Chromosomal localisation of a gene(s) for Turner stigmata on Yp

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Abstract

Although recent cytogenetic and molecular studies in patients with Turner stigmata are consistent with a gene(s) for Turner stigmata being present on both Xp and Yp, the precise location has not been determined. In this report, we describe a phenotypically female infant with Turner stigmata and a partial Yp deletion and review genotype-phenotype correlations of the putative Turner gene(s) in non-mosaic patients with Y chromosome rearrangements resulting from chromosomal breakage at Yp or Yc (pericentromeric region). The results indicate that the putative Turner gene(s) on Yp is located in the Y specific region from interval 1A1A to interval 2B. In addition, assessment of ZFX/ZFY and RPS4X/RPS4Y in the context of the Turner gene(s) suggests that ZFX/ZFY rather than RPS4X/RPS4Y could be a candidate gene for the Turner stigmata.

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Turner syndrome is associated with characteristic somatic features such as webbed neck, low posterior hair line, lymphoedema, and cubitus valgus. 1-3 Since such Turner stigmata are frequently manifested by patients with 45,X, 46,X,Xp-, and 46,X,i(Xq),4 it has been suggested that Xp carries a gene(s) for Turner stigmata which escapes X inactivation.4 In addition, Turner stigmata have also been reported in patients with 46,X,Yp-1 indicating that Yp also contains a gene(s) for Turner stigmata.4 These findings imply that the gene(s) for Turner stigmata is shared by Xp and Yp, and that haplinsufficiency of the gene(s) results in the development of Turner stigmata.4 Although patients with 46,X,Xq- also sometimes have Turner stigmata, this could be explained by assuming that the putative Turner gene(s) on Xp escapes X inactivation on normal X chromosomes but is prone to undergo X inactivation on structurally abnormal X chromosomes.5

The putative Turner gene(s) has been located in the sex specific regions of Xp and Yp.6 Although genes in the pseudoautosomal region (PAR) share homology between the X and the Y chromosome and are expected to escape X inactivation, genetic evidence currently available argues against the Turner gene(s) being present in the PAR. It has been shown by cytogenetic and molecular studies that the putative Turner gene(s) on Xp is present in the middle part of Xp.6 It has also been shown that sex reversed patients with 46,XY caused by an abnormal Xp;Yp inter-
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Figure 1  Southern blot analysis (F = father, P = patient, * = normal female, & = normal male). (1) EcoRI digests hybridised with 29Cl (DXYS14). The probe detects bands specific to the patient and to the father, together with those shared by them. (2) TaqI digests hybridised with 19B (MIC2). RFLP pattern shows the presence of two copies of MIC2 in the patient. (3) SstI digests hybridised with H0.2 (PABX/PABY). PABY is absent in the patient, although PABX is present. (4) EcoRI digests hybridised with pY53.3 (SRY) pattern. The patient is negative for SRY. (5) EcoRI digests hybridised with H0.2 (PABX/PABY) (top panel), MIA (DXS31) (second panel), pG15 (DXYS61) (third panel); and probe for autosomal TK gene as an internal control (bottom panel) same filter; NB, the EcoRI filter is different from that used for 29Cl, pY53.3, 50f2, and 52d. Band intensity ratios are (F, P, * , & , &; ) PABX/TK (1.53, 1.67, 1.63, 1.45, 1.40, 1.52); DXS31/TK (0.15, 0.18, 0.35, 0.30, 0.12, 0.99); and DXYS61/TK (0.47, 0.51, 1.15, 1.21, 1.05, 0.91). The results indicate that, in both the patient and the father, PAB is present in two copies and DXS31 and DXYS61 are present in a single copy. (6) EcoRI digests hybridised with 50f2 (DYST7). DYST7/A and DYST7/B are absent in the patient. (7) EcoRI digests hybridised with 52d (DYF27). The patient is negative for DYF27/B. Intensity ratio between DYF27/C band and the X specific band (the second upper band) is 1.39 for the father, 0.74 for the patient, and 1.65 and 1.76 for the two control males, implying that one copy of DYF27/C in interval 3 is deleted whereas the other copy in interval 4 is preserved in the patient.

Discussion

The present study indicates that the Yq specific loci from interval 1A1A to interval 3 were deleted, whereas those assigned to interval 4 were preserved. Although PABY was absent, PABX was present in two copies as were other pseudoautosomal loci. DXS31 was present in a single copy. Both the patient and the father had a single copy of DXYS61, as expected from the cytogenetic findings of the Yq chromosomes.

In summary, the results of this study support the hypothesis that the gene(s) for Turner stigmata are located on the pseudoautosomal region of the Yq chromosome.
mosome imbalance being absent. Although our patient inherited the satellite Y chromosome from the father, the apparently normal phenotype of the father suggests that the structural abnormality of Yq's has no phenotypic effect.

For a more precise localisation of the putative Turner gene(s) on Yp, it is useful to review genotype-phenotype correlations in persons with Y chromosome rearrangements resulting from chromosomal breakage at Yp or Yq (pericentromeric region). For this purpose, we surveyed published reports for informative patients using the following criteria: (1) analysis of the rearranged Y chromosomes by molecular studies; (2) absence of numerical or structural abnormalities of the X chromosome; (3) lack of demonstrable mosaicism; and (4) description of somatic features. Consequently, a total of 18 informative patients was identified (fig 2). Before the correlations, however, two matters should be considered, that is, the number of genes involved and problems inherent in phenotypic assessment.

The number of Turner genes is unknown, but there are some indicators. Most Turner stigmata can be classified into three groups: (1) features attributable to lymphatic stasis, such as webbed neck, low posterior hair line, rotated ears, lymphoedema, redundant skin, nail dysplasia, and characteristic dermatoglyphics; (2) those attributable to skeletal anomalies, such as short neck, micrognathia, cubitus valgus, and short metacarpals and metatarsals; and (3) those attributable to vascular dysplasia, such as cardiac anomalies and, possibly, renal malformations. Since lymphovascular and skeletal systems are derived from mesenchyme, disruption of mesenchymal development might lead to the various Turner stigmata. Alternatively, lymphatic malformation alone might cause the various Turner stigmata. The possible contribution of lymphatic malformation to skeletal anomalies has been speculated upon. In fact, skeletal anomalies are detectable in the regions where there is retention of lymphatic fluid. A potential relationship of lymphatic stasis to cardiac and renal malformations has also been suggested.17,18 Thus, despite the phenotypic diversity, Turner stigmata could most simply be explained as sequelae of an impairment of a
patients with characteristic Turner stigmata than in those with no or equivocal stigmata.

Genotype-phenotype correlations in 18 informative patients are shown in Fig. 2. The simplest explanation is to assume a single Turner gene in the Y specific region from 1A1A to 2B. This location is based on the results of cases 1 to 9. All nine females had lymphoedema during fetal or infant life, three of them (cases, 4, 8, and 9) exhibited skeletal manifestations, and three of them (cases 1, 6, and 8) had cardiac or renal malformations. It might be possible that other Turner genes are present in the more proximal region. If this is the case, a gene(s) for lymphatic development is located in this region. The assignment is consistent with absent Turner stigmata in cases 10 to 15, although lack of stigmata, especially in male patients with a partial autosomal monosomy, does not necessarily imply the presence of the Turner gene(s). The results of cases 16 to 18 may be confounding, but they do not provide direct evidence against the above location. The lack of Turner features in case 16 could be explained by assuming that expressivity was severely reduced or that some features remained undetected. Although case 17 has a high arched palate, short and slightly webbed neck, and shield chest, it is uncertain whether such non-characteristic or equivocal manifestations are directly caused by an impairment of the Turner gene(s). Rather, they could be the result of autosomal involvement. Although case 18 has a low hair line, high arched palate, pigmented naevi, and horseshoe kidney, the features also appear somewhat equivocal. In addition, latent mosaicism with a 45,X cell line is possible in case 18, since the patient has partial gonadal dysgenesis in the presence of SRY. Furthermore, it might be possible that, because of a cryptic complex deletion, the Turner gene(s) is preserved in case 16 and affected in cases 17 and 18.

Two genes of unknown function, ZFY and RPS4Y, have been cloned from the region of the Turner gene(s). Both genes are associated with the homologous genes on the X chromosome, ZFX and RPS4X, which normally escape X inactivation. Since ZFX is present at Xp21.3–Xp22.1,44 the position of ZFX/ZFY appears to satisfy the condition for the chromosomal location of the Turner gene(s). Although Page et al.28 have reported that a female with 46,X,t(Y;22) missing ZFY (case 15) has no Turner stigmata, and Hecht et al.25 have described a female with 46,X,t(X;Y)(p11.2q11) and no apparent Turner stigmata, the findings based on the patients lacking Turner stigmata would not provide compelling evidence against ZFX/ZFY being the Turner gene. Since, to our knowledge, there has been no report documenting a patient with characteristic Turner stigmata in the presence of two copies of ZFX/ZFY, the possibility that ZFX/ZFY could be a candidate Turner gene has not been excluded formally. By contrast, RPS4X/RPS4Y is unlikely to be the Turner gene. The position of RPS4X at Xq13 is inappropriate for the Turner gene. Furthermore, Just et al.18 have reported that the transcription rate of RPS4X

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**Figure 3** A schematic representation of the generation of the patient's Yqs chromosome. White, striped, and stippled areas depict the pseudoautosomal, X specific, and Y specific regions, respectively. The area indicated by horizontal lines denotes the chromosomal satellite. The patient's Yp chromosome is formed by an aberrant Xp:Yp interchange during paternal meiosis, with the breakpoints being between PABX and DXS31 in the X specific region and at the border of intervals 3 and 4 in the Y specific region. Consequently, SRY and the putative Turner gene(s) in the Y specific region were lost, whereas the pseudoautosomal growth gene(s) was present in two doses.

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is normal or increased in Turner patients with 46,XX,XP- and 46,XX,i(Xq). Although detailed phenotype features are not described in the report, this would provide strong evidence against
RPS4X/RPS4Y being the Turner gene.

In summary, although genotype-phenotype
analysis of the putative Turner gene(s) on Yp
is still not conclusive, we propose that the
Turner gene(s) is located in the Y specific region from 1A1A to 2B. In addition, assessment
of ZFX/ZFY and RPS4X/RPS4Y in the context of the Turner gene(s) suggests that
ZFX/ZFY rather than RPS4X/RPS4Y could be a candidate for the Turner gene.

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