SHORT REPORT

Germline CDKN2A/P16INK4A mutations contribute to genetic determinism of sarcoma

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ABSTRACT

Background Sarcomas are rare mesenchymal malignancies whose pathogenesis is poorly understood; both environmental and genetic risk factors could contribute to their aetiology. Methods and results We performed whole-exome sequencing (WES) in a familial aggregation of three individuals affected with soft-tissue sarcoma (STS) without TP53 mutation (Li-Fraumeni-like, LFL) and found a shared pathogenic mutation in CDKN2A tumour suppressor gene. We searched for individuals with sarcoma among 474 melanoma-prone families with a CDKN2A/p16INK4A genotype and for CDKN2A mutations in 190 TP53-negative LFL families where the index case was a sarcoma. Including the initial family, eight independent sarcoma cases carried a germline mutation in the CDKN2A/p16INK4A gene. In five out of seven formalin-fixed paraffin-embedded sarcomas, heterozygosity was lost at germline CDKN2A mutations sites demonstrating complete loss of function. As sarcomas are rare in CDKN2A/p16INK4A carriers, we searched in constitutional WES of nine carriers for potential modifying rare variants and identified three in platelet-derived growth factor receptor (PDGFRα) gene. Molecular modelling showed that two never-described variants could impact the PDGFRα extracellular domain structure. Conclusion Germline mutations in CDKN2A/P16INK4A, a gene known to predispose to hereditary melanoma, pancreatic cancer and tobacco-related cancers, account also for a subset of hereditary sarcoma. In addition, we identified PDGFRα as a candidate modifier gene.
<table>
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<tr>
<th>Collections*</th>
<th>Family ID</th>
<th>Patient ID</th>
<th>Cases Clinical context</th>
<th>P16 exon</th>
<th>P16(^{\text{INK4A}}) mutation(^{\dagger})</th>
<th>p14(^{\text{INK4A}})AA change</th>
<th>Sarcoma LOH at CDKN2A/P16(^{\ddagger})</th>
<th>Melanoma/pancreatic cancer reports</th>
<th>P16(^{\text{INK4A}}) Loss of function</th>
<th>Other candidate modifiers(^{3,6})</th>
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<td>7389</td>
<td>I-1</td>
<td>LPS (57)</td>
<td>IVS 1</td>
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<td>c.194-2A&gt;G</td>
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<td>Yes</td>
<td>Yes (unpublished data)</td>
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<td>(Walker GJ, 1995;(^{29}) Goldstein A, 2007(^{28}))</td>
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<td>ND</td>
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<td>(McKenzie HA, 2010(^{30}))</td>
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\*All subjects provided written informed consent for participation in these oncogenetic research studies, which were approved by the local research ethics committees. Collection (A) comprised 190 families with suspected Li-Fraumeni syndrome that included at least one member with sarcoma. Collection (B) comprised 296 melanoma-prone French families CDKN2A/p16INK4A+. Collection (C) comprised 178 CDKN2A/p16INK4A+ melanoma-prone families from the international GenoMEL database.

\(\dagger\)CDKN2A/P16\(^{\text{INK4A}}\) exons 1\(\alpha\), 2 and 3 were sequenced by Sanger method based on transcript NM_000077.4 to screen for mutations in collections A, B and C. None were present in public controls databases such as 1000 genomes or ExAC.

\(\ddagger\)LOH analyses were performed by Sanger sequencing at germline CDKN2A mutations sites in DNA extracted from sarcoma FFPE samples.

Ages (years) at diagnosis appears in parentheses

AGS, angiosarcoma; FS, fibrosarcoma; LPS, liposarcoma; MM, cutaneous melanoma; NA, not analysed; ND, not determined; OS, osteosarcoma; STS, soft-tissue sarcoma; SVS, synovialosarcoma; UCS, uterine carcinosarcoma; RMS, rhabdomyosarcoma.
Figure 1  Whole-exome sequencing in a three sarcoma cases family without TP53 germline mutation: identification of CDKN2A and PDGFRA germline mutations, co-segregating with sarcomas (A) Pedigree of the Li-Fraumeni-like family. Cancer diagnosis and age at onset are indicated for affected members; hatched circles/squares indicate sarcoma: AGS, angiosarcoma; LPS, liposarcoma; STS, soft-tissue sarcoma. Genotypes of CDKN2A and PDGFRA for all samples available for testing are shown. Patients with WES data are indicated with a black star. (B) Whole-exome sequencing (WES) germline SNV filtering and interpretation, for two patients of Family 7389. We used Ingenuity Variant Analysis software (v.2.1.20130711, IVA, Qiagen) and predetermined filters (see Bioinformatics analysis, online supplementary material). Starting with 307 690 variants spanning 17 673 genes, successive filters lead to 3 variants spanning 3 genes (CDKN2A, PDGFRA and SKA3). (C) Structural properties of platelet-derived growth factor receptor α (PDGFRα) wild-type and variants. (Top row) the PDGFRα protein has a modular structure composed of five Ig-like domains (D1, D2, D3, D4 and D5), a trans-membrane domain (TMD) and a cytoplasmic region. The cytoplasmic region consists of a regulatory juxtamembrane region (JM) and a catalytic kinase domain, with an N-lobe and a C-lobe, which harbours a kinase insert domain (KID). (Bottom row) The X-ray analysis structures are represented as ribbon diagrams, based on the KIT oncogene structural data. D1 and D5 are denoted as ovals. (Middle row) Schematic representations of D1 and D5 topologies. (Bottom figures) Superimposed conformations of wild-type PDGFRα (blue) and PDGFRα germline variants (pink), obtained from molecular dynamics (MD) simulations. Representative conformations were selected by RMSDs clustering and are presented as ribbon diagrams.
were partially described previously \(^{10}\) and found eight kindreds that contained at least one member with sarcoma. Among them, five probands with sarcoma carried the pathogenic familial \(\text{CDKN2A/P16INK4A}\) mutation \((\text{p.Ile49Ser})\), a patient diagnosed with a pleomorphic liposarcoma at the age of 32 years whose brother died of osteosarcoma at the age of 24 years (Family 18 998, table 1, online supplementary S1A and S2B). To explore further the potential connection between \(\text{CDKN2A}\) germline mutations and sarcoma, we reviewed the phenotypes in our collection of 296 melanoma-prone French families with \(\text{CDKN2A/P16INK4A}\) germline mutations (collection B); mutations were partially described previously \(^{11,12}\) and found eight kindreds that contained at least one member with sarcoma. Among them, five probands with sarcoma carried the pathogenic familial \(\text{CDKN2A/P16INK4A}\) germline mutation \((\text{table 1, families 14288, 2 225, 1 4289, 14291 and 15 118, online supplementary figure S1B})\) and three families had incomplete data (two untested index cases and one unconfirmed STS; see online supplementary figure S4A,S4C; material and methods). Overall, among the 296 families, the difference in sarcoma incidence between \(\text{CDKN2A}\) carrier and non-carrier \((5/593; 0.84%; 95\% \text{ CI 0.3\% to 2\%})\) and non-carriers \((1/298; 0.34%; 95\% \text{ CI 0.02\% to 2.16\%})\) did not reach statistical significance \((p=0.67; \text{ Fisher's exact test})\). Considering the yearly incidence in Caucasians of 5.8 per 100\,000\(^{1}\) and the mean follow-up in collection B of 46 years, the probability of observing at least five sarcomas in the 593 \(\text{CDKN2A}\) carriers population was 0.02 (assuming a binomial distribution). In the 298 \(\text{CDKN2A}\) WT populations, the mean follow-up was 39 years, and the probability of observing at least 1 sarcoma was 49\%.

Next, we searched for biological arguments. As loss of heterozygosity (LOH) is considered in tumour biology as a strong indicator to the causative role of a tumour suppressor, we performed Sanger sequencing in seven FFPE sarcoma blocs available from French patients. We identified LOH at the \(\text{CDKN2A}\) germline mutation site in five out of seven samples \((\text{table 1, online supplementary figure S2})\). These LOHs demonstrate the occurrence of a second genetic hit on \(\text{CDKN2A}\) and, therefore, complete loss of \(\text{p16INK4A}\) function in five sarcomas, in accordance with the driver role of \(\text{CDKN2A}\) tumour suppressor gene in sarcomagenesis.\(^{8}\)

Finally, we interrogated the GenoME database containing 178 \(\text{CDKN2A+}\) melanoma-prone families \((\text{collection C})\), after removal of 60 French families already included in collection B. We identified three additional independent \(\text{CDKN2A}\) mutation carriers affected with a sarcoma. One family was from Australia and carried a \(\text{CDKN2A/p16INK4A}\) \(\text{p.Leu112Arg}\) germline mutation \((\text{Family 20473, table 1, online supplementary figure S1C})\). The second family was from the UK \((21\text{kb deletion targeting CDKN2A/p14REF exon 1b})\) \((\text{data not shown})\) and the third family was from the Netherlands, but the initial diagnosis of fibrosarcoma case was revised to melanoma and, therefore, was excluded. Overall, in collections A, B and C, ascertainment for Li-Fraumeni (A) or multiple cases of melanoma and/or pancreatic cancer (B and C), we identified eight independent families in which at least a \(\text{CDKN2A/P16INK4A}\) mutation carrier had a sarcoma \((\text{table 1})\). Therefore, based on probabilistic and biological arguments, \(\text{CDKN2A/P16INK4A}\) germline mutations can be strongly suspected to increase sarcoma risk. Interestingly, in the literature, two sarcoma cases in \(\text{CDKN2A/P16INK4A}\) mutation carriers were identified in families with melanoma/pancreatic cancer and very recently germline \(\text{CDKN2A}\) mutations were identified in two independent patients presenting with LFS.\(^{11,12}\) In addition to the well-known role of \(\text{CDKN2A}\) in somatic sarcomagenesis, other observations in animals suggested a germline effect. First, in a mouse model, deletion of the \(\text{Cdkn2a}\) locus could substitute for mutations in \(\text{Tp53}\) to generate STSs.\(^{13}\) Second, in a naturally occurring, canine breed-specific histiocytic sarcoma, a genome-wide association study (GWAS) identified a haplotype near \(\text{CDKN2A}\).\(^{14}\) In conclusion to our work and published data, germline mutations in \(\text{CDKN2A/P16INK4A}\), a gene known to predispose to hereditary melanoma, pancreatic cancer and tobacco-related cancers, account also for a subset of hereditary sarcoma.\(^{7}\)

As melanoma risk in \(\text{CDKN2A}\) mutation carriers is clearly associated with \(\text{MC1R}\) frequent alleles acting as modifiers,\(^{15}\) we formulated the hypothesis that the very low frequency of sarcoma cases observed in \(\text{CDKN2A/P16INK4A}\) positive melanoma-prone families could be explained by rare modifiers alleles. In a model of oligogenic inheritance, it is challenging to identify rare germline variants that act in synergy to initiate cancer, and GWAS is unable to identify rare disease-predisposing variants.\(^{16}\) Candidate pathogenic variants for sarcoma risk in \(\text{ATM}, \text{ATR, BRCA2 and ERCC2}\) genes were identified recently in a large sarcoma case–control study as well as \(\text{POT1}\) variants in cardiac angiosarcoma, but other genes not yet identified could also play a role.\(^{15,16}\) To explore this hypothesis, we considered the two additional germline variants identified in \(\text{PDGFR}\) and \(\text{SKA3}\) genes in the WES data of patients I-2 and II-1, both sarcoma-affected \((\text{initial Family 7389})\). In \(\text{SKA3}\) gene, an insertion of 2T was supposed to have occurred in a stretch of 12T but was unconfirmed by Sanger sequencing and was also found in DNA extracted from FFPE-sarcoma tissue from the third family member, patient I-1, therefore being present in the three sarcoma-affected patients \((\text{Family 7389, figure 1A; online supplementary S7A})\). Next, we performed additional WES analyses in blood-extracted DNA from seven probands affected with sarcoma that carried germline \(\text{CDKN2A}\) mutations \((\text{family 18 998-II.1 in collection A; families 14288-II.1, 2 225-II.1, 14 289-I.1, 14 291-II.1 and 15 118-II.1 in collection B and family 20473-I.4 in collection C})\). Subsequently, we data mined the WES available for a total of nine \(\text{CDKN2A/P16INK4A}\) carriers affected with sarcoma, including two relatives. We applied classical filtering strategies using the IVA software \((\text{Qiagen})\) \((\text{online supplementary figure S6})\). For variant frequency, we defined rare variants as those with a minor allele frequency \((\text{MAF})<0.5\%\).\(^{16}\) The outcome of our filtering strategy was the selection of 82 variants spanning 76 genes. Among previously published sarcoma susceptibility genes, we found no mutations in \(\text{TP53}, \text{ATR, BRCA2 and ERCC2}\).\(^{2}\) We found a c.8584+1G>A putative splice site mutation in \(\text{ATM}\) gene in patient 7389-II.2, but this variant was absent in the sarcoma-affected relative, II.1. We also found, in patient 14 291-II.1, a \(\text{POT1}\) c.1127A>G, p.Gln376Arg missense variant, present at a frequency of 0.07\% in Euro-Amm ESP and predicted deleterious by four prediction methods \((\text{SIFT, MutationTaster, Polyphen 2 and Condel})\). This variant...
was also present in the unaffected mother. More interestingly, we detected two other germline missense mutations (verified by Sanger sequencing, online supplementary figure S7B, S7C) located in the extracellular receptor domain of the platelet-derived growth factor receptor alpha gene (PDGFRA), including one absent in public databases. The PDGFRA missense variant c.227A>G, p.Asn76Ser, predicted deleterious by four computational methods (GVGD, SIFT, Mutation Taster and Polyphen 2), was not present in unaffected mother that carried the CDKN2A p.Gly101Trp mutation (Family 14 29, online supplementary figure S1B). In the sarcoma-proband I-4 of family 20 (online supplementary figure S1C), we identified another germline PDGFRA variant, c.1388C>G, p.Thr463Ser, described with an allelic frequency of 0.02%, and predicted deleterious by two computational methods (Mutation Taster and Condel). Co-segregation analysis was not informative (online supplementary figure S1C).

The PDGFRα, composed of extracellular, trans-membrane and intracellular domains (figure 1C), is activated by the binding of its ligand, which induces dimerisation, followed by kinase domain activation.21 Germline oncogenic gain-of-function mutations in PDGFRA cause familial gastrointestinal stromal tumours (GIST) associated with other tumours.18 19 Accordingly, the variants described above were not oncogenic in the sarcoma-proband I-4 of family 20, et al. J Med Genet 0 Jouenne F, et al. Cancer Genetics

Overall, our data identified PDGFRA as a new sarcoma candidate modifier gene. Unfortunately, PDGFRA was not included in the 72 genes panel studied in the recent study of 1162 patients with sarcoma.22 PDGFRα belongs to the large family of membrane RTKs and plays primary roles in mesenchymal tissue development. Recent whole-genome or whole-exome analyses have revealed numerous somatic mutations localised in the RTK-III extracellular domain, which could have transforming potential, based on their structural and physicochemical effects on the receptor.23 These mutations in PDGFRA extra-cellular domains could affect non-canonical RTK functions. On ligand activation, RTKs are internalised and translocated into endosomal compartments for signalling.20 Overall, our genetic and molecular modelling results suggested that PDGFRA germline variants that affect the extracellular domain could play a role in sarcomagenesis, but the functional mechanism remains unknown.

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Contributors BB-deP-J-BD, LT and TF designed the study. TF, OC, OI, M-FA, AL, PB, PT, DP, AdAD, OC, GIJ, MJH, MN-B, NG, RVD, RG, CD, MG-V, GP and DS-L provided patients clinical data and samples. FJ, EB, VC, IC-de B, GB and AV performed the experiments. FJ, IC-deB, BND, BB-de B-J, LT and JB SK were involved with data analysis and interpretation. FJ, BB-deP-JF, LT, JB, AB, AE, PB, M-FA, TF and JYS wrote and reviewed the manuscript.

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Competing interests None declared.

Patient consent All patients signed informed consent for research genetic analysis, approved by the concerned IRBs.

Ethics approval CPP Nord Ouest N2015/160/HP; CPP ile de France 2, IRB#000001072, 2010-01-09.

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