I and S1 nuclease digestions and the subsequent ligation, had a 0.85-kb deletion and had lost all five restriction sites in the region from the Sac I site at 0.75 kb to the Bal I site at 1.55 kb of the linear DNA, the deletion of pSc2 was suggested to include the region from 0.75 kb to 1.6 kb of the linear DNA.

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Familial Renal Cell Carcinoma with a 3;11 Chromosome Translocation Limited to Tumor Cells

Abstract. *Cytogenetic studies were performed on the direct chromosome preparations of the renal cell carcinoma cells and the cultured peripheral blood lymphocytes of a patient with familial renal cell carcinoma. The results revealed a specific, acquired translocation (3p;11p) present in the majority of metaphases of the tumor, indicating that the development of renal cell carcinoma is associated with a deletion in the proximal end of 3p. Renal cell carcinoma is thus the third example—the first two being retinoblastoma and Wilms' tumor—of a chromosomal deletion occurring germinally or somatically in association with a specific tumor. This finding adds further support to the existence of specific human cancer genes.*

Nonrandom, tumor-specific chromosomal abnormalities have been observed in cells of many types of human tumors. At least for retinoblastoma and Wilms' tumor, chromosomal abnormalities have been observed to be both heritable and predisposing to the tumors and have been identified as tumor-specific, acquired abnormalities in tumors from persons with normal constitutional karyotypes (*1–4*). Recently, a heritable, balanced 3;8 chromosomal translocation was reported in association with familial renal cell carcinoma (RCC) (*5*). We now report a balanced 3;11 translocation in tumor cells from a patient with a normal constitutional karyotype and familial RCC.

The patient, a 32-year-old white man, was referred to the University of Texas M. D. Anderson Hospital and Tumor Institute at Houston after the diagnosis of a left papillary renal cell adenocarcinoma with extensive regional lymph node metastases. Peripheral blood was collected from the patient before chemotherapy for karyotyping and biochemical genetic markers; peripheral blood was also collected from family members. Ascitic fluid with cytologically confirmed malignant cells was obtained from the patient and processed immediately for cytological preparations (*6*). The familial occurrence of RCC over three generations was confirmed through death certificates and medical records (Fig. 1).

Of 50 metaphases, 30 showed a stemline number of 54 chromosomes. A minor peak (eight cells) occurred at 52 chromosomes. A total of 30 G-banded metaphases were analyzed for the identification of altered chromosomes. A typical G-banded karyotype of the major stem-line metaphase is shown in Fig. 2A. Among the G-banded cells, two cell lines were identified: in 22 cells (73.3 percent), a translocation involving 3p and the entire No. 11 chromosome was present, but in the other eight cells, chromosomes 3 and 11 were both normal. Four marker chromosomes were identified in the majority of metaphases of the major stemline. Putative identification of each of the marker chromosomes follows. M_1, an acrocentric, was similar in length to a D-group chromosome; the G-banding pattern identified this as the long arm of a chromosome 3. M_2 was a large, submetacentric chromosome the size of a normal chromosome 2; the G-banding pattern indicated that this marker was made of an entire chromosome 11, the distal end of whose p arm was translocated to 3p. This marker was also present in all 22 cells with a 3;11 translocation. Although M_2 sometimes exhibits the morphology of a dicentric chromosome, its C-banding pattern reveals only one centromeric region. M_2 was invariably accompanied by M_1. In cells with a 3;11 translocation only one normal chromosome 3 and one normal chromosome 11 were present. M_3 was the largest acrocentric chromosome in the complement. The proximal end, including the centromeric region, was similar to that of a chromosome 14, whereas the distal part was similar to that of a chromosome 2q in the G-banding pattern. This marker was also present in the majority of cells analyzed. M_4 was a small, metacentric chromosome present in the majority of the cells. It appeared to be an isochromosome of 5p. It was the only marker chromosome that was also present in the other eight G-banded metaphases in which other markers (M_1, M_2, and M_3) were absent.

A number of other altered chromosomes with minor rearrangements are shown paired with their normal homologs in Fig. 2A. For example, one chromosome 1 had a deletion in the distal segment of its q arm. Also, one chromosome 7 had added chromatin in its short arm. The minor hyperdiploid stem line had only the M_4 marker and normal chromosomes 3 and 11. Apparently M_4 was present before the translocation between 3p and 11p took place. Presence of M_4 might have been advantageous for the selection in vivo of the stem line with a 3p;11p translocation.

A diagrammatic sketch of the forma-

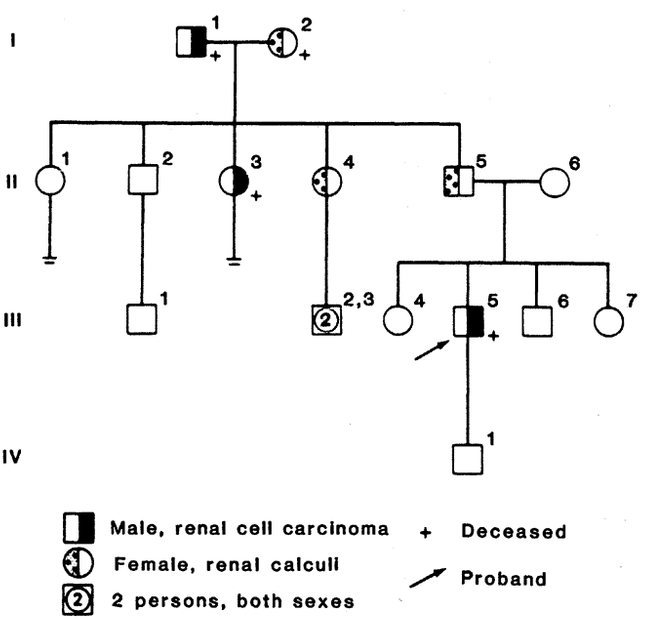

Fig. 1. Pedigree of the family members by clinical phenotype and karyotype.

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tion of M_1 and M_2 chromosomes is shown in Fig. 2B. Apparently a break took place in the proximal end of 3p (probably in the region of 3p13 or 4) and in the terminal end of 11p (11p15). The 3q, with its centromere intact, formed the M_1, and the acentric piece of 3p was translocated to the end of 11p, which gave rise to marker M_2. Whether the terminal broken piece of 11p was translocated with the M_1 marker was difficult to determine because the G-banding pattern of the tumor cells was substandard. Cultured lymphocytes of the proband and his relatives showed normal chromosome constitutions.

Familial RCC is relatively rare, but reports suggest that the characteristics of familial RCC include an early average age at diagnosis and frequent multiple primary or bilateral RCC tumors (*5, 7*), characteristics similar to those of heritable retinoblastoma, Wilms' tumor, colon cancer, and breast cancer (*8*). The suspicion that some percentage of RCC might be heritable was strengthened by a report by Cohen *et al.* (*5*), in which RCC was consistently associated with a heritable 3;8 chromosome rearrangement in seven individuals spanning three generations. This observation suggests that a putative RCC gene might be located on chromosome 3 or 8 and might be deleted or altered in function by the chromosomal rearrangement. Most familial RCC patients, however, show no constitutional chromosomal abnormality (*5*). No data have been previously available on the RCC karyotypes.

Our observation of 3p rearrangement in RCC may be important evidence for the location of a "cancer gene" related to RCC on 3p, since the same chromosomal segment was involved in a family in which this tumor was correlated with a constitutional chromosome rearrangement (*5*). Retinoblastoma and Wilms' tumor have also been associated with specific heritable or acquired chromosomal anomalies, namely, deletion of 13q14 and 11p13, respectively (*1–4*). The location of the apparent autosomal dominant heritable retinoblastoma may be in the same 13q14 region, and as in individuals with familial retinoblastoma with normal chromosomes, the predisposing gene seems to be closely linked to the 13q14 marker esterase D (*9*). In our study of the relation between 3p and RCC, no polymorphic gene markers for the 3p region were available.

If the relation of the 3p region and RCC is analogous to that of the 13q14 region and retinoblastoma, then the 3p region may be rearranged as a heritable event predisposing to RCC, as in the family reported by Cohen *et al.* (*5*); or it may be associated with some other heritable predisposing factor, with the rearrangement acquired during tumor development. The breakpoints of the 3p region observed in the tumor cells of the patient in our study (3p13 or 3p14) and those of the previously reported familial rearrangement (3p21) are different. A terminal deletion of 3p is also reported in small-cell lung cancers (*10*). Although we suspect that some common genetic region related to RCC may be affected by the rearrangements, the involvement of 3p in both RCC and small-cell lung cancer may be fortuitous. Polymorphic markers for the 3p region for linkage studies of familial RCC and karyotyping of other cases of RCC are needed.

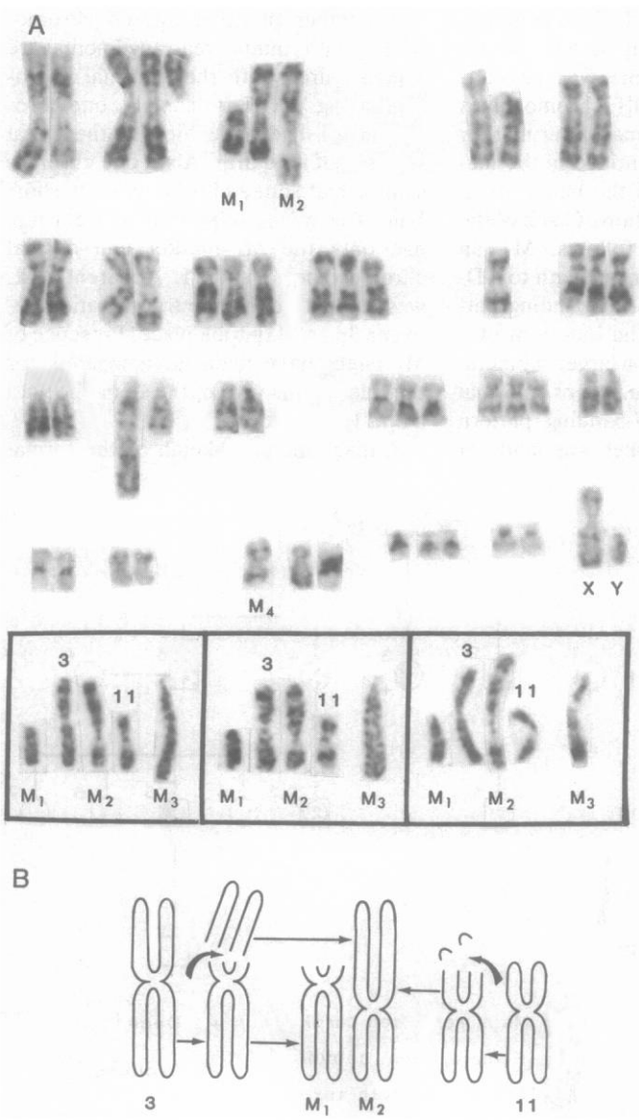

Fig. 2. (A) G-banded karyotype of a cell from renal cell carcinoma (BF-22). The four marker chromosomes (M_1, M_2, M_3, and M_4) are present. Two unidentified abnormal chromosomes are arranged by the side of M_4. (Inset) Markers M_1, M_2, M_3, and normal chromosomes 3 and 11 from three additional tumor cells. (B) Diagrammatic representation of chromosomes 3 and 11 and the formation of M_1 and M_2 markers. A break in the proximal region of 3p and in the extreme distal end of the short arm of No. 11 is marked by thick, curved arrows. M_1 represents the long arm plus the centromere with a small piece of 3p. M_2 comprises almost the entire No. 11 with a translocation of the 3p to its short arm.

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Endomycorrhizal Role for Interspecific Transfer of Phosphorus in a Community of Annual Plants

Abstract. *Phosphorus-32 applied to leaves of* Plantago erecta *in a serpentine annual grassland reached the shoots of about 20 percent of the close neighbors. Vesicular-arbuscular mycorrhizae connect the root systems of neighbors of different species and probably mediate nutrient transfers among them. Spatial patterns of transfer show that taxonomic affinity, distance from donor, and size of recipient do not serve as predictors of transfer and that models of transfer by simple diffusion are not appropriate. No alternative predictor was discovered. The results underscore the importance of belowground interactions in explaining neighbor effects, but the factors controlling nutrient transfer and its consequences for community structure appear complex.*

Despite advances in population and community ecology, little is known about the controls on production or fitness within natural populations and communities of interacting plants. In some cases, simple models of neighbor interactions based on spatial pattern have predicted production patterns rather precisely, but not all attempts to apply simple models have been so effective (*1*). To date, interactions of root systems have been ignored in studies of local controls on production in natural plant communities, even though such interactions are known to affect both growth and long-term community dynamics (*2, 3*). We report experiments performed to assess the potential role of interconnections among herbaceous plants made by mycorrhizae in shaping community structure and spatial patterns of community production.

Vesicular-arbuscular mycorrhizae are symbioses formed between fungi of the Endogonaceae and plant roots. These mycorrhizae are ubiquitous, develop best under conditions of low soil fertility (particularly low phosphorus), and generally enhance nutrient uptake by the host plant (*4*), though they may be detrimental to young hosts (*5*). Because susceptibility to colonization varies among plant taxa (*6*) and with plant life history (*2, 5, 7*), the effects of vesicular-arbuscular mycorrhizae on the nutrient economy of individual plants may structure growth relations and competitive interactions within a plant community. In addition, mycorrhizal plants may participate in a direct form of interaction that is not available to nonmycorrhizal plants. In pot culture, mycorrhizal formation may alter the balance of competition (*8*). Furthermore, a single vesicular-arbuscular fungal hypha can colonize two neighboring plants of the same or different species (*9*), facilitating movement of nutrients from one plant to another (*10, 11*).

By understanding the dynamics of nutrient transfer among plants that are functionally connected (*11*) by mycorrhizal hyphae, we may be able to predict some of the consequences of mycorrhizae for the structure of a plant community. We examined two aspects of a community having abundant vesicular-arbuscular mycorrhizae: the formation of interplant hyphal connections, and patterns of ^{32}P transfer among plants in the field. We tested the observed patterns of ^{32}P transfer against three possible predictors of nutrient exchange.

The community we examined is a California serpentine grassland dominated by small annual plants (mean density about 1×10^4 m^{-2}). Serpentine soils are characteristically low in most nutrients, including phosphorus (*12*). In preliminary harvests, all species from plant families that typically form mycorrhizae were colonized at the seedling stage by fungi of the genus *Glomus*.

To assess whether the root systems of plants from this grassland may be interconnected by fungal hyphae, a pot experiment was undertaken, and the buried slide technique was used (*13*). Agar-coat-

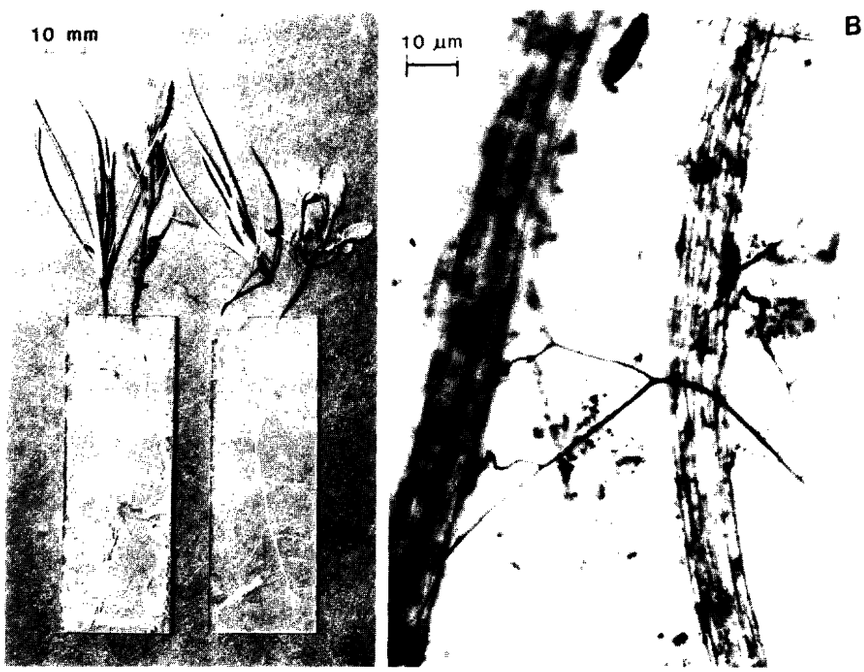

Fig. 1. Roots and mycelium on buried slides. (A) Freshly harvested slides with *Plantago erecta* (left plant on each slide) and *Clarkia rubicunda* (right). (B) At the right, a hypha branches and the right branch enters a *Clarkia* root. The left branch enters a *Plantago* root in several places.

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