1975 the summer mortality of similarly age-structured 2- and 3-year-old *Macrocystis* plants located at the main study site in the center of the forest (*5*) was 14 percent (N = 128) and 9 percent (N = 45), respectively. In 1982, summer mortality of the 2-year-old plants was 2 percent (N = 52); and during the El Niño of 1983, summer mortality of the normally robust 3-year-old plants was 59 percent (N = 27) (*7*). In other areas of the kelp forest, mortality of adult plants in 400-m^2 transects between April and November 1983 ranged from 22 percent at the northern edge, 20 percent at the southern edge, and 58 percent in the central part of the forest to 61 percent at the outer and 67 percent at the inner edge of the forest. The northern and southern edges of the forest face into long shore currents, where they may be exposed to water which has not been scrubbed of nutrients by other plants. By late summer, few plants had healthy upper fronds and most plants had lost their fronds altogether. Immediately after the winter storms there was a strong recruitment of *Macrocystis* in all but the south portion of the Point Loma kelp forest. By May 1983 we observed hundreds of *Macrocystis* per square meter in patches along the transect lines not already dominated by understory algae. However, there was also a heavy recruitment of understory algae, especially *Pterygophora* and *Laminaria*, in most areas and unusually large areas of 100 percent cover of two annuals, *Dictyopteris undulata* in deeper water and *Desmarestia ligulata* in shallow water. Thus there was a scramble competition during the spring and early summer which, under "normal" conditions of light and nutrients, *Macrocystis* would have won easily (*5*).

The massive spring recruitment of *Macrocystis* during the El Niño summer had virtually no survivors, partly because of the heavy understory canopies which are known to interfere with giant kelp recruitment in this area (*5*). Those *Macrocystis* that had escaped the understory invasion grew slowly and were discolored and often diseased, and by September the fronds in many areas had died 2 to 3 m above the bottom; this was especially pronounced in the shallow area. Recruitment was first observed in April at this site, but by September the mean plant size was only 137 cm (standard deviation = 61 cm; N = 60), poor growth for a species that can grow as much as 5 to 15 cm/day under optimal conditions (*17*).

Wind and minor storms in November 1983 accompanying the slow deterioration of the El Niño have resulted in a drop in water temperature (Fig. 1). At this point there were scattered young *Macrocystis* plants ranging from 1 to 10 m in height; these plants may survive, but dense canopies of understories were also present. Isolated *Macrocystis* plants do not survive well because they are subject to relatively heavy encrustation by invertebrates that settle on the fronds and to fish grazing (*4, 18*). If most survive to reproduce, they are sufficiently dominant to slowly displace the understory algae which have become entrenched; but the resistance of these understory patches of perennial algae (*5*) can make this a long process. However, two sites were dominated by understories of annual algae which also could have inhibited successful recruitment of perennial understories. These canopies are now breaking up, and if the few remaining young *Macrocystis* survive, these areas may yet have scramble competition favoring *Macrocystis*.

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Primary Structure of v-*raf*: Relatedness to the *src* Family of Oncogenes

Abstract. *A replication-defective, acute transforming retrovirus (murine sarcoma virus 3611) was isolated from mouse and molecularly cloned. The nucleotide sequence of 1.5 kilobases encompassing the transforming gene (v-*raf*) was determined. This sequence, which predicts the amino acid sequence of a* gag-raf *fusion protein, terminates 180 nucleotides from the 3′ end of the acquired cellular sequence. Comparison of the predicted amino acid sequence of v-*raf *with the predicted amino acid sequences of other oncogenes reveals significant homologies to the* src *family of oncogenes. There is a lack of homology within the sequence of the tyrosine acceptor domain described for the phosphotyrosine kinase members of the* src *family of transforming proteins. Phylogenetic arrangement of this family of oncogenes suggests that tyrosine-specific phosphorylation may be a recently acquired activity.*

Viral oncogenes are derived from cellular genes (proto-oncogenes) (*1*) that endow the virus with the capacity to transform cells in vitro and induce rapid tumors in vivo. The proto-oncogenes are generally single-copy sequences and are highly conserved in evolution. Viral oncogenes may be functionally grouped into those that code for a tyrosine-specific protein kinase and those that are negative for this activity. The protein kinase–negative oncogenes fall into several functional categories: v-*sis* (*2*) is derived from a growth factor; v-*myc* (*3*) and v-*myb* (*4*) encode DNA-binding proteins; v-*mil* (*4*) encodes an RNA-binding protein; and Ha-*ras* (*5*) and Ki-*ras* encode guanosine nucleotide–binding proteins. Although their physiological significance is still unclear, proto-oncogenes have been directly implicated in the development of certain human tumors because their positions are adjacent to breakpoints in tumor-specific chromosomal translocations (*6*).

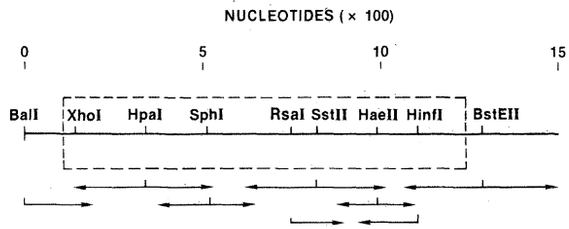
We have isolated and molecularly

cloned a replication-defective, oncogene-transducing retrovirus, murine sarcoma virus 3611 (3611-MSV) (*7*). The oncogene of 3611-MSV, v-*raf*, has homologs in eukaryotes, including cells from yeast, *Drosophila* (*8*), birds (*7*), and man (*7*). Cells transformed by 3611-MSV contain two *gag-raf* fusion proteins, P75 and P90, which represent modifications of the same core protein. Tyrosine-specific protein kinase activity has not been shown in these transformed cells (*9*). Two v-*raf* homologs are present in man—a functional gene (c-*raf*-1) on chromosome 3 and a pseudogene (c-*raf*-2) on chromosome 4 (*10*). Although v-*raf*-specific RNA has been detected in small cell lung carcinomas (which exhibit alterations in chromosome 3), it has not been found in normal human bronchial epithelial cells (*8*).

No relation between the v-*raf* oncogene and previously isolated retroviral oncogenes is observed on nucleic acid hybridization. To assess the possibility of a distant relationship between this gene and other oncogenes, we determined the nucleic acid sequence of v-*raf*. Comparison of the predicted amino acid sequence of v-*raf* with that of other oncogenes revealed significant homologies throughout the v-*raf* sequence and the oncogene family that includes v-*src* (*11*), v-*yes* (*12*), v-*abl* (*13*), v-*fps* (*14*), v-*fes* (*15*), v-*ros* (*16*), v-*erb B* (*17*), v-*fms* (*18*), and v-*mos* (*19*).

The restriction map of 3611-MSV DNA and the strategy of sequencing are shown in Fig. 1A. The 1514-base-pair (bp) nucleotide sequence of v-*raf* and adjacent viral *gag* (p30) and polymerase gene domains is shown in Fig. 1B. Examination reveals no sequences characteristic of promoter or splice acceptor regions, nor a polyadenylation signal. This is consistent with the expression of v-*raf* as a *gag-x* polyprotein that depends on the virus for transcriptional and translational controls. The single open reading frame translating the *gag-raf* gene is terminated by an amber codon approxi-

A



B

```
   A  K  V     K  G  I     T  Q  G     P  N  E  S     P  S  A     F  L  E     R  L  K  E     A  Y  R     R  Y  T     P  Y  D  P
TGGCCAAGGT  AAAAGGAATA  ACACAAGGGC  CCAATGAGTC  TCCCTCGGCC  TTCCTAGAGA  GACTTAAGGA  AGCCTATCGC  AGGTACACTC  CTTATGACCC   100
BalI
   G  T  Q     E  K  N     K  I  R  P     R  G  Q     R  D  S     S  Y  Y  W     K  M  E     A  S  E     V  M  L  S     T  R  I
TGGGACCCAG  GAAAAAAACA  AAATTAGGCC  TCGTGGGCAG  AGAGACTCGA  GTTATTACTG  GAAAATGGAA  GCCAGTGAGG  TGATGCTCTC  TACTCGGATC   200
p30                                                    XhoI
   G  S  G     S  F  G  T     V  Y  K     G  K  W     H  G  D  V     A  V  K     I  L  K     V  V  D  P     T  P  E     Q  L  Q
GGGTCAGGTT  CCTTTGGCAC  TGTGTACAAG  GGCAAGTGGC  ATGGAGATGT  TGCAGTAAAG  ATCCTAAAGG  TGGTTGACCC  AACTCCAGAG  CAACTTCAGG   300
   A  F  R  N     E  V  A     V  L  R     K  T  R  H     V  N  I     L  L  F     M  G  Y  M     T  K  D     N  L  A     I  V  T  Q
CCTTCAGGAA  CGAGGTGGCT  GTTTTGCGCA  AAACACGGCA  TGTTAACATC  CTGCTGTTCA  TGGGGTACAT  GACAAAGGAC  AACCTGGCGA  TTGTGACTCA   400
                                               HpaI
   W  C  E     G  S  S     L  Y  K  H     L  H  V     Q  E  T     K  F  Q  M     F  Q  L     I  D  I     A  R  Q  T     A  Q  G
GTGGTGTGAA  GGCAGCAGTC  TCTACAAACA  CCTGCATGTC  CAGGAGACCA  AATTCCAGAT  GTTCCAGCTA  ATTGACATTG  CCCGACAGAC  AGCTCAGGGA   500
   M  D  Y     L  H  A  K     N  I  I     H  R  D     M  K  S  N     N  I  F     L  H  E     G  L  T  V     K  I  G     D  F  G
ATGGACTATT  TGCATGCAAA  GAACATCATC  CACAGAGACA  TGAAATCCAA  CAATATATTT  CTCCATGAAG  GCCTCACGGT  GAAAATTGGA  GATTTTGGTT   600
      SphI
   L  A  T  V     K  S  R     W  S  G     S  Q  Q  V     E  Q  P     T  G  S     V  L  W  M     A  P  E     V  I  R     M  Q  D  D
TGGCAACAGT  GAAGTCACGC  TGGAGTGGTT  CTCAGCAGGT  TGAACAGCCC  ACTGGCTCTG  TGCTGTGGAT  GGCCCCAGAG  GTAATCCGGA  TGCAGGATGA   700
   N  P  F     S  F  Q     S  D  V  Y     S  Y  G     I  V  L     Y  E  L  M     A  G  E     L  P  Y     A  H  I  N     N  R  D
CAACCCGTTC  AGCTTCCAGT  CCGACGTGTA  CTCGTACGGC  ATCGTGCTGT  ACGAGCTGAT  GGCTGGGGAG  CTTCCCTACG  CCCACATCAA  CAACCGAGAC   800
   Q  I  I     F  M  V  G     R  G  Y     A  S  P     D  L  S  R     L  Y  K     N  C  P     K  A  I  K     R  L  V     A  D  C
CAGATCATCT  TCATGGTAGG  CCGCGGGTAT  GCTTCCCCTG  ATCTCAGCAG  GCTCTACAAG  AACTGCCCCA  AGGCAATAAA  GAGGTTGGTG  GCTGACTGTG   900
                        SstII
   V  K  K  V     K  E  E     R  P  L     F  P  Q  I     L  S  S     I  E  L     L  Q  H  S     L  P  K     I  N  R     S  A  P  E
TAAAGAAAGT  CAAAGAAGAG  AGACCTTTGT  TTCCCCAGAT  CCTGTCTTCC  ATCGAGCTGC  TTCAGCACTC  TCTGCCGAAA  ATCAACAGGA  GCGCCCCTGA  1000
                                                                                    HaeII
   P  S  L     H  R  A     A  H  T  E     D  I  N     A  C  T     L  T  T  S     P  R  L     P  V  F
GCCTTCCCTG  CATCGGGCAG  CTCACACTGA  GGACATCAAT  GCTTGCACGC  TGACTACATC  CCCAAGGCTA  CCAGTCTTCT AG CTGATGAT  GTAGCTGTTC  1100

TTAGGCCACC  AAGGGACGAA  AAAGACTCAG  CGGGCACCAC  TTTCTGTTTC  CTTGGGGGCA  GAATGCATGT  TTTTGGAAAA  GCTGCTGCTG  CTAAGGACCT  1200

AGACTACTCA  CAGGGCCTTA  ACTTCATATT  GCCTTCTTTT  CTACCCCTCC  TGCCCTGGAA  ATGGAAGCAG  TCTCTTACAA  GAGGGACAGC  GTAAGGCGGG  1300
                                                              polymerase

AGCTGCGGTG  ACCACCGAGA  CCGAGGTAAT  CTGGGCTAAA  GCCCTGCCAG  CCGGGACATC  CGCTGAGCGG  GCTGAACTGA  TAGCACTCAC  CCAGGCCCTA  1400
BstEII

AAGATGGCAG  AAGGTAAGAA  GCTAAATGTT  TATACTGATA  GCCGTTATGC  TTTTGCTACT  GCCCATATCC  ATGGAGAAAT  ATACAGAAGG  CGTGGGTTGC  1500

TCACATCAGA  AGGC
```

Fig. 1. (A) Restriction endonuclease cleavage map and sequencing strategy of v-*raf*. The dashed-line box defines the v-*raf* sequences. The Bal I and Bst EII restriction sites are equivalent to the identical sites in Moloney-MuLV (*33*) (positions 1672 and 4214, respectively). Vertical lines correspond to positions of labeled termini at the indicated restriction sites. The arrow lengths reflect the number of nucleotides for which sequence was determined according to the methods of Maxam and Gilbert (*34*). (B) Nucleotide sequence and predicted amino acid sequence of v-*raf*, including the neighboring p30 and polymerase gene regions. Indicated are the proposed limits of unique v-*raf* sequence (vertical broken lines at nucleotides 111 and 1260), unique restriction endonuclease sites (underlined), and the in-frame amber termination codon (boxed). The one-letter symbols for the amino acids are A, alanine; C, cysteine; D, aspartic acid; E, glutamic acid; F, phenylalanine; G, glycine; H, histidine; I. isoleucine; K, lysine; L, leucine; M, methionine; N, asparagine; P, proline; Q, glutamine; R, arginine; S, serine; T, threonine; V, valine; W, tryptophan; and Y, tyrosine.

mately 180 nucleotides from the presumed 3′ end of the inserted cellular sequences. By analogy to the synthesis and posttranslational modification of Moloney murine leukemia virus (MuLV) $Pr65^{gag}$ (*20*), two *raf*-containing polypeptides would be expected in transformed cells. The smaller one would be initiated at the AUG (A, adenine; U, uracil; G, guanine) from which the translation of $Pr65^{gag}$ begins. This *gag-raf* polyprotein, which contains 383 *gag*-specific amino acids and 329 *raf*-specific amino acids, has a predicted molecular size of 79,000 daltons. The larger polyprotein, representing the initiation product characteristic of $gPr80^{gag}$, the glycosylated form of $Pr65^{gag}$, should migrate as if it has a

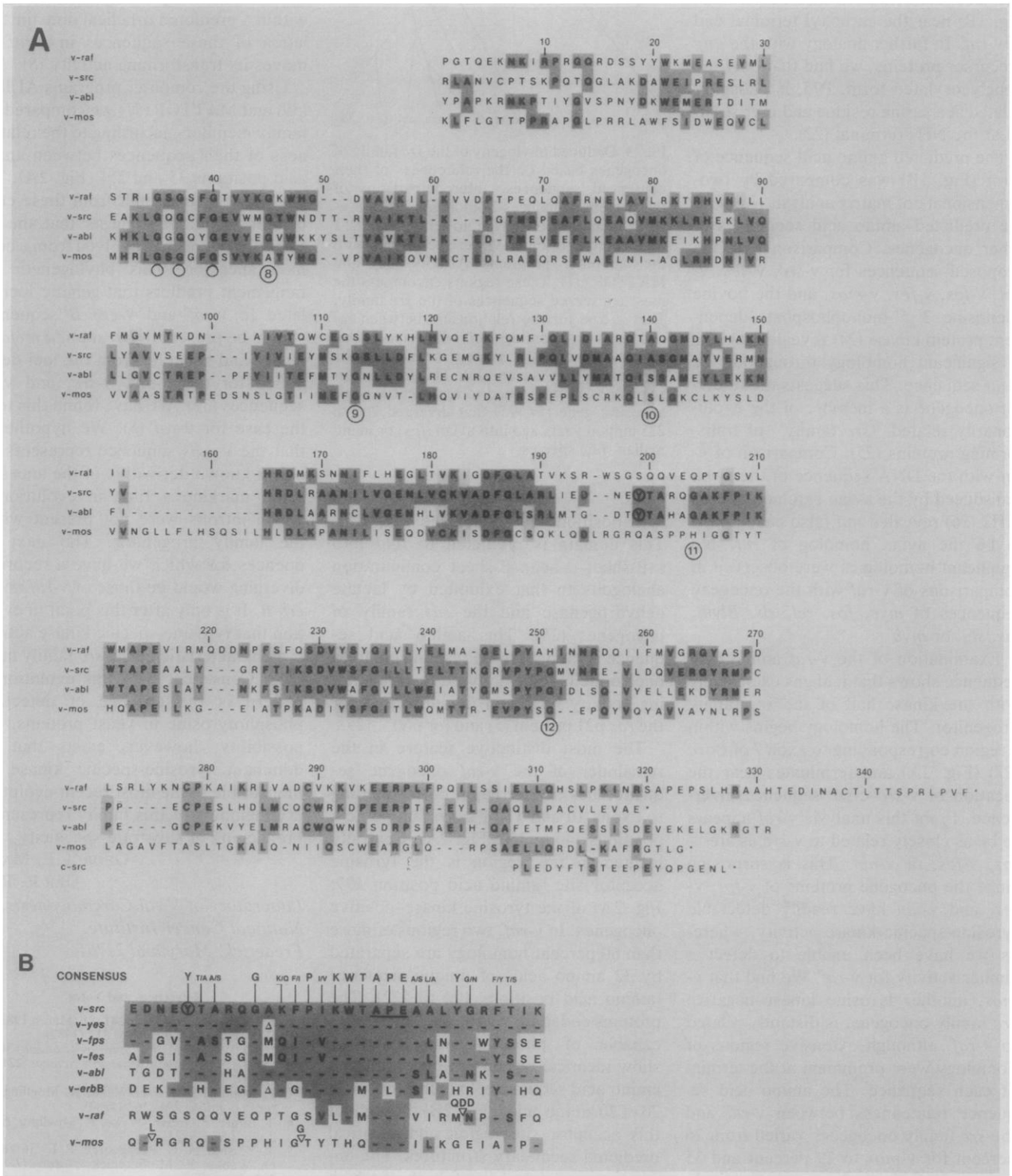


Fig. 2. (A) Comparison of the deduced amino acid sequences of the *src* family oncogenes of murine origin and that of v-*src* and its cellular homolog (c-*src*). The sequences are aligned by the computer method of Dayhoff and Barker (*30*). Amino acid homologies are shaded. Homologies not shared by v-*src* are weakly shaded. Open circles locate the canonical -Gly-X-Gly-X-X-Gly- sequence of a putative nucleotide binding region. The tyrosine acceptors of v-*src* and v-*abl* are circled. The location of the exon junctions of c-*src* are represented by circles in which the number of the exon to the right is indicated. The v-*src* (*11*) sequence begins at amino acid 240; v-*abl* (*13*) begins at amino acid 336; v-*mos* (*19*) begins at amino acid 67. (B) Comparison of the sequences surrounding the phosphotyrosine acceptor sites, or analogous domains, of the *src* family transforming proteins. The phosphotyrosine acceptor of v-*src* is circled and a sequence present in all but the v-*erb B* (*35*) protein is underlined. Identical amino acids are represented as dashes, deletions are indicated with triangles, and insertions are shown by amino acids above the linear sequences. Amino acids that conform to the consensus sequence are shaded.

molecular size of 94,000 daltons. These predictions agree well with the 90,000- and 75,000-dalton *gag*-fusion polypeptides observed in 3611-MSV transformed cells (*7, 9*). The glycosylation of P90 may involve sites on *gag* as well as a potential site (*21*) (NRS, nucleotides 984 to 992; Fig. 1B) near the carboxyl terminal end of v-*raf*. In further analogy with the *gag* precursor proteins, we find that only the nonglycosylated form, P75, is phosphorylated at a serine residue and myristilated at the NH_2 terminal (*22*).

The predicted amino acid sequence of v-*raf* (Fig. 1B) was compared by two-dimensional dot matrix analysis (*23*) with the predicted amino acid sequences of other oncogenes. Comparison with the proposed sequences for v-*src*, v-*yes*, v-*abl*, v-*fps*, v-*fes*, v-*mos*, and the bovine adenosine 3′,5′-monophosphate–dependent protein kinase (*24*) revealed regions of significant homology throughout the v-*raf* sequence. This suggests that the v-*raf* oncogene is a member of the evolutionarily related "*src* family" of transforming proteins (*25*). Comparison of v-*raf* with the DNA sequence of the v-*mil* transduced by the avian carcinoma virus MH2 (*26*) revealed *mil* (also called *mht*) to be the avian homolog of *raf*. No significant homologies were observed in comparisons of v-*raf* with the oncogene sequences of *myc, fos, rel, sis, Blym, ras, ski*, or *myb*.

Examination of the v-*raf* amino acid sequence shows that it aligns exclusively with the kinase half of the *src* family progenitor. The homology begins within a region corresponding to exon 7 of c-*src* (*27*) (Fig. 2A) and terminates near the location of v-*src*–c-*src* sequence divergence. From this analysis v-*raf* appears to be as closely related to v-*src* as are v-*fps*, v-*fes*, or v-*abl*. This is surprising since the oncogene proteins of v-*fps*, v-*fes*, and v-*abl* have readily detectable tyrosine-specific kinase activity, whereas we have been unable to detect a similar activity for v-*raf*. We find that v-*mos*, another tyrosine kinase–negative *src* family oncogene, is distantly related to v-*raf*, although extensive regions of homology were prominent at the termini of each sequence. The amino acid sequence relatedness between v-*raf* and the *src* family oncogenes varied from 26 percent for v-*mos* to 29 percent and 35 percent for v-*fes* and v-*src*, respectively (Fig. 2A). By comparison, the corresponding regions of v-*src* and v-*fes* show a 39 percent amino acid homology.

Near the amino end of the v-*raf* sequence lies one of the several regions of greater than 57 percent homology detected in the dot matrix comparisons (amino acid positions 30 to 61; see Fig. 2A). This domain is predicted to fold into a β-sheet–α-helix–β-sheet configuration analogous to that exhibited by lactate dehydrogenase and the *ras* family of oncogenes (*28*). This amino acid sequence is thought to be responsible for a nucleotide binding activity. Such a binding activity has been demonstrated for the *ras* p21 protein (*5*) and for $p60^{src}$ (*29*).

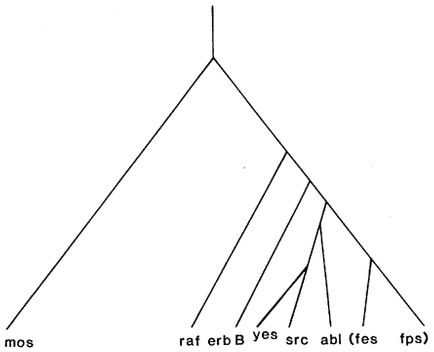


Fig. 3. Deduced phylogeny of the *src* family of oncogenes based on the relatedness of their conserved sequences. Intercomparisons of the protein sequences homologous to the v-*raf* sequences between amino acids 35 and 251 (numbered as in Fig. 2A) were performed with the computer programs ALIGN (*30*) and MATTOP (*31*). These regions encompass the most conserved sequences of the *src* family. This is true for the relationship between *raf* and its avian homolog (*mil*) where more than 95 percent of their protein sequences are identical in this region (*26*). The *fps* and *fes* sequences are presumed to represent a single ancestral gene (*14, 15*) that diverged 200 to 225 million years ago into avian (*fps*) or mammalian (*fes*) species.

The most distinctive feature in the remainder of the v-*raf* oncogene sequence lies in the region corresponding to exons 10 and 11 of c-*src* (amino acid positions 140 to 250; Fig. 2A). Centrally located in this region is the tyrosine acceptor site (amino acid position 199; Fig. 2A) of the tyrosine kinase–positive oncogenes. In v-*raf*, two regions of more than 60 percent homology are separated by 32 amino acids of unique sequence (amino acid positions 190 to 222). The proteins coded for by the five oncogenes capable of phosphorylating tyrosine show identical or conservatively altered amino acid sequences (matches occur in 20 of 20 amino acids; Fig. 2B) throughout this acceptor site region and identical predicted secondary structures. The oncogenes v-*mos* and v-*raf*, both of which lack a tyrosine acceptor, and also v-*erb B*, exhibit variations from the consensus sequence (matches in 6 of 20, 8 of 20, and 13 of 20 amino acids, respectively; Fig. 2B) as well as alterations in the predicted secondary structures. When these differences, which are multifocal, are arranged in a gradient of severity relative to the tyrosine acceptor genotype, a time table for their emergence in evolution is suggested (see below). Although all of the members of this family have unique carboxyl terminal sequences, they all contain positively charged amino acids within a predicted α-helical domain. Deletion of these sequences in v-*raf* removes its transforming activity (*8*).

Using the computer programs ALIGN (*30*) and MATTOP (*31*) we compared *src* family members according to the relatedness of their sequences between amino acid positions 35 and 251 (Fig. 2A). The phylogenetic tree built from these comparisons (Fig. 3) suggests that the *src* family of oncogenes evolved from a common ancestor. This phylogenetic arrangement predicts that genetic loci related to v-*raf* and v-*erb B* sequences should be present in *Drosophila melanogaster* and separate from the loci determined for the v-*abl*, v-*src*, and v-*fps* sequences (*32*). We have found this to be the case for v-*raf* (*8*). We hypothesize that the v-*mos* sequence represents the oldest known derivative of the ancestral gene, marking a time in evolution at which introns were not present within the family progenitor. The next sequences for which we have a record of diverging would be those of v-*raf* and v-*erb B*. It is only after this point in evolution that tyrosine-specific kinase activity is a characteristic of the *src* family members. Consistent with this evolutionary pattern is the absence of detectable phosphotyrosine in yeast proteins. The possibility, however, exists that the dominant tyrosine-specific kinase demonstrable in the most recent evolutionary members of this family represents a broadening of substrate specificity.

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Characterization of Exogenous Type D Retrovirus from a Fibroma of a Macaque with Simian AIDS and Fibromatosis

Abstract. *A novel type D retrovirus was isolated by cocultivation of explants of fibromatous tissue from a rhesus monkey (*Macaca mulatta*) with immunodeficiency and retroperitoneal fibromatosis. This type D virus, isolated from a macaque with simian acquired immunodeficiency syndrome (SAIDS-D/Washington), is exogenous and is partially related to the Mason-Pfizer and the langur monkey type D viruses. The SAIDS-D virus can be distinguished from all other primate retroviruses by antigenicity and molecular hybridization. Nucleic acid hybridization studies reveal that the origin of the SAIDS-D isolate may reside in Old World monkey (subfamily Colobinae) cellular DNA.*

Human acquired immunodeficiency syndrome (AIDS) is characterized pathologically by lymphoid depletion, depressed cellular and humoral immune functions, opportunistic infections, and unusual neoplasms, particularly Kaposi's sarcoma and, less frequently, lymphomas (*1*). An acquired immunodeficiency syndrome similar in certain respects to human AIDS has been observed in macaques at the New England (*2*) and California (*3*) Regional Primate Research Centers (RPRC). The simian AIDS (SAIDS) at the New England RPRC occurs primarily in *Macaca cyclopis* in which some of the affected animals died with lymphoproliferative lesions (*2*). SAIDS in the California facility is epidemic in *M. mulatta* and two cases of cutaneous fibrosarcomas have been reported in rhesus monkeys (*4*). At the RPRC at the University of Washington, various macaques, primarily *M. nemestrina* but also *M. mulatta, M. fuscata*, and *M. fascicularis*, show an immunodeficiency syndrome characterized by persistent diarrhea, progressive weight loss, anemia, lymphocytopenia, unusual chronic infections (noma and cryptosporidiosis), and a peculiar fibromatous tumor termed retroperitoneal fibromatosis (RF) (*5, 6*). Histologically, there is marked thymic atrophy, follicular and paracortical atrophy of lymph nodes, and variable myeloid and lymphoid hyperplasia in bone marrow. Neither RF nor immunodeficiency has been observed among colony-born or feral baboons housed at the Washington RPRC. Retroperitoneal fibromatosis, which is characterized by an aggressive proliferation of highly vascular fibrous tissue, often remains localized to the peritoneum. However, in over one-fourth of the cases it progresses to involve the entire abdominal cavity, inguinal canal, and thoracic cavity. A cutaneous form has been recognized in a small number of RF-affected animals and resembles the cutaneous fibrosarcomas seen in the California colony (*3*). Immunohistochemical studies have shown factor VIII–related antigen in endothelial and scattered fibroblast-like cells throughout the RF lesions (*6*), similar to that described for Kaposi's sarcoma (*7*). Thus, in its progressive form, SAIDS at the RPRC in Washington includes the triad of lymphoid depletion, opportunistic infections, and an unusual neoplasm (RF).

We have investigated the immune status of monkeys with RF. In an experiment involving four *M. nemestrina* monkeys with biopsy-confirmed lesions of RF and three age- and sex-matched controls, peripheral blood mononuclear cells were cultured in the presence of optimal concentrations of phytohemagglutinin (PHA), concanavalin A (Con A), or pokeweed mitogen (PWM) (*8*). Results for the RF-affected animals were expressed as the percentage of the average net [^{3}H]thymidine incorporation by lymphoid cells of the three controls. The results showed that responses of lymphoid cells of RF animals were 2 to 12 percent of the control value for PHA, 1 to 13 percent of the control value for Con A, and 5 to 66 percent of the control value for PWM. Antibody responses to the T-cell–dependent antigen bacteriophage ϕX174 (*9*) were measured in two rhesus monkeys with biopsy-confirmed RF and two age- and sex-matched controls. Control monkeys showed a typical primary immunoglobulin M (IgM) response and a brisk and amplified secondary response consisting mainly of immunoglobulin G (IgG) antibody. In contrast, RF-affected animals had a markedly depressed primary response (both animals less than 1 percent of controls) and failed to amplify and switch from IgM to IgG during the secondary response. Similarly depressed immune responses have been observed in homosexual men with lymphadenopathy and reversed ratios of helper to suppressor lymphocytes (*10*).

To examine the etiology of SAIDS at the Washington RPRC, RF tissue from an immunodeficient rhesus monkey was cocultivated with heterologous mammalian cells known to support the replication of a wide variety of primate viruses (*11*). After only 2 weeks, a Mg^{2+}-dependent reverse transcriptase activity was detected in the conditioned medium from a dog thymus cell line (FCf2Th). Electron microscopic examination of the virus (Fig. 1) revealed typical (*12*) type D retroviral particles, indistinguishable from Mason-Pfizer monkey virus (MPMV), in which intracytoplasmic type A particles were common (Fig. 1A), and budding occurred by envelopment of preformed A particles (Fig. 1B). Budding of virions with incomplete nucleoids was also observed (Fig. 1C) and, characteris-