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# L-*myc* Allele Polymorphism and Prognosis for Metastases in Russian Gastric Cancer Patients

**N.M. Mironov, A.-M. Aguelon, G.I. Potapova, O.V. Gorbunov, A.A. Klimenkov and H. Yamasaki**

During recent years, several attempts have been made to use restriction fragment length polymorphism (RFLP) of proto-oncogenes, e.g. c-Ha-*ras* and L-*myc*, as a marker for prognosis in human cancers [1]. L-*myc* has L and S alleles, and the presence of two S-S alleles has been reported to be associated with metastases of lung [2] and stomach cancer [3] in Japanese patients, although another study of lung cancer in Caucasians showed no such association [4]. Stomach cancer is common among the Russian population and a good prognostic marker is greatly needed. We performed L-*myc* RFLP analysis of stomach cancer samples from 21 newly diagnosed patients in Russia. DNA from tumour samples and corresponding mucosa was amplified by polymerase chain reaction, before single strand conformation polymorphism analysis or EcoRI digestion [4]. 9 patients had metastases in regional lymph nodes. All the tumours contained the same L-*myc* genotypes as the corresponding normal mucosa. Among the 21 patients, the ratio of L-*myc* genotypes between L-L, L-S and S-S was 0.24:0.62:0.14, which is very close to that found for a healthy white Caucasian population [4]: 0.25:0.62:0.13 ($P=0.9865$, $\chi^2$). Among the nine patients with metastases, only 1 patient was found to have the S-S genotype, and distribution of L-*myc* alleles was 0.33:0.56:0.11. The distribution of alleles in patients without metastases was 0.17:0.66:0.17, which did not significantly differ from the patients with metastases ($P=0.8137$, $\chi^2$). Thus, no excess prevalence of S-S L-*myc* allele genotype was found in these Russian patients with metastases. If the reported association between the S-S genotype and metastases in Japanese patients could be confirmed in future studies, such an association might be explained by the presence of some specific factor(s) (internal or external) modulating the metastatic process. Among such factors could be ethnic differences in genotypes in the L-*myc* gene and environmental risk factors. However, because loss of heterozygosity is infrequent in stomach cancer at the L-*myc* locus [5], the loss of putative metastasis suppressor gene near this locus is improbable. In addition, it appears that the L-*myc* gene itself is not activated in stomach cancer. It seems that L-*myc* polymorphism is not suitable as a prognostic marker of metastasis development in stomach cancer patients.

Correspondence to N.M. Mironov
N.M. Mironov, A.-M. Aguelon and H. Yamasaki are at the Multistage Carcinogenesis, International Agency for Research on Cancer, Lyon 69372 Cedex 08, France; G.I. Potapova is at the Laboratory of Tumour Biochemistry and O.V. Gorbunov and A.A. Klimenkov are at the Abdominal Department, Cancer Research Centre, 115478, Moscow, Russia.
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# Male Breast Cancer: Incidence, Mortality and Survival Rates From an Italian Population-based Series

**E. Crocetti and E. Buiatti**

The Tuscany Tumour Registry (RTT) [1] is a population-based cancer registry which has been operating since 1984 in the province of Florence (3814.5 km$^2$), central Italy. The male breast cancer series from the RTT is one of the largest available from the Mediterranean area [2–4].

Between 1985 and 1989, 32 cases of malignant breast cancer (ICD-0 T = 175) had been diagnosed in the male population resident in the province of Florence (male population at 1 January 1988 = 573 957).

The crude incidence rate was 1.1 × 100 000; the age-adjusted (world standard) incidence rate was 0.64 [95% confidence interval (C.I.) 0.44–0.84]. The age-adjusted (world standard) sex ratio (female versus male) was 102.1. The median age at diagnosis was 66.3 (range 27.1–94.0) and the rates increased sharply with age. The cumulative risk increased consistently with age being 0.1 (x 1 000) from 0 to 49 years, 0.4 from 0 to 64 years, 0.7 from 0 to 74 years and 1.0 for the whole lifespan. There was a slight

Correspondence to E. Crocetti.
The authors are at U.O. Epidemiologia, Servizio Multizonale di Prevenzione Oncologica. Via di S. Salvi 12, 50135 Firenze, Italy.
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