# CHAPTER V

## Results

Twenty three samples were obtained from 21 primary tumours and 2 samples from recurrence patients. The clinical staging of the tumours was stage II, III and IV. All biopsy specimens were histopathologically proven to be NPC type II and type III according to the WHO classification. The tumours specimens were analyzed for Epstein-Barr virus (EBV) genome and identified EBV type by using PCR assay (Hording et al., 1993; Rajadurai et al., 1995). The detail of pateints data were shown in Table 7.

**Table 7** : Patient details ; Age, sex, presence of EBV genome, EBV type, tumour histology type, and TNM stage.

| Patient No | Age | Sex | Histological type | EBV/ Type* | TNM stage | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | T | N | M | Stage |
| 11 | 59 | M | II | +/A | 3 | 0 | 0 | III |
| 18 | 80 | F | II | +/A | 3 | 26 | 0 | IV |
| 19 | 31 | F | II | +/A | 2 | 20 | 0 | IV |
| 24 | 32 | M | III | +/A | 4 | 30 | 0 | IV |
| 31 | 40 | F | III | +/A | Recurrence | | | |
| 34 | 52 | M | III | +/A | 4 | 26 | 0 | IV |
| 35 | 48 | F | III | +/A | 2 | 20 | 0 | IV |
| 38 | 71 | M | II | +/A | 2 | 0 | 0 | II |
| 44 | 73 | M | II | +/A | 2 | 1 | 0 | III |
| 45 | 38 | M | II | +/A | 1 | 26 | 1 | IV |
| 46 | 62 | F | III | +/B | 2 | 0 | 0 | II |
| 47 | 36 | M | III | +/A | Recurrence | | | |
| 50 | 42 | M | II | +/A | 4 | 0 | 0 | IV |
| 51 | 63 | F | III | +/A | 3 | 3 | 0 | IV |
| 53 | 65 | M | II | +/A | 3 | 1 | 0 | III |
| 56 | 44 | M | II | +/A | 3 | 3 | 0 | IV |
| 57 | 55 | M | III | +/A | 1 | 20 | 0 | IV |
| 67 | 30 | F | II | +/A | 2 | 2 | 0 | IV |
| 70 | 73 | M | III | +/A | 4 | 2 | 0 | IV |
| 72 | 59 | F | II | +/A | 3 | 0 | 0 | III |
| 76 | 70 | M | III | +/A | 2 | 2 | 0 | IV |
| 83 | 48 | M | II | +/B | 3 | 3 | 0 | IV |
| 86 | 58 | M | II | +/A | 3 | 0 | 0 | III |

* : Tumour specimens were found to be positive for EBV genome and were identified the EBV type by PCR assay.

T: Primary tumour ; N: Regional lymph nodes ; M:Distant metastasis

Note : Histological typing or Tumour typing is based on the histological scheme of the WHO,Stage is according to the TNM stage by AJCC 1988. The definition of histological type and TNM type are listed in appendix A.

PCR analysis

The twenty-three cases of nasopharyngeal cancer were examined for LOH with STRPs. Using 89 STRPs, all 17 autosomal short arms and 22 autosomal long arms were analyzed with at least 1-3 markers per arm. The results of all loci studied in twenty three nasopharyngeal specimens were shown in details in Table 8, Figure 9. The autoradiographs showing LOH of some loci studied were presented in Figure 10. The autoradiographs of some multiplex PCR analysis were shown in Figure 11.

All chromosome arms were subjected to LOH in at least one tumour. The frequency of LOH for each chromosome arms varied from 0% (2p, 4q, 8p, 10p 19q, 20p, and 21q), to 77% (9p). Thirteen tumours (57%) exhibited LOH in 1-5 chromosomal arms, while ten tumours (43%) displayed LOH in 6 or more chromosomal arms.

The regions with significant LOH together with the percentage of LOH found in the informative cases were as followed : 3p, 65.20%(15 of 23), 9p,77% (17 of 22) that considered to be a common sites of LOH. LOH at 11q, 36.4% (8 of 23) ; 13q, 38% (8 of 21) ; 14q, 37% (7 of 19) ; and 20q, 30% (6 of 20) were considered to be a moderate frequent of LOH. In addition, several chromosome arms exhibited 20-29% LOH : 1p, 23% (5/22); 6p, 27.30% (6/22); and 17p, 22% (5/23). These arms were considered to be less frequent of LOH.

The regions of LOH on chromosome 3p were analyzed using 7 STRPs ( D3S1038, 3p25 VHL; D3S192, 3p25 VHL; D3S1600, 3p14; D3S966, 3p21.3; D3S1480, 3p; D3S1255, 3p25VHL; D3S1217, 3p13-14 ; D3S1481, 3p14 ; and D3S1241, 3p21.3). Fourteen of 23 informative tumour specimens had LOH more than one markers at the VHL loci, 4 of 18 showed LOH at D3S1600, 4 of 6 showed LOH at D3S966, 1 of 5 showed LOH at D3S1217, but there was not any LOH at D3S1480, D3S1481 and D3S1241. There was no LOH presented in six tumours from patients no. 11, 34, 45, 47, 50 and 51 with 9 markers. The typical feature of LOH at 3p VHL loci is shown in Figure 10.

The most frequently affected region of LOH at chromosome 9p was analysed by using 3 markers D9S169, 9p21 ; D9S165, 9p ; and IFNA, 9p21-22. Seventeen of 23 informative tumour specimens revealed LOH at one or more of these 3 markers. Patient no.46 and 50 appeared to have lost all 3 markers. Figure 10 showed the LOH of paient no.38 at D9S169 locus.

The regions of LOH on chromosome 11q were analyzed using 5 STRPs markers (D11S534, 11q13; D11S956, 11q13; D11S976, 11q23; D11S897, 11q23 ; and INT2, 11q13.3). Eight of 23 informative tumour specimens had shown LOH at one or more loci according to the 5 markers analyzed for 11q arm. Six of 23 tumour specimens showed LOH at 11q23 loci and 3 of 23 informative tumour specimens showed LOH at 11q13 locus(Figure 10). But there was no LOH at locus D11S534 in all the informative tumour specimens studied.

The LOH on chromosome 13q were observed in 8 of 21 (38%) informative cases when analyzed with two STRPs marker :D135284,13q 13RBI; D13S119, 13q. Eight tumours showed LOH at D13S284(Figure 10), while D13S119 locus did not present any LOH.

The chromosome 14q was analyzed for LOH with two STRPs markers : TCRD, 14q11.2 ; D14S118,14q. Seven of 19 (37%) informative cases showed LOH in more than one markers used. Five of 19 informative cases had shown lost of heterzygosity at the TCRD locus (Figure 10), and 4 of 19 informative cases tumours exhibited lost of heterozygosity at D14S118 locus. Frequent LOH on 20q (D20S17) was noted in 6 out of the 20 (30%) informative cases. Figure 10 presented the LOH on chromosome 20q arm.

Two of the 23 (8%) tumour specimens (no.38, 51) analyzed were characterized by microsatellite instability (MSI) which had been evidenced by the presence of allelic fragments not found in the matched normal DNA. Only tumour no. 38 showed MSI at 25 locus, while tumour no.51 had showed MSI at 1 locus (D11S956). No.38 showed both MSI and LOH at loci D3S1600 (3p), IGF2R (6q), D13S284 (13q), and D16S511 (16q). The apparence of MSI in this study is similar to that described for MSI-positive colorectal tumours (Aaltonen et al., 1993; Thibodeau et al., 1993). Figure 12 presented the feature of MSI found in the nasopharyngeal cancer DNA.

**TABLE 8 : Allelotyping results for all tumours at all loci**

| | | | | | | | | | | T | U | M | O | U | R | S | | N | O | | | | | | | | LOCUS | ARM : %LOH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Chromosome | Arm | Locus | Location | 11 | 18 | 19 | 24 | 31 | 34 | 35 | 38 | 44 | 45 | 46 | 47 | 50 | 51 | 53 | 56 | 57 | 67 | 70 | 72 | 76 | 83 | 86 | (%LOH) | (no.of LOH/no.of INF) |
| 1 | 1P | D1S243 | 1p36.1-36.2 | 0 | 0 | 0 | • | • | 0 | 0 | • | 0 | u | • | 0 | 0 | • | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 23% | **23%(5/22)** |
| | 1Q | D1S103 | 1q31-q32 | 0 | 0 | • | 0 | 0 | 0 | 0 | 0,i | 0 | 0 | 0 | 0 | u | • | 0 | u | • | 0 | 0 | 0 | 0 | 0 | 0 | 14.30% | **14.30%(3/22)** |
| 2 | 2P | D2S131 | 2p | | | 0 | | 0 | 0 | 0 | 0,i | 0 | 0 | | 0 | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0% | **0%** |
| | | D2S405 | 2p | u | 0 | | | | | | | | | 0 | | u | | | | | | | | | | | 0% | |
| | 2Q | D2S102 | 2q33-q37 | 0 | 0 | • | 0 | • | 0 | 0 | u,i | • | 0 | u | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | u | 0 | 14.30% | **14.30%(3/21)** |
| 3 | 3P | D3S1038 | 3p25VHL | u | • | u | • | • | u | • | • | • | 0 | u | 0 | 0 | 0 | • | 0 | | 0 | • | • | • | • | • | 67% | |
| | | D3S192 | 3p25VHL | u | | | | | 0 | | | | 0 | | | | 0 | • | | u | u | | | | • | • | 50% | |
| | | D3S1600 | 3p14 | | | | • | 0 | u | 0 | •,i | | 0 | • | 0 | u | 0 | 0 | u | 0 | • | 0 | 0 | 0 | | u | 29% | |
| | | D3S966 | 3p21.3 | 0 | | • | • | | 0 | | | | | | | | | | | | • | | | • | | | 67% | |
| | | D3S1480 | 3p | 0 | | u | | | | 0 | | | | | | 0 | | | u | | | | | | | | 0% | **65.20%(15/23)** |
| | | D3S1255 | 3p25VHL | 0 | | 0 | 0 | | | 0 | 0 | u | | u | 0 | | | | | 0 | • | 0 | 0 | • | | | 18% | |
| | | D3S1217 | 3p13-14 | | 0 | | | 0 | | • | | | | | | 0 | | | 0 | | | | | | | | 20% | |
| | | D3S1481 | 3p14 | | 0 | | | | | | | 0 | | | | | | | | | | | | | | | 0% | |
| | | D3S1241 | 3p21.3 | | | | | | | | | | | | | 0 | | | 0 | | | | | | | | 0% | |
| | 3Q | GLUT2 | 3q26.1-q26.2 | u | 0 | 0 | | 0 | 0 | 0 | 0,i | 0 | • | 0 | 0 | u | 0 | 0 | u | u | 0 | 0 | 0 | 0 | 0 | 0 | 6% | **4.50%(1/23)** |
| | | D3S1744 | 3q23-q24 | 0 | | | 0 | | | | | | | | | 0 | | | 0 | 0 | | | | | | | 0% | |
| 4 | 4P | D4S174 | 4p11-p15 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,i | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | u | 0 | 0 | 0% | **9%(2/23)** |
| | | D4S1599 | 4p | 0 | 0 | u | 0 | • | 0 | 0 | u,i | 0 | 0 | 0 | 0 | u | 0 | | • | 0 | u | 0 | u | 0 | | | 12.50% | |

**TABLE 8 : Allelotyping results for all tumours at all loci (continue)**

| | | | | | | | | | | T | U | M | O | U | R | S | | N | O | | | | | | | | LOCUS | ARM : %LOH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Chromosome | Arm | Locus | Location | 11 | 18 | 19 | 24 | 31 | 34 | 35 | 38 | 44 | 45 | 46 | 47 | 50 | 51 | 53 | 56 | 57 | 67 | 70 | 72 | 76 | 83 | 86 | (%LOH) | (no.of LOH/no.of INF) |
| 4 | 4Q | D4S1554 | 4q11-q35 | | u | | | 0 | 0 | 0 | u,i | 0 | 0 | | 0 | | 0 | u | 0 | 0 | 0 | 0 | 0 | u | 0 | 0 | 0% | 0% |
| | | D4S1625 | 4q | u | 0 | u | | | | | 0 | | | 0 | | u | | 0 | | | | | | 0 | | | 0% | |
| 5 | 5P | D5S392 | 5p | 0 | 0 | | | 0 | | | | 0 | u | 0 | | 0 | | | | 0 | 0 | | | • | 0 | 0 | 9.10% | 10%(2/21) |
| | | D5S819 | 5p | u | u | 0 | | • | 0 | 0 | 0 | u | u | | 0 | | 0 | 0 | 0 | u | u | 0 | 0 | u | | u | 9.10% | |
| | 5Q | D5S82 | 5q14-21 | • | 0 | 0 | u | • | 0 | 0 | 0 | 0 | u | 0 | u | u | u | 0 | 0 | 0 | • | 0 | 0 | 0 | 0 | 0 | 18% | 15%(3/20) |
| | | D5S346 | 5q21-q22 | | 0 | | u | 0 | 0 | 0 | 0,i | | 0 | | | 0 | u | | 0 | 0 | | | 0 | 0 | | 0 | 0% | |
| 6 | 6P | D6S309 | 6p | • | 0 | 0 | • | 0 | 0 | u | u,i | • | 0 | 0 | 0 | 0 | • | u | 0 | u | u | 0 | u | 0 | u | u | 27% | 27.30%(6/22) |
| | | D6S477 | 6p | • | 0 | 0 | | u | 0 | u | 0 | • | 0 | 0 | 0 | u | u | 0 | 0 | 0 | • | 0 | 0 | 0 | 0 | • | 22% | |
| | 6Q | IGF2R | 6q27 | u | 0 | u | u | 0 | u | u | •,i | 0 | u | | 0 | | 0 | | 0 | 0 | | | u | u | | | 13% | |
| | | D6S503 | 6q | 0 | | u | | | 0 | 0 | | | 0 | u | | u | | u | | | 0 | 0 | u | u | u | 0 | 0% | 5%(1/20) |
| | | D6S292 | 6q | | | 0 | | | | | | | | | | 0 | | 0 | | | | | 0 | 0 | | | 0% | |
| 7 | 7P | D7S517 | 7p | 0 | • | 0 | 0 | 0 | 0 | 0 | • | • | 0 | 0 | 0 | 0 | 0 | • | 0 | 0 | 0 | u | 0 | 0 | 0 | u | 19% | 18%(4/22) |
| | | D7S460 | 7p | | | | | | | | | | | 0 | | | | | | | | 0 | | | 0 | | 0% | |
| | 7Q | D7S486 | 7q31 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | • | 0 | 0 | 0 | 0 | 0 | u | u | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 5.30% | 4.35%(1/23) |
| | | D7S821 | 7q | | | | | | | | | | | 0 | | | | 0 | 0 | | | | | | 0 | | 0% | |
| 8 | 8P | NEFL | 8p | u | u | 0 | u | 0 | 0 | u | 0 | 0 | 0 | 0 | 0 | u | u | 0 | 0 | 0 | u | 0 | 0 | 0 | | u | 0% | |
| | | D8S87 | 8p21.3-p22 | 0 | 0 | | | | | 0 | | | | | | 0 | u | | | | u | | | | 0 | u | 0% | 0% |
| | | D8S110 | 8p | 0 | | | | | | | | | | | | | 0 | | | | 0 | | | | | u | 0% | |

**TABLE 8 : Allelotyping results for all tumours at all loci (continue)**

| | | | | | | | | | | T | U | M | O | U | R | S | | N | O | | | | | | | | LOCUS | ARM : %LOH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Chromosome | Arm | Locus | Location | 11 | 18 | 19 | 24 | 31 | 34 | 35 | 38 | 44 | 45 | 46 | 47 | 50 | 51 | 53 | 56 | 57 | 67 | 70 | 72 | 76 | 83 | 86 | (%LOH) | (no.of LOH/no.of INF) |
| 8 | 8Q | D8S88 | 8q22 | 0 | 0 | • | 0 | 0 | 0 | 0 | 0,i | 0 | 0 | 0 | u | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | u | 0 | 5% | 5%(1/21) |
| | | MCC | 8q24 | u | | u | | | | u | 0 | u | | 0 | u | | | | | | | | | | | | 0% | |
| 9 | 9P | D9S169 | 9p21 | • | • | • | • | • | 0 | u | • | • | u | • | • | • | 0 | • | u | 0 | | u | • | u | | | 80% | |
| | | D9S165 | 9p | | | | | | | | | | | • | | • | 0 | u | 0 | | | | | | u | • | 60% | 77%(17/22) |
| | | IFNA | 9p22 | | | | | | 0 | 0 | | | • | • | u | • | 0 | • | • | 0 | • | u | u | • | 0 | u | 54% | |
| | 9Q | D9S51 | 9q | 0 | 0 | 0 | 0 | u | | u | u,i | 0 | 0 | 0 | • | u | 0 | | u | 0 | 0 | | u | u | 0 | 0 | 8% | |
| | | D9S290 | 9q34 | | | | | | u | 0 | | | | | | 0 | | u | 0 | | | 0 | u | 0 | 0 | | 0% | 5%(1/20) |
| | | ABL1 | 9q34 | | | | | u | 0 | | u | | | | | u | | 0 | u | | | u | u | u | u | 0 | 0% | |
| 10 | 10P | D10S89 | 10p11.2-pter | 0 | | | | 0 | | | | 0 | 0 | 0 | 0 | 0 | | | | | | | | 0 | | | 0% | 0% |
| | | D10S249 | 10p | | 0 | 0 | | 0 | u | 0 | 0 | u | u | | u | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 | | 0% | |
| | 10Q | D10S169 | 10q11.2-qter | u | 0 | 0 | u | u | 0 | u | 0,i | 0 | u | u | 0 | 0 | u | u | u | u | 0 | u | 0 | u | 0 | • | 9% | 5%(1/22) |
| | | D10S677 | 10q | 0 | | | | 0 | | 0 | | | 0 | 0 | | | 0 | 0 | 0 | 0 | | 0 | | 0 | | | 0% | |
| 11 | 11P | WT1 | 11p13 | u | u | 0 | | 0 | 0 | 0 | u | u | 0 | u | 0 | u | 0 | 0 | 0 | u | 0 | 0 | 0 | u | | 0 | 0% | 9%(1/22) |
| | | D11S554 | 11p | 0 | 0 | | | | | | • | 0 | 0 | 0 | | 0 | | | | 0 | | | | 0 | 0 | | 20% | |
| | 11Q | D11S534 | 11q13 | u | 0 | | | 0 | 0 | 0 | 0 | 0 | 0 | | u | u | 0 | u | 0 | 0 | u | u | 0 | 0 | 0 | 0 | 0% | |
| | | D11S956 | 11q13 | u | 0 | u | u | | 0 | 0 | | | 0 | 0 | 0 | 0 | 0,i | • | | | u | 0 | 0 | 0 | | 0 | 15.40% | |
| | | D11S976 | 11q23 | | | | | | | • | • | | | | | | | u | | 0 | | | | | | 0 | 66.66% | 36.4%(8/23) |

**TABLE 8 : Allelotyping results for all tumours at all loci (continue)**

| | | | | | | | | | | T | U | M | O | U | R | S | | N | O | | | | | | | | LOCUS | ARM : %LOH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Chromosome | Arm | Locus | Location | 11 | 18 | 19 | 24 | 31 | 34 | 35 | 38 | 44 | 45 | 46 | 47 | 50 | 51 | 53 | 56 | 57 | 67 | 70 | 72 | 76 | 83 | 86 | (%LOH) | (no.of LOH/no.of INF) |
| 11 | 11Q | D11S897 | 11q23 | 0 | 0 | 0 | 0 | • | 0 | u | | • | u | u | 0 | u | 0 | u | • | u | • | 0 | 0 | 0 | 0 | 0 | 24% | |
| | | INT2 | 11q13.3 | 0 | | 0 | | • | | u | | 0 | | | | | | | 0 | u | | | | | | | 20% | |
| 12 | 12P | D12S341 | 12p | 0 | 0 | 0 | 0 | 0 | 0 | 0 | • | u | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | u | | 0 | | 0 | 5.00% | **5%(1/23)** |
| | | D12S62 | 12p | | | | | | | | | 0 | | | | | | | | | | 0 | 0 | | 0 | | 0% | |
| | 12Q | MFD133 | 12q | u | 0 | u | 0 | 0 | 0 | 0 | 0,i | • | u | 0 | u | • | 0 | u | • | 0 | 0 | 0 | u | 0 | 0 | 0 | 18% | **13%(3/23)** |
| | | D12S86 | 12q | | | 0 | | | | | | | 0 | | 0 | | | 0 | | | | | 0 | | | | 0% | |
| 13 | 13Q | D13S284 | 13qRBI | • | u | • | • | 0 | 0 | 0 | •,i | 0 | 0 | 0 | u | 0 | • | • | • | 0 | • | 0 | 0 | 0 | 0 | 0 | 38% | **38%(8/21)** |
| | | D13S119 | 13q | 0 | u | 0 | | 0 | 0 | | 0 | 0 | | 0 | u | | 0 | 0 | 0 | 0 | 0 | | 0 | 0 | 0 | 0 | 0% | |
| 14 | 14Q | TCRD | 14q11.2 | 0 | u | u | u | • | u | u | u | u | u | 0 | 0 | • | 0 | 0 | • | 0 | • | u | 0 | 0 | 0 | • | 36% | **37%(7/19)** |
| | | D14S118 | 14q | 0 | • | u | | 0 | 0 | 0 | u | • | u | 0 | 0 | u | 0 | u | u | u | u | 0 | 0 | u | 0 | 0 | 15% | |
| 15 | 15Q | GABRB3 | 15q11-13 | 0 | 0 | 0 | | u | u | 0 | u,i | u | 0 | u | 0 | 0 | u | 0 | 0 | • | u | 0 | 0 | 0 | 0 | 0 | 7% | |
| | | D15S131 | 15q | | | | | 0 | 0 | | | 0 | | 0 | | | 0 | | | | 0 | | | | | | 0% | **5%(1/22)** |
| | | D15S123 | 15q | | | | | 0 | u | | | 0 | | 0 | | | 0 | | | | 0 | | | | | | 0% | |
| 16 | 16P | D16S287 | 16p13.11 | 0 | u | 0 | 0 | • | 0 | 0 | 0 | 0 | 0 | 0 | 0 | • | 0 | u | 0 | 0 | u | 0 | u | u | 0 | 0 | 11.11% | **10%(2/21)** |
| | | D16S748 | 16p13.2-13.13 | | u | | | | | | | | | | | | | u | | | 0 | | 0 | 0 | | | 0% | |
| | 16Q | D16S511 | 16q22-24 | 0 | 0 | 0 | 0 | u | 0 | 0 | •,i | • | u | 0 | u | 0 | 0 | u | 0 | 0 | 0 | 0 | 0 | 0 | u | 0 | 11.11% | **11%(2/19)** |
| | | D16S539 | 16q24.2-q24.3 | | | | | u | | | | | u | | u | | | 0 | | | | | | | | | 0% | |

**TABLE 8 : Allelotyping results for all tumours at all loci (continue)**

| | | | | | | | | | | T | U | M | O | U | R | S | | N | O | | | | | | | | LOCUS | ARM : %LOH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Chromosome | Arm | Locus | Location | 11 | 18 | 19 | 24 | 31 | 34 | 35 | 38 | 44 | 45 | 46 | 47 | 50 | 51 | 53 | 56 | 57 | 67 | 70 | 72 | 76 | 83 | 86 | (%LOH) | (no.of LOH/no.of INF) |
| 17 | 17P | D17S520 | 17p12 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | u | 0 | • | 0 | u | 0 | 0 | 0 | 0 | 0 | u | 0 | 0 | 0 | u | u | 6% | |
| | | D17S945 | 17p13 | | | | | | | | 0,i | | | | | 0 | | | | 0 | | | | | | | 0% | 22%(5/23) |
| | | D17S1176 | 17p | • | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | • | 0 | 0 | 0 | 0 | • | • | 0 | • | 0 | 0 | 0 | 0 | 0 | 22% | |
| | 17Q | KRT9 | 17q21NME1 | • | u | 0 | 0 | 0 | u | 0 | u,i | 0 | 0 | 0 | 0 | 0 | 0 | 0 | u | 0 | u | 0 | 0 | 0 | | u | 6.30% | 5%(1/22) |
| | | NFI | 17q11.2 | | u | | | | 0 | | 0 | | | | | | | | 0 | | 0 | | | | 0 | 0 | 0% | |
| 18 | 18P | D18S59 | 18pter-p11.22 | u | 0 | u | 0 | 0 | 0 | 0 | 0 | • | 0 | 0 | • | 0 | 0 | u | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 10% | 10%(2/20) |
| | 18Q | D18S35 | 18q21.2-q21.3 | u | u | 0 | u | 0 | 0 | 0 | • | 0 | 0 | 0 | 0 | u | 0 | | u | u | u | 0 | u | 0 | | 0 | 8% | |
| | | DCC | 18q21.1 | u | 0 | u | | 0 | 0 | 0 | 0,i | u | 0 | | 0 | • | 0 | 0 | 0 | 0 | u | 0 | u | | | 0 | 7% | 10%(2/21) |
| | | D18S535 | 18q | 0 | | | | | | | | | | | | | | | | | 0 | | 0 | | u | | 0% | |
| 19 | 19P | D19S221 | 19p | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0,i | • | 0 | 0 | 0 | 0 | 0 | • | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 9% | 9%(2/23) |
| | 19Q | D19S412 | 19q | u | 0 | 0 | | u | 0 | 0 | 0,i | 0 | u | 0 | 0 | u | u | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | 0 | 0% | 0% |
| | | D19S246 | 19q | u | | | | 0 | | | | | u | | | 0 | 0 | | | | | | | | 0 | | 0% | |
| 20 | 20P | D20S470 | 20p | 0 | 0 | 0 | | 0 | u | u | 0,i | 0 | 0 | 0 | | | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0% | 0% |
| | | D20S27 | 20p12 | | | | | | u | 0 | | | | | 0 | u | | | | | | | | | | | 0% | |
| | 20Q | D20S17 | 20q12-q13.1 | 0 | 0 | u | • | 0 | 0 | 0 | 0 | • | • | u | 0 | • | 0 | 0 | 0 | • | • | 0 | 0 | u | 0 | 0 | 30% | 30%(6/20) |
| 21 | 21Q | D21S258 | 21q | u | u | u | u | 0 | 0 | 0 | 0 | 0 | 0 | u | 0 | 0 | 0 | | 0 | 0 | 0 | u | u | 0 | 0 | 0 | 0% | 0% |
| | | D21S11 | 21q21 | 0 | 0 | 0 | | | | | | | | 0 | | | | 0 | | | | u | 0 | | | | 0% | |

**TABLE 8 : Allelotyping results for all tumours at all loci (continue)**

| | | | | | | | | | | T | U | M | O | U | R | S | | N | O | | | | | | | | LOCUS | ARM : %LOH |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Chromosome | Arm | Locus | Location | 11 | 18 | 19 | 24 | 31 | 34 | 35 | 38 | 44 | 45 | 46 | 47 | 50 | 51 | 53 | 56 | 57 | 67 | 70 | 72 | 76 | 83 | 86 | (%LOH) | (no.of LOH/no.of INF) |
| 22 | 22Q | D22S446 | 22q11NF2 | 0 | | 0 | | • | 0 | | | | | | | | u | 0 | u | | u | | u | | 0 | 0 | 25% | 18%(3/18) |
| | | IL2RB | 22q | u | 0 | | | u | • | 0 | 0,i | 0 | 0 | 0 | 0 | 0 | u | u | u | 0 | u | 0 | u | 0 | u | u | 15.40% | |

**NOTE**

• ; Loss of heterozygosity
0 ; Retaintion of heterozygosity
u ; Uninformative
i ; Microsatellite instability
blank ; Failed or no detect

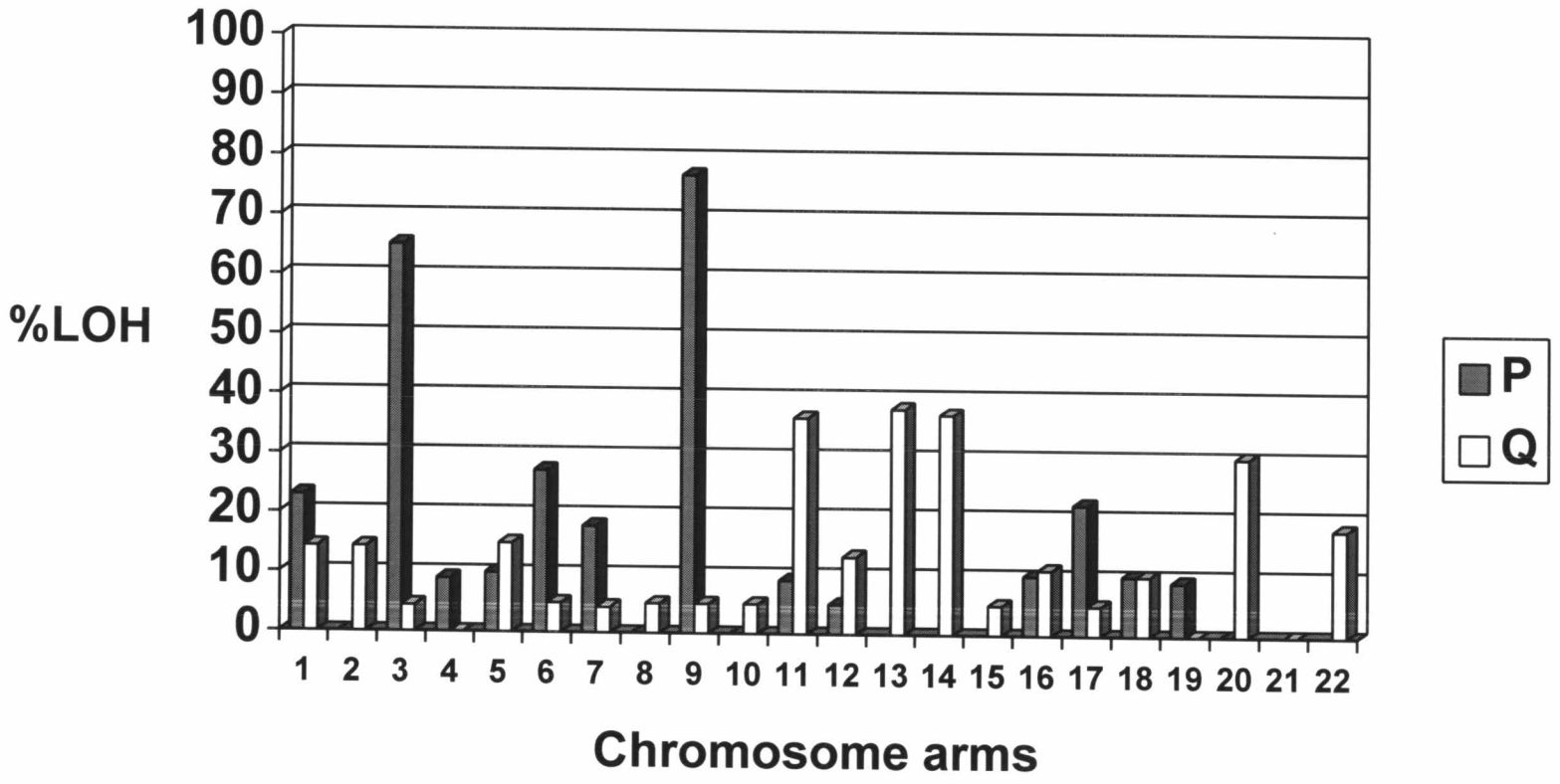


**Figure 9** : Percentage of loss of heterozygosity on individual chromosome arms

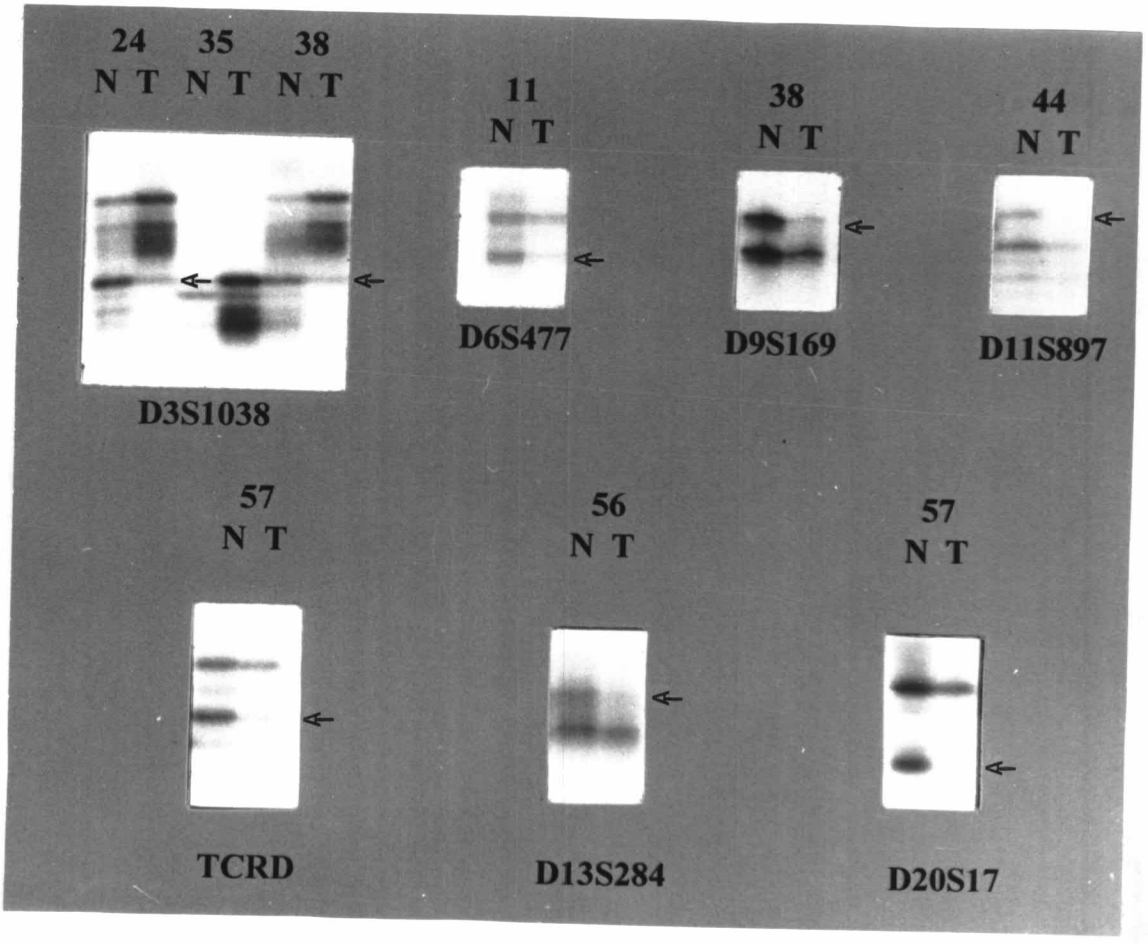


**Figure 10 :** Autoradiographs of PCR products separated by polyacryamide gel eletrophoresis, showing examples of LOH in tumour specimens N, normal lymphocyte DNA; T, tumour DNA; ➡, loss of heterozygosity.

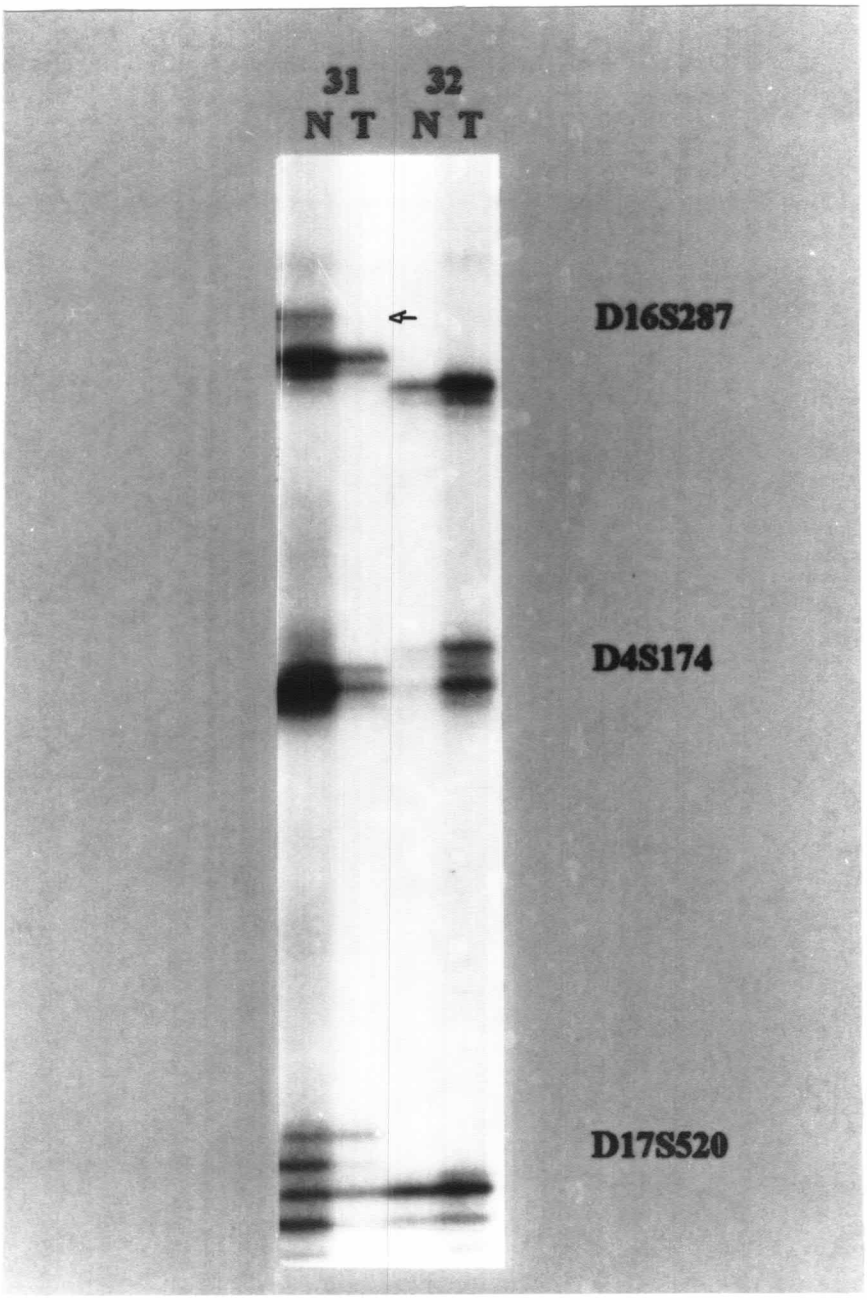


**Figure 11 :** An example of multiplex PCR at loci D4S174, D16S287, D17S520 in tumour no.31, 32. N, normal lymphocyte DNA; T, tumour DNA; ➡, loss of heterozygosity (LOH). In tumour no. 31 showed LOH at locus D16S287.

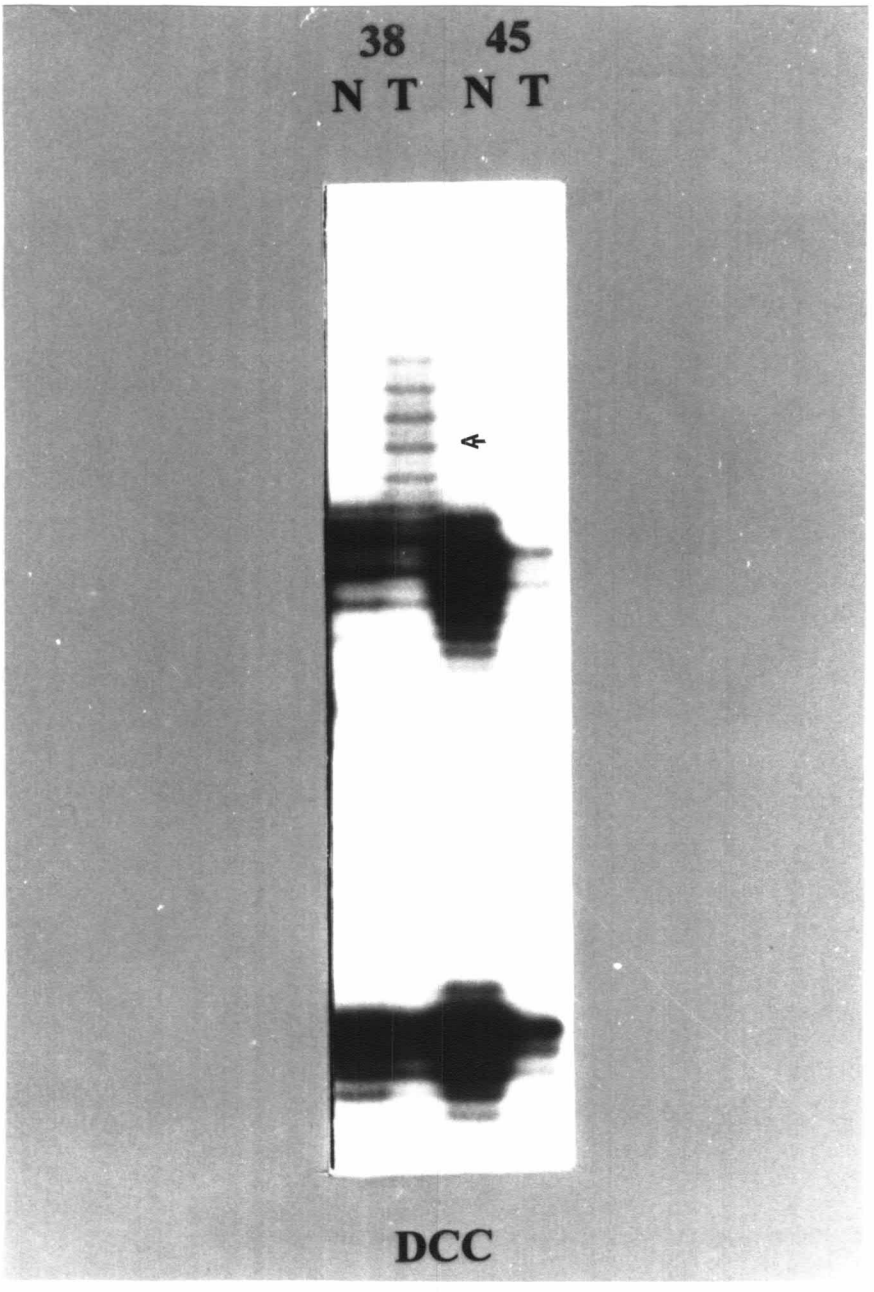


**Figure 12 :** Microsatellite instability (MSI) observed in tumour no.38 at DCC locus. N, normal lymphocyte DNA; T, tumour DNA; ➡, MSI.