

PublisherInfo		
PublisherName	:	BioMed Central
PublisherLocation	:	London
PublisherImprintName	:	BioMed Central

Finding the bug in the system

ArticleInfo		
ArticleID	:	4376
ArticleDOI	:	10.1186/gb-spotlight-20020115-01
ArticleCitationID	:	spotlight-20020115-01
ArticleSequenceNumber	:	42
ArticleCategory	:	Research news
ArticleFirstPage	:	1
ArticleLastPage	:	2
ArticleHistory	:	RegistrationDate : 2002-01-15 OnlineDate : 2002-01-15
ArticleCopyright	:	BioMed Central Ltd2002
ArticleGrants	:	
ArticleContext	:	130593311

Tudor Toma

Email: t.toma@ic.ac.uk

After *Helicobacter pylori* was implicated in the development of peptic ulcers, other common diseases - such as asthma and atherosclerosis - were screened for known and unknown pathogens, but the available detection methods failed to reveal causative microorganisms. In the January 14 online issue of [Nature Genetics](#), Griffin Weber and colleagues from [Dana-Farber Cancer Institute](#), Boston, Massachusetts, USA describe a novel method to detect microbial causes behind infectious diseases by sequence transcript filtering against the human genome.

Weber *et al.* developed an *in silico* approach that employed the draft sequence of the human genome to identify nonhuman DNA sequences in expressed-sequence tag (EST) libraries of human origin. Using this method (called computational subtraction) they identified known viral pathogens such as HPV-18 in cervical carcinoma tissues (*Nat Genet* 2002, DOI: 10.1038/ng818).

"We therefore propose to generate, sequence and filter cDNA libraries from tissues of diseases such as systemic lupus erythematosus and extraintestinal Crohn disease, which are candidates for infectious etiology. [...] Further experiments could then distinguish sequences of benign commensal organisms from pathogen sequences by assessing the strength of their association with disease", concluded the authors.

References

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2. Dana-Farber Cancer Institute, [<http://www.dana-farber.org/>]