Perfil familial da fluência da fala - estudo linguístico, acústico e eletromiográfico**

Speech fluency family profile - a linguistic, acoustic and electromyographic study

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Abstract

Background: genetic factors as a possible cause of stuttering. Aim: to identify the speech fluency family profile (linguistic, electromyographic and acoustic aspects) in children with and without a close family history of stuttering. Method: the study included a total of 127 individuals, 32 children (probands) and 95 members of the immediate family (father, mother, sisters and brothers). The individuals were divided in two groups: GI (SC) was composed of 17 probands with a diagnosis of stuttering, 17 fathers, 17 mothers, 10 brothers, and 13 sisters, and GII (NSC) was composed of 15 fluent probands, 15 fathers, 15 mothers, no brothers, and 8 sisters. All testing procedures were applied to all participants as follows: 1) identification of disruption typology; 2) electromyographic analyses; and 3) acoustic analyses. Results: the percentage of affected mothers was 41.1%, and the percentage of affected fathers was 35.3%. In addition, the percentage of affected sisters was 6.7%, and 40% of the brothers were affected. Similarity was observed in the typology of speech disruptions in all of the affected individuals of the same family; however, a trend towards a greater severity of the disorder in probands was observed. Similarity was found in muscle activation for diadochokinesia rates in all the affected individuals in the same family. This suggests the existence of a speech motor pattern within the same family that can be measured by capturing peripheral muscle activation. Similarity was found in the acoustic variation for diadochokinetic rates in all affected individuals of the same family. Conclusion: this study represents one of the first endophenotypic research proposals on stuttering characterized by two aspects: objective inclusion criteria and the type of stuttering symptomatology manifested.

Key Words: Speech; Language and Hearing Sciences; Stuttering; Genetics.

Resumo

Tema: fatores genéticos como possíveis responsáveis pela gagueira. Objetivo: identificar o perfil familial da fluência da fala - aspectos linguísticos, eletromiográficos e acústicos - em crianças com e sem história familiar próxima para a gagueira. Método: participaram do estudo 127 indivíduos, 32 crianças (probandos) e 95 membros da família imediata (pai, mãe, irmãs e irmãos) divididos em dois grupos: GI (CCG): 17 probandos com diagnóstico de gagueira; 17 pais, 17 mães, 10 irmãos e 13 irmãs; e GII (CSG): 15 probandos fluentes; 15 pais, 15 mães, 0 irmãos e 8 irmãs. Todos os procedimentos de testagem foram aplicados em todos os participantes: 1. Coleta das tipologias das rupturas; 2. Coleta eletromiográfica; 3. Coleta acústica. Resultados: foi encontrado o percentual de 41,1% de mães afetadas; 35,3% de pais afetados; 16,7% de irmãs afetadas e 40% de irmãos afetados. Foi observada similaridade na tipologia das rupturas da fala em todos os afetados de uma mesma família, mesmo havendo uma tendência a maior gravidade do distúrbio nos probandos. Foi encontrada similaridade na ativação muscular para as taxas de diadococinesia em todos os afetados de uma mesma família. Sugere-se um padrão motor para a fala, numa relação passível de ser mensurada pala captação da ativação muscular periférica, dentro de uma mesma família. Foi encontrada similaridade na variação acústica para as taxas de diadococinesia em todos os afetados de uma mesma família. Conclusão: esta pesquisa se caracteriza como uma primeira proposta de estudo endofenotípico da gagueira, em dois aspectos: critérios objetivos de inclusão e tipo de sintomatologia manifesta da gagueira.

Palavras-Chave: Fonoaudiologia; Gagueira; Genética.

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Introduction

Stuttering is a disorder of unknown cause characterized by involuntary interruptions of the flow of speech (repetitions, hesitations and prolongations).1-4 Genetic factors have been identified as a cause of some types of stuttering.5-30

Phenotypic studies indicate a pattern of segregation of stuttering in families, and the disorder occurs more often in certain families. Male individuals with first-degree relatives that stutter have a greater risk of developing the disease, and stuttering occurs more frequently in biological relatives of individuals who are predisposed to stuttering than in adopted relatives. Studies show a higher correlation of stuttering between monozygotic twins compared to dizygotic twins. Both the polygenic multifactorial model (many genes with a small effect) and the isolated locus model (one gene with a large effect) appear to be applicable to genetic studies of stuttering. The transmission model indicates genetic differences that vary between gender, suggesting that female individuals have more susceptible alleles necessary for phenotypic expression than male individuals. 5-14

Genotypic studies of stuttering have not yet clearly identified its mode of inheritance and have not yet indicated an obvious overlap of the chromosomal regions involved in the disorder. Genomic analyses performed indicate the following possible chromosomal candidates regions: 18,1,12,5,15,2,9,13,1, and 3. 15-29 A recent study suggests an association between susceptibility to stuttering and variations in genes responsible for lysosomal metabolism (genomic region 12q23.3).

A critical component of the evolution of genetic studies in stuttering has been criteria for the selection of affected and unaffected family members. In this regard, a significant proportion of previous studies were based on questionnaires and/or personal and family accounts. Few studies have been developed with a type of objective and professional assessment. 9,11,12,18

The accuracy and reliability of the classification of both probands and other affected family members is an important phenotypic measure because it ensures the sensitivity and specificity of the diagnosis. Although large sample studies and research including different populations can be advantageous to the generalization of the potential genetic findings, data from more homogeneous samples may also be of interest because they are genetically more similar (micro or endophenotypes) and, therefore, more closely or directly linked to gene expression.18

The objective of this study was to identify the speech fluency family profile consisting of linguistic, electromyographic and acoustic aspects in two distinct groups of children, with (GI) and without (parents and siblings - GII) a close family history of stuttering.

The hypotheses were as follows:

. H1 - Child/family relationship - the direct genetic antecedent implies similarity in the typology of speech disruptions in all affected individuals in the same family. This hypothesis is based on the assumption that the activity of the gene is directly reflected on the speech pattern, or, in other words, it is linked to the speech symptomatology manifested.
. H2 - Child/family relationship - the direct genetic antecedent implies similarity in muscular activation of the diadochokinesia rates in all affected members of the same family. This hypothesis is based on the assumption that the activity of the gene is directly reflected on the speech motor pattern, which can be measured by capturing peripheral muscle activation.
. H3 - Child/family relationship - the direct genetic antecedent implies similarity in acoustic variation of the diadochokinetic rates in all affected individuals in the same family. This hypothesis is based on the assumption that the activity of the gene is directly reflected in the acoustic speech pattern, or in other words, it is linked to factors influencing the production of the sound signal.
. H4 -Proband GI/GII relation - the final scores for typology, muscular activation and speech acoustic variation will be negatively differentiated in the GI children. This hypothesis is based on the assumption that the activity of the stuttering heredity gene is responsible for the occurrence of the phenomenon or the observed results.

Method

Participants

A total of 127 individuals participated in the study. The participants consisted of 32 children between 4.0 and 11.11 years of age (probands) and 95 immediate family members (father, mother, sisters, and brothers). The participants were chosen irrespective of race and gender, were enrolled in public school elementary and secondary education,

and resided in São Paulo and Greater São Paulo. The selection and evaluation processes followed the relevant ethical processes: Assessment of the Ethics Commission (CAPPesq HCFMUSP, 266/05) and the signing of free and informed consent by the proband families. Participants were divided into two groups:

. GI (stuttering child - SC): 17 probands, 17 fathers, 17 mothers, 10 brothers and 13 sisters. Total number of participants: 74:
. GII (non-stuttering child - NSC): 15 probands, 15 fathers, 15 mothers, no brothers and 8 sisters. Total number of participants: 53.

The inclusion criteria for GI probands and considerations for affected family members were:

. presented with a fluency profile score not within the reference values for the age group;31,32;
. obtained 11 points or more on the Stuttering Severity Instrument - 3 (SSI-3);33;
. presented with at least 3% stutter disfluency per 100 syllables;
. presented with persistent stuttering for at least six months.8.

The inclusion criteria for probands in GII and considerations for non-affected family members were:

. presented with a fluency profile score in accord with the reference values for the age group; 31,32;
. obtained a total of 10 points or less in the SSI-3; 33;
. presented with less than 2% stutter disfluency per 100 syllables;
. presented with no family history for recovered or persistent stuttering. 8.

Materials

All participants were filmed using a Sony DRC-SR62 digital camera. The recordings of the muscular responses were collected using four-track equipment, with an analog to digital conversion plate and software for signal collection and processing (Windows platform - EMG System, Brazil) installed in a high-resolution computer. The electrodes used were the MedTrace Mini Ag/AgCl (10-mm diameter) disposable type. The acoustic analysis software used was the PRAAT.

Procedures

The test procedures applied to all participants were as follows:

. disruption typology collection - speech pattern disruptions (both common and stutter) from a sample of spontaneous speech were analyzed. 31;
. EMG collection - the rate of the speed of movement (diadochokinesia) was studied, including both alternate (papapa) and sequential (pataka) tasks, with three repetitions per rate.34 To capture muscular electric activity of the perioral region, electrodes were placed in the following positions: inferior orbicularis oris; right masseter; suprahyoid region (anterior digastric branch); and above the thyroid proeminence.35 The objective was to evaluate muscular activation relative to force, speed, range, accuracy, and stability of the movement;
. acoustic collection - the rate of the speed of movement (diadochokinesia) was studied, including both alternated (papapa) and sequential (pataka) tasks, with three repetitions per rate.34 The objective was to evaluate the duration, VOT, pitch, and loudness.

Results

Stuttering distribution profile

Table 1 shows the distribution of the affected and unaffected family members in GI.

Gender distribution of G1 includes 13 male probands and 4 female probands, with a ratio of 3.25/1 (Table 2).

Distribution profile by disorder severity

For GI (SC), according to the SSI-3 classification, 29.4% of the probands showed mild stuttering, 53% showed moderate stuttering, and 17.6% showed severe stuttering. When analyzing the degree of similarity of stuttering severity between the probands and their affected relatives, it was observed that the severity of affected family members was not similar to that of the probands, with 95% of the relatives showing mild stuttering.

III. Typology of the disruptions

For GI (SC), the similarity observed in the types of disruptions (stutter) between probands and affected fathers was 44.8%. Between the probands and affected mothers, the similarity observed was

64.3%, and between probands and affected siblings, the similarity was 64.8%. The analysis of the degree of similarity of the disruptions between probands and affected relatives was 12% for a low degree of similarity (0-24% similarity), 35.3% for a medium degree of similarity (25-49%), 35.3% for a high degree of similarity (50-74%), and 17.4% for an extremely high degree of similarity (75-100%).

Electromyographic response

Using the Mann-Whitney U test with a significance level of 0.95, the analysis of GI (SC) probands and affected relatives revealed no significant statistical difference between probands/brothers, probands/father and probands/mother regarding both the sequential and the alternate rates.

Between-group analysis of GI (SC) and GII (NSC) probands by ANOVA and Mann-Whitney showed a statistically significant difference (p.037 and 0.015) regarding the sequential rate (pataka), or, in other words, that GI presents lower efficiency in the task.

Acoustic response

Regarding GI (SC), the analysis between probands and affected relatives, using the Mann-Whitney U test with a significance level of 0.95, revealed no statistically significant difference between probands and siblings. Statistical significance was found between probands and fathers ($p = 0.009$) and between probands and mothers ($p < 0.01$) regarding pitch variable. For the other variables (duration, loudness and VOT), no statistically significant differences were found.

Between-group analysis of GI (SC) and of GII (NSC) probands by ANOVA and Mann-Whitney showed no statistically significant difference for the variables studied.

TABLE 1. Distribution of affected and unaffected family members in GI.

Family member	Affected	% Affected	Unaffected	% Unaffected	Total
father	6	35.3%	11	64.7%	17
mother	7	41.2%	10	58.8%	17
sisters	3	23%	10	77%	13
brothers	4	40%	6	60%	10
total	20	35%	37	65%	57

TABLE 2. Proportion of male and female proband immediate family members with a stutter.

Family member	Male proband (n=13)	Female proband (n=4)
parents	5/31.3%	1/25%
brothers	4/25%	0
total males	9/56.3%	1/25%
mothers	5/31.3%	2/50%
sisters	2/12.5%	1/25%
total females	7/43.8%	3/75%
total in the immediate family	16/80%	4/20%

Discussion

A literature search did not reveal any studies similar to work presented here; therefore, comparisons are only partially possible between the findings regarding the distribution of stuttering in families due to the scope of the phenotypic study.

Although the comparison of the results should be carefully analyzed due to the different methodologies applied and based on the study by Yairi et al., it is apparent that the more elaborate the inclusion criteria, the higher the proportion of affected members of the same family. As noted in our study, according to the criteria used in our methodology, most of the affected family members presented with mild stuttering, which, within the context of an interview, may not have been considered stuttering by the individual.

Regarding the study hypotheses for H1, a similarity was observed in the typology of speech disruptions in all affected individuals in the same family; however, a tendency for greater severity of the disorder in probands was observed. This finding confirms the hypothesis, but further studies are necessary because stuttering manifests differently in children and adults.

Regarding H2, a similarity was found in the muscular activation of diadochokinetic rates in all affected individuals of the same family. A difference was observed when comparing the probands of the study group and members of the control group. This result should be carefully considered because it is only a preliminary finding on the issue. A suggested speech motor pattern within the same family was observed; therefore, a pattern can be measured by capturing peripheral muscular activation. This aspect requires further studies before it can be effectively considered.

For H3, it is pertinent that we use the same reasoning applied for H2. A similarity was found in acoustic variation of the diadochokinetic rates in all the affected individuals in the same family. This finding is relevant but needs further studies before it can be effectively considered.

For H4, the results of the study were unable to confirm the hypothesis due to the sample size, the evaluation methodology adopted, and inconsistent results, which are not amenable to comparisons in the literature.

Conclusion

The research is characterized as a first proposal from an endophenotypic study of stuttering considering two reproducible aspects: objective inclusion criteria and the evaluation of manifest symptomatology of stuttering. The study has obvious limitations and should not be generalized, but constitutes an interesting suggestion for further studies. The study also contributes as a model for the standardized evaluation of participants in genetic studies of stuttering.

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