Abstract: Renal cell carcinoma (RCC) is the 10th most common cancer in United States. It is a heterogeneous disease with various histologic types. Since high-throughput technologies such as microarrays have been introduced, molecular confirmation of previously known findings in RCC has been made and new molecular findings have emerged. We review the accumulating advances in this field and their clinical implications. The published data so far have proved to be significant and promising, and numerous microarray studies with larger number of cases are currently ongoing or being planned. Although various clinical parameters are being refined for diagnosis and prognosis, these data obtained by microarray studies will undoubtedly contribute to both and eventually impacts the treatment of RCC.

Keywords: gene expression profiling, renal cell carcinoma, prognosis
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(A)

Stage I + II (n = 13)

Stage III + IV (n = 16)

P = 0.0049

Cause-specific survival (months)

(B)

Grade 1 (n = 15)

Grade 2 (n = 6)

Grade 3 (n = 8)

P < 0.0001

Cause-specific survival (months)

(C)

Low risk (n = 17)

High risk (n = 12)

P < 0.0001

Cause-specific survival (months)

(D)

Low risk (n = 5)

High risk (n = 11)

P < 0.03

Cause-specific survival (months)
Molecular sub-classification of kidney tumors

- **clear cell**
  - GST-α↑
  - IGFBP-3↑
  - VEGF↑

- **aggressive type**

- **type 1**
  - class 1 — type 2, low grade
  - Mixed type (type 1 and type 2, low grade)
  - chromophobe
    - carbonic anhydrase II↑
  - oncocytooma

- **type 2, high grade**
  - topo IIα↑
  - mitochondria-related genes↑
  - c-Kit↑

- **granular cell**

- **renal medullary carcinoma**
  - topo IIα↑

- **good outcome**
- **poor outcome**

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In vivo

et al.