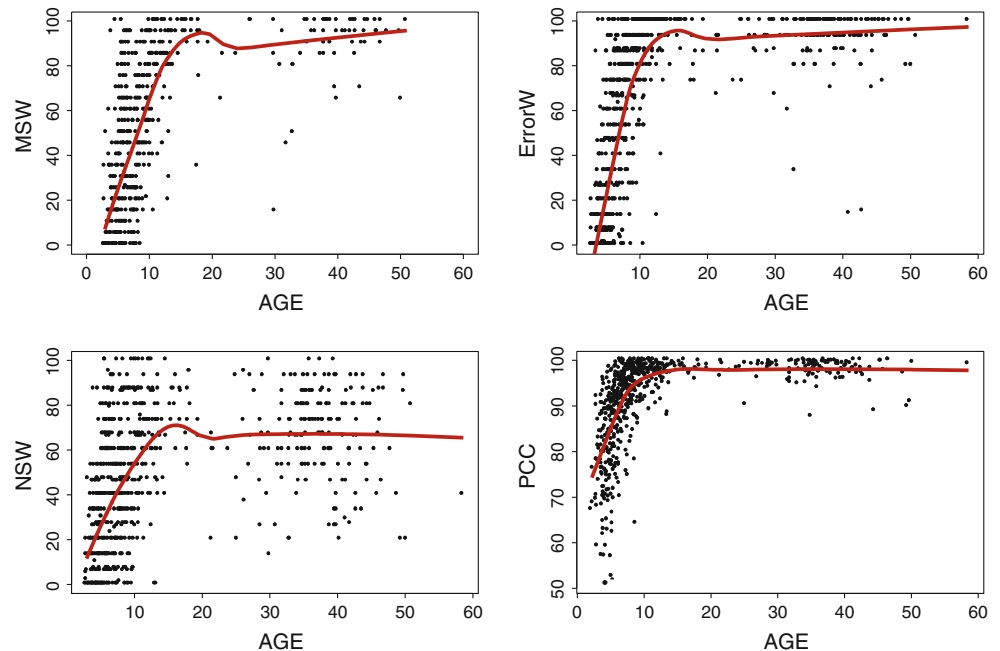
difference between ages 5 and 6 is much different than the difference between ages 15 and 16 or 30 and 31, for example. We also see that the familial correlations for MSW and ERRORW obtained with no age adjustment or simple age adjustment are higher overall, suggesting that the spline fitting model reduces a potential upward bias. Finally, it is interesting that some of the parent–offspring correlations obtained with simple age adjustment (ERRORW and PCC) were actually negative, which may be due to the varying ages of the children. We also compared the correlations obtained for all sibling pairs with simple age adjustment to those obtained in a

subsample of sibling pairs age ≤15 years, the age at which the ceiling effects begin to occur (Fig. 1). The correlations in the sibpairs age ≤15 years were only slightly lower, further illustrating that proper age adjustment is necessary to appropriately estimate the similarity between siblings for measures where performance increases non-linearly with age (data not shown).

Examination of familial correlations obtained after spline fitting shows that all of these relative pair correlations were greater than zero (Table 4). Though the sib–sib correlation was greatest for NSW and PCC, the parent–offspring correlation was greatest for MSW and ERRORW. In addition, the spousal correlations were non-zero, emphasizing the importance of accounting for these correlations properly (Stein et al. 2003) and implying that the adjustments made produce measures that would be predictive of children’s values later in life. These results illustrate the importance of transforming the trait values for the parental generation, so that accurate relative pair correlations can be obtained for heritability estimation.

Parent–offspring, sibling, and spousal correlations were then used to estimate heritability. These results can be found in Table 4 as well. Both PCC and MSW had

Fig. 1 Trait (MSW, ERRORW, NSW, and PCC) is plotted against age. The best fitting spline is shown with the datapoints



heritability estimates above 40%, which is relatively high for a complex trait. The heritability for ERRORW was 14.3 and 28.4% for NSW. Given their standard errors, these heritabilities are all significantly greater than zero.

Discussion

In this study, we developed a strategy to estimate heritability estimates for traits subject to age-related change. Traits that measure developmentally driven trajectories tend to have skewed distributions, making variance component-based analyses challenging. Heritability estimation is an important component in planning linkage and association studies. Though heritability may be estimated using sibling pair and twin data, including the parent–offspring correlation in the heritability estimation allows for a more precise estimate of the additive component of genetic variance. In addition, incorporation of the spousal correlation allows for the estimation of the proportion of variance due to shared environmental effects. Since the spousal correlations in these data were nonzero, we have evidence that shared environment also plays a role in trait similarity among relatives. However, parent–offspring and spousal correlations are inaccurate unless the developmental trajectory is appropriately specified. Here, we provide a method to model this developmental trajectory and present the corrected fitted means of these values and heritability estimates.

As expected, the developmental trajectories for these speech production measures were nonlinear. When children are younger, they rely more on oral presentation of words, but as they age, they are able to successfully use other inputs. They may rely on the visual written mechanism, as well. In this study, children acquiring the speech sound system demonstrated rapid improvement in the percentage of consonants correct (PCC) in conversational speech, and in the repetition of multisyllabic real words (MSW), and nonsense words (NSW). Developmental norms for individual speech sound acquisition have consistently reported that over 90% of children produce all speech sounds correctly by 8 years of age (Prather et al. 1975; Sander 1972; Shriberg 1993; Smith et al. 1990; Templin 1957). In fact, there is remarkable similarity in the age of acquisition of speech sounds cross-linguistically (McLeod 2007). As seen in the trajectory obtained for the PCC, very few individuals beyond the age of 10 years make speech-sound errors in conversational speech. Measures developed to evoke speech sound errors such as the repetition of multisyllabic real (MSW) and non-words (NSW) and difficult to articulate phrases (ERRORW) show a similar developmental trajectory, although the age at which development plateaus for these skills is slightly

older and a greater number of individuals continue to make errors on these tasks throughout the lifespan. Repetition of nonsense words, a task related to SSD, RD and LI, shows the greatest amount of variability in acquisition, with many individuals presenting with persistent errors throughout adulthood (Estes et al. 2007; Lewis et al. 2006) and with substantial variability in scores at all ages (see Shriberg et al. 2009 for discussion of methodological and substantive issues in the use of nonword repetition tasks in speech genetics and other studies).

Our findings suggest that these traits are heritable, with PCC ($h^2 = 0.44$) and MSW ($h^2 = 0.45$) demonstrating the highest heritability. PCC and MSW are based on the articulation of real words in conversation and in repetition, respectively. NSW differs from PCC and MSW as it requires the individual to encode phonemes presented in novel non-word sequences that are presumably not stored in verbal memory. The Error Phrases (ERRORW), on the other hand, are difficult to articulate sequences of real words that are designed to evoke errors. Thus, these measures tap different aspects of phonological processing and speech sound production.

The heritability estimates reported above are difficult to interpret relative to the published literature because many studies have used composite measures derived solely from factor analysis and/or twin data. Most of the twin analyses employed the ACE model (Neale and Cardon 1992) so it can be assumed that those are narrow-sense heritability estimates (using only the additive genetic variance). Within the articulation domain, published estimates of heritability include 0.37 for GFTA from a twin study (Kovas et al. 2005a), and locus-specific heritability of a composite measure containing Percentage of Consonants Correct-Revised (PCCR), among other traits, ranging between 0.29 and 0.45 (McGrath and Pennington 2005). Our measures of articulation yielded heritability estimates of 0.143 for ERRORW, and 0.438 for PCC. Otherwise, these heritability estimates are similar to published estimates. The heritability of ERRORW is considerably lower than heritability of other articulation measures, but this task may also tap other cognitive domains.

Within the phonological memory domain, a composite variable containing a nonword repetition task had a locus-specific heritability of 0.61 (McGrath and Pennington 2005), and a twin study found a heritability of nonword repetition of 0.41 (Kovas et al. 2005b). Our estimate of heritability for NSW was considerably lower (0.284). However, these various nonword repetition measures may not be comparable, as McGrath used the measure by Dollaghan and Campbell (1998), and the study by Kovas used the measure by Gathercole and Baddeley (1996). This result is subject to several interpretations. First, our measure of NSW may tap a different and less heritable

cognitive process than the other two aforementioned non-word repetition measures. Second, adjustment for the developmental trajectory puts the measure on the proper scale and our estimate of heritability may thus be more appropriate. Inclusion of parent data may also affect the estimate, perhaps by providing a more accurate estimate of the cross-age heritability of traits. Third, other factors such as level of education may influence these traits and contribute to study-to-study fluctuation in estimates. Finally, the other two studies also used different ascertainment criteria to select participants than ours which may also lead to differences in outcome. Further study is needed to clarify those hypotheses, since these measures are used in linkage analyses and a genome-wide association study has been published on nonsense word repetition in language impaired children (Newbury et al. 2009). Nevertheless, our estimate of heritability for MSW approximated the published estimates.

There are some limitations to this study. We focused our analyses on four measures because these had the most available data (particularly for adults) and because they did not have published age normative data. This analysis may be relevant to the other measures we collect, and as our longitudinal follow-up continues, we will repeat this analysis on other measures. Another limitation is the possibility of an ascertainment bias. However, the single ascertainment scheme used by this study required that only one child in the family have SSD, so there should not be a predominance of outlying observations that would skew the LOESS model. Also, our heritability estimates may not be directly comparable to the aforementioned studies; because twins are the same age, a developmental trajectory would not be evident in a twin design. In studies like ours that include siblings of varying ages, it is critical to account for the non-linear association with age. Finally, our heritability estimates may not be directly comparable to those estimated in twin studies, because of the assumptions made by the twin design (Elston and Boklage 1978).

In sum, we have developed an approach to modeling developmental trajectories applicable to behavioral trait data. This model enables the incorporation of parental data into heritability estimation, which could not have been done without properly accounting for the non-linear change in trait with age. We also show that this method yields some heritability estimates that are different from the published literature, suggesting that age-dependant trajectories may bias the analysis of similar measures where parents and children are both assessed but age trajectories have not been accounted for. Properly modeling parental phenotypes for phenotypes such as these will be key in the analysis of parent-of-origin effects, which have been shown in SSD (Stein et al. 2006).

Acknowledgments This research was supported by the National Institutes of Health, National Institute on Deafness and Other Communication Disorders, Grant R01 DC00528 Barbara A. Lewis, Principal Investigator, NIH-NIDCD 1 R03 DC004005, Sudha K. Iyengar, Principal Investigator, and Multidisciplinary Clinical Research Career Development Programs Grant (KL2RR024990) to Catherine Stein from the NCRR. We wish to express our appreciation to the speech-language pathologists who assisted us in recruiting subjects, and to the families who generously agreed to participate. We also wish to acknowledge Dr. Zhiying Xu, who helped perform the data analyses. Some of the analyses were performed using the program package S.A.G.E., release 4.5, which is supported by the U.S. Public Health Resource Grant RR03655 from the National Center for Research Resources.

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