

*Review*

**Molecular basis of inherited predispositions for tumors<sup>★</sup>**

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**On the basis of literature data and own experience the authors review the current knowledge about the molecular basis of inherited predispositions for tumors. They hypothesize that in the near perspective 5–10 years studies using existing registry data/material and the latest novel technology will allow the identification of the molecular background for the majority of hereditary cancers which will have enormous practical consequences especially for the prevention of malignancies.**

**CONSTITUTIONAL MUTATIONS IN GENES RELATED TO PREDISPOSITION FOR TUMORS**

It is now well recognized that 5–10% of all tumors including so-called common malignancies such as cancers of the breast, colon and ovaries occur as a result of high monogenic predispositions. It is estimated that an addi-

tional 30–50% of malignancies are also „inherited tumors”, however they occur due to polygenic predispositions. The molecular basis of polygenic tumors is not known, although its existence is strongly suggested by results of studies on monozygotic twins. In contrast, monogenic background has already been proven for a significant proportion of hereditary cancers (Lichtenstein *et al.*, 2000).

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**Abbreviations:** HNPCC, hereditary non-polyposis colorectal cancer.

Genes/syndromes most frequently examined for the occurrence of constitutional mutations are summarized in Table 1.

Although the number of known genes related to cancer predisposition with detected unequivocal constitutional mutations has

**Table 1. Genes/syndromes most frequently examined for the occurrence of constitutional mutations**

Gene	Syndrome	Predisposition to tumors	References
<i>BRCA1</i>	Hereditary Breast-Ovarian Cancer, BRCA1 type	breast, ovary	de los Rios <i>et al.</i> , 2001; Górski <i>et al.</i> , 2000; Jakubowska <i>et al.</i> , 2001
<i>BRCA2</i>	Hereditary Breast-Ovarian Cancer, BRCA2 type	breast, ovary	de los Rios <i>et al.</i> , 2001
<i>ERBB2</i>	Familial Clustering of Breast Cancer	breast	McKean-Cowdin <i>et al.</i> , 2001
<i>ESR</i>	Familial Clustering of Breast Cancer	breast	Anderson <i>et al.</i> , 1997
<i>ATM</i>	Ataxia Telangiectasia	leukemia, breast	Broeks <i>et al.</i> , 2000
<i>MSH2</i>	Hereditary Non-Polyposis Colorectal Cancer	colorectum, endometrium	Dębniak <i>et al.</i> , 2001; Jakubowska <i>et al.</i> , 2001a; Kurzawski <i>et al.</i> , 2002a; Park <i>et al.</i> , 1999; Peltomäki <i>et al.</i> , 1997
<i>MLH1</i>	Hereditary Non-Polyposis Colorectal Cancer	colorectum, endometrium	Dębniak <i>et al.</i> , 2001; Jakubowska <i>et al.</i> , 2001a; Kurzawski <i>et al.</i> , 1999; Kurzawski <i>et al.</i> , 2002a; Park <i>et al.</i> , 1999; Peltomäki <i>et al.</i> , 1997
<i>MSH6</i>	Hereditary Non-Polyposis Colorectal Cancer	colorectum, endometrium	Berends <i>et al.</i> , 2002; Huang <i>et al.</i> , 2001
<i>MSH3</i>	Hereditary Non-Polyposis Colorectal Cancer	colorectum, endometrium	Huang <i>et al.</i> , 2001
<i>PMS1</i>	Hereditary Non-Polyposis Colorectal Cancer	colorectum, endometrium	Olschwang, 1999
<i>PMS2</i>	Hereditary Non-Polyposis Colorectal Cancer	colorectum, endometrium	De Rosa <i>et al.</i> , 2000
<i>TGFRBR2</i>	Hereditary Non-Polyposis Colorectal Cancer	colorectum, endometrium	Lu <i>et al.</i> , 1998
<i>EXO1</i>	Hereditary Non-Polyposis Colorectal Cancer	colorectum, endometrium	Wu <i>et al.</i> , 2001
<i>APC</i>	Familial Adenomatous Polyposis	colon	Zajac <i>et al.</i> , 2000
<i>p53, CHK2</i>	Li-Fraumeni syndrome	sarcoma, leukemia, suprarenal gland, breast	Bell <i>et al.</i> , 1999; Sullivan <i>et al.</i> , 2002
<i>VHL</i>	von Hippel Lindau	hemangioblastoma of the brain, eye and renal	Cybulski <i>et al.</i> , 1999; Hes <i>et al.</i> , 2000
<i>Rb-1</i>	Retinoblastoma	retinoblastoma	Jakubowska <i>et al.</i> , 2001b; Zajaczek <i>et al.</i> , 1999
<i>RET</i>	Familial Medullary Thyroid Cancer	medullary thyroid	Menko <i>et al.</i> , 2002; Rey <i>et al.</i> , 2001
<i>CDH1</i>	Hereditary Diffuse Gastric Cancer	stomach	Salahshor <i>et al.</i> , 2001
<i>SMAD4</i>	Juvenile Polyposis	colon	Howe <i>et al.</i> , 1998; Kim <i>et al.</i> , 2000
<i>PTEN</i>	Cowden disease	breast, thyroid	De Vivo <i>et al.</i> , 2000
<i>STK11</i>	Peutz-Jegers syndrome	breast, pancreas	Westerman <i>et al.</i> , 1999; Yoon <i>et al.</i> , 2000

reached about 50, there is still a large proportion of strong tumor aggregations without known molecular defects. For example:

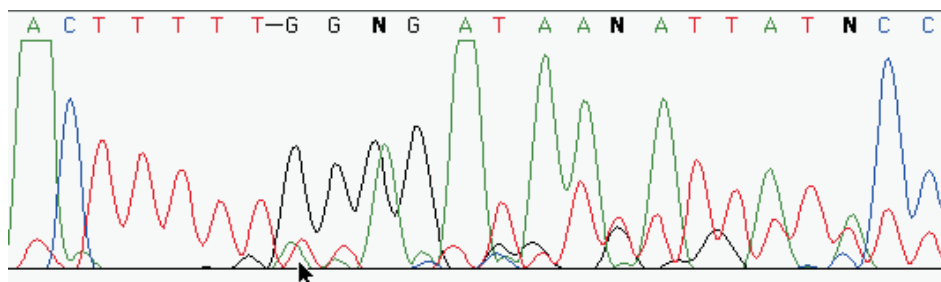
a) Since 2001 we performed the first worldwide population screening for familial cancers in West-Pomerania. During the first year of this programme we performed a complete diagnostic process including pedigree analysis, DNA testing and clinical examination of about 400 000 individuals. About 2600 families with at least three first degree relatives affected by tumors, thus showing the most characteristic feature of monogenic dominant genetic disorders, have been identified, but constitutional mutations were detected in only about 5% of them (Lubiński *et al.*, 2002).

b) We performed sequencing in 200 families with at least three cases of breast/ovarian cancers. Constitutional mutations of the

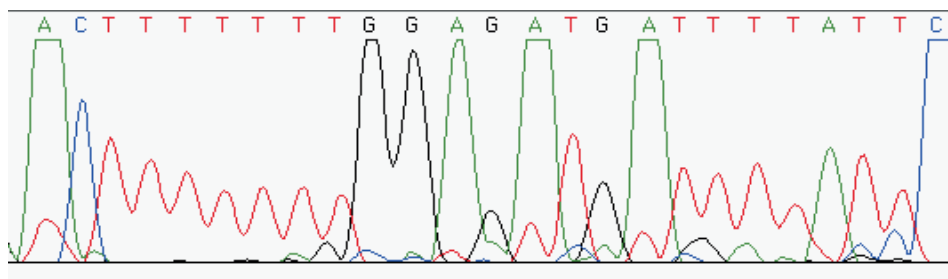
*BRCA1* gene were found in 63% (126/200) and of the *BRCA2* gene in 3% (6/200) of families. Most probably about 30% of cancer aggregations are caused by *BRCAX* gene/genes mutations. Large *BRCA1/BRCA2* deletions were found only in five cases (Górski *et al.*, 2002).

c) Sequencing of the *MSH2/MLH1* genes in families with Lynch syndrome diagnosed definitely or with high probability allowed us to detect constitutional mutations in about 34% of cases. We screened 101 HNPCC kindreds from Poland and Baltic States fulfilling the Amsterdam II diagnostic criteria (17/101) or suspected HNPCC criteria for mutations in *MSH2* and *MLH1* (84/101). Suspected HNPCC families were diagnosed if among first degree relatives of patient with colorectal cancer at least one cancer of the colon or

a)



b)



**Figure 1. The first Polish *MSH6* mutation c.3311-3312 delTT.**

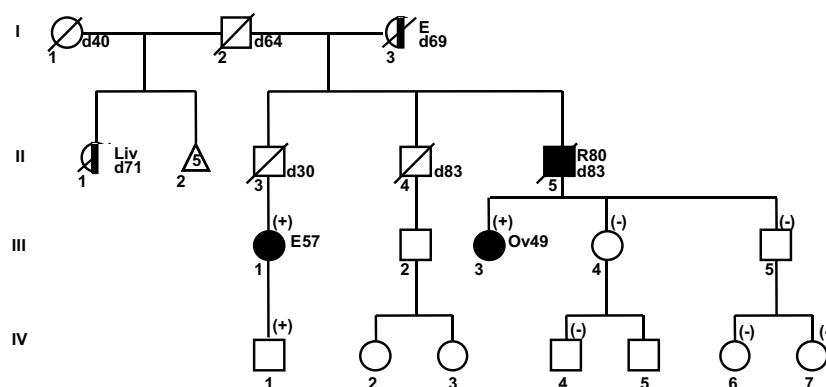
Detection of a germline *MSH6* mutation by sequence analysis; arrow indicates the site of deletion; a) mutant; b) wild type (Suchy *et al.*, 2002). Using of lower case "c" in front of the nucleotide number is recommended for cDNA by the Nomenclature Working Group (Antonarakis SE and the Nomenclature Working Group (1998) Recommendations for a Nomenclature System for Human Gene Mutations. *Hum Mutat.*; **11**: 1-3).

endometrium have been recognised and at least one of these tumors has been diagnosed under age of 50 (Kurzwski *et al.*, 2002a). Thus, again there is very high probability that in a significant proportion of families with strong aggregation of colorectal/ endometrial cancers the genes responsible for a major molecular defect are not known yet. We were able to show that one of such genes may be *MSH6*. The *MSH6* gene is one of the mismatch repair genes. Mutations in this gene, in opposite to *MSH2/MLH1* genes, are much rarer and exhibit distinct phenotype. In our *MSH6* family tumor spectrum include endometrioid ovarian cancer, colon cancer and two endometrial cancers. In patient, with previously excluded germline mutation in *MSH2/MLH1* genes, we identified in exon 5 of *MSH6* gene the frameshift mutation (Figs. 1 and 2) (Suchy *et al.*, 2002).

of 50) and in no case the E-cadherin constitutional mutations have been found (A. Jakubowska, unpublished data).

#### IDENTIFICATION OF MOLECULAR BASIS OF STRONG CANCER FAMILY AGGREGATIONS

Major work has still to be performed in order to identify molecular basis of strong cancer family aggregations. A promising methodology is linkage analysis with intragenic markers for candidate genes. It is reasonable to expect that for example for strong cancer aggregations with the involvement of breast cancer genes known to be connected with *BRCA1/BRCA2*, and for cancer aggregations with the involvement of colon cancer genes known for their aggregation with



**Figure 2.** Pedigree of an *MSH6* family with c.3311-3312 delTT mutation.

E, endometrial cancer; R, rectal cancer; Ov, ovarian cancer; Liv, liver cancer; number after the abbreviation indicates the age at diagnosis; d, death age; (+), *MSH6* mutation positive; (-), *MSH6* mutation negative.

d) One of the genes recognized as a cause of stomach cancer familial aggregations is E-cadherin. We sequenced 53 patients with stomach cancers from families with clinical features of hereditary gastric tumors (at least three relatives affected by stomach cancer at any age or two relatives affected by stomach cancer with at least one diagnosed under age

*MSH2/MLH1* should be considered (Tables 2–5, Fig. 3). Interactions between *BRCA1*, *BRCA2*, *MSH2* and *MLH1* and associated gene proteins have been recognised using different systems, mainly by immunoprecipitation and mass spectrometric analysis of associated proteins (Deng & Brodie, 2000; Wang *et al.*, 2000).

**Table 2. *BRCA1* associated genes**

Genes	References
<b>BASC:BRCA1-ASSOCIATED GENOME SURVEILLANCE COMPLEX:</b> - <i>RAD50-MRE11-NBS1</i> , - <i>ATM</i> , - <i>BLM</i> , - <i>MSH2-MSH6</i> HETERODIMER - <i>MLH1-PMS2</i> HETERODIMER - <i>MSH3</i> , - <i>REPLICATION FACTOR C</i>	Deng & Brodie, 2000; Futaki & Liu, 2001; Kerr & Ashworth, 2001; Wang <i>et al.</i> , 2000; Wang <i>et al.</i> , 2001a; Welch <i>et al.</i> , 2000; Yoshikawa <i>et al.</i> , 2000
<i>RAD51</i>	Kerr & Ashworth, 2001; Wang <i>et al.</i> , 2000; Wang <i>et al.</i> , 2001a; Welch <i>et al.</i> , 2000; Yoshikawa <i>et al.</i> , 2000
<i>BACH1</i>	Kerr & Ashworth, 2001
<i>FANCD2</i>	Futaki & Liu, 2001; Kerr & Ashworth, 2001
<i>BARD1</i>	Ghimenti <i>et al.</i> , 2002; Kerr & Ashworth, 2001; Wang <i>et al.</i> , 2001a; Welch <i>et al.</i> , 2000; Yoshikawa <i>et al.</i> , 2000
<i>CtIP</i>	Deng & Brodie, 2000; Kerr & Ashworth, 2001; Welch <i>et al.</i> , 2000
<i>GADD45</i>	Kerr & Ashworth, 2001
<i>BRCA2</i>	Deng & Brodie, 2000; Welch <i>et al.</i> , 2000
<i>GADD153</i> , <i>Cyclin B1</i> , <i>P1N1</i> , <i>PCNA</i> , <i>zbrk1</i> , <i>p300</i> , <i>P/CAF</i> (RNA Polymerase II holoenzyme), <i>Ki-67</i> , <i>Bax</i> , <i>p21</i> , <i>STAT1</i> , <i>STAT3</i> , <i>JAK1</i> , <i>JAK2</i> ,	Kerr & Ashworth, 2001
<i>BAP1</i>	Welch <i>et al.</i> , 2000
<i>RB</i>	Deng & Brodie, 2000; Welch <i>et al.</i> , 2000
<i>p53</i>	Deng & Brodie, 2000; Welch <i>et al.</i> , 2000; Yoshikawa <i>et al.</i> , 2000
<i>MYC</i>	Deng & Brodie, 2000; Welch <i>et al.</i> , 2000
<i>HDAC1</i> , <i>HDAC2</i>	Deng & Brodie, 2000; Welch <i>et al.</i> , 2000
<i>RHA</i>	Deng & Brodie, 2000; Welch <i>et al.</i> , 2000
<i>BRG1</i>	Kerr & Ashworth, 2001
<i>casein kinase</i>	Deng & Brodie, 2000
<i>E2F</i>	Deng & Brodie, 2000

## MODIFIERS

The cancer risk in *BRCA1*, *MSH2* and *MLH1* mutation carriers is at the level of about 50–80%. It has been shown recently that the risk heterogeneity may be related to modifying environmental and genetic factors (Table 6).

The results of studies on modifying features are not consistent. In our opinion this is caused by methodology problems: short series

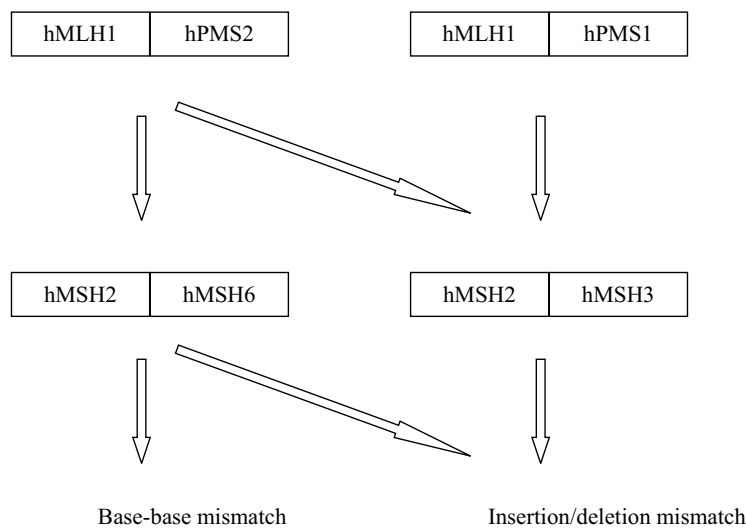
of cases studied, differences in ethnic origin and mutation types, the lack of matching for environmental features. Recently, we performed studies on the modifying effect of the polymorphic 135C→G *Rad51* allele on breast cancer risk in carriers of *BRCA1* 5382insC. Analyses on 83 pairs matched very carefully for reproductive factors allowed us to show more than 2x risk reduction in women with the 135C→G form of *Rad51*. This form has been found in 37% of the unaffected *BRCA1*

**Table 3. BRCA2-associated genes**

Genes	References
<i>RAD51</i>	Kerr & Ashworth, 2001; Welch <i>et al.</i> , 2000
<i>p300</i> , <i>CtIP</i> , <i>P/CAF</i> (RNA Polymerase II holoenzyme)	Kerr & Ashworth, 2001
<i>BRAF35</i>	Kerr & Ashworth, 2001
<i>BRCA1</i>	Welch <i>et al.</i> , 2000
<i>BARD1</i>	Ghimenti <i>et al.</i> , 2002
<i>BCCIP</i>	Liu <i>et al.</i> , 2001

**Table 4. MSH2-associated genes**

Genes	References
<i>MSH3</i>	Guerrette <i>et al.</i> , 1998; Peltomäki <i>et al.</i> , 2001
<i>MSH6</i>	Guerrette <i>et al.</i> , 1998; Peltomäki <i>et al.</i> , 2001
<i>Exo1</i>	Schmutte <i>et al.</i> , 2001
<i>BRCA1</i>	Wang <i>et al.</i> , 2001a
<i>BARD1</i>	Wang <i>et al.</i> , 2001a

**Figure 3. Interactions between mismatch repair genes.**

The complex hMSH2-hMSH6 is responsible for the repair of base-base mismatches and base insertion/deletion mismatches, whilst the complex hMSH2-hMSH3 is only responsible for the repair of base insertion/deletion mismatches (Kolodner & Marsischky, 1999)

**Table 5. MLH1-associated genes**

Genes	References
<i>PMS1</i>	Schmutte <i>et al.</i> , 2001
<i>PMS2</i>	Guerrette <i>et al.</i> , 1999; Peltomäki <i>et al.</i> , 2001, Schmutte <i>et al.</i> , 2001; Yuan <i>et al.</i> , 2002
<i>Exo1</i>	Schmutte <i>et al.</i> , 2001

**Table 6. Genes modifying cancer risk**

Gene		Risk		References
Modified	Modifier	Increased	Decreased	
<i>BRCA2</i>	<b><i>Rad51</i></b> 135C→G	Breast cancer	Ovarian cancer	Levy-Lahad <i>et al.</i> , 2001; Wang <i>et al.</i> , 2001b
<i>BRCA1/2</i>	<b><i>ATM</i></b> T7271G IVS10-6T→G	Breast cancer		Chenevix-Trench <i>et al.</i> , 2002; Maillet <i>et al.</i> , 2000; Teraoka <i>et al.</i> , 2001
<i>MLH1/MSH2</i>	<b><i>ATM</i></b> 1853N polymorphism vs. 1853D polymorphism	Colorectal cancer and other HNPCC-related cancers		
<i>BRCA1</i>	<b><i>AR</i></b> ≥28 CAG repeats	Breast cancer		Rebbeck <i>et al.</i> , 1999
<i>BRCA1</i> <i>BRCA2</i>	<b><i>AIB1</i></b> At least 28 or 29 polyglutamine repeats	Breast cancer		Rebbeck <i>et al.</i> , 2001
<i>MLH1/MSH2</i>	<b><i>CCND1</i></b> alternatively spliced transcript "b" vs. transcript "a"	Lower age at onset of colon cancer		Bala & Peltomäki, 2001

carriers (31/83) and in 17% of the affected carriers (14/83) and in 26% among 189 healthy population controls (Jakubowska *et al.*, 2002).

## CONCLUSIONS

The molecular basis of the genetic background for hereditary cancers has been discovered for a significant proportion of tumors. However, for the majority of hereditary cancers there is still lack of fundamental knowledge. Summarised results indicate directions of studies on identification of novel genes involved in pathogenesis of cancer family syndromes, which can be planned in the near future. It can be expected that in the near perspective of 5–10 years studies using existing registry data/material and the latest novel technology will allow the identification of the molecular background for the majority of hereditary cancers which will have enormous practical consequences especially for the prevention of malignancies.

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