

Diagnosis of Xeroderma Pigmentosum by Measuring Unscheduled DNA Synthesis

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The unscheduled DNA synthesis assay has become the most important laboratory method for confirmative diagnosis of xeroderma pigmentosum (XP). Cases of XP diagnosed on clinical grounds alone have been reported in Korea.

We experienced a boy who showed typical features of XP clinically and tried to confirm the diagnosis of XP experimentally.

Fibroblasts were cultured from the patient and from a normal healthy volunteer. Unscheduled DNA synthesis (UDS) after UVB irradiation to the fibroblasts was measured autoradiographically. In addition, polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) with AlwNI in exon 4 of XP group A complementing (XPAC) gene was done after an extraction of genomic DNA from the patient and his parents.

The level of UDS in our patient was 63% of that of the normal control. No cleavage site for the AlwNI was found in the PCR samples.

The diagnosis was confirmed *in vitro* by measuring UDS autoradiographically. Our patient was believed to belong to the variant group based on clinical findings and on our experimental results. (*Ann Dermatol* 8:(2)135~139, 1996).

Key Words : Xeroderma pigmentosum, Unscheduled DNA synthesis assay, PCR-RFLP with AlwNI

Xeroderma pigmentosum (XP) is a rare genetic disease with clinical and cellular hypersensitivity to ultraviolet (UV) radiation and defective DNA repair. Clinically patients with XP show typical pigmentary changes on the exposed skin in the early stage of XP but soon experience UV-induced cutaneous and ocular abnormalities, in-

cluding neoplasia¹⁻³.

Cleaver⁴ found that XP cells in culture showed markedly diminished rates of unscheduled DNA synthesis (UDS), which represents excision repair, following ultraviolet exposure. Epstein et al⁵ demonstrated reduced UDS *in vivo* in patients with XP. Ever since the UDS assay has become the most important laboratory method for confirming a diagnosis of XP.

De Weerd-Kastelein et al⁶ reported genetic heterogeneity of XP demonstrated by cell fusion technique and seven genetic complementation groups, A through G, of excision repair-deficient types and one excision repair-proficient type, variant group, have been identified³. Recently, a human gene, designated as XP group A complementing (XPAC) gene was cloned, three types of mutations in the XPAC gene were elucidated, and a rapid diagnostic method for group A using

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Fig. 1. Multiple freckles on the face.



Fig. 2. Slightly scaly papule on the nasal bridge.

polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) was reported in Japan⁷⁻⁹. However, in Korea only cases of XP diagnosed on clinical grounds alone have been reported¹⁰⁻²⁰.

We experienced a boy who showed quite typical features of XP clinically and tried to confirm the diagnosis of XP experimentally by measuring the rate of excision repair after UV irradiation, i.e. UDS. We also applied the PCR-RFLP technique which proven useful for the rapid diagnosis of XP group A in our patient.

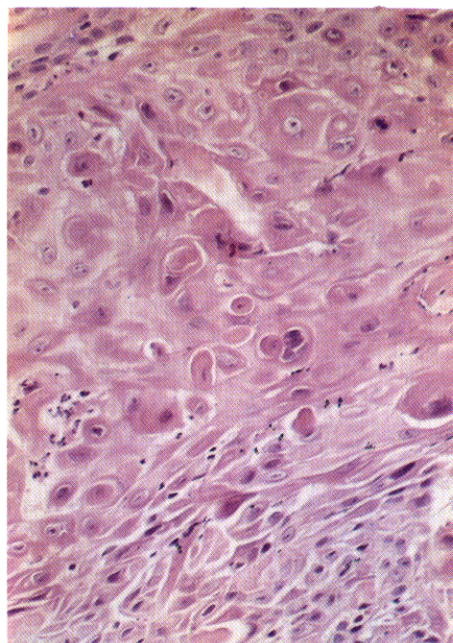


Fig. 3. Histopathologic examination of the papule on the nasal bridge showed squamous cell carcinoma (H&E, $\times 400$).

REPORT OF A CASE

A boy at the age of 3 years and 10 months presented to our hospital complaining of multiple pigmented macules on his face which had appeared since 7-8 months after birth. He had a history of severe sunburning and photophobia. A tumor was found at his initial visit and his growth was normal. His parents were not consanguineous and looked clinically normal. His elder sister looked completely normal without any freckles on her face. However, his father had a few adult relatives with similar pigmented skin lesions.

Physical examination showed multiple freckles on his face (Figure. 1) and a mild conjunctival injection. One month after his initial visit two slightly scaly papules developed on the nasal bridge and the left cheek (Figure. 2), which were proved to be squamous cell carcinomas by histopathologic examination (Figure. 3). Neither ophthalmologic examination nor neurologic examination showed specific abnormalities except for the conjunctival injection.

Fibroblasts were cultured from the patient and from a normal healthy volunteer. Unscheduled

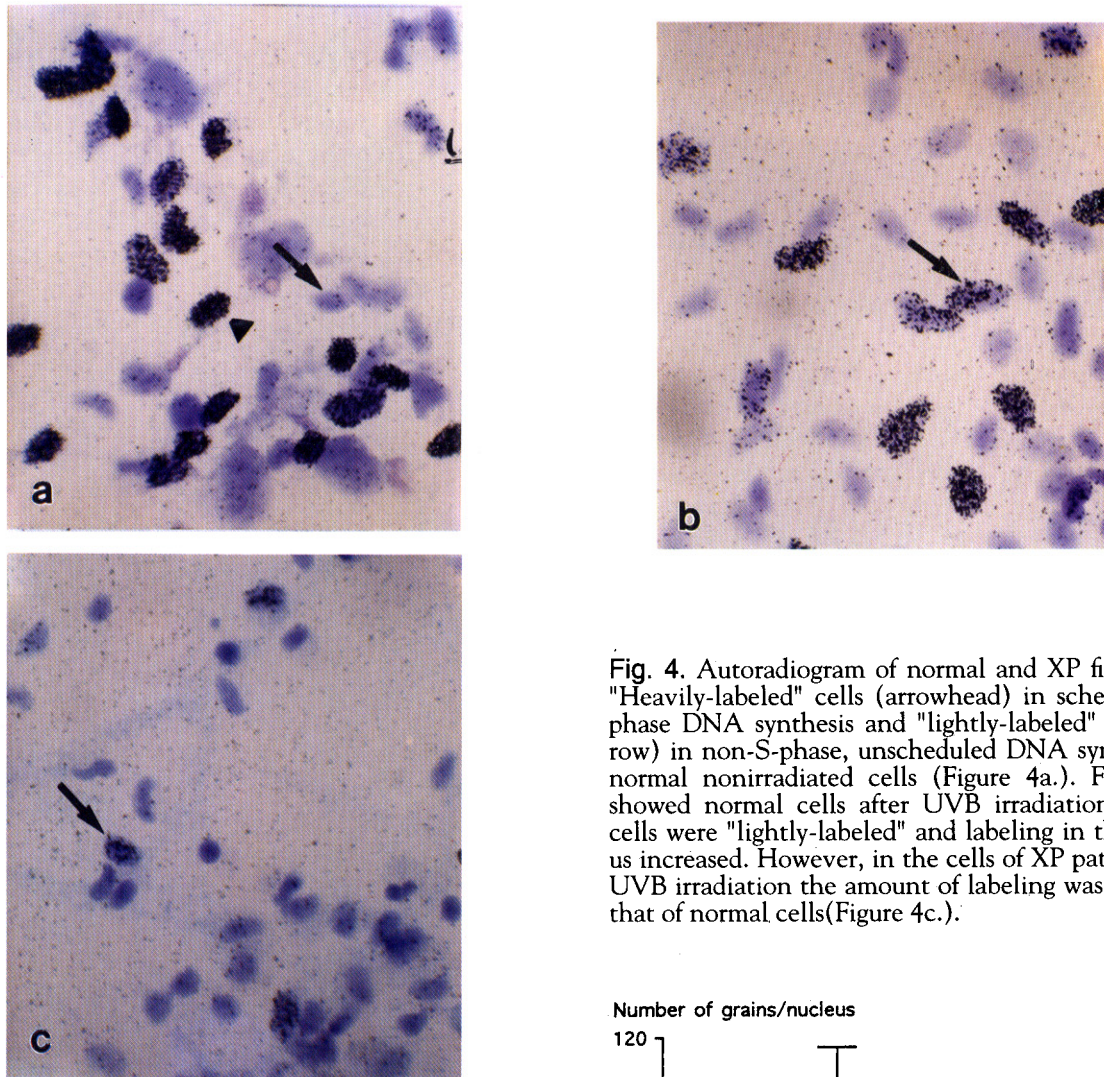


Fig. 4. Autoradiogram of normal and XP fibroblasts. "Heavily-labeled" cells (arrowhead) in scheduled, S-phase DNA synthesis and "lightly-labeled" cells (arrow) in non-S-phase, unscheduled DNA synthesis in normal nonirradiated cells (Figure 4a.). Figure 4b. showed normal cells after UVB irradiation; all the cells were "lightly-labeled" and labeling in the nucleus increased. However, in the cells of XP patient after UVB irradiation the amount of labeling was less than that of normal cells (Figure 4c.).

DNA synthesis (UDS) after UVB irradiation to the fibroblasts was measured autoradiographically with a slight modification as described by Cleaver. The average number of grains per nucleus was determined by counting 50 nuclei in each specimen. Figure 4 showed an autoradiogram of normal and XP fibroblasts. Normal nonirradiated cells after a 3-hour incubation with tritiated thymidine ($^3\text{HTdR}$) showed "heavily-labeled" cells (arrowhead) in scheduled, S-phase DNA synthesis and "lightly-labeled" cells (arrow) in non-S-phase, unscheduled DNA synthesis representing excision repair synthesis (Figure 4a.). Figure 4b showed normal cells after a 3-hour postirradiation incubation with $^3\text{HTdR}$; all the cells were "lightly-labeled" and labeling in the nucleus increased owing to the UV-induced incorpora-

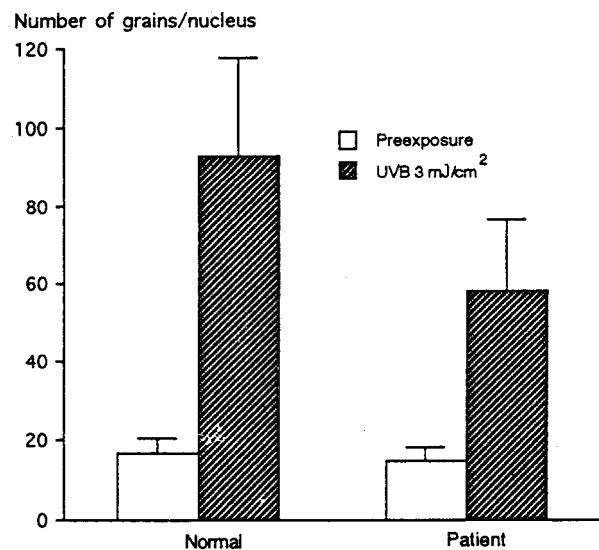


Fig. 5. Unscheduled DNA synthesis (UDS) after 3 mJ/cm² of UVB irradiation to the cultured fibroblasts was measured by counting grains in 50 nuclei in each specimen. The level of UDS in our patient was 63% of normal control.

tion of ³HTdR during DNA repair synthesis. However, in the cells of the XP patient after a 3-hour postirradiation incubation with ³HTdR the amount of labeling was less than that of the normal cells (Figure 4c) of the control.

The number of grains of the nonirradiated normal fibroblasts were 16.52 ± 4.26 and those of the nonirradiated fibroblasts of patient were 14.80 ± 3.34 . However, following UVB irradiation the number of grains of normal fibroblasts increased to 92.72 ± 24.94 compared to 58.50 ± 18.11 of XP fibroblasts. The level of UDS in our patient was 63% of that of the normal control (Fig. 5).

Also polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) with AlwNI in exon 4 of XP group A complementing (XPAC) gene was done after an extraction of genomic DNA from the patient and his parents. PCR products of the DNAs from the normal subject, the patient, and his parents gave uniform 328-base pair bands (data not shown).

A point mutation at the splicing junction of intron 3 and exon 4 that was found to be the most predominant mutation in Japanese patients with XP group A (XPA) creates a new cleavage site for the AlwNI by transversion (G to C) at the 3' splice acceptor site of intron 3 of XPAC gene, and thus 2 bands of 244 and 84 base pairs would appear in the mutated homozygote state with AlwNI. However, in our normal subject, the patient and his parents no PCR samples were digested with AlwNI indicating that our XP patient is less likely to belong to the XPA.

DISCUSSION

Our patient showed the typical clinical features of XP and the diagnosis was confirmed *in vitro* by measuring UDS autoradiographically.

To know a patient belongs to a certain complementation group depends on complementation group analysis. Testing standard XP cell lines against sample cells by measuring UDS autoradiographically after cell fusion allows groups of patients whose cells fail to complement each other in culture to be grouped within a single complementation group¹. We could not perform complementation group analysis and classify our patient exactly.

Among 8 subtypes (A through G, and variant) groups A, C, D, and variant comprised 90% of reported XP patients. Group A, the most common type in Japan, is characteristically accompanied by an early onset of severe neurologic abnormality and group D shows a clinical diversity ranging from patients with no neurologic symptoms to patients with a late onset of neurologic symptoms. Group C, E, F, and variant show no neurologic abnormality¹⁻³.

Each complementation group has a characteristic range of UDS rates and variant group shows proficient UDS³. Group C is not associated with neurologic symptoms but shows a very low rate of UDS of 10-20%, and group D also shows a low rate of UDS (25-50% of normal control)³. Our patient had skin cancer but no neurologic symptoms at least until now and showed the level of UDS to be 63% of that of the normal control.

A rapid diagnostic method for group A using polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) reported in Japan^{8,9} was also applied to our case but no cleavage site for the AlwNI by transversion (G to C) at the 3' splice acceptor site of intron 3 of XPAC gene was found. This was another indirect evidence that our XP patient is less likely to belong to the XPA. We concluded that our patient belonged to the variant group based on clinical findings and our experimental results.

From now on the diagnosis of XP in Korea must be made by typical clinical features and confirmed by laboratory methods *in vitro*. Laboratory confirmation especially in cases with ambiguous clinical features will make the early diagnosis of XP and early genetic counseling possible. In the future we will be able to subgroup Korean patients with XP according to their genetic heterogeneity by doing complementation group analysis.

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