A twofold increase in BRCA mutation related prostate cancer among Ashkenazi Israelis is not associated with distinctive histopathology


To estimate the risk of prostate cancer (PrC) associated with the common Ashkenazi founder mutations of the BRCA1 and BRCA2 genes, and to investigate the histopathology characteristics of mutation related PrC, we identified 979 Ashkenazi Jewish men diagnosed with PrC during 1994-1995 in 16 Israeli hospitals and reference laboratories.

DNA obtained from paraffin sections was tested for the three founder mutations in 940 (96%) cases, and a mutation was identified in 30/940 (3.2%), a two fold increase compared with a referent group of Ashkenazi men over 50 years old with no history of prostate cancer (21 of 1344 (1.6%); OR = 2.1; 95% CI = 1.2–3.6).

In the entire cohort, no difference was found in the mean age at diagnosis between cases with and without a founder mutation.

A representative histology slide was blindly reviewed from 29/30 (97%) of Israeli BRCA associated PrC cases and 145 individually matched non-carrier PrC cases.

No differences were noted between the two sets of cases regarding: the mean Gleason score; presence of prostatic intraepithelial neoplasia or atypical adenomatous hyperplasia; or other histopathology features.

These results are consistent with a doubling of the risk of PrC among carriers of an Ashkenazi BRCA founder mutation, and do not suggest that mutation related PrC is characterised by early age at diagnosis or distinct histopathology features.

Key points

- To estimate the risk of prostate cancer (PrC) associated with the common Ashkenazi founder mutations of the BRCA1 and BRCA2 genes, and to investigate the histopathology characteristics of mutation related PrC, we identified 979 Ashkenazi Jewish men diagnosed with PrC during 1994–1995 in 16 Israeli hospitals and reference laboratories.
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- No differences were noted between the two sets of cases regarding: the mean Gleason score; presence of prostatic intraepithelial neoplasia or atypical adenomatous hyperplasia; or other histopathology features.
- These results are consistent with a doubling of the risk of PrC among carriers of an Ashkenazi BRCA founder mutation, and do not suggest that mutation related PrC is characterised by early age at diagnosis or distinct histopathology features.

Abbreviations: PSA, prostate specific antigen
Participants were then assigned a unique study identifier linked to the pathology specimens. The pathology material was anonymised prior to pathology review and data analysis. Due to the anonymous nature of the study design, medical records were not abstracted, and no information concerning stage or PSA levels at the time of diagnosis was obtained. The study was done under a waiver of the requirement for Institutional Review Board review granted by the National Institutes of Health Office of Human Subjects Research.

We estimated the population founder mutation carrier frequency in Ashkenazi men over 50 years old using data from two study populations: (a) Ashkenazi Jewish male volunteers with no personal history of prostate cancer in the Washington Ashkenazi Study (WAS) (Struwing et al. and J Struwing, unpublished data), and (b) Israeli men enrolled in the Molecular Epidemiology of Colorectal Cancer (MECC) study, an Israeli case-control study with phenotype and genotype data available for 901 population-based controls (Struewing, unpublished data), and (b) Israeli men enrolled in the Molecular Epidemiology of Colorectal Cancer (MECC) study, an Israeli case-control study with phenotype and genotype data available for 901 population-based controls (Struewing, unpublished data), and (b) Israeli men enrolled in the Molecular Epidemiology of Colorectal Cancer (MECC) study, an Israeli case-control study with phenotype and genotype data available for 901 population-based controls (Struewing, unpublished data). Controls were individually matched by sex, year of birth, and clinic to incident cases of colorectal cancer diagnosed in northern Israel between March 1998 and December 2002.

For the pathology review, each prostate cancer case was identified as positive for one of the three Ashkenazi founder mutations. The best available match for each carrier case was made using a four-tiered system: (a) an exact match by age and pathology laboratory; (b) the closest age match (within 5 years) from the same pathology laboratory; (c) the closest age match (within 5 years) from the same type of laboratory (hospital based or referral laboratory); or (d) the closest age match (within 3 years) from any laboratory type. To select five controls per case, we first selected one control per case, selecting a control from the most optimal tier. A second control for each case was then selected, and so forth. Controls were selected without replacement. Thus, once a control was selected as a match for a case, it was unavailable for selection for another case. Histology slides from carrier and non-carrier cases were randomly arranged, and reviewed by a single pathologist (PD). Mutations were identified as positive, using DNA from the founder mutation, and a total of 992 eligible cases of prostate cancer were identified, representing approximately two-thirds of all prostate cancer cases diagnosed in Israel during the study period. In 13 cases (1%), no pathology material could be retrieved. In the remaining 979 cases, a haematoxylin and eosin stained slide was obtained for review, and five unstained 5 µm paraffin fixed sections were obtained as the DNA source for mutation testing. DNA was extracted and mutation testing was successfully completed for all three of the founder BRCA mutations on 940 (96%) of these cases.

In the entire cohort, although the BRCA2 related cases were slightly younger at diagnosis than the non-carriers and the BRCA1 related cases, there were no statistical differences in the mean ages of these three groups (BRCA2 71.6 years, non-carriers 73.6 years, and BRCA1 74.2 years). One prostate cancer case, a non-carrier, was diagnosed at the age of 49 years. All other cases were diagnosed at 50 years of age or later. Among the prostate cancer cases, mutation carriers were more frequently diagnosed by core needle biopsy (29/30 (93%) v 625/910 (69%)) than non-carriers. This difference in the mode of diagnostic tissue acquisition was significantly different between mutation carriers and non-carriers ($\chi^2 = 9.03, p = .01$).

The overall founder mutation prevalence among Israeli prostate cancer cases was 30/940 (3.2%). Of these, 16 (1.7%) had a BRCA1 mutation [185delAG, 14 (1.5%); 5382insC, 2 (0.2%)] and 14 (1.5%) had a BRCA2 6174delT mutation. In the WAS and MECC studies, the mutation frequencies found among Ashkenazi men over the age of 50 years with no history of prostate cancer were 1.49 and 1.69 respectively (table 1). The difference between these two frequencies was not statistically significant (OR = 0.88; 95%CI = 0.3–2.3). When the two comparison groups were combined (WAS+MECC), the increased frequency of any of the founder mutations and of the BRCA1 185delAG founder mutation among Israeli PCa cases reached statistical significance (table 1).

Cases and controls in the pathology review were well matched. An exact match was found for 85% of the first selected controls and for 62%, 54%, 50% and 39% of the second to fifth controls, respectively. In only four cases was a fourth tier control selected for inclusion. Of the 30 identified mutation carriers (with a BRCA1 185delAG mutation) and his five matched controls were eliminated from the pathology case-control study, because the reviewing pathologist was not able to confirm the diagnosis of prostate cancer based on the limited material available for review. The remaining 29 confirmed prostate cancer cases with an identified BRCA1 or BRCA2 founder mutation, and a total of 145 individually matched non-carrier cases constituted the pathology review group.
Mutation carriers and non-carriers were comparable with respect to all the histological characteristics evaluated. While prostate cancer among carriers was more likely to arise in the setting of chronic prostatitis and to be associated with neuroendocrine features than was prostate cancer in non-carriers, these findings were not statistically significant. No significant differences were noted in either the mean primary or secondary Gleason grades or in the Gleason sum (table 2).

A number of case series have examined the carrier frequency among Ashkenazi men with prostate cancer (4–6) (table 3). While the numbers of mutation carriers included in these studies have been very small, these studies have not suggested a large increase in prostate cancer risk associated with founder mutations. One small case-control study of Israeli prostate cancer cases and matched controls did not suggest an increased carrier frequency among cases, but provide a suggestion of a more aggressive phenotype among mutation carriers.

Two larger studies have estimated risk of prostate cancer indirectly, based on the history of prostate cancer in relatives of founder mutation carriers and non-carriers. 12 Struewing and colleagues used a kin cohort analytic approach to estimate the cumulative incidence of cancer associated with Ashkenazi founder mutations in a study of over 5000 American Ashkenazi Jewish volunteers from the Washington DC area [the Washington Ashkenazi Study (WAS)].1 In this study, the founder mutations were found at a similar frequency to that reported in previous studies of Ashkenazi Jews. The risk of prostate cancer by 70 years of age was estimated to be 16% (95% CI 4%–30%) among male carriers of any founder mutation, compared with 3.8% among non-carriers (95% CI 3.3%–4.4%), a risk equal to that of

<table>
<thead>
<tr>
<th>Pathological feature</th>
<th>Carriers</th>
<th>Non-carriers</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Benign and pre-neoplastic features</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Atrophy</td>
<td>3/29</td>
<td>11/145</td>
</tr>
<tr>
<td>Benign prostatic hyperplasia</td>
<td>5/16</td>
<td>19/13</td>
</tr>
<tr>
<td>Chronic prostatitis</td>
<td>9/23</td>
<td>23/16</td>
</tr>
<tr>
<td>Basal cell hyperplasia</td>
<td>1/3</td>
<td>10/7</td>
</tr>
<tr>
<td>Atypical adenomatous hyperplasia</td>
<td>0/2</td>
<td>2/1</td>
</tr>
<tr>
<td>Atypical small acini proliferation</td>
<td>1/3</td>
<td>9/6</td>
</tr>
<tr>
<td><strong>Prostatic intraepithelial neoplasia</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Low grade</td>
<td>3/1</td>
<td>17/12</td>
</tr>
<tr>
<td>High grade</td>
<td>4/14</td>
<td>38/26</td>
</tr>
<tr>
<td><strong>Adverse pathological features</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Perineural invasion</td>
<td>16/55</td>
<td>77/53</td>
</tr>
<tr>
<td>Lymphovascular invasion</td>
<td>0/2</td>
<td>5/3</td>
</tr>
<tr>
<td>Neuroendocrine features</td>
<td>6/21</td>
<td>13/9</td>
</tr>
<tr>
<td>Extra prostatic extension</td>
<td>3/10</td>
<td>6/4</td>
</tr>
<tr>
<td>Seminal vesicle involvement</td>
<td>1/3</td>
<td>2/1</td>
</tr>
<tr>
<td>Any adverse feature</td>
<td>21/72</td>
<td>95/66</td>
</tr>
<tr>
<td>Mean Gleason Score</td>
<td>7.1</td>
<td>7.0</td>
</tr>
</tbody>
</table>
The incidence of prostate cancer in carriers in the WAS was elevated by the age of 50 years, was statistically significantly elevated by 67 years, and increased thereafter with age, approaching 30% by 80 years, suggesting both an overall excess in prostate cancer risk, and an increased risk of early onset disease among founder mutation carriers. While confidence limits were widely overlapping in the WAS analysis, the risk of prostate cancer appeared higher among individuals with BRCA1 mutations than those with BRCA2 mutations, and there was some suggestion of early onset disease among those with a BRCA1 5382insC mutation. In that study, the number of individuals with a family history of prostate cancer was 5/40 (12%), 5/20 (25%), 6/54 (11%), 16/114 (14%), and 364/4759 (8%) for 185delAG, 5382insC, 6174delT, BRCA1 mutations, and there was some suggestion of early onset disease among those with a BRCA1 5382insC mutation. In this study, we did observe an overall twofold increased risk of PrC (p<0.01).

Warner and colleagues studied the risk of breast, ovarian and other cancers in the first degree relatives of 412 Ashkenazi Jewish women with breast cancer unselected for age or family history, who elected to undergo mutation testing. Among first degree relatives of carriers of any founder mutation, the risk of breast cancer was estimated to be 34% by the age of 85 years compared with 12.6% among non-carriers (p = .05). Interestingly, this study appeared to enrich for carriers of the BRCA1 185delAG mutation, despite the nearly equal frequencies of the BRCA1 185delAG and the BRCA2 6174delT mutations in the general Ashkenazi population. Only 15 (3.6%) of breast cancer patients in this study carried a 6174delT mutation compared with 26 (6.3%) patients who carried a 185delAG mutation, perhaps reflecting variable penetrance of these two mutations for breast cancer. Differences in subject ascertainment could account for the observed differences in the estimated risk of prostate cancer in these two studies.

In our population based series, 3.2% of Israeli Ashkenazi men with an incident diagnosis of prostate cancer, unselected for family history of breast and/or ovarian cancer, carried an Ashkenazi founder mutation. No population controls were obtained as part of this study. This represents a major limitation of our study design. We have attempted to address this limitation though comparison with existing Ashkenazi groups for which age and sex specific estimates of the founder mutation rate are available, i.e., the WAS and the MECC.

The MECC data are derived from a population based study of Israeli men and, while relatively small, is the best available Israeli comparison group. There is no statistical difference in the mutation frequency among participants in the MECC (1.69%), which may over-represent Ashkenazi Jews immigrating from the former Soviet Union, and in that observed in the WAS (1.49%), composed predominantly of immigrants from Germany, Poland and Austria. Estimates of the Ashkenazi BRCA1 founder mutation prevalence have been reported for several populations. These rates are strikingly similar across Ashkenazi populations living in various geographical regions. We therefore thought it reasonable to combine the data from the MECC and WAS studies.

In the current study, we did observe an overall twofold risk of prostate cancer among founder mutation carriers.

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**Table 3** Risk of prostate cancer associated with BRCA1/2 Ashkenazi Jewish (AJ) founder mutations (literature review)

<table>
<thead>
<tr>
<th>Study</th>
<th>Population</th>
<th>BRCA1</th>
<th>BRCA2</th>
<th>Outcomes</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Number (%) of individual subjects tested</td>
<td>185delAG</td>
<td>5382insC</td>
<td>6174delT</td>
</tr>
<tr>
<td>Kin cohort</td>
<td>N. American AJ volunteers; mutation carriers and non-carriers</td>
<td>5318 41 (0.8)</td>
<td>20 (0.4)</td>
<td>59 (1.2)</td>
</tr>
<tr>
<td>Foulkes et al</td>
<td>N. American AJ women with breast cancer</td>
<td>412 26 (6.3)</td>
<td>8 (1.9)</td>
<td>15 (3.6)</td>
</tr>
<tr>
<td>Case-control</td>
<td>Unselected Israeli AJ prostate cancer cases.</td>
<td>87 2/87</td>
<td>—</td>
<td>1/87</td>
</tr>
<tr>
<td>Hubert et al</td>
<td>Elderly Israeli AJ male controls</td>
<td>87 2/87</td>
<td>—</td>
<td>1/87</td>
</tr>
<tr>
<td>Case series</td>
<td>Unselected Israeli AJ men with prostate cancer</td>
<td>95 2/87(2.3)</td>
<td>2/60(3.3)</td>
<td>1/86 (1.2)</td>
</tr>
<tr>
<td>Lehrer et al</td>
<td>prostate cancer recruited from urology/radiation oncology clinics</td>
<td>60 0/60</td>
<td>—</td>
<td>0/60</td>
</tr>
<tr>
<td>Nastiuk et al</td>
<td>N. American AJ with prostate cancer; pathology review</td>
<td>83 1(1.2)</td>
<td>—</td>
<td>2 (2.4)</td>
</tr>
<tr>
<td>Vazina et al</td>
<td>Unselected Israeli AJ men with prostate cancer; pathology review</td>
<td>95 2/87(2.3)</td>
<td>2/60(3.3)</td>
<td>1/86 (1.2)</td>
</tr>
</tbody>
</table>

AJ, Ashkenazi Jew.
While increased risk of prostate cancer among carriers of the \textit{BRCA1} 185delAG and the \textit{BRCA2} 6174delT mutations appeared to be comparable (within the constraints of small numbers), only the estimate for the all mutations combined achieved statistical significance (p<0.05). No increased risk was associated with the 5382insC mutation in this study. The mean age at diagnosis among \textit{BRCA1} mutation carriers did not differ significantly from that of the \textit{BRCA2} mutation carriers, and neither differed significantly from the age at diagnosis among non-carriers. We found no evidence in this study to suggest an earlier than usual age of diagnosis in \textit{BRCA} associated prostate cancer.

Interestingly, data from both the WAS and the MECC suggest that the \textit{BRCA} founder mutation prevalence rate may decrease with age. This would suggest that employing the overall \textit{BRCA} founder mutation frequency of approximately 2.4%~^{+}~^{7}~^{8}~^{11} as the comparison, rather than an age specific prevalence estimate, will result in an underestimation of the risk of prostate cancer. If one takes into account a possible decline in founder mutation prevalence with age, our findings are consistent with at most a 2–4 fold increase in the risk of prostate cancer among carriers of an Ashkenazi \textit{BRCA} founder mutation.

Differences in the reported mutation specific risks probably represent statistical fluctuation related to small sample sizes. While a well designed, population based case-control study testing the hypotheses we explore here would be desirable, a study sufficiently powered to detect mutation specific risks is probably unfeasible. To detect reliably (with a power of 90%) an odds ratio of 1.5 for the separate mutations 185delA, 5382 insC, and 6174delT, one would need total sample sizes of approximately 25 000, 100 000 and 25 000 respectively, assuming equal numbers of cases and controls. However, there would be little clinical interest in such small odds ratios, as risks at this level would result in a very low population attributable risk (%), (calculated by 100.P.OR/ (P.OR + 1–P), where P = prevalence of mutation in the general population and OR = odds ratio) associated with \textit{BRCA} founder mutation status. In our study, P = 0.0156 and OR = 2.08, so that the population attributable risk = 3.2%. Thus, although the relative risk of prostate cancer among carriers of \textit{BRCA} Ashkenazi Jewish founder mutations is significantly elevated, founder mutations explain only a small percentage of all prostate cancers occurring among Ashkenazi men. In view of the moderately high incidence of prostate cancer among Ashkenazi Jews, the absolute number of cases attributable to the founder mutations is not inconsequential, but alternative aetiological explanations must be sought for the majority of prostate cancers.

This study represents the largest reported series of \textit{BRCA} related prostate cancer to have undergone detailed, blinded histopathological review. Only one study to date has examined the clinical characteristics of prostate cancer diagnosed in Ashkenazi mutation carriers. In a small case-control study of Israeli Ashkenazi Jewish men with prostate cancer, Hubert and colleagues reviewed the pathology of three \textit{BRCA} associated prostate cancers (two patients with \textit{BRCA1} 185delAG mutations and one patient with a \textit{BRCA2} 6174delT mutation). They suggested that these tumours appeared to be associated with biologically more aggressive disease. These cancers presented with higher PSA levels, higher Gleason scores and more advanced stage at diagnosis than did prostate cancers diagnosed in men without mutations.\footnote{While data on initial stage and PSA at diagnosis were not available in our study, we found no evidence for distinctive clinical or pathological features among prostate cancer cases associated with an Ashkenazi founder mutation compared with prostate cancers occurring among non-carriers. It is interesting to note that the majority of carriers were diagnosed by needle biopsy rather than at prostatectomy. We have insufficient information to address the basis for this association. We selected prostate cancer cases diagnosed from 1994–1995, a time period antedating the widespread use of PSA screening in Israel. Therefore, we believe it unlikely that a detection bias due to differential PSA screening among men with a family history of breast and/or ovarian cancer could account for this association. Some clustering of chronic prostatitis was noted among cases with mutations, which may suggest a predilection for \textit{BRCA} associated prostate cancers to arise in this setting. We did not find a higher Gleason Score among mutation positive cases.}

In summary, our findings are consistent with previous reports of a modest increase in the risk of prostate cancer associated with the Ashkenazi founder mutations. This risk is unlikely to exceed a fourfold increase. This level of risk may warrant consideration of male carriers of Ashkenazi founder mutations as candidates for inclusion in high risk prostate cancer screening and/or risk reduction studies. Our review of the pathological characteristics of founder mutation \textit{BRCA} associated prostate cancer, while based on a relatively small number of cases, does not suggest that these cases display a more aggressive phenotype.

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ECHO

Genotype-phenotype analysis of the Crohn’s disease susceptibility haplotype on chromosome 5q31

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Background and aims: Recent molecular data suggest that genetic factors may underlie the disease heterogeneity observed in both ulcerative colitis (UC) and Crohn’s disease (CD). A locus on chromosome 5q has been implicated in susceptibility to CD, and recently refined by linkage disequilibrium mapping to a conserved 250 kb haplotype (5q31). No data regarding the contribution of this locus to clinical phenotype exist. In this case control study, we investigated the contribution of this haplotype to both susceptibility and phenotype of CD and UC.

Patients and methods: We studied 330 Caucasian CD and 457 UC patients recruited from one single UK centre. Association with disease susceptibility and phenotype was analysed with genotype-phenotype analysis of the Crohn’s disease susceptibility haplotype on chromosome 5q31.

Results: Linkage disequilibrium across this region was confirmed, with two haplotypes comprising 88% of all chromosomes. Susceptibility to CD, but not to UC, was associated with homozygosity for a common haplotype, H2 (p = 0.0022; relative risk (RR) 2.0). Genotype-phenotype analyses demonstrated that this association was particularly strong in patients with perianal disease (p = 0.0005; RR 1.7), especially in individuals homozygous for this haplotype (p = 0.0005; RR 3.0). Importantly, no association with H2 was found in 186 patients without perianal disease. No evidence of epistasis between IBDS and NOD2/CARD15 was sought.

Conclusions: The IBDS risk haplotype is associated with CD only. Genotype-phenotype analysis reveals that the strongest association is observed in patients with perianal CD. While the precise gene involved is unclear, these data provide further molecular evidence for a genetic basis of the clinical heterogeneity of CD.
A twofold increase in BRCA mutation related prostate cancer among Ashkenazi Israelis is not associated with distinctive histopathology


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The formation of intracellular amyloid-like inclusions by mutant proteins is a feature of two groups of codon reiteration diseases, for which there are currently no treatments. The first group that was described includes the nine known neurodegenerative conditions caused by polyglutamine (polyQ) repeat expansions resulting from CAG trinucleotide repeat mutations, exemplified by Huntington’s disease (HD). HD is caused by a tract of more than 37 uninterrupted polyglutamines in exon 1 of the HD gene product, huntingtin. Genetic and transgenic studies are consistent with a model where expanded polyglutamines cause disease by conferring a novel toxic function on the disease proteins.\(^1\)\(^2\)\(^3\)

The second type of codon reiteration mutation results in autosomal dominant oculopharyngeal muscular dystrophy (OPMD).\(^4\) OPMD is caused by the abnormal expansion of a \((\text{GCG})_n\) trinucleotide repeat in the coding region of the polyadenine binding protein 2 gene (\(\text{PABP2}\)). \((\text{GCG})_n\) repeat is expanded to \((\text{GCG})_{6–13}\) in most patients. In some rare cases, insertion mutations such as \((\text{GCG})_6\text{GCA}\text{(GCG)}_2\), \((\text{GCG})_6\text{GCA}\text{(GCG)}_3\) and \((\text{GCG})_6\text{(GCA)}_3\text{(GCG)}_2\) are seen.\(^5\)\(^6\)

In \(\text{PABP2}\), \((\text{GCG})_n\) codes for the first six alanines in a homopolymeric stretch of 10 alanines. Thus, disease is associated with expansions of 12 or more uninterrupted alanines in this nuclear protein. OPMD is characterised by aggregates in muscle cell nuclei comprising mutant \(\text{PABP2}\) as a major component.\(^7\)\(^8\)\(^9\)

The role of inclusions in these diseases has been vigorously disputed.\(^1\) Nevertheless, strategies that target protein misfolding frequently reduce aggregate formation and cell death in parallel. In mammalian cell based models of both polyglutamine and polyalanine diseases, the mutant proteins are much more prone to aggregate formation than their wild-type counterparts and cause significantly more cell death.\(^10\)\(^11\)\(^12\) In such models, aggregate formation and cell death can be reduced by overexpressing yeast and bacteria derived chaperones that do not appear to protect against some other cell death pathways.\(^13\)\(^14\)\(^15\) A causal role for aggregation in cell death in tissue culture models of OPMD is supported by complementary data from our lab and Rouleau’s group.\(^16\)\(^17\)\(^18\) Rouleau and colleagues found that oligomerisation of \(\text{PABP2}\) is mediated by two potential oligomerisation domains (ODs)—deletions in either of these domains inactivated oligomerisation of mutant \(\text{PABP2}\) and also reduced the cell death caused by this protein.\(^19\)

The similarities between polyglutamine diseases and OPMD have led us to explore whether strategies that protect against polyglutamine aggregation or toxicity are also effective in OPMD models. Our previous studies suggested that mammalian heat shock proteins might be able to play similar roles in both diseases.\(^11\)\(^15\) Members of the \(\text{HSP70}\) and \(\text{HSP40}\) family members are recruited to polyQ inclusions in vivo and in cell models.\(^11\)\(^15\)\(^16\)\(^17\)\(^18\)\(^19\) We have tested if this is the case in OPMD patients, as we had previously shown that this occurred in a cell model of OPMD.\(^20\) We have previously shown that HDJ1, an \(\text{HSP40}\) family member, reduced aggregate formation and cell death in cell models of HD and OPMD.\(^11\)\(^15\) Since HDJ1 is a co-chaperone for \(\text{HSP70}\), we have now tested if \(\text{HSP70}\) chaperone is effective in cell models of OPMD, as it can be effective in HD.\(^25\)

Since it may be possible to treat these diseases with compounds that reduce aggregate formation, we have been testing a number of anti-amyloid compounds in cell based models of OPMD (where no animal models have been published). We tested Congo red, as data from Ross and colleagues suggested that it blocked the conversion of mutant huntingtin protofibrils into mature fibrils\(^20\) and Sanchez et al showed that Congo red reduced aggregation and cell death in HD cell models.\(^21\) The latter study also reported that infusion of Congo red into an HD mouse model by the intraperitoneal and intracerebroventricular routes improved survival, weight loss, and motor function, compared with untreated mutant mice.\(^22\) These data provided important insights into the role of inclusions polyglutamine disease pathology and suggested that the beneficial effects of Congo red were due to its

**Key points**

- Intracellular amyloid-like inclusions formed by mutant proteins result from polyglutamine expansions in Huntington’s disease (HD) and polyalanine expansions in polyadenine binding protein 2 (PABP2) in oculopharyngeal muscular dystrophy (OPMD).
- Here we show further parallels between these diseases and suggest therapeutic strategies for OPMD. Like polyglutamine diseases, HSP70 and HDJ-1 colocalised with PABP2 aggregates in OPMD patient muscle tissue and overexpression of HSP70 reduced mutant PABP2 aggregate formation. Aggregate formation and cytotoxicity in cell models of OPMD were reduced by Congo red or doxycycline.
- Our data highlight the therapeutic potential of these compounds in oculopharyngeal muscular dystrophy.

**Abbreviations:** DAPI, 4’, 6-diamidino-2-phenylindole; DMEM, Dulbecco’s modified Eagle’s medium; Dox, doxycycline hydrochloride; EGFP, enhanced green fluorescent protein; GFP, green fluorescent protein; HD, Huntington’s disease; HSP, heat shock protein; OD, oligomerisation domain; OPMD, oculopharyngeal muscular dystrophy; PABP2, polyadenine binding protein 2; polyQ, polyglutamine
anti-aggregate properties. Unfortunately, the therapeutic potential for Congo red in HD may be minimal, because of its very poor blood brain barrier permeability. On the other hand, brain penetration would not be an issue for a muscle disease like OPMD. We also tested doxycycline as an anti-aggregate compound, since previous studies had suggested that tetracyclines were anti-amyloidogenic.

MATERIALS AND METHODS

Cell culture and transfection

African green monkey kidney (COS-7) cells were grown in Dulbecco’s modified Eagle’s medium (DMEM 5471 (Sigma) supplemented with 10% fetal bovine serum, 100 units/ml penicillin/streptomycin, and 2 mM L-glutamine at 37°C, 5% CO2. For transfection of plasmid DNA, cells were seeded on coverslips at 0.6–1×105 per well, in 6-well plates, the day before transfection. Cells were transfected with Lipofectamine (Life Technologies) according to the manufacturer’s instructions. Constructs are described in refs 11 (PABP2) and 15 (HSP70).

Compounds and treatment

Congo red (Sigma) was dissolved in DMEM 5671(Sigma) with a stock concentration of 10 mg/ml. Doxycycline hydrochloride (Dox) (Sigma) was dissolved in water with a stock concentration of 100 mg/ml. All the stock solutions were sterilised through a filter with a 0.2 µm pore diameter. The compounds were diluted to the required concentration in the cell culture medium immediately before use. At 24 h after transfection, the compounds were added to the cells at different concentrations. The cells were incubated with the compounds for another 24 h and then washed with 1 x phosphate buffered saline, fixed in 4% paraformaldehyde for 20 min, mounted in antifadent reagent supplemented with 3 µg/ml of 4’, 6-diamidino-2-phenylindole (DAPI) to allow visualisation of nuclear morphology.

Western blotting analysis

Cells were lysed with Laemml buffer (0.0625 M Tris-HCl, pH 6.8, 2% SDS, 5% β-Mercaptoethanol, 10% Glycerol, 0.01% Bromophenol Blue). Lysates were subjected to SDS-polyacrylamide gel (10%) electrophoresis and transferred to a nitrocellulose membrane (Amersham Pharmacia Biotech, UK). The membrane was incubated with mouse polyclonal anti-HSP70 (StressGene, 1:1000), mouse polyclonal anti-HDJ-1 (StressGene, 1:1000) and rabbit anti-actin (Sigma, anti-HSP70 (StressGene, 1:1000), mouse polyclonal anti-actin (Sigma, UK). The membrane was incubated with mouse polyclonal antibody together with the monoclonal mouse anti-HSP70 (1:200), or by using anti-PABP2 antibody together with the monoclonal mouse anti-

Measurement of aggregate formation and abnormal cell nuclei

Cells were fixed with 4% paraformaldehyde at 72 h after transfection and counterstained with DAPI. Aggregate formation and nuclear morphology were assessed with a fluorescence microscope. Two hundred enhanced green fluorescent protein (EGFP) expressing cells were counted (with the observer blinded to the slide identity) across the centre region of the slides, to quantify all types of polyalanine aggregates in the cells. We assessed the proportions of PABP2-A17 expressing cells that contained one or more inclusions. We considered cells to have inclusions if the green fluorescent protein (GFP) was abnormally concentrated and differed from the nuclear speckled appearance typically seen with the normal PABP2-A10. Cells were considered dead if the DAPI-stained nuclei showed apoptotic morphology (fragmentation or pyknosis). Pyknotic nuclei are typically <50% diameter of normal nuclei and show obvious increased DAPI intensity. We have demonstrated that these criteria are specific for cell death, as they show a very high correlation with propiodium iodide staining in live cells.

Confocal microscopy

Fluorescently labelled samples were analysed using the laser scanning microscope Zeiss LSM410 equipped with an argon ion laser (wavelength, 488 nm) to excite FITC fluorescence, and a helium neon laser (wavelength, 543 nm) to excite Texas red fluorescence. For double labelling experiments, images from the same focal plane were sequentially recorded in different channels and merged to confirm colocalisation.

Statistical analysis

As we and others have described previously, pooled estimates for the changes in inclusion formation resulting from perturbations assessed in multiple experiments were calculated as odds ratios with 95% confidence intervals:

\[
\frac{\text{% cells expressing construct with inclusions in perturbation conditions}}{\text{% cells expressing construct without inclusions in perturbation conditions}}
\]

\[
\frac{\text{% cells expressing construct with inclusions in control conditions}}{\text{% cells expressing construct without inclusions in control conditions}}
\]

Odds ratios and p values were determined by unconditional logistical regression analysis using the general log/linear analysis option of SPSS ver 6.1 software (SPSS, Chicago, USA). p<0.05 was considered to be statistically significant.

RESULTS

To test if the intranuclear inclusions in OPMD patients sequester heat shock proteins (HSPs) in a manner similar to what we described in cell models, we used double staining
immunohistochemistry to allow simultaneous analysis of both mutant PABP2 and the relevant HSPs. Fig 1 shows colocalisation of HSP70 and HDJ-1 (HSP40 family) in inclusions in the DAPI stained nuclei of OPMD muscle. Similar findings were observed in samples from two OPMD patients. No colocalisation of these HSPs with PABP2 was seen in two control muscle samples (data not shown). The anti-PABP2 antibody we have used has been previously used to distinguish between cells with and without PABP2 aggregates. The strong nuclear staining for the chaperones correlated strongly with the cells with nuclear aggregates (fig 1).

Previously, we showed that GFP tagged mutant PABP2 with 17 alanines (PABP2-A17) resulted in increased intranuclear aggregate formation and cell death, compared with otherwise identical constructs with 10 alanines. HSP70 co-expression with GFP tagged mutant PABP2 with 17 alanines (PABP2-A17) significantly reduced the proportion of GFP positive cells with aggregates, compared with cells cotransfected with an empty vector control (pFlag-empty) (fig 2). HSP70 overexpression reduced the toxicity of mutant PABP2 in parallel with the reduction in aggregates (fig 2). Fig 2B shows that total HSP70 levels increase in cells transfected with HSP70, or in cells treated with sodium arsenite, which induces a heat shock response (as a positive control).

We considered Congo red and doxycycline as chemical chaperones with the potential to reduce mutant PABP2 aggregation and toxicity. COS-7 cells (the only cell model that has been reported to show aggregation and cell death as a readout for mutant OPMD toxicity) were transfected with GFP-tagged mutant PABP2 with 17 alanines (PABP2-A17). Twenty four hours after transfection, we added different concentrations of Congo red and doxycycline for the next 24 h and then assessed the proportions of GFP positive cells with aggregates and cell death (as scored by apoptotic nuclear morphology). We found that both Congo red and doxycycline reduced aggregation and cell death caused by mutant PABP2 (fig 3A). These effects were not caused by these compounds inducing raised levels of stress inducible HSPs, like HSP70 (fig 3B). While Congo red did not protect against cell death caused by incubating cells in staurosporine (2.5 μM) or H2O2 (400 μM), protective effects were observed with doxycycline (fig 3C). In these experiments,
Figure 3 Congo red and doxycycline (Dox) reduce aggregation and cell death in cell models of OPMD and HD. (A) COS-7 cells were transfected with PABP2-A17. Congo red or Dox with different doses were added 24 h after transfection. Cells were incubated with the compounds for another 24 h and then fixed and stained with DAPI. The proportions of cells with aggregates and nuclear fragmentation or condensation were determined. The odds ratios were derived from 2-4 independent experiments, each done in triplicate. The error bars represent the 95% confidence intervals for the odds ratios. p<0.05; **p<0.001; ***p<0.0001; not significant, p>0.05. The 95% confidence intervals for 50 μg/ml and 100 μg/ml Congo red overlap, suggesting that there are no significant differences between these doses. (B) Congo red and Dox do not stimulate the expression of HSP70. COS7 cells were transfected with PABP2-A17. 100 μg/ml of Congo red or 100 μM of Dox was added to the cells 24 h after transfection. Cells were harvested after another 24 h, Western blotting was carried out, and the expression level of HSP70 was detected. (C) Effects of Congo red (100 μg/ml) and Dox (100 μM) on cell death caused by pro-apoptotic agents. COS-7 cells were transfected with the vector pEGFP-C1 and the Congo red and doxycycline were added 24 h after transfection. After another 24 h, either H2O2 or Staurosporine were added to the cells (for 4 h and 6 h, respectively) before fixing the cells. Nuclear fragmentation and condensation were determined in GFP positive cells. The odds ratios were derived from 2-4 independent experiments, each done in triplicate. The error bars represent the 95% confidence intervals for the odds ratios. p<0.05; **p<0.001; ***p<0.0001; not significant, p>0.05.

cells were treated in the same protocol as described previously11, and staurosporine and H2O2 were added in the final 6 h and 4 h, respectively, of the experiment.

Discussion
Both polyglutamine diseases like HD and polyalanine expansion mutations in PABP2 are associated with intracellular inclusions, whose appearance correlates with cell death in model systems. In this study we have extended the parallels between these different types of codon reiteration mutations by demonstrating HSP70 and HDJ-1 colocalisation in PABP2 inclusions in vivo, which has been previously observed in HD and related polyglutamine diseases15–21. The failure to detect colocalisation of these HSPs with PABP2 in wild-type samples or outside the nucleus in OPMD tissues is likely to be because the HSP preferentially associate with the aggregated protein and because PABP2 is predominantly nuclear in steady state. HSP70 overexpression resulted in a reduction of mutant PABP2 and HD exon 115 aggregation and cytotoxicity. While this paper was being written, Abu-Baker et al published data also showing colocalisation of HSP70 with OPMD aggregates and reduction of these aggregates with overexpression of this chaperone.27 Since HSP70 can directly protect against certain apoptotic pathways, for instance by inhibiting cytochrome c-mediated caspase activation,28,29 it is important to be cautious about inferring a causal relationship between reduced aggregation and cell death in this context. Indeed, this cell death pathway is activated and contributes to the cytotoxicity in HD cell models.11

The reduction in aggregation and cell death mediated by Congo red and doxycycline against mutant PABP2 suggests that these compounds may have therapeutic potential, especially for OPMD. The concentrations that we have used are compatible with previous studies in HD models. We obtained significant reductions in aggregation and cell death caused by mutant PABP2 with 50 μg/ml (70 μM) Congo red, while Sanchez and colleagues reported reduction in their HD cell models with 100μM.32 Recently, Smith et al reported that doxycycline reduced aggregation in a slice culture model of HD at 30μM,30 while we observed protection in our OPMD model with 100μM. Doxycycline appears to be protective by reducing aggregation and also by reducing susceptibility to cell death pathways induced by apoptotic inducers like staurosporine and H2O2, the latter effect compatible with the data of Chen et al who showed minocycline reduced caspase activation in a mouse model of HD.31 However, since tetracyclines are predicted to protect against apoptosis by inhibiting caspases and caspase 1 is interleukin-1β-converting enzyme, the effects of tetracyclines may also be due to anti-inflammatory activity in certain in vivo disease models. While Congo red may have limited utility in HD due to its poor blood brain barrier permeability,32 it may be useful for diseases associated with aggregation outside the central nervous system, such as OPMD. Congo red appears to be a general amyloid protein ligand.33 In the case of HD, it blocks the conversion of protofibril to mature fibre formation in the aggregation process.34 Modelling studies reveal that Congo red is likely to break the continuity of the ordered structures of the β-sheets characteristic of polyalanine expansions,35,36 thus providing a molecular explanation for the effect we observed with the mutant PABP2 protein. The parallel protection that Congo red affords against the cytotoxicity of expanded polyglutamines and polyalanines is consistent with the idea that abnormal protein aggregation and accumulation may be deleterious in all intracellular amyloidoses, irrespective of the primary mutation.

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During the production process errors were introduced into Table 1 of this paper. The odds ratio value for the BRCA1 3382insC mutation in the WAS + MECC studies should read 0.95. The 95% CI for the BRCA2 6174delT and the total positive frequency should read 0.89–4.56 and 1.18–3.65, respectively.