A database on cytogenetics in haematology and oncology

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ABSTRACT

The aim of ‘Atlas of Genetics and Cytogenetics in Oncology and Haematology’ (http://www.infobiogen.fr/services/chromcancer) is to present summarized information on chromosome abnormalities in cancer, with extensions to genes involved in cancer and to cancer-prone diseases. Information is to be updated. This database is made for and by cytogeneticists, molecular biologists, clinicians in oncology and in haematology, and pathologists.

INTRODUCTION

Aim

The spectrum of chromosome anomalies in cancer—often associated with a prognosis—is increasing to a point where it appeared necessary to take a census of the relevant items, review and summarize on each of them, and update both the information contained in the items and the census itself. The ‘Atlas of Genetics and Cytogenetics in Oncology and Haematology’ (http://www.infobiogen.fr/services/chromcancer) is an in-progress database, available via free access on the Internet, devoted to cytogenetics in cancer which includes data on genes and somatic genetics, cytogenetics and clinical entities in cancer, and on cancer-prone diseases. It is made for and by cytogeneticists, molecular biologists and geneticists in general, clinicians in oncology and in haematology, pathologists, cytologists and other related specialists, who are encouraged to contribute.

Organisation

The Atlas is being developed by INFOBIOGEN (INFOrmatique, BIOmolecules, GENomes) (http://www.infobiogen.fr), the CHU POITIERS (University Hospital of Poitiers) (http://www.chu-poitiers.fr) and the GFCO (French Group for the study of Cytogenetics in Oncology). Various scientific societies in the fields under study from various countries, are, or will be welcome as, informal partners.

STRUCTURE OF THE DATABASE

Cards

Cards on (i) genes, (ii) cytogenetic/clinical entities in haematology, (iii) solid tumours: cytogenetic/clinical entities, and (iv) cancer prone diseases represent the body of this Atlas. The purpose is to summarize and review on the main entities in the above mentioned fields; these cards are to evolve with further improvements and updates from various contributions. Rare entities (e.g., at least two cases of a given chromosome anomaly, or only one case if the gene is described) will also be reported. Cards are entry points; they are concise.

Aside

Deep insights, introductory items (Fig. 1), addresses of journals, addresses of databases, scientific societies’ presentations, and other possible developments are surrounding parts of the Atlas. Deep insights are papers focusing on a specific aspect when of particular interest. Introductory items may be used for teaching purposes.

Collaborations

Contributors are experts in the fields under study. Contributions are reviewed before acceptance. Guidelines for collaborations can be found in the ‘how to contribute’ section.

Navigation

We have designed the user interface to ease the navigation between all the objects described. The entities (genes and abnormalities) can be accessed by cytogenetic position or according to medical classification. The degree of cross referenc- ing will be increased with the next release.

CONTENTS OF THE CARDS

Cards on genes include data on: contributors; name(s) of the gene, location; DNA/RNA description; protein description; mutations; where this gene is implicated: diseases, with the prognosis and data on oncogenesis; a selected bibliography with hyperlinks to Medline abstracts (http://www.ncbi.nlm.nih.gov/Entrez/medline.html); and other external links towards: GENE CARD (http://bioinfo.weizmann.ac.il/cards/), the best cross-roads, GDB

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Figure 1. Diagrams of chromosome abnormalities (such as above), diagrams of genes and proteins will be available; photographs of chromosomes and other relevant images are planned to be included.

(1) for the necessary nomenclature, GenBank (2) where the DNA sequence is described, SWISS-PROT (3), which gives extensive data concerning the protein, HGMD (4) for the screening of mutations and OMIM (http://www.ncbi.nlm.nih.gov/Omim/) for clinical data on inherited diseases.

Cards on cytogenetic entities and on clinical entities in haematology, cards on solid tumours include data on: contributors; name of the disease; clinics, pathology description, treatment and prognosis; cytogenetics; genes involved: description and proteins description; result of the chromosomal anomaly; hybrid gene and fusion protein; a selected bibliography with hyperlinks to Medline (http://www4.ncbi.nlm.nih.gov/Entrez/medline.html) and another external link towards Resources for Molecular Cytogenetics (http://bioserver.uniba.it/fish/rocchi/welcome.html).

Cards on cancer-prone diseases include data on: contributors; name(s) of the disease with inheritance mode/epidemiology; clinics: phenotype and clinics, neoplastic risk, prognosis; cytogenetics: inborn condition, cytogenetics of cancers; other findings (ex: cell metabolism); genes and proteins description; mutations: germinal (inborn condition), somatic (tumourigenesis); a selected bibliography with hyperlinks to Medline (http://www.ncbi.nlm.nih.gov/Entrez/medline.html) and other external links towards: GENECARD (http://bioinfo.weizmann.ac.il/cards/), GDB (1), GenBank (2), SWISS-PROT (3), HGMD (4), OMIM (http://www.ncbi.nlm.nih.gov/Omim/) and also, whenever possible, external links towards registries and family associations.

COMMENTS

To contribute to the understanding of the expression of nucleic sequences, it is important to create links between these sequences and information on their function as well as on the diseases in which they are implicated.

To our knowledge, the Atlas of Genetics and Cytogenetics in Oncology and Haematology is the first database in free access and with open contributions devoted to cytogenetics in cancer on the Internet. It also contains data on the diseases and their prognoses. This repository gives the cross-references to the nucleic and proteinic sequences involved in these pathologies. It will be a link to other databases such as the probe resources and other various actors of the genome program.

At the present time, about half of the items which should be included are available in our database.

This database is intended to give assistance to cytogeneticists and clinicians, students and teachers in oncology as an entry point.

REFERENCES