

# Assessing educational priorities in genetics for general practitioners and specialists in five countries: factor structure of the Genetic-Educational Priorities (Gen-EP) scale

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**Purpose:** A scale assessing primary care physicians' priorities for genetic education (The Gen-EP scale) was developed and tested in five European countries. The objective of this study was to determine its factor structure, to test scaling assumptions and to determine internal consistency. **Methods:** The sample consisted of 3686 practitioners (general practitioners, gynecologists-obstetricians, pediatricians) sampled in France, Germany, the Netherlands, Sweden, and United Kingdom. We first determined the factor structure of the Gen-EP scale (30 items) on the whole sample. Scaling assumptions were then tested on each country using multitrait scaling analysis. Internal consistency was assessed across the five countries. **Results:** Six factors were identified accounting for 63.3% of the variance of the items. They represented the following priorities for genetic education: "Genetics of Common Diseases"; "Ethical, Legal, and Public Health Issues"; "Approaching Genetic Risk Assessment in Clinical Practice"; "Basic Genetics and Congenital Malformations"; "Techniques and Innovation in Genetics" and "Psychosocial and Counseling Issues." In each country, convergent and discriminant validity were satisfactory. Internal-consistency reliability coefficients (Cronbach's  $\alpha$ ) were all above the acceptable threshold (0.70). **Conclusion:** The Gen-EP scale could be a helpful instrument in different countries to organize and evaluate the impact of genetic educational programs for primary care providers. *Genet Med* 2008;10(2):99–106.

**Key Words:** genetics, continuing education, factor analysis, reliability

The implications for health service provision of genetic knowledge in all fields of medicine have been expanding since the mapping of the human genome.<sup>1–4</sup> It has been established in many surveys that knowledge of genetics among primary care providers is poor,<sup>5–9</sup> but physicians' willingness to be educated regarding genetic aspects of diseases has been poorly documented and only in qualitative surveys.<sup>5,8</sup> The topics doctors would consider to be training priorities for themselves are still unclear. Genetics in medicine is a very broad and hetero-

geneous field including biology, many disorders and conditions in clinical medicine, ethics, law, public health, psychology, but also computer techniques such as software for pedigree analysis, and innovations such as preimplantation diagnosis or pharmacogenomics. The use of a common assessment tool developed with the doctors themselves and defining more precisely some specific needs in core groups of competencies in genetics would be very helpful for different countries and different educational health care systems. Adapting the content of educational lectures to doctors' priorities may be relevant in improving the organization of teaching in genetic medicine.

As far as we know, no quantitative instrument to measure educational priorities in genetics is available in the literature. We have developed an instrument which will be helpful in adapting and evaluating the impact of continuing medical education training to actual clinical practice.

The doctors surveyed were general practitioners (GPs), pediatricians, and gynecologists-obstetricians. The latter two specialties can be considered as "2nd"-order primary care providers because children or pregnant women may use them to access genetic services.

In the context of the European project, GenEd,<sup>10</sup> which assessed the educational needs in genetics of primary care pro-

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viders, we developed a specific scale of 30 items called the Genetic Education Priorities (Gen-EP) scale. The objective of this article is to determine the factor structure of this scale and how it applied in each of the five European countries involved (France, Germany, the Netherlands, Sweden, and United Kingdom) assessing data quality, scaling assumptions, and internal consistency of the items.

## MATERIALS AND METHODS

### Design and sample

The GenEd study was carried out in 2004 in five European countries (France, Germany, the Netherlands, Sweden and United Kingdom) to assess the genetic educational priorities of GPs, gynecologists, and pediatricians. It was a postal survey with a self-administered questionnaire and small monetary incentive for the respondents (10€). In every country, at least one reminder was mailed. Some countries organized a second reminder and a telephone recall to achieve, if possible, a minimal size of 200 doctors by type of practice. This number was calculated for a precision of 10% for a 95% confidence interval of an outcome measure of 65% (high educational priority).

The doctors' samples were randomly selected either from representative databases of the practitioners (France, United Kingdom, the Netherlands, Sweden) or from professional organizations (Germany).

### The Genetic Educational Priority questionnaire (Gen-EP)

The complete questionnaire included 122 items, and 30 of them related to educational priorities in clinical genetics: the Gen-EP scale (Fig. 1).

The items were generated by a consortium of European experts composed of clinical geneticists (5), general and hospital practitioners (2), nurses (2), representatives of patients associations (2), and methodologists (5). Practicing GPs, pediatricians, and gynecologists were consulted about content. Every country was involved in the questionnaire design which was carried out in specific workshops. The first draft contained as many items as possible to maximize content validity and relevance to the field of genetics in medical practice. A five-point Likert scale response format was used to select each item priority ("lowest," "low," "moderate," "high," and "highest"). The first English version of the questionnaire was piloted in each country with English-speaking practitioners (GPs, pediatricians and gynecologists) to adapt the content and phrasing of the items. A new version was adapted consensually, and was translated following the "translation/back-translation" process. The translated versions were piloted among a small number of practitioners in every country.

### Statistical analyses

SPSS 12.0 software was used for all statistical analyses.

### Factor analysis

A principal components analysis was carried out on complete cases of the whole sample, i.e., on the GPs, gynecologists, and pediatricians who had answered the whole set of items. The aim of this analysis was to investigate the pattern underlying doctors' responses to the 30 items by allowing the detection of independent dimensions that explained the majority of the variance in the sample.

According to Kaiser's criterion, only components with eigenvalues  $>1$  were retained. The retained components corresponded to the different scales subsequently described, established, and named according to the items included. The names were given at a specific workshop between the partners to obtain a consensus. An orthogonal rotation (Varimax) was then performed to ease the interpretation of the different components. The variance explained by the selected components was evaluated.

For each component, every item's loading values were checked. A given item was taken to load on a single factor with a loading value  $>0.40$ .

Scaling assumptions, data quality, and check of internal consistency of the scales were investigated. The approach used in the International Quality of Life Assessment (IQOLA) project was chosen as a reference.<sup>11</sup> It is described in depth elsewhere.<sup>11</sup> We first determined the extent of missing and out-of-range data in item-level descriptive statistics. Second, we carried out a multitrait scaling analysis for the whole sample and for every country sample assessing item convergent and discriminant validity. Finally, we used the internal consistency method to assess the reliability of scale scores and interscale correlations across the countries.

### Item-level descriptive statistics: Likert assumptions

Likert assumptions at the item-level were first tested. The extent of missing data in the sample was evaluated. For a given item, a missing data rate lower than 5% was considered satisfactory. In addition, for each item, distribution of response choices was examined. A good item should have on one hand all its response choices used and on the other hand a symmetrical, if not normal, distribution. Items' mean and standard deviation were also examined in each scale to check their equivalence. Standard deviations values should be around 1.0.<sup>11</sup>

### Multitrait scaling analysis

The extent to which the items could be combined into the multi-item scales determined by the previous factor analysis was examined using multitrait scaling analysis. Multitrait scaling analyses were performed on the French, German, Dutch, Swedish, and British samples. Internal consistency of the scale (item convergent validity) was assessed by checking that each item was substantially linearly related to the scale of which it was supposed to be a part. Pearson's correlation coefficients were computed between items and their hypothesized scale (taking into account item-scale overlap). Evidence of convergent validity was defined as a correlation  $>0.40$ .

	Lowest	Low	Moderate	High	Highest
	priority	priority	priority	priority	priority
Chromosomes and chromosomal disorders	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Genes and mutations	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Mitochondrial inheritance	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Understanding of DNA results	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Taking a family history	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Drawing a pedigree	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Recognising that a condition is genetic	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Recognising inheritance patterns	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Numerical risk assessment...	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Genetics of cancer	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Genetics of malformations	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Genetics of cardiovascular diseases	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Genetics of pulmonary diseases	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Genetics of psychiatric/neurodegenerative disorders	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Genetics of diabetes	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Basic risk communication and counselling skills	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Psychosocial issues relating to genetic testing	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
How to identify and access patient support	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Informed consent process	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Population genetic screening (inc. newborn)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Sub-populations at increased risk (inc. minorities)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Current legal framework within your country relating to genetic testing	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Insurance issues and genetic testing	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Testing minors for late onset disorders	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Protecting genetic information: confidentiality and privacy	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Genetic variation in drug response (pharmacogenetics)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
New laboratory techniques	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Gene therapy	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Preimplantation genetic diagnosis (PGD)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
Use of computer databases for clinical diagnosis	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

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**Fig. 1.** The Gen-EP scale. Physicians were asked: We would like some information about your preferences for priorities for your own genetic education. Please indicate using the scale.

**Table 1**  
Response rates

	France	Germany	The Netherlands	Sweden	United Kingdom	Overall
General practitioners	48.7%	20.8%	37.0%	38.7%	23.1%	30.2%
Obstetricians and Gynecologists	45.8%	29.6%	51.5%	50.0%	29.9%	37.9%
Pediatricians	56.1%	41.9%	58.6%	49.0%	35.6%	45.9%
Overall	50.2%	30.8%	47.2%	45.2%	29.1%	37.7%

**Table 2**  
Item descriptive statistics

Item	N	Mean	SD	Missing (%)	Response values frequency (%)				
					Very low	Low	Moderate	High	Very high
Genetics of Common Diseases (GCD)									
Genetics of cardiovascular diseases	3589	3.07	1.06	2.63	8.40	20.90	33.60	29.80	7.40
Genetics of pulmonary diseases	3592	2.98	1.04	2.55	9.10	22.40	35.70	27.10	5.80
Genetics of psychiatric/neurodegenerative disorders	3596	3.01	1.04	2.44	8.40	22.60	34.60	28.40	6.00
Genetics of diabetes	3584	3.11	1.05	2.77	7.60	20.00	33.50	31.30	7.50
Genetics of cancer	3601	3.32	1.10	2.31	6.30	17.50	26.80	36.70	12.70
Ethical, Legal and Public Health Issues (ELPHI)									
Subpopulations at increased risk (including minorities)	3564	2.91	1.02	3.31	9.10	25.20	35.80	25.60	4.30
Testing minors for late onset disorders	3588	2.98	1.07	2.66	9.60	23.00	33.80	27.00	6.50
Insurance issues and genetic testing	3585	2.77	1.10	2.74	14.00	27.40	31.90	21.40	5.30
Current legal framework within your country relating to genetic testing	3588	2.98	1.06	2.66	9.30	22.40	36.20	25.40	6.80
Population genetic screening (including newborn)	3586	2.95	1.12	2.71	11.00	25.00	29.70	26.70	7.60
Protecting genetic information: confidentiality and privacy	3595	3.19	1.12	2.47	8.10	19.20	30.60	30.00	12.00
Approaching Genetic Risk Assessment in Clinical Practice (AGRACP)									
Taking a family history	3583	3.40	1.14	2.79	6.50	15.7	26.20	34.4	17.10
Drawing a pedigree	3577	3.03	1.12	2.96	9.50	23.1	31.70	25.9	9.80
Recognizing inheritance patterns	3581	3.57	0.95	2.85	2.80	10.20	28.00	44.7	14.30
Recognizing that a condition is genetic	3590	3.80	0.95	2.60	2.30	7.40	21.10	46.20	23.10
Numerical risk assessment	3574	2.93	1.04	3.04	9.10	25.00	35.10	25.50	5.20
Basic Genetics and Congenital Malformations (BGCM)									
Genes and mutations	3576	3.42	0.97	2.98	4.10	12.10	31.60	41.90	10.20
Chromosomes and chromosomal disorders	3567	3.48	0.99	3.23	3.7	12.2	29.7	41.7	12.8
Mitochondrial inheritance	3553	2.84	1.02	3.61	9.60	27.90	35.40	22.60	4.50
Understanding of DNA results	3569	3.59	0.95	3.17	3.10	9.9	26.10	46.7	14.20
Genetics of malformations	3590	3.50	0.98	2.60	3.30	12.40	28.20	43.00	13.00
Techniques and Innovation in Genetics (TIG)									
Gene therapy	3587	2.97	1.09	2.69	10.50	22.80	33.50	26.00	7.20
New laboratory techniques	3582	2.84	1.11	2.82	13.30	25.20	32.10	23.20	6.30
Preimplantation genetic diagnosis	3572	2.81	1.15	3.09	14.60	26.90	28.30	23.60	6.70
Use of computer databases for clinical diagnosis	3575	3.00	1.18	3.01	12.80	21.20	28.60	27.40	9.90
Genetic variation in drug response (pharmacogenetics)	3567	3.01	1.07	3.23	9.20	22.60	33.60	27.50	7.20
Psychosocial and Counseling Issues (PCI)									
Psychosocial issues relating to genetic testing	3587	3.24	1.01	2.69	5.10	17.50	35.80	31.90	9.70
How to identify and access patient support	3580	3.15	1.02	2.88	5.80	20.10	35.30	31.00	7.70
Basic risk communication and counseling skills	3578	3.38	1.05	2.93	5.00	14.90	30.60	36.30	13.10
Informed consent process	3575	3.12	1.03	3.01	6.80	19.70	35.90	29.80	7.90

Item-scale correlations were examined to see if each item contributed to its hypothesized scale roughly in the same proportion.

Item discriminant validity was supported and a scaling success counted whenever the correlation between an item and its hypothesized scale was more than two standard errors higher than its correlation with other scales. The standard error was here approximated to 1 divided by the square root of the sample size. A scaling failure was identified when

an item correlated lower with its hypothesized scale than with other scales.

#### Internal consistency

To establish internal consistency of the set of items, Cronbach's  $\alpha$  coefficients were computed for each scale. A Cronbach's  $\alpha$  value above 0.70 was considered satisfactory.

Pearson's correlation coefficients were computed among the six scales. For each pair of scales, the correlation coefficient was

**Table 3**  
Factor structure and factor loadings (>0.40) after Varimax rotation of 30 items ( $n = 3164$ )

Items	Components					
	1	2	3	4	5	6
Genetics of cardiovascular diseases	0.87	—	—	—	—	—
Genetics of pulmonary diseases	0.86	—	—	—	—	—
Genetics of psychiatric/neurodegenerative disorders	0.78	—	—	—	—	—
Genetics of diabetes	0.78	—	—	—	—	—
Genetics of cancer	0.51	—	—	—	—	—
Subpopulations at increased risk (including minorities)	—	0.69	—	—	—	—
Testing minors for late onset disorders	—	0.67	—	—	—	—
Insurance issues and genetic testing	—	0.67	—	—	—	—
Current legal framework within your country relating to genetic testing	—	0.66	—	—	—	—
Population genetic screening (including newborn)	—	0.65	—	—	—	—
Protecting genetic information: confidentiality and privacy	—	0.53	—	—	—	0.42
Taking a family history	—	—	0.80	—	—	—
Drawing a pedigree	—	—	0.78	—	—	—
Recognizing inheritance patterns	—	—	0.72	—	—	—
Recognizing that a condition is genetic	—	—	0.71	—	—	—
Numerical risk assessment	—	—	(0.36)	—	—	—
Genes and mutations	—	—	—	0.84	—	—
Chromosomes and chromosomal disorders	—	—	—	0.77	—	—
Mitochondrial inheritance	—	—	—	0.69	—	—
Understanding of DNA results	—	—	—	0.55	—	—
Genetics of malformations	—	—	—	0.53	—	—
Gene therapy	—	—	—	—	0.77	—
New laboratory techniques	—	—	—	—	0.75	—
Preimplantation genetic diagnosis	—	—	—	—	0.72	—
Use of computer databases for clinical diagnosis	—	—	—	—	0.54	—
Genetic variation in drug response (pharmacogenetics)	—	—	—	—	0.50	—
Psychosocial issues relating to genetic testing	—	—	—	—	—	0.81
How to identify and access patient support	—	—	—	—	—	0.74
Basic risk communication and counseling skills	—	—	—	—	—	0.69
Informed consent process	—	—	—	—	—	0.67
Eigenvalue before rotation	9.88	2.46	2.38	1.97	1.17	1.12
% of variance	32.90%	8.20%	7.90%	6.60%	3.90%	3.70%

then compared to the corresponding two Cronbach's  $\alpha$  coefficient. If the scale consistency reliability coefficients were greater than the Cronbach's  $\alpha$ , the scales were considered to measure a different concept.

## RESULTS

### Sample characteristics

The response rates to the postal survey differed significantly across the countries ( $P < 0.001$ ) (Table 1). GPs had the lowest response rates across the countries ranging between 21% in Germany and 49% in France ( $P < 0.001$ ). National samples from every country were compared with national statistics (when available). These comparisons have shown that women were under-represented in the German samples and that young doctors were also under-represented in nearly all the countries.

3686 doctors responded: 1168 GPs, 1167 gynecologist-obstetricians, and 1351 pediatricians. Their age was 50 on average (range, 25–70) and 39% were female. The five countries differed for these characteristics. Doctors from the Netherlands were the youngest, and the German and Swedish ones were the oldest.

### The Gen-EP scale

#### Missing data

Missing data occurred in  $<5\%$  of every item. The median percentage of item omission was 2.8% (range, 2.3–3.6%) with the highest omission rate for “mitochondrial inheritance.” Details are presented in Table 2.

#### Factor analysis

Principal components analysis was first performed on the overall 30 items. The doctors who answered the whole set of items ( $n = 3164$  of the 3686; 85.7%) were included in the analysis. Six independent components were identified because their eigenvalue was  $>1$ . Each component was named according to the items selected and included in the dimension (see

below in the subsequent paragraph on item descriptive statistics). They explained 63.3% of the variance. The factor loadings are displayed in Table 3.

Of the 30 items, 28 (93%) loaded on a single component with a loading value  $>0.40$ . The item “numeric risk assessment” had a loading value slightly lower than 0.40 (0.36). The item “protecting genetic information: confidentiality and privacy” loaded on two dimensions with loading values  $>0.40$  (0.54 on the “Ethical, Legal, and Public Health Issues” dimension and 0.43 on the “Psychosocial and Counseling Issues” dimension).

#### Item-level descriptive statistics

Based on the results of the factor analysis which demonstrated the existence of six components, the overall 30 items were grouped into six scales, each representing a particular field of genetics education. These subscales were named “Genetics of Common Diseases”; “Ethical, Legal, and Public Health Issues”; “Approaching Genetic Risk Assessment in Clinical Practice”; “Basic Genetics and Congenital Malformations”; “Techniques and Innovation in Genetics”; and “Psychosocial and Counseling Issues.”

The means and standard deviations of the items of every scale were comparable (Table 2). However, two items had a notably lower mean than the other items of their corresponding scale (“mitochondrial inheritance” and “numerical risk assessment”).

The distribution of the five available response choices for the 30 items was symmetrical and shown to be quasi-normal (Table 2).

#### Multitrait scaling analysis

*Convergent validity.* Across the five countries, nearly all the Pearson's correlation estimates were higher than 0.40, the value considered as satisfactory for convergent validity (Table

**Table 4**  
Item convergent validity, scaling failures and scale reliability

Scales	Convergent validity <sup>a</sup>					Scaling failures <sup>b</sup> (discriminant validity)				
	F	D	NL	S	UK	F (%)	D (%)	NL (%)	S (%)	UK (%)
GCD	0.61–0.86	0.49–0.80	0.31–0.76	0.40–0.81	0.45–0.84	0	0	4	0	0
ELPHI	0.54–0.70	0.55–0.70	0.54–0.73	0.56–0.70	0.51–0.72	0	0	0	0	0
AGRACP	0.43–0.75	0.33–0.64	0.59–0.73	0.42–0.73	0.35–0.78	0	16	0	12	20
BGCM	0.45–0.72	0.48–0.71	0.50–0.77	0.62–0.81	0.41–0.68	4	0	0	0	0
TIG	0.49–0.70	0.47–0.66	0.54–0.70	0.46–0.67	0.52–0.69	0	4	4	4	0
PCI	0.57–0.76	0.59–0.68	0.67–0.78	0.56–0.77	0.70–0.73	0	0	0	0	0
Overall						0.07	3.3	1.3	2.7	3.3

<sup>a</sup>Range of item-scale Pearson's correlation (corrected for overlap).

<sup>b</sup>Percentages of cases in which an item correlates lower with its own scale (corrected for overlap) than with other scales.

GCD, Genetics of Common Diseases; ELPHI, Ethical, Legal, and Public Health Issues; AGRACP, Approaching Genetic Risk Assessment in Clinical Practice; BGCM, Basic Genetics and Congenital Malformations; TIG, Techniques and Innovations in Genetics; PCI, Psychosocial and Counseling Issues; F, France; D, Germany; NL, The Netherlands; S, Sweden; UK, United Kingdom.

4). For three items, the correlations were not completely satisfactory with values of 0.33 and 0.35 for the German and British samples respectively (scale “Approaching Genetic Risk Assessment in Clinical Practice”) and 0.31 for the Dutch sample (scale “Genetics of Common Diseases”).

Within each scale, the range of item-scale correlations was comparable except for the scales including the three items mentioned above.

*Discriminant validity.* Overall scaling successes were noted in 95.3%, 93.3%, 94%, 96%, and 92.7% of the cases in the French, German, Dutch, Swedish, and British samples, respectively. Scaling failures were observed for 0.07%, 3.3%, 1.3%, 2.7%, and 3.3% of the cases in the French, German, Dutch, Swedish, and British samples, respectively (Table 4). The item “numerical risk assessment” represented 70.6% of the overall scaling failures.

*Scale-level descriptive statistics: reliability.* In each country, Cronbach’s  $\alpha$  estimates were above the recommended threshold of 0.70 (Table 5). Every interscale correlation coefficient was lower than its own Cronbach’s  $\alpha$ .

## DISCUSSION

We describe a 30-item scale (Gen-EP) constructed by a multidisciplinary and international team of clinical practitioners and researchers to assess the Genetic Educational Priorities perceived by different types of primary care providers. After the usual steps to construct this scale and to determine its content validity for different countries, we have shown its multifactor structure on the overall sample and that this structure applied to the five country samples studied (France, Germany, the Netherlands, United Kingdom, and Sweden). Convergent and discriminant characteristics of the items of the six factors extracted from the analysis are acceptable.

The development of such a scale is a multistep process. Here we present the first steps of this process but others remain to be carried out. The process of validation involves hypothesis testing and in particular confirmation that this scale does measure actual primary care doctors’ educational priorities in genetics. Generalizability studies will complement our approach, as will studies to assess more widely the ability of the Gen-EP scale to measure change. This may be of particular interest to measure the impact of vocational training on doctors’ assessment of their educational priorities in the context of their own practice. Priorities could be considered as a proxy of expectations about suitable training.

The six dimensions of the priorities mentioned by the practitioners represented complementary fields and specific contents of courses for genetic education in medical practice: They can be considered a homogeneous set of competencies necessary for clinical practice which could be organized in specific lectures “Genetics of Common Diseases”; “Ethical, Legal, and Public Health Issues”; “Approaching Genetic Risk Assessment in Clinical Practice”; “Basic Genetics and Congenital Malfor-

**Table 5**  
Reliability coefficients and interscale correlations

Scale	GCD	ELPHI	AGRACP	BGCM	TIG	PCI
France						
GCD	0.91					
ELPHI	0.44	0.85				
AGRACP	0.48	0.47	0.86			
BGCM	0.45	0.43	0.52	0.79		
TIG	0.42	0.57	0.3	0.46	0.8	
PCI	0.31	0.57	0.54	0.42	0.34	0.84
Germany						
GCD	0.86					
ELPHI	0.47	0.85				
AGRACP	0.43	0.38	0.76			
BGCM	0.4	0.48	0.38	0.79		
TIG	0.42	0.64	0.3	0.51	0.81	
PCI	0.4	0.56	0.48	0.38	0.41	0.81
The Netherlands						
GCD	0.87					
ELPHI	0.47	0.85				
AGRACP	0.49	0.53	0.87			
BGCM	0.32	0.52	0.51	0.83		
TIG	0.38	0.6	0.38	0.54	0.81	
PCI	0.46	0.64	0.56	0.47	0.47	0.87
Sweden						
GCD	0.86					
ELPHI	0.37	0.85				
AGRACP	0.43	0.49	0.82			
BGCM	0.23	0.49	0.53	0.87		
TIG	0.3	0.63	0.36	0.56	0.82	
PCI	0.34	0.62	0.55	0.5	0.45	0.85
United Kingdom						
GCD	0.87					
ELPHI	0.38	0.83				
AGRACP	0.36	0.36	0.85			
BGCM	0.25	0.38	0.44	0.76		
TIG	0.29	0.52	0.19	0.44	0.82	
PCI	0.31	0.62	0.55	0.32	0.26	0.87

Scale internal consistency reliability (Cronbach’s  $\alpha$  coefficient) is presented in bold in the diagonal.

mations”; “Techniques and Innovations in Genetics”; and “Psychosocial and Counseling Issues.” Clusters of topics, such as the ones described in the 30 items of the Gen-EP scale, instead of a list of heterogeneous topics offer a structure for training. We show that educational priorities in genetics are not a

unidimensional dimension of training to be covered comprehensively. Future analyses will allow comparison of these priorities by country and by specialty. Because no comparable instrument on doctors' educational needs in genetic education was available in the medical and educational literature through a Pubmed search, we could not compare our results to previous surveys. In two previous qualitative studies, it was shown that testing and counseling were areas of particular need for GPs,<sup>8,12</sup> and this priority is included in the "Psychosocial and Counseling Issues" scale. However, a standardized instrument such as the "Gen-EP" scale can give a more comprehensive assessment of educational needs in genetics to help the organization and assessment of training.

In the construction of the six factors, only one item was problematic: "numerical risk assessment." This item had a loading value lower than 0.40, the lowest threshold usually considered. As recommended by some methodologists,<sup>13</sup> to preserve content validity of the subscale we decided to keep this item in the scale "Approaching Genetic Risk Assessment in Clinical Practice." In justification, we considered that the development of software to assess genetic risks numerically is likely to be an issue for primary care providers in the years to come.

We developed this scale to be used for primary care doctors whatever their field of practice. We tested its performance for GPs, pediatricians, and gynecologists, but it could also apply to other medical specialists such as neurologists or cardiologists because the majority of the issues investigated cover common skills in genetics for every provider. However, using the Gen-EP scale for other specialists would require further confirmatory factorial analysis. The Gen-EP scale was validated for five European countries and the factors seemed to be adequate for each of them. Its suitability for other countries should also be confirmed by further analysis, but there is no reason to anticipate that these dimensions would not apply.

The availability of a specific scale to assess genetic educational priorities seems to be a new tool that could be very useful for organizing postgraduate continuous medical education in genetics and for assessing the impact of this training on a priori expectations. It also represents an original instrument for investigating doctors' interests in developing their knowledge

and skills in the field of medical genetics. This kind of approach is often used in medical education.<sup>14,15</sup> This will be helpful to anticipate whether primary care providers are ready (or not) to: update their knowledge; inform families about genetic risks and testing; and to adequately refer their patients to more specialized genetic services.

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