Large deletion causing the TSC2-PKD1 contiguous gene syndrome without infantile polycystic disease

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Key points

- The characteristic phenotype of patients with the TSC2-PKD1 contiguous gene syndrome is dominated by severe juvenile polycystic disease, combined with variable phenotypic expression of tuberous sclerosis.
- We describe the case of a women who presented with renal angiomyolipoma at the age of 13 years. Unilateral nephrectomy was performed at the age of 19 years. No significant polycystic disease was present at this time. At the age of 26 years, pulmonary lymphangioleiomyomatosis was diagnosed, which prompted a full evaluation of the tuberous sclerosis phenotype, resulting in confirmation of the clinical diagnosis. In this period, the remaining kidney showed only moderate polycystic disease.
- FISH analysis of the 16p13.3 region disclosed a deletion spanning the entire TSC2 and PKD1 region, larger than previously described deletions in the contiguous gene syndrome.
- This case illustrates the marked phenotypic heterogeneity of the TSC2-PKD1 contiguous gene syndrome. Although the deletion was exceptionally large, significant polycystic disease did not develop until early adulthood. The contention that severe juvenile polycystic disease is a hallmark of the TSC2-PKD1 contiguous gene syndrome appears to be incorrect.
imaging of the brain showed two small subependymal nodules. Fundoscopy was normal. Echocardiography showed a type II atrial septal defect, but no intracardiac hamartomas. Based on these clinical criteria, the likely diagnosis of TSC was confirmed.

At this time, the renal cysts were considered to be part of the TSC syndrome.

Cytogenetics

Cytogenetic and FISH (fluorescence in situ hybridisation) studies were performed on metaphases derived from a culture of PHA stimulated peripheral blood lymphocytes. The cultures were synchronised by using an excess amount of thymidine for 16 hours. The block was released by change of medium six hours before harvesting. Standard karyotyping performed on GTG banded chromosomes showed a normal female karyotype (46,XX). To detect a possible submicroscopic deletion in the TSC2 region, subsequent FISH analysis was performed according to the protocol of Pinkel et al with minor modifications. The DNA probes cc1-2, cw9d, cw23, (fig 1A), ZDS5, and cGGG4 hybridising to the 16p13.3 region showed a large deletion on one of the two chromosomes 16. The number of metaphases analysed with the different DNA probes were respectively 30, 30, 10, 10, 20, and 20. A subtelomeric probe GS-52-M11 located in the 16pter region was still present (fig 1C, a total of 10 metaphases was investigated), indicating that the deletion was interstitial. The proximal breakpoint was, on the other hand, similar to the one previously found in the patient described by Eussen et al.

Why did significant polycystic disease develop later in life in our patient? The answer remains speculative. Somatic mosaicism, which occurs frequently in tuberous sclerosis complex, and has also been reported in the TSC2-PKD1 contiguous gene syndrome, does not appear to play a role in our patient. Mosaicism at organ level, particularly in the kidney, cannot be

DISCUSSION

The case presented is remarkable in two ways. Firstly, as outlined in the introduction, it is very unusual for the TSC2-PKD1 contiguous gene syndrome to present itself without severe congenital or juvenile polycystic disease with grossly enlarged kidneys. Secondly, the deletion found in our patient is exceptionally large, at least 200 kb, which is the probe contig surrounding the TSC2 and PKD1 genes. It is, to our knowledge, the largest interstitial deletion reported in the TSC-PKD contiguous gene syndrome in an otherwise normal subject.

Previously, the α globin gene cluster was mapped to chromosome band 16p13.3 distal to the TSC2 locus. Patients with α thalassaemia/mental retardation syndrome (ATR-16) have been reported to show terminal deletions, variable in extent. The deletion present in the proband proved to be interstitial, since the subtelomeric probe GS-52-M11 located at the 16pter region was still present. This was expected considering the normal α thalassaemia trait and absence of mental retardation in the proband. The proximal breakpoint was, on the other hand, similar to the one previously found in the patient described by Eussen et al.

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Figure 1 Representative FISH results showing (A) a deletion of the 16p13.3 region using the cw23 probe (7q11.23) and D7S427 control probe (7q36). Only one normal chromosome 16 shows signals at p13.3; no signals are visible on the deleted chromosome 16 (arrow). (B) A partial deletion (diminished signals) of the 16p13.3 region using the 1.8F probe (small arrow) and normal signals on the other chromosome 16 (large arrow). (C) On both chromosomes 16 the subtelomeric probe GS-S2-M11 is still visible (arrows).

Figure 2 The molecular map of the TSC2 and PKD region on chromosome 16p (not drawn to scale). The deletion detected in the proband is indicated by the solid bar.
ruled out. In both ADPKD and TSC, loss of heterozygosity has been suggested as the mechanism responsible for disease expression. Loss of heterozygosity implies that a “second hit” is required before disease develops. The nature of this “second hit” causing loss of heterozygosity is unknown. Whether it is usually the same for the adjacent genes PKD1 and TSC2 is also uncertain. Since PKD1 and TSC2 mutations are apparently both recessive at the cellular level, loss of heterozygosity is probably responsible for disease manifestations in the contiguous gene syndrome as well, although this remains to be proven. We speculate that, in our patient, either a single “second hit” caused loss of heterozygosity for both PKD1 and TSC2 at a later stage than is common in the contiguous gene syndrome, or two “second hits” were responsible for her disease, one of which, conceivably the one causing loss of heterozygosity for the PKD gene, occurred at a later stage in life.

In conclusion, this case illustrates that marked heterogeneity exists in the clinical presentation of the TSC2-PKD contiguous gene syndrome. In contrast to what is commonly thought, severe juvenile polycystic disease is not an obligatory sign.

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REFERENCES
12 Burn TC, Connors TD, Raay TVJ, Dockowski WR, Millhallion JD, Klinger KW, Landers GM. Generation of a transcriptional map for a 700 kb region surrounding the polycystic kidney disease type 1 (PKD1) and tuberous sclerosis type 2 (TSC2) disease genes on human chromosome 16p13. Genome Res 1996;6:525-37.