BITS :: Call for Abstracts 2021 - Poster

Type	Poster
Session	Biological Databases
Title	KuNG FU, an interactive database for exploring kinase gene fusions landscape in human cancer cell lines
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Motivation

Kinases are a family of enzymes involved in key cellular functions, often found altered in cancer as a consequence of activating mutations, overexpression or gene fusions. Inhibition of kinase gene fusions (KGFs) is proven successful in cancer treatment as demonstrated by drugs targeting driver kinases activated due to KGF such as imatinib, entrectinib or larotrectinib. The advent of NGS analysis has extraordinarily increased the number of KGF candidates identified in patients and cancer cell lines, the latest thus representing a useful model for target validation and drug development. However, KGFs information is sparse in literature and public databases, often lacking extensive annotation and experimental evidences. To overcome these issues, we have implemented KuNG FU (KiNase Gene FUsion) database, a manually curated, free-available, interactive resource collecting potentially actionable and experimentally validated KGFs in cancer cell lines with detailed annotation, thus providing a tool in support to cancer research and drug discovery.

Methods

Abstracts published in Pubmed between 2013 and 2020 were automatically retrieved and filtered using a Python script for the presence of specific keywords. Automated searches of KGFs features in public databases combined with an extensive manual literature curation was applied in order to extract and collect detailed KGF information from the data mining of thousands of filtered scientific abstracts. Resulting dataset was stored in a MySQL relational database and provided with a web graphical interface developed using AngularJS (a Javascript framework) and powered by JQuery and Bootstrap. Stored data can be exported as txt or sql files. Graphical representation of the KGF constructs is visualized through AGFusion plot tool (Murphy, C. et al., 2016). Statistics related to KGFs are also available through graphs implemented in PHP and Javascript.

Results

In this work we describe the implementation of KuNG FU, a curated, user-friendly repository of experimentally validated KGFs in cancer cell lines. Only in-frame KGFs retaining an intact kinase domain are collected in KuNG FU, offering a set of potential biologically relevant and druggable targets. KuNG FU interface supports free-text searches and filtering by means of keywords, allowing quick interrogation among a broad panel of tumor-derived cell lines. KuNG FU output is organized in sub-sections and provides detailed information on each KGF, such as predicted breakpoints, transcripts and exons/introns involved in the rearrangement along with a graphical representation of the gene fusion construct and protein domain structure. The method used for experimental validation with PMID references and link to the Tumor Fusion Gene Data Portal database (https://www.tumorfusions.org/) are reported. KuNG FU also provides a 'statistics' section with a graphical representation of database content.
In the current release, kuNG FU database contains 108 KGFs belonging to 104 cancer cell lines, supported by experimental evidences. Overall, the cell lines included in KuNG FU are derived from 14 different tissue types. The database is update regularly and it is exportable as txt or sql files.
Open contributions from users are welcome through a dedicated web submission form.
KuNG FU is available at: http://www.kungfudb.org/

Info

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Figure

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Availability	http://www.kungfudb.org/
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