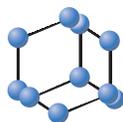


## RESEARCH ARTICLE

BENTHAM  
SCIENCE

## Genetic Imbalance in Patients with Cervical Artery Dissection



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**Abstract: Background:** Genetic and environmental risk factors are assumed to contribute to the susceptibility to cervical artery dissection (CeAD). To explore the role of genetic imbalance in the etiology of CeAD, copy number variants (CNVs) were identified in high-density microarrays samples from the multicenter CADISP (Cervical Artery Dissection and Ischemic Stroke Patients) study and from control subjects from the CADISP study and the German PopGen biobank. Microarray data from 833 CeAD patients and 2040 control subjects (565 subjects with ischemic stroke due to causes different from CeAD and 1475 disease-free individuals) were analyzed. Rare genic CNVs were equally frequent in CeAD-patients (16.4%; n=137) and in control subjects (17.0%; n=346) but differed with respect to their genetic content. Compared to control subjects, CNVs from CeAD patients were enriched for genes associated with muscle organ development and cell differentiation, which suggests a possible association with arterial development. CNVs affecting cardiovascular system development were more common in CeAD patients than in control subjects ( $p=0.003$ ; odds ratio (OR) =2.5; 95% confidence interval (95% CI) =1.4-4.5) and more common in patients with a familial history of CeAD than in those with sporadic CeAD ( $p=0.036$ ; OR=11.2; 95% CI=1.2-107).

**Conclusion:** The findings suggest that rare genetic imbalance affecting cardiovascular system development may contribute to the risk of CeAD. Validation of these findings in independent study populations is warranted.

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## INTRODUCTION

Copy number variations (CNVs) are structural genetic variants (deletions or duplications), leading to genetic imbalance.

CNVs are widespread in the human genome and play an important role in multiple phenotypes [1-3] including vascular diseases [4, 5]. The contribution of structural genetic variation to the risk of ischemic stroke (IS) has not been explored thoroughly: In a CNV study of 263 patients with IS of different causes [6], no common genomic structural variant was unequivocally linked to IS. A pilot study of 70 patients with cervical artery dissection (CeAD) [7] identified several rare

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CNVs affecting genes involved in arterial development or in connective tissue disorders. CeAD is a bleeding within the arterial wall of the carotid artery or the vertebral artery. CeAD is a rare cause of IS in old patients, but it causes IS in about 10% of patients <50 years [8, 9]. A recent genome-wide association study identified a common variant in the PHACTR1 gene (encoding the phosphatase and actin regulator 1) that increased the risk for CeAD [10]). In the current study we explore rare CNVs in a large set of SNP-microarray data that genome-wide association study [10]. Our findings suggest that rare structural variation associated with different biological functions including muscle organ development, cell differentiation and cardiovascular system development contribute to the risk of CeAD.

## MATERIAL AND METHODS

### Patients and Controls Subjects

A total of 983 patients with a diagnosis of CeAD based upon predefined criteria were included in the CADISP (Cervical Artery Dissection and Ischemic Stroke Patients) study between 2004 and 2009 [11]. After the exclusion of CeAD patients with (i) confirmed diagnosis of vascular Ehlers-Danlos syndrome (vEDS), (ii) non-European origin, or (iii) insufficient DNA quality, 883 patients were successfully genotyped using an Illumina Human 610-Quad or Human 660W-Quad Bead Chip at the Centre National de Génotypage in Evry, France, and passed genotyping quality control.

As control subjects, 658 patients with ischemic stroke attributable to a cause other than CeAD (non-CeAD-IS patients) and 269 Finnish healthy subjects from the CADISP study [11, 12] were included in the study. After the exclusion of individuals with (i) non-European origin or (ii) insufficient DNA quality, 585 control patients and 237 healthy controls passed genotyping quality control. Ancestry of all CADISP subjects (patients as well as controls) was inferred from places of birth of both parents as well as of self-reported information during the interview upon recruitment. Principal component analysis and stringent Hardy-Weinberg Equilibrium filtering during quality control preceding the genome-wide association study [10] enabled identification of population stratification. As additional controls, we used 1262 high-quality Affymetrix 6.0 datasets from Caucasian subjects in the German PopGen biobank [13].

### Baseline Characteristics of CeAD Patients

The following clinical variables were derived from the CADISP-database: age, sex, vascular risk factors (as defined before [14]), site of dissection (internal carotid artery, vertebral artery or both), presence or absence of ischemic stroke, familial history of CeAD, defined as self-reported history of CeAD in first-degree relatives (parents, siblings or children). Since the CeAD study sample comprised two families with two affected relatives each, analysis of the familial history of CeAD was also performed by including only one affected individual from each family.

### CNV Discovery and Prioritization

CNVs were identified with the PennCNV software (version May 2010) [15]. CNVs comprising >10 SNPs (Illumina

data) or >20 SNPs (Affymetrix data) were analyzed further. Datasets with outlier numbers of CNV calls (i.e., >125 or < 15 CNVs) or with a variance >0.2 of the normalized LRR values taken over all autosomal SNPs were excluded from the analysis [16]. The final study sample comprised microarray data from 833 CeAD patients, 565 control patients, and 215 Finnish and 1260 German healthy subjects.

Published CNV data were used to identify common CNVs in the study subjects. CNVs were considered as rare if less than three copies were found among the 3703 disease-free subjects in two published CNV databases [17, 18]. CNVs overlapping > 50% of their physical length were considered as similar.

### CNV Validation and Mapping

Signal intensity and B-allele frequencies of all rare CNVs were visualized (<http://noise-free-cnv.sourceforge.net/contact.php>) to identify putative false-positive calls and to inspect and map the breakpoints. CNV validation was performed in two-steps as described before [7, 16], including visual inspection of each CNV finding in noise-reduced datasets, followed by molecular analysis of a few selected CNVs. For molecular validation by quantitative PCR [19], we randomly selected 10 rare CNVs from the CeAD patients. For each CNV, PCR was carried out in six replicates with DNA of the CNV carrier and three control subjects in 96-well plates with a Bio-Rad SYBR-Green PCR system following standard procedures. Five additional CNVs from CeAD patients were validated by identification and sequence analysis of the joining fragment [20].

The first and the last SNPs of each CNV were mapped onto the human genome (GRCh38) ([http://www.ensembl.org/Homo\\_sapiens](http://www.ensembl.org/Homo_sapiens)). CNVs were classified as genic if they comprised the deletion of at least one coding exon or a duplication that either encompassed an entire coding region or internal exons [21]. Duplications with both breakpoints within genes of similar chromosomal orientation were also considered as genic, because they might encode a fusion protein [22].

CNV findings located in heterochromatic pericentromeric regions, in the short arms of the acrocentric chromosomes (numbers 13,14,15,21 and 22), in the subtelomeric regions of chromosomes 9q and 14q, in the MHC region of chromosome 6p and in the Y-chromosome were *a-priori* excluded from the current analysis.

### Functional Enrichment Analysis / Case Control Studies

All genes identified in all rare CNVs from the CeAD patients sample were analyzed for enrichment of predefined gene sets with the Set Distiller software package (<http://www.genecards.org/index.php?path=/GeneDecks>). Top enrichments for the category “GeneOntology biological process” were analyzed. P-values for enrichment were Bonferroni-adjusted for multiple testing of the total set of tested biological processes (n=7780) by default.

For each analyzed enriched gene set, all rare CNVs affecting one or more genes belonging to the gene set were identified in both study groups (CeAD patients and control subjects). The prevalence of CNVs affecting a selected gene



**Table 1. Functional enrichment analysis (FEA) and specificity analysis of rare genic CNVs in CeAD patients. Left hand columns show top findings of GeneDecks enrichment analysis for genes covering rare CNVs of CeAD patients with adjusted p-values. The frequency of rare CNVs at genes belonging to the enriched gene sets was compared between CeAD patients and control subjects (non-CeAD IS disease controls plus population controls). Since the findings suggested CeAD to be associated with cardiovascular system development, this candidate gene set was subsequently tested formally for disease association (see table 2). P-values of FEA were Bonferroni-corrected for multiple testing by default. Crude P-values of Case/Control comparisons were multiplied by 10 to adjust for multiple testing.**

Functional Enrichment Analysis		Case/Control Comparison		
Identified gene sets in GeneOntology – biological processes	adjusted p-value	CeAD (n=833)	Controls (n=2040)	adjusted p-value
Small molecule metabolic process	1.23e-10	29	41	0.234
Muscle organ development	3.57e-07	9	3	<b>0.013</b>
Multicellular organismal development	4.91e-07	18	16	0.036
Xenobiotic catabolic process	9.17e-07	1	0	1.000
Regulation of transcription, DNA-templated	1.44e-06	18	41	1.000
Cell differentiation	1.61e-05	18	13	<b>0.010</b>
Signal transduction	1.93e-05	19	28	1.000
Proteolysis	3.12e-05	8	5	0.145
Cell adhesion	3.21e-05	13	12	0.147
Cell surface receptor signaling pathways	3.59e-05	8	5	0.145
Apoptotic process	3.86e-05	12	14	0.791

tients and in 22 (1.1%) control subjects (Table 2:  $p=0.006$ ; odds ratio = 2.38; 95% confidence interval = 1.30-4.35). Exclusion of Finnish subjects from the analyses didn't lead to different results.

CeAD patients carrying rare CNVs of genes associated with cardiovascular system development did not differ from non-carriers with regard to baseline characteristics, clinical symptoms or risk factors (Table 3). However, patients with a family history of CeAD were significantly more likely to carry a rare CNV affecting cardiovascular system development than patients without a family history. The association between familial CeAD and CNVs affecting cardiovascular system development remained significant after exclusion of related CeAD patients (two pairs of affected sibs were enrolled in the CeAD sample). A rare genic duplication in two affected CeAD siblings (Table 4) comprised the MKL2 gene (encoding myocardin-like 2) which is associated with muscle organ development as well as with muscle phenotype.

The rare CNVs from the CeAD patients that are associated with cardiovascular system development are listed in (Table 4). A large duplication in chromosome 16p including MYH11 and ABCC6 was found in three CeAD patients and in a single control subject. A deletion of the same locus was identified in one further CeAD patient.

## DISCUSSION

This large genome-wide analysis of rare genetic variants in CeAD patients yielded the following key findings: 1) patients with CeAD were more likely to carry rare CNVs asso-

ciated with muscle development, cell differentiation, or cardiovascular system development than control subjects; 2) patients with a family history of CeAD more often carried a rare CNVs associated with cardiovascular system development than patients with sporadic (non-familial) CeAD and 3) CNVs in CeAD patients were highly heterogeneous, even though three patients carried a recurrent 16p duplication including MYH11 and ABCC6 and one further patient had a deletion of the same region.

The association between CeAD and rare genetic variants affecting cardiovascular system development observed in our study is in agreement with earlier findings of rare COL3A1 and TGFBR2 mutations in some patients [23-26]. Moreover, our pilot study of 70 CeAD patients revealed a rare CNV of the COL3A1/COL5A2 locus and some additional CNVs affecting cardiovascular system development or muscle organ development [7]. In patients with aortic aneurysms and dissections, enrichment of rare copy number variants in similar predefined gene groups has been reported (including enrichment of CNVs in genes associated with smooth muscle cell contraction and in genes associated with cardiovascular diseases) [27]. Interestingly, one patient from our pilot study sample [7] carried the 16p duplication that we identified in three additional patients from the current study. Furthermore, one CeAD patient from the current study had a large deletion of this same region. This 16p duplication is rare in the human population [28] but was previously found to be significantly more common among patients with aortic dissection than in healthy subjects [4]. Our findings suggest that this rare CNV also increases the risk for CeAD. Taken

**Table 2. Carriership of rare CNVs affecting cardiovascular system development in the study samples. *p*-adj.: *p*-values (unadjusted) and OR (odds ratio) were calculated for a comparison between patients and all control subjects. 95% CI = 95% confidence interval. \*) The CeAD samples included two families with two affected siblings, but only one sibling of each family was included in this analysis.**

	CeAD Patients*	Ischemic Stroke Controls	Finnish Healthy Controls	German Healthy Controls	All Controls	<i>p</i> -value	OR	95% CI
	n=831	n=565	n=215	n=1260	n=2040			
<b>Carriership of rare CNVs</b>								
CNVs affecting muscle organ development	8	2	0	1	3	0.003	6.60	1.75-24.9
CNVs affecting cell differentiation	18	0	1	12	13	<0.001	3.45	1.68-7.08
CNVs affecting cardiovascular system development	21	5	2	15	22	0.006	2.38	1.30-4.35

**Table 3. Baseline characteristics and risk factors in CeAD patients with or without rare CNV affecting cardiovascular system development. Adjusted *p*-values and OR (odds ratio) are from a logistic regression analysis adjusted for age and sex. 95% CI = 95% confidence interval of OR. Values are n (%) or mean ± standard deviation, CeAD = cervical artery dissection, ICAD = internal carotid artery dissection, FH = family history, unrelated = related patients were excluded.**

	Patients with rare CNVs affecting cardiovascular system development	Other patients				
	(n=22)	(n=811)	<i>p</i> -value	Adjusted <i>p</i> -value	OR	[95% CI]
Age	42.8 ± 10.4	44.3 ± 9.9	0.494			
Female sex	10 (45.5)	343 (42.3)	0.828			
Stroke	16 (72.7)	522 (64.4)	0.503	0.425	1.47	[0.57 – 3.81]
ICAD	13 (59.1)	547 (67.4)	0.490	0.501	0.74	[0.30 – 1.79]
Multiple CeAD	1 (4.5)	124 (15.3)	0.230	0.184	0.25	[0.03 – 1.91]
Hypertension	5 (22.7)	214 (26.6)	0.810	0.815	0.88	[0.31 – 2.51]
Hypercholesterolemia	4 (18.2)	153 (19.3)	1.000	0.955	1.03	[0.33 – 3.23]
Migraine	9 (40.9)	300 (37.5)	0.824	0.811	1.12	[0.46 – 2.72]
BMI	25.0 ± 6.4	24.6 ± 3.9	0.743	0.469	1.04	[0.94 – 1.15]
Previous trauma	8 (36.8)	328 (41.2)	0.827	0.592	0.78	[0.32 – 1.91]
Previous infection	7 (31.8)	150 (18.9)	0.165	0.134	2.02	[0.81 – 5.04]
smoking	1 (50.0)	418 (52.2)	1.000	0.916	0.96	[0.41 – 2.25]
FH of CeAD	2 (10.5)	5 (0.7)	0.011	0.001	18.5	[3.3 – 103]
FH of CeAD (unrelated)	1 (5.6)	4 (0.5)	0.110	0.036	11.2	[1.17 – 107]

together, these findings also point towards shared risk factors for dissections of different arterial beds [29].

We are aware of several limitations. The analysis of microarrays data enables the identification of deletions and duplications, but other types of disease-causing mutations (point mutations, indels, translocations, inversions) cannot be detected. Furthermore, smaller CNVs (<50 kb) may have been overlooked, due to the insufficient probe density of the

used microarray platforms. The use of different microarray platforms for the analysis of the control groups is a further limitation of our study. Moreover, some of the patient characteristics (including history of trauma, and smoking) were self-reported and not validated by medical records. Familial history of CeAD was also self-reported and not confirmed by molecular analysis. The lack of independent patient and control samples to confirm the current findings is another limitation of this study.

**Table 4. CNVs associated with cardiovascular system development in the patient' sample. \*) Patients B00ACFQ and B00ACKL are siblings.**

Patient ID	CN-state	Locus	Genes
B00ADIK	loss	chr 1: 10.0-12.0	C1orf127, TARDBP, MASP2, SRM, MTOR, EXOSC10, ANGPTL7, UBIAD1, FBXO44, FBXO6, MAD2L2, DRAXIN, C1orf1
B00ADIC	gain	chr1:12.3-12.8	AADAACL3, AADAACL4, DHRS3, PRAMEF1, PRAMEF11, PRAMEF12, C1orf158, HNRNPCL1
B00ADMI	gain	chr1:12.3-12.8	AADAACL3, AADAACL4, DHRS3, PRAMEF1, PRAMEF11, PRAMEF12, C1orf158, HNRNPCL1
B00AE14	gain	chr2:68.9-69.4	BMP10, GKN1, GKN2, ANTXR1
B00AD9N	gain	chr3:185.5-185.9	CLCN2, POLR2H, THPO, RP11-433C9.2, EPHB3
B00ACGF	gain	chr5:0.3-0.5	SDHA, PDCD6, EXOC3, AHRR, C5orf55, CCDC127
B00ACGZ	gain	chr7:16.9-17.4	AHR
B00AD2L	loss	chr7:19.0-19.1	TWIST1, HDAC9
B00ACEI	gain	chr8:143.8-144.8	LY6K, THEM6, SLURP1, LYPD2, LYNX1, LY6D, CYP11B2, LY6E, C8orf31, LY6H, GPIHBP1, ZFP41, GLI4, ZNF696, TOP1MT, RHPN1, MAFA
B00ACJC	loss	chr8:23.2-23.4	R3HCC1, ENTPD4, LOXL2
B00ADHH	loss	chr15:82.9-83.5	ZSCAN2, WDR73, NMB, SEC11A, ZNF92, ALPK3, SLC28A1, PDE8A
B00ACFQ*	gain	chr16:14.0-15.6	MKL2, PARN, BFAR, PLA2G10, NOMO1, NPIP
B00ACKL*	gain	chr16:14.0-15.6	MKL2, PARN, BFAR, PLA2G10, NOMO1, NPIP
B00AEME	gain	chr16:15.2-16.2	PKD1P1, MPV17L, C16orf45, KIAA0430, NDEI, MYH11, FOPNL, ABCC1, ABCC6
B00AEON	gain	chr16:15.2-16.2	PKD1P1, MPV17L, C16orf45, KIAA0430, NDEI, MYH11, FOPNL, ABCC1, ABCC6
B00ACG3	loss	chr16:15.4-16.2	PKD1P1, MPV17L, C16orf45, KIAA0430, NDEI, MYH11, FOPNL, ABCC1, ABCC6
B00ACRB	gain	chr16:15.4-16.2	PKD1P1, MPV17L, C16orf45, KIAA0430, NDEI, MYH11, FOPNL, ABCC1, ABCC6
B00AE12	gain	chr16:2.8-3.4	ZG16B, PRSS22, FLYWCH1, FLYWCH2, KREMEN2, PKMYT1, CLDN9, PAQR4, CLDN6, TNFRSF12A, HCFC1R1, THOC6, CCDC64B, MMP25, ZSCAN10, ZNF205, ZNF213, OR1F1, ZNF263, TIGD7, ZNF75A, OR2C1, MTRNR2L4, ZNF434, ZNF174
B00ADC0	gain	chr16:84.9-85.3	MTHFSD, FOXL1, FOXC2, FOXF1
B00ADWH	gain	chr17:0.7-0.9	TIMM22, NXN, ABR
B00AEP8	gain	chr17:29.0-29.7	CCL1, CCL2, CCL7, CCL8, CCL11, CCL13
B00AD77	gain	chr17:75.7-75.8	GAA, EIF4A3, CARD14, SGSH, SLC26A11

A major strength of our study was the large study sample of patients recruited according to uniform criteria with a single, well-characterized stroke etiology, the utilization of large samples of control subjects as well as the careful inspection and validation of each PennCNV finding in noise-reduced datasets in order to reject all artificial CNV findings [7, 16]. Visual inspection of noise-reduced datasets enabled a critical evaluation of PennCNV findings, including their presence, their length and the position of the breakpoints. Moreover, split calls (consecutive calls that in reality represent one single CNV) were identified as CNVs with copy number state = 4, or mosaicism. Last but not least, visual inspection of a dataset gave an immediate impression of the data-quality, including the amplitude of GC-waves and the noise across the BAF-values. For the prioritization of rare CNV findings we compared our data with control subjects from high-quality public databases, to avoid misclassifica-

tions [30]. A further strength of our study was the analysis of predefined gene sets associated with biological functions, instead of focusing upon single candidate CNVs. Association of predefined gene sets was identified by different methods: 1) functional enrichment was detected by comparing the frequency of gene sets in the patient sample and in the human genome; 2) genetic association was detected by comparing the frequency of rare CNVs affecting a predefined gene set in patients and control subjects and 3) genetic association was confirmed by comparing the frequency of rare CNVs affecting a predefined gene set in patients with sporadic and familial CeAD.

In summary, our findings suggest that rare genetic imbalance affecting different biological functions contributes to the risk of CeAD. Moreover, the imbalanced genes in this study suggest that developmental defects of the arterial sys-

tem may predispose to CeAD. To further explore the role of rare genetic variants in the etiology of CeAD, a whole-exome sequencing study of patients with familial CeAD is currently ongoing [31].

### CONFLICT OF INTEREST

The authors confirm that this article content has no conflict of interest.

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### SUPPLEMENTARY MATERIAL

Supplementary material is available on the publisher's web site along with the published article.

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