Fibroblast growth factors (FGFs) are essential molecules for mammalian development. The nine known FGF ligands and the four signaling FGF receptors (and their alternatively spliced variants) are expressed in specific spatial and temporal patterns. The activity of this signaling pathway is regulated by ligand binding specificity, heparan sulfate proteoglycans, and the differential signaling capacity of individual FGF receptors. To determine potentially relevant ligand-receptor pairs we have engineered mitogenically responsive cell lines expressing the major splice variants of all the known FGF receptors. We have assayed the mitogenic activity of the nine known FGF ligands on these cell lines. These studies demonstrate that FGF 1 is the only FGF that can activate all FGF receptor splice variants. Using FGF 1 as an internal standard we have determined the relative activity of all the other members of the FGF family. These data should serve as a biochemical foundation for determining developmental, physiological, and pathophysiological processes that involve FGF signaling pathways.

Fibroblast growth factor (FGF) was identified as an activity that stimulates the proliferation of NIH3T3 cells (1). Currently, FGFs comprise a family of nine structurally related proteins (FGF 1–9). FGFs are expressed in specific spatial and temporal patterns and are involved in developmental processes, angiogenesis, wound healing, and tumorigenesis (2-5).

FGFs bind and activate high-affinity receptor tyrosine kinases. The cloning of FGF receptors (FGFRs) has identified four distinct genes (6–13). These receptors bind members of the FGF family with varying affinity (13–16), and alternative mRNA splicing leads to isoforms of these receptors which have unique ligand binding properties (15, 17, 18). An additional mechanism regulating FGF activity involves heparan or heparan sulfate proteoglycans, molecules which facilitate ligand-receptor interactions (12, 19, 20). FGFRs contain an extracellular ligand binding domain, a single transmembrane domain, and an intracellular tyrosine kinase domain. The extracellular domain determines ligand binding specificity and mediates ligand-induced receptor dimerization. Dimerization in turn results in one or more trans-phosphorylation events and the subsequent activation of the receptor (21).

The extracellular region of the FGFR contains three immunoglobulin-like (Ig-like) domains (6). Alternative mRNA splicing creates several forms of the FGF receptor which differ in their extracellular sequence and have unique ligand binding properties. One splicing event results in the skipping of exons encoding the amino-terminal Ig-like domain (domain I) resulting in a "short" two Ig-like domain form of the receptor (22). The ligand binding properties of the short (two Ig-like domain) and long (three Ig-like domain) FGFRs are similar. However, the short form of the receptor may have a higher affinity for some FGFs than the long form (23). Changes in this alternative splicing pattern may correlate with the progression of several tumors toward malignancy (24, 25).

Another RNA splicing event utilizes one of two unique exons and results in three alternative versions of Ig-like domain III (referred to as domains IIIa, IIIb, IIIc) in FGFRs 1–3 (15, 18, 22). FGFRs containing alternatively spliced Ig-like domains IIIb ("b") and IIIc ("c") are expressed on the cell surface and bind FGF ligands. The IIIa ("a") splice form of the FGFR terminates within Ig-like domain III to yield a secreted extracellular FGF-binding protein with no known signaling capability (26). DNA encompassing the carboxyl-terminal half of Ig-like domain III in FGFRs 1, 2, and 3 have a remarkable conservation in both the number and arrangement of the intron/exon boundaries (18, 27–29). Expression of these receptor isoforms appears to be regulated in a tissue-specific manner with b exon expression restricted to epithelial lineages and c exon expression restricted to mesenchymal lineages (29–33). Unlike FGFRs 1–3, FGFR 4 is not alternatively spliced in this region (34).

Receptor binding specificity is an essential mechanism for regulating FGF activity. Specificity is determined by sequence differences among individual FGFRs, by alternative splicing, and by sequence differences among the nine FGF ligands. Knowledge of the paired interactions between the nine known FGFs and the major splice forms of the four known FGF receptors is essential to begin to discern the functions of FGFs during development. In this report we analyze the mitogenic activity of each FGF on BaF3 cell lines that express unique FGFRs. For the known FGFs, we have assembled the available published mitogenic activity data for BaF3 cells (35–37) and have filled in all the gaps for the remaining FGFs. We present a paired analysis of the activity of each FGF (1–9) on the b and c splice forms of the FGFRs 1–3 and on FGFR 4.
**FGF Specificity**

15293

**Table 1**

| FGFR | % Amino acid identity<sup>a</sup> | Species used<sup>b</sup> | Ref. | GenBank accession numbers<sup>c</sup> |
|------|---------------------------------|--------------------------|------|--------------------------------------|
| 1    | 98                              | M                        | 12,15| X51803                               |
| 2    | 96                              | M                        | 16,40| U22324                               |
| 3    | 92                              | M                        | 14,18| M58051                               |
| 4    | 88                              | M                        | 41   | X57205                               |

<sup>a</sup> <sup>b</sup> <sup>c</sup> splice forms were used in this analysis.

<sup>M</sup>, mouse; <sup>H</sup>, human.

<sup>GenBank accession numbers for sequences used in this analysis.

**EXPERIMENTAL PROCEDURES**

Materials—Human recombinant FGF 1 was a gift from K. Thomas, Merck Inc.; human recombinant FGF 2 was a gift from J. Abraham, Sigma Novo Inc.; mouse FGF 3 was a gift from M. Mathieu and C. Dickson and was purified from NIH3T3 cells expressing the murine FGF 3 cDNA (35). Human recombinant FGF 4 was a gift from Genetics Institute Inc.; human recombinant FGF 5 was purified from Escherichia coli as described (38). Human recombinant FGF 6 was purified from E. coli as described (39). Human recombinant FGF 7 was a gift from Amgen Inc.; mouse FGF 8b was purified from E. coli as described (36). Human recombinant FGF 9 was obtained from Pepro Tech Inc. (37).

The source of the FGFR cDNAs are: FGFR 1b (15), FGFR 1c (12), FGFR 2 (36); mouse recombinant FGF 9 was obtained from Pepro Tech Inc. (37). The sequence of the FGFR cDNAs are: FGFR 1b (15), FGFR 1c (12), FGFR 2 (36), FGFR 3b (18), FGFR 3c (14), and FGFR 4 (41).

FGFR Expression Plasmids—Full-length cDNAs encoding the three immunoglobulin-like domain of FGFR 1b, 1c, and 2c were cloned into the MIRB expression vector as described in Refs. 18, 36, and 37. The FGFR 3 cDNAs were re-engineered to enhance signaling in BaF3 cells by constructing chimeric cDNAs encoding the extracellular region of FGF 3 fused to the cDNA encoding the intracellular region and tyrosine kinase domain of FGF 1. FGFR 3c has the extracellular region from FGFR 3c (14) and the transmembrane and tyrosine kinase domain from FGF 1. The cDNA sequences were assembled using polymerase chain reaction-directed mutagenesis and polymerase chain reaction-mediated ligations. The amino acid sequence joining FGFR 3c (bold) to FGFR 1 (plain) is: 

TDEAGRSLYLIEYCTGA--; the transmembrane domain is underlined, the lower case "r" (Arg) is an exogenous amino acid added in the cloning. FGF 3b has the extracellular region and transmembrane domain derived from FGF 3b (18) and the tyrosine kinase domain derived from FGF 1. The amino acid sequence joining FGFR 3b (bold) to FGFR 1 (plain) is: VVAAVIL-CRLKSGTKK--; the transmembrane domain is underlined.

FR4/R1C and FR4/R1C contain the extracellular domains of murine FGFR 4 and FGFR 4c, respectively, fused to the transmembrane and cytoplasmic domains of murine FGFR 1 (41). The amino acid sequence joining FGFR 4c (bold) to FGFR 1 (plain) is: PEARYTDYLCGTKA--; the transmembrane domain is underlined, and the tyrosine kinase domain derived from FGF 1. The amino acid sequence joining FGFR 4b (bold) to FGFR 1 (plain) is: VVAAVIL-CRLKSGTKK--; the transmembrane domain is underlined.

FR4/R1C and FR4/R1C contain the extracellular domains of murine FGFR 4 and FGFR 4c, respectively, fused to the transmembrane and cytoplasmic domains of murine FGFR 1 (41). The amino acid sequence joining FGFR 4c (bold) to FGFR 1 (plain) is: PEARYTDYLCGTKA--; the transmembrane domain is underlined, and the tyrosine kinase domain derived from FGF 1. The amino acid sequence joining FGFR 4b (bold) to FGFR 1 (plain) is: VVAAVIL-CRLKSGTKK--; the transmembrane domain is underlined.

Overall, the sequence derived from the signal peptide is in bold type. FR4/R1C and FR4/R1C cDNAs were inserted into the pMX expression vector (42).

Cell Culture and Mitogenic Assays—Suspension cultures of BaF3 (43, 44) were maintained in RPMI 1640 media (Life Technologies, Inc.) supplemented with 10% neonatal bovine serum, 10% conditioned media from WEHI-3 cells, 1-glutamine, and penicillin-streptomycin/mercaptoethanol. To express FGFRs in BaF3 cells, 10<sup>6</sup> cells were electroporated with 20 μg of Cial linearized MIRB-FGFR plasmids or 50-μl linearized pMX-FGFR 4 plasmids as described previously (14, 19, 42). Cells were selected in media containing 600 μg/ml G418 (Life Technologies, Inc.) and 10% WEHI-conditioned media for 10–12 days. Pods of transfected cells were checked for mitogenic responsiveness to FGF 1 and then subcloned by limiting dilution. The cell lines used in this study are designated FR1b-5 (FGFR 1b), FR1c-11 (FGFR 1c), FR2b-7 (FGFR 2b), FR2c-2 (FGFR 2c), FR3b-1 (FGFR 3b), FR3c1-4 (FGFR 3c), and FR4/R1C-4 (FGFR 4a).

For mitogenic assays, BaF3 cells expressing specific FGFRs were washed and resuspended in RPMI, 10% neonatal bovine serum, 1-glutamine. 22,500 cells were plated per well in a 96-well assay plate in media containing 2 μg/ml heparin. FGFRs, diluted in media containing 2 μg/ml heparin, were added to each well for a total volume of 200 μl/well.

![Figure 1](image_url)

**FIG. 1. FGFR receptor expression in BaF3 cells.** A, BaF3 cell lines expressing FGFRs 1–3 were cross-linked to 125I-FGF 1 in the presence of heparin. B, BaF3 cells expressing FGFR 4-FGFR 1 chimeric molecules were visualized by Western blotting with antibodies directed against the carboxyl terminus of FGFR 1.

The cells were then incubated at 37 °C for 36–48 h. To each well, 1 μCi of [125I]thyminide was added in 50 μl of media. Cells were harvested after 4–5 h by filtration through glass fiber paper. Incorporated [125I]thyminide was counted on a Wallac 

**RESULTS**

FGFR-expressing Cell Lines—The BaF3 cell line has been used extensively to investigate the activity of a variety of receptor tyrosine kinases (19, 45–48). This cell line is dependent on interleukin 3 for growth. This dependence upon interleukin 3 can be replaced by ligands for receptor tyrosine kinases if the appropriate receptor tyrosine kinase is expressed in the BaF3 cell (19, 45). Wild-type BaF3 cells do not express FGFRs (14, 19, 41). However, BaF3 cells transfected to express FGFRs can be propagated in the presence of FGF 1 (19, 41). To determine the relative mitogenic activity of FGFRs 1–9 on different FGFRs, BaF3 cell lines have been engineered to express each of the three Ig-like domain, b and c splice forms, of FGFRs 1–3 or the two Ig-like domain forms of FGFR 4. The FGFRs used have been derived from either mouse or human cDNA clones. In the region encompassing Ig-like domain II to the transmembrane domain (the region thought to determine ligand binding specificity) there is a high degree of sequence conservation between these two species (92–99%) (Table 1). It is therefore unlikely that species differences influence the ligand specificity of these
receptors. Analysis of the FGFR-expressing BaF3 cell lines, by cross-linking of cell surface receptors to labeled FGF 1 or by Western blotting, demonstrates that all cell lines express comparable levels of cell surface receptor (Fig. 1).

FGFR 1 and 2 expressing-BaF3 cells consistently demonstrate a robust mitogenic response to FGF. However, FGFR 3 or FGFR 4 expressing cells respond poorly or not at all to FGF (18, 41). To overcome this diminished signaling capacity, chimeric receptors were engineered to contain the entire extracellular domain of FGFR 3 and FGFR 4 and the tyrosine kinase domain of FGFR 1 (see “Experimental Procedures”). Comparison of the specificity of full-length FGFR 3 expressed in BaF3 cells for FGFs 1, 2, 4, 5, 6, and 7 (18) to chimeric FGFR 3/FGFR 1 (this study) demonstrates complete agreement (see below). We conclude that ligand binding specificity is determined by the extracellular domains of FGFRs and that chimeric receptors mimic their wild-type counterparts with respect to ligand binding specificity.

For FGFRs 1–3 the “long” or three Ig-like domain receptor was used. Unlike for FGFRs 1–3, BaF3 cells expressing the long form of FGFR 4/FGFR 1 chimera demonstrate a significant mitogenic response to anionic polysaccharides, including heparin (42). Therefore, the two Ig-like domain form of FGFR 4 was used. This receptor has a small response to heparin alone but remains responsive to FGF. Preliminary analysis of the long and short forms of FGFRs 1 and 3 demonstrate no significant difference in responsiveness to FGFs, although all nine FGFs have not been examined (4). The long and short forms of FGFR 4 expressed in BaF3 cells show no significant differences in their ability to bind different FGFs (5).

Mitogenic Response to FGF—To directly compare the activity of each FGF with a single FGFR, dilutions of FGFs were simultaneously assayed on FGFR-expressing BaF3 cell lines by monitoring [3H]thymidine incorporation into DNA after 36–48 h (Figs. 2–5). All FGFs were bacterially expressed recombinant proteins except for FGF 3, which has not been successfully expressed in bacteria. The FGFs tested were derived from either mouse or human clones. Sequence conservation between mouse and human varies between 80 and 100% amino acid identity (Table II). The higher sequence variability between FGFs 3, 4, and 5 can be accounted for in part by divergence in the region of the sequence encoding the signal peptide (FGF 4 and 5) and the extreme carboxyl terminus (FGF 3 and 5).

3 D. M. Ornitz, J. Xu, G. Cao, and M. Goldfarb, unpublished data.
4 A. Chellaiah and D. M. Ornitz, unpublished data.
5 G. Gao and M. Goldfarb, unpublished data.
Concentrations of FGFs ranging from 5 nM to 20 pM were used for these assays. The concentration of heparin, a cofactor required for FGF activity in BaF3 cells (14, 19, 37) was held constant at a concentration of 2 μg/ml. This concentration of heparin is optimal for FGF 1 and FGF 9 (14, 37, 49) and does not demonstrate any inhibitory activity toward FGF2 (data not shown). Half-maximal activity for the most active FGFs was in the range of 20–300 pM, consistent with the established affinities of the FGFRs for ligand (7, 16). Consistent with previous data in other systems (7, 14–16, 18, 19, 26, 34, 40, 41, 50–55), all forms of FGFRs expressed in BaF3 cells respond to FGF 1. To assess the relative mitogenic activity of FGFs on individual FGFR splice variants and to make comparisons between different FGF receptor variants, we normalized the data in Figs. 2–5 to that of FGF 1. To reduce sampling error, the relative mitogenic activity of FGFs on individual FGFR splice variants and to make comparisons between different FGF receptor variants, we normalized the data in Figs. 2–5 to that of FGF 1. To reduce sampling error, the relative mitogenic activity of FGFs on individual FGFR splice variants and to make comparisons between different FGF receptor variants, we normalized the data in Figs. 2–5 to that of FGF 1. To reduce sampling error, the relative mitogenic activity of FGFs on individual FGFR splice variants and to make comparisons between different FGF receptor variants, we normalized the data in Figs. 2–5 to that of FGF 1. To reduce sampling error, the relative mitogenic activity of FGFs on individual FGFR splice variants and to make comparisons between different FGF receptor variants, we normalized the data in Figs. 2–5 to that of FGF 1. The mitogenic activity reported here is in general agreement with the reported receptor binding properties of FGFs. However, there are some notable exceptions. Binding studies on FGF 4 demonstrate that FGF 2 binds with 10-fold lower affinity than FGF 1 (34), whereas our data indicates that FGF 1 and FGF 2 have similar mitogenic activities (Fig. 5). Similarly, soluble FGFR 3c does not bind FGF 2 (14, 18), whereas BaF3 cells expressing FGFR 3c molecules responds equally well to both FGF 1 and FGF 2 (Ref. 18; Fig. 4b). The mitogenic data must therefore be interpreted in the context of the BaF3 cell, the assay conditions used (which include 2 μg/ml heparin) and the absence of endogenous heparan sulfate proteoglycans on the BaF3 cell surface. Different cell types, heparin concentrations, and heparan sulfate proteoglycans may modify the relative specificities reported here.

DISCUSSION

FGFs compose a family of growth factors that play key roles in a variety of developmental events. Many of the FGFs are expressed only in embryonic tissues. However, some of the FGFs continue to be expressed in adult tissues and may be important for maintaining normal tissue homeostasis. FGFs are also involved in mediating a physiological response to injury (3). Diffusion of FGFs from their site of synthesis is limited by their affinity for cell surface and extracellular matrix heparan sulfate (56). Therefore, the tissue-specific expression of FGFs and FGFR receptors are critical factors that regulate the activation of the FGF receptor signaling pathway.

Ectopic expression of an FGF ligand or aberrant splicing of an FGF receptor can result in the activation of an autocrine signaling pathway and ensuing uncontrolled cell proliferation. Consistent with this, several of the FGFs are oncogenic when aberrantly expressed in humans or mice (57–59). Additionally, switching in expression from FGF 2b to FGF 2c has been implicated in the progression of prostate cancer from a nonmalignant, stromal-dependent, epithelial tumor to an invasive, stromal-independent, undifferentiated tumor (32). This splice form change alters the ligand binding profile of FGF 2 for both FGF 2 and FGF 7. Coincident with the change in receptor expression, up-regulation of alternative ligands such as FGF 2 has been observed within these epithelial cells (32).

All seven FGFR-expressing BaF3 cell lines respond to FGF 1. This observation is consistent with previously published data (7, 14–16, 18, 19, 26, 40, 50–55). FGF 1 thus appears to be a universal FGF ligand and may functionally define a core FGF-binding domain. FGF 1 was therefore used as a positive

Fig. 4. BaF3 cell mitogenic assays.

CONGRUENCY

FGFR 3. A, FGFR 3b expressing cells; B, FGFR 3c expressing cells. The symbols used to represent FGFs are the same as those shown in Fig. 2.

Fig. 5. BaF3 cell mitogenic assays using cells expressing the two Ig-like domain form of FGFR 4. The symbols used to represent FGFs are the same as those shown in Fig. 2.

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control and to normalize the mitogenic activity of the other FGFs. Notably, no other FGF ligand could activate all FGFs.

The expression patterns of FGF receptors 1, 2, and 3 are distinct and analysis of the alternative splicing pattern of these receptors demonstrates that the utilization of either the b or c exon is dependent upon cell lineage. The b exon appears to be expressed in epithelial tissues while the c exon is expressed in mesenchymal tissues (29, 32, 33). The activity of several of the FGFs toward FGFR isoforms can be divided along these lines. FGF 3 activates the b splice forms of FGFRs 1 and 2, and FGF 7 activates the b splice form of FGFR 2. Expression studies demonstrate that FGF 3 and FGF 7 are expressed in mesenchymal tissues and thus may be paracrine effectors of the overlying epithelium (60–62). FGFs 4, 5, 6, and 8 demonstrate that FGF 3 and FGF 7 are expressed in mesenchymal tissues while the c exon is expressed in epithelial tissues (36, 63, 64). Expression studies localize FGF 8 to epithelial tissues and thus FGF 8 may be a paracrine inducer of underlying mesenchyme (36, 63, 64). FGFs 4, 5, and 6 are expressed in both epithelial and mesenchymal lineages and may therefore have either autocrine or paracrine roles (65–68). FGFs 2 and 9 preferentially activate c splice forms; however, FGF 2 shows some activity toward FGFR 1b, and FGF 9 shows some activity toward FGFR 3b. Like FGFs 4, 5, and 6, these FGFs may have both autocrine and paracrine roles.

The diversity in the binding specificity of FGF receptors for FGFs clearly can lead to a large combinatorial set of possible interactions. In addition to the interactions shown in Table III, heterodimers may form between FGF ligands and between FGF receptors. Heterodimers may further increase the repertoire of interactions between FGFs and FGF receptors. Furthermore, the interactions of FGF ligands with heparan sulfate proteoglycans may further affect specificity toward FGF receptors. The concentration of heparin chosen for these studies was such that the activity of FGFs that are known to require relatively high heparin concentrations is optimal. Also, at this concentration, heparin is unlikely to have significant inhibitory activity toward an FGF since the maximum mitogenic activity of individual FGFs is comparable to that of FGF 1 on one or more of the receptor-specific cell lines. With these caveats in mind, this study is nevertheless the first attempt to compare the receptor-specificity of all the FGFs under identical experimental conditions. The important next step will be to determine which ligand-receptor pairs are important in development, in tissue homeostasis and in disease.

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Amino acid sequence identity between mouse and human FGFs

| FGF | % Amino acid identity | Species used | Ref./source | GenBank accession numbers
|-----|----------------------|--------------|-------------|-------------------------|
| 1   | 96                   | H            | Merck       | X51943 M30641 |
| 2   | 94                   | H            | Scios Nova  | 104513 M30644 |
| 3   | 90                   | M            | Genetics Institute | X14445 M26284 |
| 4   | 80                   | H            |            | 163638 X18489 |
| 5   | 84                   | H            |            | 37825 M30643 |
| 6   | 93                   | H            |            | 63545 X51552 |
| 7   | 94                   | H            | Arogen      | 227203 U35295 |
| 8   | 100                  | M            |            | 36 U36223 D12482 |
| 9   | 99                   | M            | Pepro Tech  | 41843 U33535 |

Footnotes a and b are the same as in Table I.
