

(12) STANDARD PATENT
(19) AUSTRALIAN PATENT OFFICE

(11) Application No. **AU 2004232459 B2**

- (54) Title
Analysis and use of PAR 1 polymorphisms for the risk estimation of cardiovascular diseases
- (51) International Patent Classification(s)
C07K 14/72 (2006.01) **C12Q 1/68** (2006.01)
- (21) Application No: **2004232459** (22) Date of Filing: **2004.04.16**
- (87) WIPO No: **WO04/094470**
- (30) Priority Data
- (31) Number (32) Date (33) Country
103 18 496.1 **2003.04.24** **DE**
- (43) Publication Date: **2004.11.04**
(44) Accepted Journal Date: **2010.11.11**
- (71) Applicant(s)
Sanofi-Aventis Deutschland GmbH
- (72) Inventor(s)
Kozian, Detlef;Siegler, Karl-Ernst;Ricard, Sylvain;Mace, Sandrine;Czech, Joerg;Deleuze, Jean-Francois
- (74) Agent / Attorney
Watermark Patent and Trade Marks Attorneys, Level 2 302 Burwood Road, Hawthorn, VIC, 3122

(12) NACH DEM VERTRAG ÜBER DIE INTERNATIONALE ZUSAMMENARBEIT AUF DEM GEBIET DES
PATENTWESENS (PCT) VERÖFFENTLICHTE INTERNATIONALE ANMELDUNG

(19) Weltorganisation für geistiges Eigentum
Internationales Büro



(43) Internationales Veröffentlichungsdatum
4. November 2004 (04.11.2004)

PCT

(10) Internationale Veröffentlichungsnummer
WO 2004/094470 A1

(51) Internationale Patentklassifikation⁷: **C07K 14/72**,
C12Q 1/68

(21) Internationales Aktenzeichen: PCT/EP2004/004035

(22) Internationales Anmeldedatum:
16. April 2004 (16.04.2004)

(25) Einreichungssprache: Deutsch

(26) Veröffentlichungssprache: Deutsch

(30) Angaben zur Priorität:
103 18 496.1 24. April 2003 (24.04.2003) DE

(71) Anmelder (für alle Bestimmungsstaaten mit Ausnahme
von US): **AVENTIS PHARMA DEUTSCHLAND
GMBH** [DE/DE]; Brüningstrasse 50, 65929 Frankfurt am
Main (DE).

(72) Erfinder; und

(75) Erfinder/Anmelder (nur für US): **KOZIAN, Detlef**
[DE/DE]; Schulstrasse 23, 67595 Hattersheim (DE).
CZECH, Joerg [DE/DE]; Kreuzacker 2a, 35041
Marburg (DE). **SIEGLER, Karl-Ernst** [DE/DE];
Horst-Schorck-Strasse 19, 67069 Ludwigshafen (DE).
DELEUZE, Jean-Francois [FR/FR]; 4, rue de l'Yer-
res, F-77380 Combs La Ville (FR). **RICARD, Sylvain**
[FR/FR]; 120 Boulevard Vincent Auriol, F-75013 PARIS
(FR). **MACE, Sandrine** [FR/FR]; 11, rue Louis Chagnot,
F-78350 Jouy-en-Josas (FR).

(81) Bestimmungsstaaten (soweit nicht anders angegeben, für
jede verfügbare nationale Schutzrechtsart): AE, AG, AL,
AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
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TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM,
ZW.

(84) Bestimmungsstaaten (soweit nicht anders angegeben, für
jede verfügbare regionale Schutzrechtsart): ARIPO (BW,
GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM,
ZW), eurasisches (AM, AZ, BY, KG, KZ, MD, RU, TJ,
TM), europäisches (AT, BE, BG, CH, CY, CZ, DE, DK,
EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT,
RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA,
GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Veröffentlicht:

- mit internationalem Recherchenbericht
- vor Ablauf der für Änderungen der Ansprüche geltenden
Frist; Veröffentlichung wird wiederholt, falls Änderungen
eintreffen

Zur Erklärung der Zweibuchstaben-Codes und der anderen Ab-
kürzungen wird auf die Erklärungen ("Guidance Notes on Co-
des and Abbreviations") am Anfang jeder regulären Ausgabe der
PCT-Gazette verwiesen.



WO 2004/094470 A1

(54) Title: ANALYSIS AND USE OF PAR 1 POLYMORPHISMS FOR THE RISK ESTIMATION OF CARDIOVASCULAR DISEASES

(54) Bezeichnung: ANALYSE UND VERWENDUNG VON PAR 1 POLYMORPHISMEN ZUR RISIKOABSCHÄTZUNG FÜR KARDIOVASKULÄRE ERKRANKUNGEN

(57) Abstract: The invention relates to polynucleotide sequences comprising genetic variations of PAR 1 gene on positions 3090 and/or 3329. Surprisingly, the presence of said variants in humans correlates with specific cardiovascular diseases. The invention also relates to methods for the detection of said genetic variations.

(57) Zusammenfassung: Die Erfindung betrifft Polynukleotidsequenzen umfassend genetische Variationen des PAR 1 Gens an den Positionen 3090 und/oder 3329. Das Auftreten dieser Varianten ist beim Menschen korreliert mit erhöhter Auffälligkeit für bestimmte Herzkreislaufkrankungen. Die Erfindung bezieht sich weiterhin auf Verfahren zum Nachweis dieser genetischen Variationen.

Description

Analysis and use of PAR1 polymorphisms for evaluating the risk of cardiovascular disorders.

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The invention relates to polynucleotide sequences comprising genetic variations of the PAR1 gene at positions 3090 and/or 3329.

10 The protease-activated receptor 1 (PAR1) is a thrombin receptor which belongs to the class of G protein-coupled receptors (GPCR). The gene for PAR1 is located on chromosome 5q13, consists of two exons and covers a region of approx. 27 kb. PAR1 is expressed in, inter alia, endothelial cells, smooth muscles cells, fibroblasts, neurons and human platelets. In platelets, PAR1 is an important signal transduction receptor which is
15 involved in the initiation of platelet aggregation.

PARs are activated via proteolytic removal of a part of the N terminus of said PARs, whereby a new N-terminal sequence is exposed which then activates the receptor.

20 PAR1 and PAR4 play a central part in the activation of platelets; the activation of these receptors in platelets leads to morphological changes, release of ADP and aggregation of said platelets.

A connection of coronary heart diseases with single nucleotide polymorphisms (SNP) in the promoter region of PAR1 in a group of Korean
25 patients was not confirmed. In another study, a PAR1 promoter variant was shown to have a protective action for the development of venous thromboembolisms.

30 The sequence of the human PAR1 gene is known. The polynucleotide sequence of this gene can be accessed under the number NM-001992 at the NCBI nucleotide database. Likewise, the protein sequence is available under the number NP-001983 at the NCBI protein database. NCBI is the National Center for Biotechnology Information (postal address: National Center for Biotechnology Information, National Library of Medicine, Building
35 38A, Bethesda, MD 20894, USA; Web address: www.ncbi.nlm.nih.gov). The cloning of the PAR1 gene has been described, inter alia, in "Schmidt et al., J. Biol. Chem. 271, 9307-9312, 1996".

There are various new polymorphisms of the PAR1 gene, by means of which it is possible to determine a relatively strong disposition of an individual for coronary heart diseases. The affected individuals are thus enabled to counteract this risk factor in time by adapting their life style
5 accordingly, for example by compensating via increased control of other damaging influences such as smoking, alcohol consumption, cholesterol-rich food, high blood pressure etc.

Such health-related preventive mechanisms would not be possible without
10 knowledge of the PAR1 polymorphisms which are explained in more detail below and the use thereof in corresponding methods.

Variants of a particular nucleotide sequence with substitutions at individual positions are known to the skilled worker under the term SNP (= single
15 nucleotide polymorphism).

The invention relates to an isolated polynucleotide sequence of the PAR1 gene, which comprises a C for T substitution at position 3090 of the PAR1 sequence according to NM-001992 which, as prior art, is publicly available.
20 In a preferred embodiment, the polynucleotide sequence of the PAR1 gene having a T to C substitution at position 3090 encompasses a sequence according to SEQ ID NO: 2 and, in a particularly preferred embodiment of said polynucleotide sequence, the latter comprises a sequence of SEQ ID
NO: 2.

25 The invention furthermore relates to an isolated polynucleotide sequence of the PAR1 gene, which comprises an C for A substitution at position 3329 of the PAR1 sequence according to NM-001992 which, as prior art, is publicly available. In a preferred embodiment, the polynucleotide sequence of the
30 PAR1 gene having an A to C substitution at position 3329 encompasses a sequence according to SEQ ID NO: 3 and, in a particularly preferred embodiment of said polynucleotide sequence, the latter comprises a sequence of SEQ ID NO: 3.

35 The invention also relates to an isolated polynucleotide sequence of the PAR1 gene, which comprises a C for T substitution at position 3090 of the PAR1 sequence according to NM-001992 and, simultaneously, a V for A substitution at position 3329 of said PAR1 sequence. In a preferred embodiment, the polynucleotide sequence of the PAR1 gene having a T to

C substitution at position 3090 and a simultaneous A to C substitution at position 3329 encompasses a sequence according to SEQ ID NO: 4 and, in a particularly preferred embodiment of said polynucleotide sequence, the latter comprises a sequence of SEQ ID NO; 4.

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The invention also relates to an isolated part of the polynucleotide sequence of the PAR1 gene, which comprises a sequence according to SEQ ID NO: 5.

10 The invention also relates to an isolated part of the polynucleotide sequence of the PAR1 gene, which sequence comprises a C for T substitution at position 3090, based on the PAR1 sequence according to NM-001992, which part comprises a sequence according to SEQ ID NO: 6.

15 The invention also relates to an isolated part of the polynucleotide sequence of the PAR1 gene, which sequence comprises a C for A substitution at position 3329, based on the PAR1 sequence according to NM-001992, which part comprises a sequence according to SEQ ID NO: 7.

20 The invention also relates to an isolated part of the polynucleotide sequence of the PAR1 gene, which sequence comprises a C for T substitution at position 3090, based on the PAR1 sequence according to NM-001992, and simultaneously a C for A substitution at position 3329 of said PAR1 sequence, which part comprises a sequence according to SEQ
25 ID NO: 8.

The invention furthermore comprises the preparation of a 3592 base pair polynucleotide sequence of the PAR1 cDNA gene, which sequence may or may not comprise the polymorphisms at positions 3090 and 3329, as
30 defined above, individually or in combination, which preparation comprises the following method steps:

- a) Providing human DNA comprising a PAR1 sequence according to SEQ ID NO: 2 and/or a PAR1 sequence according to SEQ ID NO: 3 and/or a PAR1 sequence according to SEQ ID NO: 4,
- 35 b) Providing a primer pair having a sequence according to SEQ ID NO: 9 and SEQ ID NO: 10 .
- c) Amplifying the PAR1 polynucleotide sequence by the polymerase chain extension reaction (PCR),
- d) Isolating and/or purifying the 3.56 kb fragment obtained from c],

- e] Sequencing the fragment from d].

The invention also relates to the preparation of a polynucleotide sequence according to SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7 or SEQ ID NO: 8, which preparation comprises the following method steps:

- a] Providing human genomic DNA comprising a PAR1 sequence according to SEQ ID NO: 1 and/or a PAR1 sequence according to SEQ ID NO: 2 and/or a PAR1 sequence according to SEQ ID NO: 3 and/or a PAR1 sequence according to SEQ ID NO: 4
- 10 b] Providing a primer pair according to SEQ ID NO: 11 and SEQ ID NO: 12
- c] Amplifying the fragment of the PAR1 polynucleotide sequence by the polymerase chain extension reaction (PCR),
- d] Isolating and/or purifying the fragment obtained from c],
- 15 e] Sequencing the fragment from d].

The invention furthermore relates to a method for detecting whether or not there is in a PAR1 gene a T to C substitution at position 3090 of the sequence according to NM-001992 and/or an A to C substitution at position 3329 of the sequence according to NM-001992, which method comprises the following method steps:

- a] Providing biological material comprising human cells,
- b] Obtaining chromosomal DNA from the material of a],
- c] Amplifying a polynucleotide fragment by means of the primers according to SEQ ID NO: 11 and SEQ ID NO: 12, using a PCR reaction,
- 25 d] Sequencing the polynucleotide fragment from c].

The invention furthermore relates to a method for detecting, whether or not there is in a PAR1 gene a T to C substitution at position 3090 of the sequence according to NM-001992 and/or an A to C substitution at position 3329 of the sequence according to NM-001992, which method comprises the following method steps:

- a] Providing biological material comprising human cells,
- 35 b] Obtaining RNA from the material of a],
- c] Transcribing said RNA to cDNA by means of reverse transcriptase,
- d] Possibly amplifying a polynucleotide fragment by means of the primers according to SEQ ID NO: 10 and SEQ ID NO: 11, using said PCR reaction,

- e] Sequencing the cDNA from c] and/or the polynucleotide fragment from d].

5 The invention also relates to a method for detecting whether or not there is in a PAR1 gene a T to C substitution at position 3090 of the sequence according to NM-001992 and/or an A to C substitution at position 3329 of the sequence according to NM-001992, which method comprises the following method steps:

- 10 a] Providing biological material comprising human cells,
b] Obtaining chromosomal DNA from the material of a],
c] Southern blotting the chromosomal DNA from b],
d] Providing a probe according to SEQ ID NO: 5 and/or SEQ ID NO: 6 and/or SEQ ID NO: 7 and/or SEQ ID NO: 8,
15 e] Hybridizing the Southern blot from c] with the probe from d] under stringent hybridization conditions,
f] Determining the presence or absence of a genetic variation in the PAR1 gene at position 3090 and/or 3329 according to NM-001992 by comparing the results of the hybridization from e].

20 The invention furthermore relates to a method for detecting whether or not there is in a PAR1 gene a T to C substitution at position 3090 of the sequence according to NM-001992 and/or an A to C substitution at position 3329 of the sequence according to NM-001992, which method comprises the following method steps:

- 25 a] Providing biological material comprising human cells,
b] Obtaining RNA from the material of a],
c] Northern blotting the RNA from b],
d] Providing a probe according to SEQ ID NO: 5 and/or SEQ ID NO: 6 and/or SEQ ID NO: 7 and/or SEQ ID NO: 8,
30 e] Hybridizing the Northern blot from c] with the probe from d] under stringent hybridization conditions,
f] Determining the presence or absence of a genetic variation in the PAR1 gene at position 3090 and/or 3329 according to NM-001992 by comparing the results of the hybridization.

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Detection of the genetic variations or polymorphisms in the PAR1 gene at positions 3090 and/or 3329 may be used as (a) genetic marker for evaluating the risk of atrial fibrillation, acute coronary syndrome, cardiomyopathy and/or unstable angina, as (b) marker for preventive

treatment for atrial fibrillation, acute coronary syndrome, cardiomyopathy and/or stable angina of the carriers of the corresponding genetic variants, as (c) marker for adjusting the dose of a pharmaceutically active substance to be administered for atrial fibrillation, acute coronary syndrome, 5 cardiomyopathy and/or unstable angina, as (d) marker for determining the high throughput-screening strategy for identifying a pharmaceutically active substance for atrial fibrillation, acute coronary syndrome, cardiomyopathy and/or unstable angina, as (e) marker for identifying the relevant individuals or patients for clinic studies in order to test the tolerability, safety and 10 efficacy of a pharmaceutical substance for atrial fibrillation, acute coronary syndrome, cardiomyopathy and/or unstable angina, and as (f) basis for developing assays systems for analyzing the genetic variation in the PAR1 gene at the DNA, RNA or protein level.

15 The invention also relates to an isolated polynucleotide sequence having from 21 to 50 nucleotides, which comprises a sequence according to SEQ ID NO: 11. Said sequence preferably comprises SEQ ID NO: 11. The invention furthermore relates to an isolated polynucleotide sequence having from 20 to 50 nucleotides, which comprises a sequence according 20 to SEQ ID NO: 12. Said sequence preferably comprises SEQ ID NO: 12.

The invention also relates to the use of an isolated polynucleotide sequence having from 21 to 50 nucleotides, which encompasses or comprises a sequence according to SEQ ID NO: 11, in combination with an 25 isolated polynucleotide sequence having from 20 to 50 nucleotides, which encompasses or comprises a sequence according to SEQ ID NO: 12, for amplifying a corresponding fragment of the PAR1 gene by means of the polymerase chain extension reaction (PCR). This use preferably relates to the amplification of a fragment of a PAR1 gene having a T to C substitution 30 at position 3090 of the sequence according to NM-001992 and/or having an A to C substitution at position 3329 of the sequence according to NM-001992.

Moreover, the invention comprises a kit of parts which comprises

- 35 a) an isolated polynucleotide sequence of from 21 to 50 nucleotides in length, which encompasses or comprises a sequence according to SEQ ID NO: 11,
- b) an isolated polynucleotide sequence of from 20 to 50 nucleotides in length, which encompasses or comprises a sequence according to

SEQ ID NO: 12,

- c] at least one enzyme for carrying out the polymerase chain extension reaction (PCR),
- d] possibly substances and/or solutions for carrying out the polymerase chain extension reaction,
- e] possibly polynucleotide sequences encompassing the PAR1 gene with or without substitution at position 3090 of the PAR1 sequence according to NM-001992 and/or position 3329 according to NM-001992 in full length and/or parts thereof
- f] and possibly reagents for carrying out the sequencing reaction.

Kit of parts here and below means the combination of said components which have been combined into a functional unit in spatial juxtaposition to each other.

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The invention furthermore relates to the preparation of the above-described kit of parts, which comprises

- a] providing an isolated polynucleotide sequence of from 21 to 50 nucleotides in length, which encompasses or comprises a sequence according to SEQ ID NO: 11,
- b] providing an isolated polynucleotide sequence of from 20 to 50 nucleotides in length, which encompasses or comprises a sequence according to SEQ ID NO: 12,
- c] providing an enzyme for carrying out the polymerase chain extension reaction (PCR),
- d] providing, where appropriate, reagents for carrying out a sequencing
- e] possibly providing substances and/or solutions for carrying out said polymerase chain extension reaction (PCR)
- f] possibly providing polynucleotide sequences comprising the PAR1 gene with or without a T to C substitution at position 3090 of the PAR1 sequence according to NM-001992 and/or an A to C substitution at position 3329 according to NM-001992, in each case in the full length, or parts thereof,
- g] introducing the components from a] to f] in each case separately into suitable containers,
- h] combining, where appropriate, the containers from g] in one or more pack units.

The above-described kit of parts may be used for amplifying a fragment of

the PAR1 gene.

The technical aspects of the invention are discussed in more detail in the following embodiments.

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Isolated polynucleotide sequences of the PAR1 gene may be prepared, for example, by amplification by means of the polymerase chain extension reaction (PCR). Suitable primers for this purpose are described in SEQ ID NO: 9 and SEQ ID NO: 10.

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The PCR is an in-vitro technique which may be used to selectively duplicate polynucleotide sections which are flanked by two known sequences. Amplification requires short, single-stranded DNA molecules which are complementary to the ends of a defined sequence of a DNA or RNA template (primers). A DNA polymerase extends the primers, under the

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correct reaction conditions and in the presence of deoxynucleotide triphosphates (dNTPs), along the single-stranded and denatured polynucleotide template and thus synthesizes new DNA strands whose sequence is complementary to said template. During this process, the

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temperature is changed at regular intervals so that, time after time, the polynucleotide strands are denatured and the primers can be attached and extended. Heat-stable DNA polymerases, for example Taq polymerase, are used. A typical PCR reaction mixture contains, apart from a polynucleotide template, two suitable primer nucleotides, for example at concentrations

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between 0.2 to 2 μ M, furthermore dNTPs, for example at concentrations of 200 μ M per dNTP, furthermore $MgCl_2$ having a concentration of 1 – 2 mM, and 1 – 10 units of a heat-stable DNA polymerase such as, for example, Taq polymerase (*Thermus aquaticus* polymerase). Heat-stable DNA polymerase and the components for carrying out the same, and also

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protocols, are commercially supplied by numerous companies such as, for example, Roche Diagnostics, Clontech, Life Technologies, New England Biolabs, Promega, Stratagene, etc.

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The polynucleotide template for amplifying the polynucleotide sequence to be isolated may be present in the form of RNA or DNA. If the polynucleotide template is RNA, then the latter is transcribed to DNA by means of reverse transcriptase, prior to the actual PCR reaction. The amount of polynucleotide template for carrying out the PCR reaction may be from 0.01 to 20 ng, for example.

The polynucleotide template is obtained using techniques known to the skilled worker for obtaining DNA and/or RNA from biological material. Biological material should include here, inter alia, the cells of a tissue or organ (e.g. brain, blood, liver, spleen, kidney, heart, blood vessels) of a vertebrate, including humans, or cells from a eukaryotic cell culture (e.g. Hela cells, CHO cells, 3T3 cells) or cells comprising bacteria or yeasts in which the DNA sequence to be isolated is present in cloned form.

Cells of a tissue assemblage or organ of a vertebrate, including humans, may be obtained by taking blood, tissue puncture or surgical techniques. A polynucleotide template may be obtained therefrom, for example, by disrupting the cells, possibly concentrating individual organelles, in particular the nucleus, and recovering the DNA or RNA by precipitation and centrifugation.

Another method for preparing isolated polynucleotide sequences of the PAR1 gene comprises cloning the PAR1 gene, subsequently expressing it in bacteria or yeast and purifying the expressed polynucleotide. The previously mentioned PCR reaction, for example, is suitable for preparing a polynucleotide fragment which is clonable. It is advantageous to use, for a fragment to be cloned, primers which carry the recognition sequence of a reaction enzyme 5' of the complementary sequence. The two primers may use in each case the same or different recognition sequences for restriction enzymes.

Examples of common restriction enzymes are: BamHI (GGATCC), ClaI (ATCGAT), EcoRI (GAATTC), EcoRV (GATATC), HindIII (AAGCTT) NcoI (CCATGG) Sall (GTCGAC), XbaI (TCTAG1).

For cloning, a vector is treated with the restriction enzymes which correspond to the recognition sequences attached to the primers. The fragment is connected to the vector by means of ligase by isolation and treatment with the same restriction enzymes. Vector means a DNA molecule such as, for example, a plasmid, bacteriophage or a cosmid, with the aid of which it is possible to clone genes or other DNA sequences and to introduce them into a bacterial or eukaryotic cell for replication. Examples of vectors are DNA molecules such as pBR322, pUC18/19, pBluescript, pcDNA3.1. Vectors are commercially available from specialist companies for biotechnological material, such as Roche Diagnostics, New England Biolabs, Promega, Stratagene etc.

The instructions required for carrying out the PCR reaction, for providing polynucleotides or for carrying out cloning procedures can be found by the skilled worker in the form of recipes and protocols in standard manuals such as, for example, in a] "Current Protocols in Molecular Biology by Frederick M. Ausubel (Editor), Roger Brent (Editor), Robert E. Kingston (Editor), David D. Moore (Editor), J. G. Seidman (Editor), Kevin Struhl (Editor), loose leaf edition, continuously updated, John Wiley & Sons, Inc., New York or in b] Short Protocols in Molecular Biology, 5th edition, by Frederick M. Ausubel (Editor), Roger Brent (Editor), Robert E. Kingston (Editor), David D. Moore (Editor), J. G. Seidman (Editor), John A. Smith (Editor), Kevin Struhl (Editor), October 2002, John Wiley & Sons, Inc., New York" or in c] "Molecular Cloning by J. Sambrock, E. F. Fritsch, T. Maniatis; Cold Spring Harbor Laboratory Press".

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Suitable primer sequences are provided, for example, via chemical synthesis thereof which may be carried out commercially to order by companies such as MWG Biotech, etc.

20 Human cDNA from different organs is commercially available from companies such as, for example, Promega, Stratagene or others.

The sequencing of a polynucleotide is carried out by means of routine methods known to the skilled worker by using, for example, laboratory robots from companies such as, for example, Life Technologies, Applied Biosystems, BioRad or others.

Isolated polynucleotide sequences of the PAR1 variant and fragments therefrom may also be used for hybridization at different stringencies. Stringency describes reaction conditions which influence the specificity of hybridization or attachment of two single-stranded nucleic acid molecules. The stringency and thus also specificity of a reaction can be increased by increasing the temperature and lowering the ionic strength. Low stringency conditions are present, for example, if the hybridization is carried out at room temperature in 2 x SSC solution. High stringency conditions are present, for example, if hybridization is carried out at 68°C in 0.1 x SSC/0.1% SDS solution.

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Hybridization under stringent hybridization conditions in accordance with

the present application means:

- 1] Hybridizing the labeled probe with the sample to be studied at 65°C (or, in the case of oligonucleotides, 5°C below the melting temperature) overnight in 50 mM Tris pH 7.5, 1NaCl, 1% SDS, 10% dextran sulfate, 0.5 mg/ml denatured salmon sperm DNA.
- 2] Washing at room temperature in 2 x SSC for 10 min.
- 3] Washing at 65°C (or, in the case of oligonucleotides, 5°C below the melting temperature) in 1 x SSC/1% SDS for 30 min.
- 4] Washing at 65°C (or, in the case of oligonucleotides, 5°C below the melting temperature) in 0.2 x SSC/0.1% SDS for 30 min.
- 5] Washing at 65°C (or, in the case of oligonucleotides, 5°C below the melting temperature) in 0.1% SSC/0.1% SDS for 30 min.

DNA fragments of 20 nucleotides in overall length are to be regarded as being oligonucleotides for this purpose. The melting temperature results from the formula $T_m = 2 (\text{number of A+T}) + 4 (\text{number of G+C})^\circ$.

A 2 x SSC or 0.1 x SSC solution is prepared by diluting a 20 x SSC solution accordingly. The 20 x SSC solution comprises a 3M NaCl/0.3 sodium citrate 2 H₂O solution. SDS is sodium dodecyl sulfate.

The hybridization is carried out by transferring the polynucleotides to be studied to a nylon or nitrocellulose membrane (Southern blot – DNA; Northern blot – RNA), after electrophoretic fractionation and subsequent denaturation. The hybridization is carried out using a probe which is radio-labeled or has been labeled in another way, for example with the aid of fluorescent dyes. The probe comprises a usually single-stranded and/or denatured DNA or RNA polynucleotide sequence which binds to the complementary nucleotide sequence of the once again single-stranded and/or denatured DNA or RNA polynucleotide sequence to be studied.

Single nucleotide polymorphisms of the PAR1 gene may be detected with the aid of the primers of the invention, also by SSCP analysis. SSCP stands for Single Stranded Conformation Polymorphism which is an electrophoretic technique for identifying individual base pair substitutions. The polynucleotides to be studied are amplified by PCR by means of labeled primers and, after denaturation into single strands, fractionated in a polyacrylamide gel electrophoresis (PAGE). If the DNA fragments to be

studied exhibit individual base pair substitutions, they then possess different conformations and thus migrate in the PAGE at different rates.

5 Examples of substances for carrying out the PCR are buffers such as Hepes or Tris, furthermore dAPP, dGTP, dTTP, dCTP, and Mg^{2+} and possibly further divalent or monovalent ions. Solutions contain these substances in dissolved form.

Examples

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Amplification of genomic regions of the PAR1 gene

15 The T to C nucleotide substitution at position 3090 and the A to C substitution at position 3329 in the PAR1 sequence were detected using the following primers:

Primer 1: 5'-ACAGAGTGAATAAGACAGAG-3' (SEQ ID NO: 11)

Primer 2: 5'-CCAGTGCTAGCTTCTACTTAC-3 (SEQ ID NO: 12)

20 Primer 1 (SEQ ID NO: 11) corresponds to positions 2767 to 2789 of the NM-001992 reference sequence. Primer 2 is derived from Exon No. 1 of the PAR1 gene.

PCR protocol for the amplification:

25 The reagents used are from Applied Biosystems (Foster City, USA): 20 ng of genomic DNA; 1 unit of TaqGold DNA polymerase; 1 x Taq polymerase buffer; 500 μ M of dNTPs; 2.5 mM $MgCl_2$; 200 nM of each amplification primer pair; H_2O to 5 μ l.

30 PCR amplification program for the genotyping

95°C for 10 min x 1 cycle

95°C for 30 sec

70°C for 30 sec

x 2 cycles

95°C for 30 sec

65°C for 30 sec

x 2 cycles;

95°C for 30 sec
60°C for 30 sec x 2 cycles;

95°C for 30 sec
56°C for 30 sec
72°C for 30 sec x 40 cycles;

72°C for 10 min
4°C for 30 sec x 1 cycle;

Identification of SNPs

Protocol for the minisequencing and detection of the SNPs.

- 5 All reagents are from Applied Biosystems (Foster City, USA). 2 µl of purified PCR product, 1.5 µL of BigDye Terminator Kit, 200 nM sequencing primer; H₂O to 10 µl.

Amplification program for the sequencing:

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96°C for 2 min x 1 cycle

96°C for 10 sec
55°C for 10 sec
65°C for 4 min x 30 cycles

72°C for 7 min
4°C for 30 sec x 1 cycle;

Analysis of the sequencing products:

- 15 The sequences were first analyzed using the sequence analysis software (Applied Biosystems, Foster City, USA) to obtain the raw data, then processed using Phred, Phrap, Polyphred and Consed. Phred, Phrap, Polyphred and Consed are software written by Phil Green at Washington University (<http://www.genome.washington.edu>).

- 20 Assigning PAR1 SNPs to coronary disorders

In a clinical study, two PAR1 polymorphisms from the 3'-noncoding region of the gene were studied for a connection with thrombotic and cardiovascular complications in a cohort of patients.

- 5 The following abbreviations are used below (all positions indicated refer to the nucleotide positions in the reference sequence NM-001992).

10 PAR1 T3090T describes the group of individuals whose alleles of the PAR1 gene both have a thymidine (T) at position 3090. These individuals are homozygous with respect to this PAR1 variant.

PAR1 T3090C describes the group of individuals whose one allele of the PAR1 gene has a cytidine (C) at position 3090 and whose other allele of the PAR1 gene has a thymidine (T) at position 3090. These individuals are heterozygous with respect to this PAR1 variant.

15 PAR1 C3090C describes the group of individuals whose alleles of the PAR1 gene both have a cytidine (C) at position 3090. These individuals are homozygous with respect to this PAR1 variant.

20 PAR1 A3329A describes the group of individuals whose alleles of the PAR1 gene both have an adenosine (A) at position 3329. These individuals are homozygous with respect to this PAR1 variant.

PAR1 A3329C describes the group of individuals whose one allele of the PAR1 gene has a cytidine (C) at position 3329 and whose other allele of the PAR1 gene has an adenosine (A) at position 3329. These individuals are heterozygous with respect to this PAR1 variant.

25 PAR1 C3329C describes the group of individuals whose alleles of the PAR1 gene both have a cytidine (C) at position 3329. These individuals are homozygous with respect to this PAR1 variant.

30 In the group of patients analyzed (Fig. 1), statistically significant associations of the homozygous carriers of the PAR1 variant C3090C with atrial fibrillation and cardiomyopathy were observed. After carrying out a logistic regression, a 1.97 fold increased risk of atrial fibrillation and a 1.84 fold increased risk of cardiomyopathy were found in homozygous carriers of the PAR1 variant C3090C compared to carriers of the PAR1 variants
35 T3090/T3090T (Fig. 3).

It was shown that, for carriers of the PAR1 variant C3329C, said variant is associated with a 2.35 fold increased risk of atrial fibrillation compared to carriers of the PAR1 variants C3329A/A3329A. In carriers of the PAR1 variant C3329C, said variant seems, in addition, to be protective with

respect to the appearance of acute coronary syndrome and unstable angina. Carriers of the PAR1 variant C3329C have a 2.78 fold reduced risk of the appearance of acute coronary syndrome and/or unstable angina compared to carriers of the PAR1 variants A3329C/A3329A (Fig. 4).

5

It is therefore possible, by means of a method of the invention and using an isolated PAR1 sequence of the particular SNP type or a fragment thereof, to determine for human individuals whether there is as assignment a risk group in accordance with the results presented.

10

Preparation of plasmid DNA

1 ml of a bacterial overnight culture is transferred to an Eppendorf tube and centrifuged (5 000 rpm for 5 min) in a Heraeus Biofuge. The bacterial cell pellet is to be resuspended in 100 μ l of cooled solution I and then to be placed on ice for 5 min.

15

Solution I: 25 mM tris-HCl, pH 8.0, 50 mM glucose (sterile-filtered) 10 mM EDTA 100 μ g/ml Rnase A.

20

After addition of 200 μ l of solution II, the entire mixture is mixed well, resulting in alkaline denaturation of the DNA.

Solution II: 200 mM NaOH, 1% SDS.

25

After subsequent incubation for 5 min on ice, 150 μ l of solution III are added to the mixture. This is followed by mixing once more and incubating on ice for a further 15 min.

30 Solution III: 3 M sodium acetate (pH 4.8).

35

Centrifugation in the Heraeus Biofuge at 12 000 rpm for 15 minutes removes the cell debris, the genomic DNA and the denatured proteins. The supernatant produced, which contains the plasmid DNA, is decanted into a second Eppendorf tube and admixed with 1 ml of 96% strength EtOH (or 300 μ l of isopropanol). The precipitation mixture is mixed thoroughly and again centrifuged (15 min at 12 000 rpm in Heraeus Biofuge). This results in precipitation of the plasmid DNA. The plasmid DNA sediment is washed with ice-cold 70% strength EtOH and then dried in air. Finally, the dry

sediment is taken up in 50 μ l of sterile distilled water.

Alcohol precipitation of DNA

- 5 Precipitation mixture: DNA solution, 1/10 volume of 3 M sodium acetate (pH 5.4), 2 to 3 volumes of 96% EtOH (1 volume of isopropanol).

The mixture is mixed well and can be stored at -20°C, although this does not increase the precipitation yield. The plasmid DNA is sedimented by
10 centrifugation at 12 000 rpm for 20 minutes.

In order to remove residues of the sodium acetate used, the plasmid DNA must be washed once more with 1 ml of 70% strength EtOH after precipitation.

15

Phenol extraction of DNA

A DNA solution is admixed with the same volume of phenol (Rotiphenol[®], equilibrated with TE buffer, pH 7.6, Roth, Karlsruhe, Germany), shaken for
20 5 min and centrifuged at 5000 rpm. Most of the now denatured proteins accumulate in the interface. The upper, aqueous phase contains the DNA and is carefully removed by suction, and then mixed with a chloroform/isoamyl alcohol mixture (24:1) in order to remove phenol residues. This is followed by another centrifugation, after which the
25 aqueous supernatant is removed and the DNA is isolated from the solution by alcohol precipitation.

Purification of amplified DNA molecules

30 DNA amplicons are purified using a PCR purification kit (Qiagen). This removes the starter molecules, nucleotides (dNTPs), polymerases and salts. For this purpose, the PCR reaction mixture is admixed with five times the volume of PB buffer, mixed well and applied to the Qiaquick column. The amplified DNA is then selectively bound to the column material, and
35 the dNTPs are removed by washing twice with 750 μ l of PE buffer. The amplified DNA is then eluted with the desired volume of water, with the best volume being the same as that of the PCR reaction mixture starting material.

DNA cleavage with restriction enzymes

Mix: 3 μ l of DNA, 2 μ l of 10 x cleavage buffer, 2.5-5 U of restriction enzyme (e.g. EcoRI, BamHI, Sall, XbaI, XhoI etc.), add distilled water to a volume of 20 μ l.

Depending on the restriction enzyme, the cleavage reaction runs at 25-55°C for 1-2 h. For analysis, the fragments are electrophoretically fractionated in an agarose or polyacrylamide gel in parallel with a length standard. If the reaction is a double cleavage, then first one enzyme is added to the mixture. After 1 hour, an aliquot is applied to an appropriate gel, and, if the cleavage has occurred, the second enzyme can be added. If the second enzyme does not cleave in the same cleavage buffer, then an alcohol precipitation is required first.

15

Agarose gel electrophoresis of DNA

The agarose (Roth) is dissolved in 1 x agarose buffer at the desired concentration and boiled in a microwave oven, until the agarose has completely dissolved. The solution is then poured into a sealed Plexiglass flat bed gel chamber.

The DNA samples are admixed with 1/10 volume of loading blue (50% v/v glycerol; 50 mM EDTA; 0.005% w/v BPB [Merck, Darmstadt, Germany] and 0.005% xylene cyanol) and pipetted into the gel pockets which are generated by means of a comb.

The electrophoresis is carried out horizontally in 1 x agarose buffer as running buffer at a constant voltage of 80-140 V, depending on the size of the gel and the distance between the electrodes.

30

1 x agarose buffer: 40 mM Tris-HCl (pH 7.8), 5 mM sodium acetate, 1 mM EDTA.

Polyacrylamide gel electrophoresis of DNA

35

7.5% polyacrylamide gel solution; 0.94 ml of 40% strength acrylamide-bisacrylamide stock solution, 0.5 ml of 10 x TBE buffer (400 mM Tris-HCl, pH 8.3; 200 mM sodium acetate, 20 mM EDTA), 0.25 ml of 1% AMPS, 10 μ l of TEMED, 3.33 ml of distilled water.

This mixture is poured between well-cleaned, vertical glass plates mounted in vertical apparatuses for polymerization (approx. 10-20 min). The gel is run in 1 x TBE buffer at a constant voltage of 140 V.

5

DNA sequencing

1-2 μg of DNA are to be dissolved in 81 μl of distilled H_2O and 9 μl of NaOH (2 N) is to be added for denaturation. After incubation at room temperature for 10 minutes, the mixture is precipitated, with thorough washing of the resulting DNA sediment with ice-cold 80% strength ethanol being important for the subsequent sequencing reactions. 2 μl of 5 x Sequenase buffer (200 mM Tris-Cl pH 7.5/100 mM MgCl_2 /250 mM NaCl), 1 μl of oligonucleotide (1 pM/ μl) and, finally, distilled H_2O are to be added to the sediment to a total volume of 10 μl . During the subsequent incubation in a 37°C water bath for 30 minutes, the starter oligonucleotide hybridizes to the DNA.

Reagents added to the hybridization mixture for the sequencing reaction: 1.0 μl of DTT (0.1 M), 2.0 μl of labeling mixture (diluted 1:5), 0.5 μl of [α - ^{35}S]dATP, 2 μl of Sequenase™ (13 U/ μl ; United States Biochemical), (diluted 1:8 with enzyme dilution buffer).

During the subsequent incubation at room temperature for 5 minutes, the counter strand is synthesized, with the synthetic DNA being labeled by incorporation of the radiolabeled dATP. This is followed by adding in each case 3.5 μl of the labeling mixture to 2.5 μl of the four different termination mixtures. Another incubation at 37°C for 5 minutes results in the randomly distributed termination reactions of counter stand synthesis. The reactions are stopped by adding 4 μl of stop buffer, after which the mixtures are denatured at 80-90°C and then applied to a 6% strength denatured sequencing gel. After loading the samples, the main run is carried out at 30-50 W and, respectively, 1300-1600 V for 2-5 h. The gel is then fixed in a 10% strength acetic acid bath (15 min), freed of urea residues under running water and then dried (for 45 min, using a heat gun, or for 2 h, in a 70°C incubator). The subsequent autoradiography is carried out at 4°C for 16-24 h (Fuji Medical X-ray-Film RX, 30 x 40; Kodak Scientific Imaging Film X-omat AR).

Labeling-mixture stock solution: in each case 7.5 μ M dATP, dTTP, dGTP, dCTP

5 Termination mixtures: in each case 80 μ M dATP, dTTP, dGTP, dCTP and in each case 8 μ M of the respective ddNTP

Sequenase dilution buffer: 10 mM Tris/HCl; pH 7.5, 5 mM DTT, 0.5 mg/ml BSA

10 Stop buffer: 95% formamide, 20 mM EDTA, 0.005% (w/v) xylene cyanol FF

Automated DNA sequencing

15 Mix: 1 μ g of plasmid DNA (in the case of PCR fragments, for example, 100ng/500 nucleotides), 3-5 pmol of starter molecule (PCR primer, T_m of 55°C, if possible), 4 μ l of Dye Terminator ready-mix (FddNTPs-Ampli-TaqFS mixture), add distilled water to a volume of 20 μ l.

20 The PCR reaction [25 x (15 sec at 94°C, 15 sec. at 50°C, 4 min at 60°C)] is precipitated with alcohol and taken up in 4 μ l of loading buffer. The samples are then denatured at 95°C for 3 min, removed by centrifugation and applied to a vertical polyacrylamide gel (34 cm in length, provided with 24 parallel lanes).

25 After excitation by an argon laser beam at 488 nm, the dyes emit light of different wavelengths of between 525 nm and 605 nm which is separated into its spectral colors via a grating, a "spectrograph". The spectral colors are subsequently detected simultaneously with the aid of the high-resolution pixel field of a CCD camera. The data are recorded with the aid of a computer (Macintosh Quadra/650 MacIIcx Apple Share) and the
30 corresponding data analysis software (PE Biosystems, Weiterstadt, Germany).

35 Sequencing gel: 30 g of urea (Sigma), 21.5 ml of distilled H₂O, 6 ml of 10 x TBE

The mixture is dissolved in a wide-necked flask on a heating block at 50°C, with the following being added: 9 ml of 40% bisacrylamide (filtered), 180 μ l of 10% APS, 24 μ l of Temed.

Polymerase chain reaction (PCR reaction)

The following DNA polymerases may be used:

- 5 Taq (*Thermus aquaticus*) DNA polymerase (recombinant, Gibco/BRL) and
10 x PCR buffer

[200 mM Tris/HCl (pH 8.4), 500 mM KCl]

Tfl (*Thermus flavus*) DNA polymerase (Master Amp™, Biozym, Oldendorf,
Germany) and 20 x PCR

Buffer [20 mM (NH₂)SO₄, 1 M Tris/HCl (pH 9.0)]

10

PCR reaction mixture:

PCR components	Amount
DNA template	10-100 ng
Starter molecule 1	25 μM
Starter molecule 2	25 μM
Nucleotide mixture (dNTPs)	20 mM (from a mixture containing 10 mM of each dNTP)
DNA polymerase buffer	1 x: 5.0 μl in the case of Taq DNA polymerase buffer 2.5 μl in the case of Tfl DNA polymerase buffer
MgCl ₂	75 mM
DNA polymerase	2 U in the case of Taq DNA polymerase 1 U in the case of Tfl DNA polymerase
Distilled H ₂ O	to 50 μl total volume

- 15 The following applies here: 1 U catalyses the conversion of 10 nM
deoxyribonucleoside triphosphates, at 74°C within 30 min, to an acid-
insoluble DNA product. The PCR reaction usually commences with the "hot
start": the mixture is incubated first without the polymerase at 94°C in order
to enable the DNA to be denatured for the first time. After the temperature
has reached 80°C, the DNA polymerase is added to the mixture in order to
20 avoid nonspecific amplification at a still low temperature. Thereafter, the
actual PCR reaction is carried out over 25-35 cycles.

For each cycle, the following reaction conditions apply:

Reaction	Temperature	Time
Denaturation	94°C	30-60 sec
Hybridization (annealing)	$T_m - 5^\circ\text{C}$	30-60 sec
Extension	72°C	1 min/1 kb

Finally and in addition, the chain extension is carried out at 72°C for 10 min, finally followed by cooling.

5

Isolation of total RNA

All centrifugation steps are carried out at 13 000 rpm and 16°C.

10 Cells are lysed with 600 μl of lysis buffer (100 RLT buffer: 1 mercaptoethanol). The cell lysate is applied to a QiaSchredder column and removed by centrifugation for 2 min.

15 The eluate is admixed with 600 μl of 70% ethanol, mixed well, and the DNA is applied to an RNAeasy mini spin column and centrifuged for 15 s (binding of RNA to the silica matrix). The column is washed three times (once with 700 μl of RW1 buffer and twice with 500 μl of RPE buffer). The column is then transferred to an autoclaved 1.5 ml Eppendorf tube and the RNA is eluted with 15 μl of distilled H_2O . The average concentration of total RNA obtained in this way is 1 $\mu\text{g}/\mu\text{l}$.

20 RNA fractionation via agarose gel electrophoresis

Denaturing agarose gel:

1 g of agarose, 37 ml of distilled water, 10 ml of 10 x MOPS (0.2 mM MOPS, 10 mM EDTA, 100 mM NaAc),
25 the mixture is boiled and cooled to 60°C
16 ml of 37% strength formaldehyde are added.

30 After it has solidified, the gel is inserted with RNA gel running buffer into the electrophoresis apparatus. The RNA is applied together with a special sample buffer.

RNA gel running buffer: 40 ml of 10 x MOPS, 65 ml of 37% strength formaldehyde, 295 ml of distilled water

RNA sample buffer: 1-5 μg of RNA, 5 μl of RNA-NEW buffer (7.5 μl 37% strength formaldehyde, 4.5 μl of 10 x MOPS, 25.9 μl of formamide, 7.5 μl of distilled water), 2 μl of formamide dye marker [50% (v/v) glycerol, 1 mM EDTA (pH 8.0), 0.25% (v/v) bromophenol blue, 0.25% (v/v) xylene cyanol].

5

The gel runs at 80 V for approx. 3 h. Since this work uses only eukaryotic RNA isolates, the dominant bands visible on the gel should be those of 28S and 18S rRNA.

10 Reverse Transcriptase with MMLV-RT

(Moloney murine leukemia virus – Reverse Transcriptase)

Reverse transcriptase mixture: 5 μg of RNA, 100 μM of starter molecule

15 The RNA preparation and the starter molecule are incubated at 75°C for 10 min, in order to avoid possible formation of secondary structures in the RNA template as factors interfering with the transcriptase. However, even without this step, a transcription reaction usually takes place.

20 Reverse transcriptase reaction mixture: 28 U of Rnasin[®] (Promega), 25 mM dNTPS, 5 μl of 10 x reverse transcriptase buffer [10 m Tris/HCl (pH 8.3), 75 mM KCl, 3 mM MgCl₂], 50 U of reverse transcriptase (StrataScript[™], Stratagene), to 50 μl with distilled water.

25 The reverse transcription is carried out by incubating the mixture at 42°C for 15 min and at 37°C for 45 min. A longer incubation of 2 h at 42°C with a 30-sec interruption at 55°C is recommended for relatively long RNA templates. Subsequent incubation of the mixture at 95°C for 5 minutes results in inactivation of said reverse transcriptase. Subsequently, 5-20 μl of the reverse transcription mixture are used for a PCR reaction.

30

Preparation of genomic DNA from tissue

35 100 mg of tissue are crushed in liquid nitrogen to give a powder. The tissue powder is introduced into a Falcon tube containing 6 ml of reaction buffer (30 μl of proteinase K [20 mg/ml] are added freshly to the buffer) and incubated with careful shaking at 56°C overnight (12-18 hours). After incubation, 100 μl of RNase A (10 $\mu\text{g}/\mu\text{l}$) are added and the mixture is incubated with further shaking at 37°C for one hour.

This is followed by adding 4 ml of phenol and turning the tube manually

upside down and up again for approximately 5 min. 4 ml of CI (chloroform/isoamyl alcohol) are added immediately and the tube is turned upside down and up again for another 5 minutes and then centrifuged for 15 min (3 000 rpm). The supernatant is carefully removed and transferred to 10 ml Falcon tubes. If the supernatant is still not clear, the phenol extraction must be repeated, otherwise another 4 ml of CI are added and the tube is manually turned upside down and up for 5 min and then centrifuged for 15 min (3 000 rpm). The supernatant is carefully removed and the CI extraction repeated. The final supernatant obtained is admixed with 1/10 volumes of sodium acetate solution (3 M, pH 6) and 2.5 volumes of ethanol (99.8%). The tube is carefully rotated, until the DNA precipitates as a tangle. This DNA tangle is transferred to approximately 25 ml of ethanol (70%) with the aid of a glass hook and left resting for 3 min. The washing was repeated twice. The DNA was then dried in air and dissolved in 0.5 ml of double-distilled water at room temperature.

Southern Blot

DNA fractionation via an agarose gel

Leave the gel on short-wave UV for approx. 5 min for strand breaks to occur in the larger DNA molecules (> 6kbp).
Continuously tilt the gel in denaturing solution for 30 min for DNA denaturation.
Continuously tilt the gel in neutralizing solution for 30 min for neutralization.

Blot construction (from bottom to top): gel, nylon membrane, dry filter paper, blotting paper, plate, weight (approx. 1 kg).

Blotting with 20 x SSC overnight.

Wash membrane in 2 x SSC for 10 min
Dry membrane on filter paper
Fixing of nucleic acid by baking at 80°C for 1 h or UV crosslinking (e.g. in "Stratalinker", automatic position). The membrane may then be stored until hybridization.
Prehybridization of membrane in hybridization solution for approx. 1 – 2 h
Covering of nonspecific binding sites on the membrane.

Hybridization solution: 5 x SSC, 5 x Denhardt's solution, 0.5% SDS,

100 µg/ml herring sperm DNA

Denaturing solution: 0.5 M NaOH (20 g), 1 M NaCl

5 Neutralizing solution: 1.5 M NaCl/0.5 M Tris pH 7.4

20 x SSC is 3 M NaCl, 0.3 M Na-citrate: 175.3 g of NaCl, 88.2 g of sodium citrate X 2 H₂O, to 1 l with double-distilled water, adjust pH to 7.0 with HCl.

10 50 x Denhard's solution: 5 g of Ficoll 400, 5 g of PVP (polyvinyl pyrrolidone), 5 g of BSA, to 500 ml with double-distilled water

Northern Blot

15 RNA fractionation using a formaldehyde agarose gel

Blot construction (from bottom to top): gel, nylon membrane, dry filter paper, blotting paper, plate, weight (approx. 1 kg).

Blotting with 20 x SSC overnight.

20 Fix RNA on filter by baking at 80°C (1 h)

Introduce filter into boiling 20 mM Tris pH 8 for RNA deglyoxylation and let cool to RT.

Description of the Figures

25

Fig. 1

Characteristics of study group

30 Fig. 2

Distribution of PAR1 variants T3090C and A3329C in 1362 individuals analyzed

35 Fig. 3

Association of PAR1 variants C3090C with atrial fibrillation and cardiomyopathy

Fig. 4

Association of PAR1 variants C3329C with atrial fibrillation, acute coronary syndrome and unstable angina.

5

Fig. 5

Polynucleotide sequence of the cDNA of the human PAR1 gene in 5'/3' orientation. The sequence corresponds to the sequence made publicly available by the NCBI Nucleotide Database under number NM-001992. The prepared sequence is identical to SEQ ID NO: 1.

10

Fig. 6

Polynucleotide sequence of the cDNA of the human PAR1 gene in 5'/3' orientation with a polymorphism at position 3090 of the sequence according to NM-001992, which polymorphism comprises a T to C substitution. The depicted sequence is identical to SEQ ID NO: 2.

15

20 Fig. 7

Polynucleotide sequence of the cDNA of the human PAR1 gene in 5'/3' orientation with a polymorphism at position 3329 of the sequence according to NM-001992, which polymorphism comprises an A to C substitution. The depicted sequence is identical to SEQ ID NO: 3.

25

Fig. 8

Polynucleotide sequence of the cDNA of the human PAR1 gene in 5'/3' orientation with a polymorphism at position 3090 of the sequence according to NM-001992, which polymorphism comprises a T to C substitution, and with a simultaneous second polymorphism at position 3329 of the sequence according to NM-001992, which polymorphism comprises an A to C substitution. The depicted sequence is identical to SEQ ID NO: 4.

30

Fig. 9

Polynucleotide sequence of a fragment of the human PAR1 gene in 5'/3' orientation. The depicted sequence is identical to SEQ ID NO: 5.

5

Fig. 10

Polynucleotide sequence of a fragment of the human PAR1 gene in 5'/3' orientation with a polymorphism at position 3090 of the sequence according to NM-01992, which polymorphism comprises a T to C substitution. The depicted sequence is identical to SEQ ID NO: 6.

10

Fig. 11

Polynucleotide sequence of a fragment of human PAR1 gene in 5'/3' orientation with a polymorphism at position 3329 of the sequence according to NM-001992, which polymorphism comprises an A to C substitution. The depicted sequence is identical to SEQ ID NO: 7.

15

20 Fig. 12

Polynucleotide sequence of a fragment of the human PAR1 gene in 5'/3' orientation with a polymorphism at position 3090 of the sequence according to NM-001992, which polymorphism comprises a T to C substitution, and with a simultaneous second polymorphism at position 3329 of the sequence according to NM-001992, which polymorphism comprises an A to C substitution. The depicted sequence is identical to SEQ ID NO: 8.

25

Fig. 13

Polynucleotide sequence in 5'/3' orientation of the 5' end of the cDNA of the human PAR1 gene. The depicted sequence is identical to SEQ ID NO: 9.

30

35 Fig. 14

Polynucleotide sequence in 5'/3' orientation of the 3' end of the cDNA of the human PAR1 gene. The depicted sequence is identical to SEQ ID NO: 10.

Fig. 15

5 Polynucleotide sequence in 5'/3' orientation of the cDNA of the human PAR1 gene, relating to positions 2767 to 2789 according to NM-001992. The depicted sequence is identical to SEQ ID NO: 11.

Fig. 16

10 Polynucleotide sequence in 5'/3' orientation of the Exon No. 1 of the human PAR1 gene. The depicted sequence is identical to SEQ ID NO: 12.

Fig. 17

15 Protein sequence of the human PAR1 receptor. The sequence corresponds to the sequence made publicly available by the NCBI Protein Database under number NP-001983. The depicted sequence is identical to SEQ ID NO: 13.

20 Comprises/comprising and grammatical variations thereof when used in this specification are to be taken to specify the presence of stated features, integers, steps or components or groups thereof, but do not preclude the presence or addition of one or more other features, integers, steps, components or groups thereof.

What is claimed is:

- 5 1. An isolated polynucleotide sequence of the PAR1 gene, which comprises a C for T substitution at position 3090 of the sequence according to NM-001992.
- 10 2. The isolated polynucleotide sequence as claimed in claim 1, wherein the polynucleotide sequence of the PAR1 gene encompasses a sequence according to SEQ ID NO: 2.
- 15 3. The isolated polynucleotide sequence as claimed in claim 1, wherein the polynucleotide sequence of the PAR1 gene comprises a sequence according to SEQ ID NO: 2.
- 20 4. An isolated polynucleotide sequence of the PAR1 gene, which comprises a C for A substitution at position 3329 of the sequence according to NM-001992.
- 25 5. The isolated polynucleotide sequence as claimed in claim 4, wherein the polynucleotide sequence of the PAR1 gene encompasses a sequence according to SEQ ID NO: 3.
- 30 6. The isolated polynucleotide sequence as claimed in claim 4, wherein the polynucleotide sequence of the PAR1 gene comprises a sequence according to SEQ ID NO: 3.
- 35 7. An isolated polynucleotide sequence of the PAR1 gene, which comprises a C for T substitution at position 3090 and a C for A substitution at position 3329, in each case based on NM-001992.
8. The isolated polynucleotide sequence as claimed in claim 7, wherein the polynucleotide sequence of the PAR1 gene encompasses a sequence according to SEQ ID NO: 4.
9. The isolated polynucleotide sequence as claimed in claim 7, wherein the polynucleotide sequence of the PAR1 gene comprises a sequence according to SEQ ID NO: 4.

10. An isolated part of the polynucleotide sequence of the PAR1 gene, comprising a sequence according to SEQ ID NO: 5.
- 5 11. An isolated part of the polynucleotide sequence of the PAR1 gene, comprising a sequence according to SEQ ID NO: 6.
12. An isolated part of the polynucleotide sequence of the PAR1 gene, comprising a sequence according to SEQ ID NO: 7.
- 10 13. An isolated part of the polynucleotide sequence of the PAR1 gene, comprising a sequence according to SEQ ID NO: 8.
14. A method for preparing a polynucleotide sequence as claimed in any of claims 1 to 9 by means of the following method steps:
 - 15 a] Providing human cDNA comprising a PAR1 sequence according to SEQ ID NO: 2 and/or a PAR1 sequence according to SEQ ID NO: 3 and/or a PAR1 sequence according to SEQ ID NO: 4,
 - 20 b] Providing a primer pair according to SEQ ID NO: 9 and SEQ ID NO: 10.
 - c] Amplifying the PAR1 polynucleotide sequence by the polymerase chain extension reaction (PCR),
 - d] Isolating and/or purifying the 3.56 kb fragment obtained from c],
 - 25 e] Sequencing the fragment from d].
15. A method for preparing a polynucleotide sequence as claimed in any of claims 10 to 13 by means of the following method steps:
 - 30 a] Providing human genomic DNA comprising a PAR1 sequence according to SEQ ID NO: 1 and/or a PAR1 sequence according to SEQ ID NO: 2 and/or a PAR1 sequence according to SEQ ID NO: 3 and/or a PAR1 sequence according to SEQ ID NO: 4
 - 35 b] Providing a primer pair according to SEQ ID NO: 11 and SEQ ID NO: 12
 - c] Amplifying the fragment of the PAR1 polynucleotide sequence by the polymerase chain extension reaction (PCR),
 - d] Isolating and/or purifying the fragment obtained from c],
 - e] Sequencing the fragment from d].

16. A method for detecting whether or not there is in a PAR1 gene a T to C substitution at position 3090 of the sequence according to NM-001992 and/or an A to C substitution at position 3329 of the sequence according to NM-001992, which method comprises the following method steps:
- 5
- a) Providing biological material comprising human cells,
 - b) Obtaining chromosomal DNA from the material of a),
 - c) Amplifying a polynucleotide fragment by means of the primers according to SEQ ID NO: 11 and SEQ ID NO: 12, using a PCR reaction,
 - d) Sequencing the polynucleotide fragment from c].
- 10
17. A method for detecting whether or not there is in a PAR1 gene a T to C substitution at position 3090 of the sequence according to NM-001992 and/or an A to C substitution at position 3329 of the sequence according to NM-001992, which method comprises the following method steps:
- 15
- a) Providing biological material comprising human cells,
 - b) Obtaining RNA from the material of a),
 - c) Transcribing said RNA into cDNA by means of reverse transcriptase,
 - d) Possibly amplifying a polynucleotide fragment by means of the primers according to SEQ ID NO: 10 and SEQ ID NO: 11, using the PCR reaction,
 - e) Sequencing the cDNA from c] and/or the polynucleotide fragment from d].
- 20
- 25
18. A method for detecting whether or not there is in a PAR1 gene a T to C substitution at position 3090 of the sequence according to NM-001992 and/or an A to C substitution at position 3329 of the sequence according to NM-001992, which method comprises the following method steps:
- 30
- a) Providing biological material comprising human cells,
 - b) Obtaining chromosomal DNA from the material of a),
 - c) Southern blotting the chromosomal DNA from b),
 - d) Providing a probe according to SEQ ID NO: 5 and/or SEQ ID NO: 6 and/or SEQ ID NO: 7 and/or SEQ ID NO: 8,
- 35

- e] Hybridizing the Southern blot from c] with the probe from d] under stringent hybridization conditions,
- f] Determining the presence or absence of a genetic variation in the PAR1 gene at position 3090 and/or 3329 according to NM-001992 by comparing the results of the hybridization from e].
- 5
19. A method for detecting, whether or not there is in a PAR1 gene a T to C substitution at position 3090 of the sequence according to NM-001992 and/or an A to C substitution at position 3329 of the sequence according to NM-001992, which method comprises the following method steps:
- 10
- a] Providing biological material comprising human cells,
- b] Obtaining RNA from the material of a],
- 15 c] Providing a probe according to SEQ ID NO: 5 and/or SEQ ID NO: 6 and/or SEQ ID NO: 7 and/or SEQ ID NO: 8,
- e] Hybridizing the Northern blot from c] with the probe from d] under stringent hybridization conditions,
- f] Determining the presence or absence of a genetic variation in the PAR1 gene at position 3090 and/or 3329 according to NM-001992 by comparing the results of the hybridization.
- 20
20. An isolated polynucleotide sequence having from 21 to 50 nucleotides, which comprises a sequence according to SEQ ID NO: 11.
- 25
21. An isolated polynucleotide sequence comprising SEQ ID NO: 11.
22. An isolated polynucleotide sequence having from 21 to 50 nucleotides, which comprises a sequence according to SEQ ID NO: 12.
- 30
23. An isolated polynucleotide sequence comprising SEQ ID NO: 12.
- 35 24. The use of an isolated polynucleotide sequence as claimed in claim 20 or 21 in combination with an isolated polynucleotide sequence as claimed in claim 22 or 23 for amplifying a fragment of the PAR1 gene by means of the PCR reaction.

25. The use as claimed in claim 24, wherein the PAR1 gene has a T to C substitution at position 3090 of the sequence according to NM-001992 and/or an A to C substitution at position 3329 of the sequence according to NM-001992.
- 5 26. A kit of parts, comprising
- a] a polynucleotide sequence as claimed in claim 20 or 21,
 - b] a polynucleotide sequence as claimed in claim 22 or 23,
 - c] at least one enzyme for carrying out the PCR reaction
 - d] and possibly substances and/or solutions for carrying out the polymerase chain extension reaction (PCR),
 - 10 e] and possibly furthermore polynucleotide sequences as claimed in one or more of claims 1 to 17
 - f] and possibly reagents for carrying out a sequencing.
- 15 27. A method for preparing the kit of parts as claimed in claim 26, which method comprises
- a] preparing a polynucleotide sequence as claimed in claim 20 or 21,
 - b] providing a polynucleotide sequence as claimed in claim 22 or 23,
 - c] providing an enzyme for carrying out the PCR reaction,
 - d] providing, where appropriate, reagents for carrying out a sequencing
 - 20 e] possibly providing substances and/or solutions for carrying out the polymerase chain extension reaction (PCR),
 - f] possibly providing polynucleotide sequences as claimed in one or more of claims 1 to 13,
 - g] introducing the components from a] to e] in each case separately
 - 25 into suitable containers,
 - h] combining, where appropriate, the containers from g] in one or more pack-units.
28. The use of the kit of parts as claimed in claim 26 or 27 for amplifying a fragment of the PAR1 gene and possibly for the further analysis, as to

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whether genetic variations are present in the PAR1 gene at positions 3090 and/or 3329 according to NM-001992.

- 29. The method of any one of claims 14 to 19 or 27, or the use according to claim 24 or 28, substantially as hereinbefore described.

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SANOFI-AVENTIS DEUTSCHLAND GMBH

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WATERMARK PATENT AND TRADE MARKS ATTORNEYS

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P26199AU00

Fig. 1

		n	%
Total		1404	
Gender	Female	406	28.9
	Male	998	71.1
Age		62.7 (30.0 – 90.7)	
BMI* (Body Mass Index)		27.8 (16.7 – 57.1)	
Hypertension		834	59.4
Smoker		923	65.7
Angina pectoris		210	62.7
Diabetic (ADA)		445	31.7
Cardiac infarction		579	41.0
CAD (> 20% stenosis)		1087	78.8
Stroke		106	7.5

* Medians and quartiles (Q1 – Q3)

5

Fig. 2

	PAR1 C3329C	PAR1 C3329A	PAR1 A3329A
PAR1 T3090T	1	0	724
PAR1 /3090C	0	371	160
PAR1 C3090C	51	47	8

10

Fig. 3

	odds ratio	95% - confidence interval		p value
		lower	upper	
Atrial fibrillation	1.97	1.18	3.30	0.0101
Cardiomyopathy	1.84	1.04	3.24	0.0353

Fig. 4

	odds ratio	95% - confidence interval		p value
		lower	upper	
Atrial fibrillation	2.35	1.18	4.68	0.0149
Cardiomyopathy	0.36	0.17	0.79	0.0107
Unstable angina	0.36	0.16	0.81	0.0142

Fig. 5

ggcggggggc gcacagagcc agaggggctt gcgagcggcg gctgagggac cgcggggagg
 gggcgccgag cggctccagc gcagagactc tcaactgcac cgggaggccc ctctctcget
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Fig. 6

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Fig. 7

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Fig. 8

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Fig. 9

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Fig. 10

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Fig. 11

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Fig. 12

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12/12

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Fig. 13

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Fig. 14

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Fig. 15

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Fig. 16

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Fig. 17

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SEQUENCE LISTING

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<120> Analysis and use of PAR1 polymorphism for
evaluating the risk of cardiovascular disorders

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<213> Homo sapiens

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<211> 939

<212> DNA

<213> Homo sapiens

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10/11

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Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser
50 55 60

Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu
65 70 75 80

Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu
85 90 95

Thr Ser Ser Trp Leu Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val
100 105 110

Phe Val Val Ser Leu Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile
115 120 125

Leu Lys Met Lys Val Lys Lys Pro Ala Val Val Tyr Met Leu His Leu
130 135 140

Ala Thr Ala Asp Val Leu Phe Val Ser Val Leu Pro Phe Lys Ile Ser
145 150 155 160

Tyr Tyr Phe Ser Gly Ser Asp Trp Gln Phe Gly Ser Glu Leu Cys Arg
165 170 175

Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu Leu
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Met Thr Val Ile Ser Ile Asp Arg Phe Leu Ala Val Val Tyr Pro Met
195 200 205

Gln Ser Leu Ser Trp Arg Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu
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Ala Ile Trp Ala Leu Ala Ile Ala Gly Val Val Pro Leu Val Leu Lys
 225 230 235 240

Glu Gln Thr Ile Gln Val Pro Gly Leu Asn Ile Thr Thr Cys His Asp
 245 250 255

Val Leu Asn Glu Thr Leu Leu Glu Gly Tyr Tyr Ala Tyr Tyr Phe Ser
 260 265 270

Ala Phe Ser Ala Val Phe Phe Phe Val Pro Leu Ile Ile Ser Thr Val
 275 280 285

Cys Tyr Val Ser Ile Ile Arg Cys Leu Ser Ser Ser Ala Val Ala Asn
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Arg Ser Lys Lys Ser Arg Ala Leu Phe Leu Ser Ala Ala Val Phe Cys
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Ile Phe Ile Ile Cys Phe Gly Pro Thr Asn Val Leu Leu Ile Ala His
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Tyr Leu Leu Cys Val Cys Val Ser Ser Ile Ser Ser Cys Ile Asp Pro
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Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys Gln Arg Tyr Val Tyr Ser
 370 375 380

Ile Leu Cys Cys Lys Glu Ser Ser Asp Pro Ser Ser Tyr Asn Ser Ser
 385 390 395 400

Gly Gln Leu Met Ala Ser Lys Met Asp Thr Cys Ser Ser Asn Leu Asn
 405 410 415

Asn Ser Ile Tyr Lys Lys Leu Leu Thr
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