

# Creating An Open-source Gene Curation Database From The Gene Curation Coalition

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## Background

Several groups and resources provide information that pertains to the validity of gene-disease relationships; however, the standards and terminologies to define the evidence base for a gene's role in disease are still evolving and the community is in need of trusted and harmonized sources that define the level of evidence for a gene's role in disease. To tackle this issue, the **Gene Curation Coalition (GenCC)** was formed.

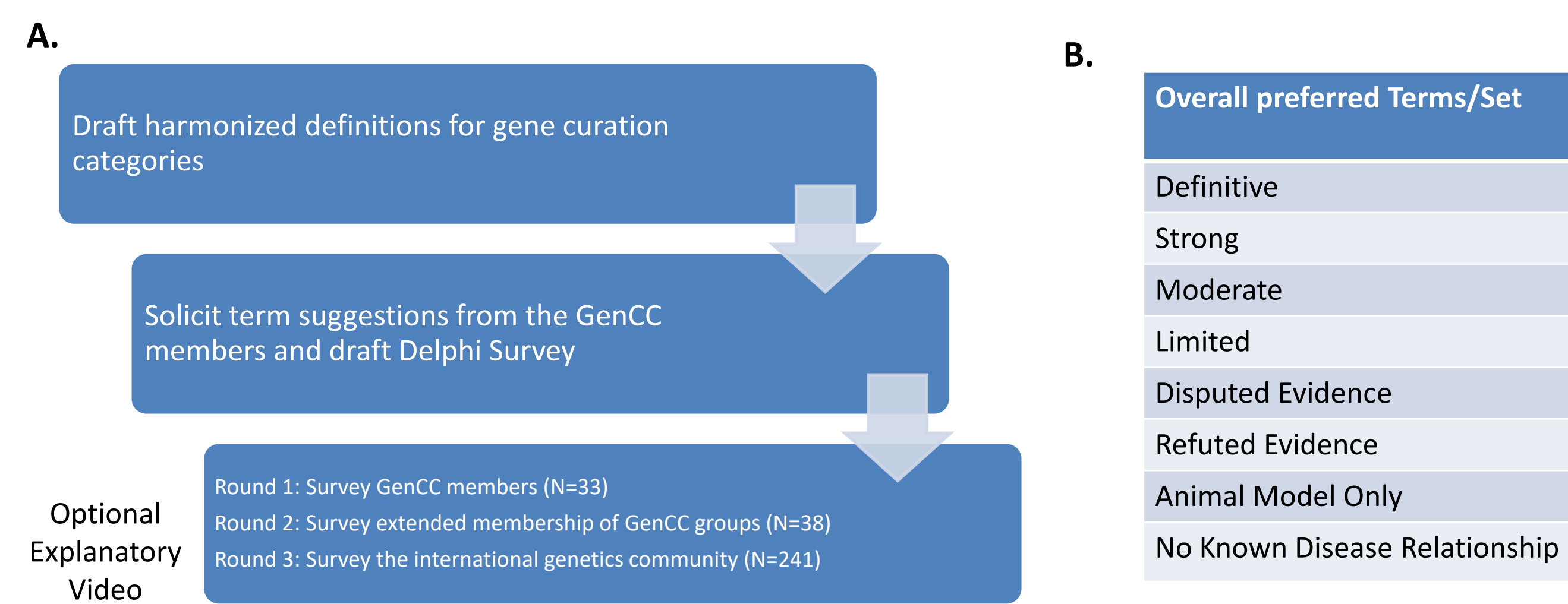
The Gene Curation Coalition brings together groups engaged in the evaluation of gene-disease validity with a willingness to share data publicly, to develop consistent terminology for gene curation activities and to facilitate the consistent assessment of genes that have been reported in association with disease.

The goals of the GenCC are as follows:

- Clarify the overlap between gene curation efforts
- Understand the aims, processes, information used, classification systems, and users of the different curation efforts
- Develop consistent terminology for validity assessment as well as inheritance, allelic requirement, and mechanism of disease
- Collaborate on gene curation projects

More information, news, and updates about the GenCC can be found on our newly launched website: [www.TheGenCC.org](http://www.TheGenCC.org)

## Clinical Validity Term Delphi Survey

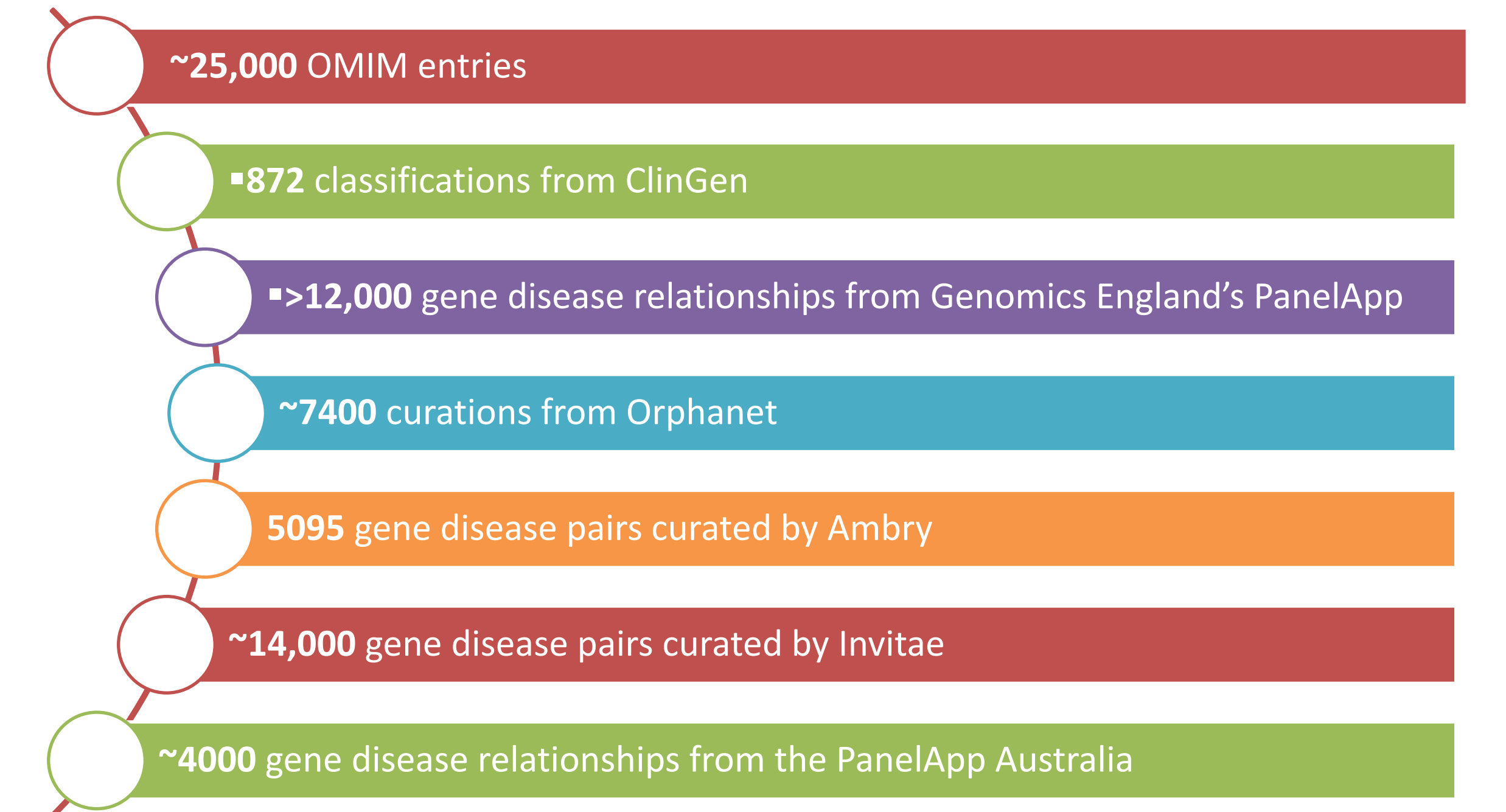


**Figure 1: A. GenCC Clinical Validity Term Delphi Survey Process.** To harmonize terms describing gene-disease validity, the GenCC used a Delphi method to survey both members of our GenCC organizations and the international genetics community. This survey was conducted in three rounds. A short introductory video describing the survey was provided to all survey takers.

**B. Standardized Clinical Validity Term Set.** Terms that were agreed upon are "Definitive, Strong, Moderate, Limited, Disputed Evidence, Refuted Evidence, Animal Model Only, and No Known Disease Relationship". GenCC groups will now use or map to relevant harmonized terms in their curation work.

## Validity Data from GenCC Members

GenCC is creating a harmonized display for the following validity data:

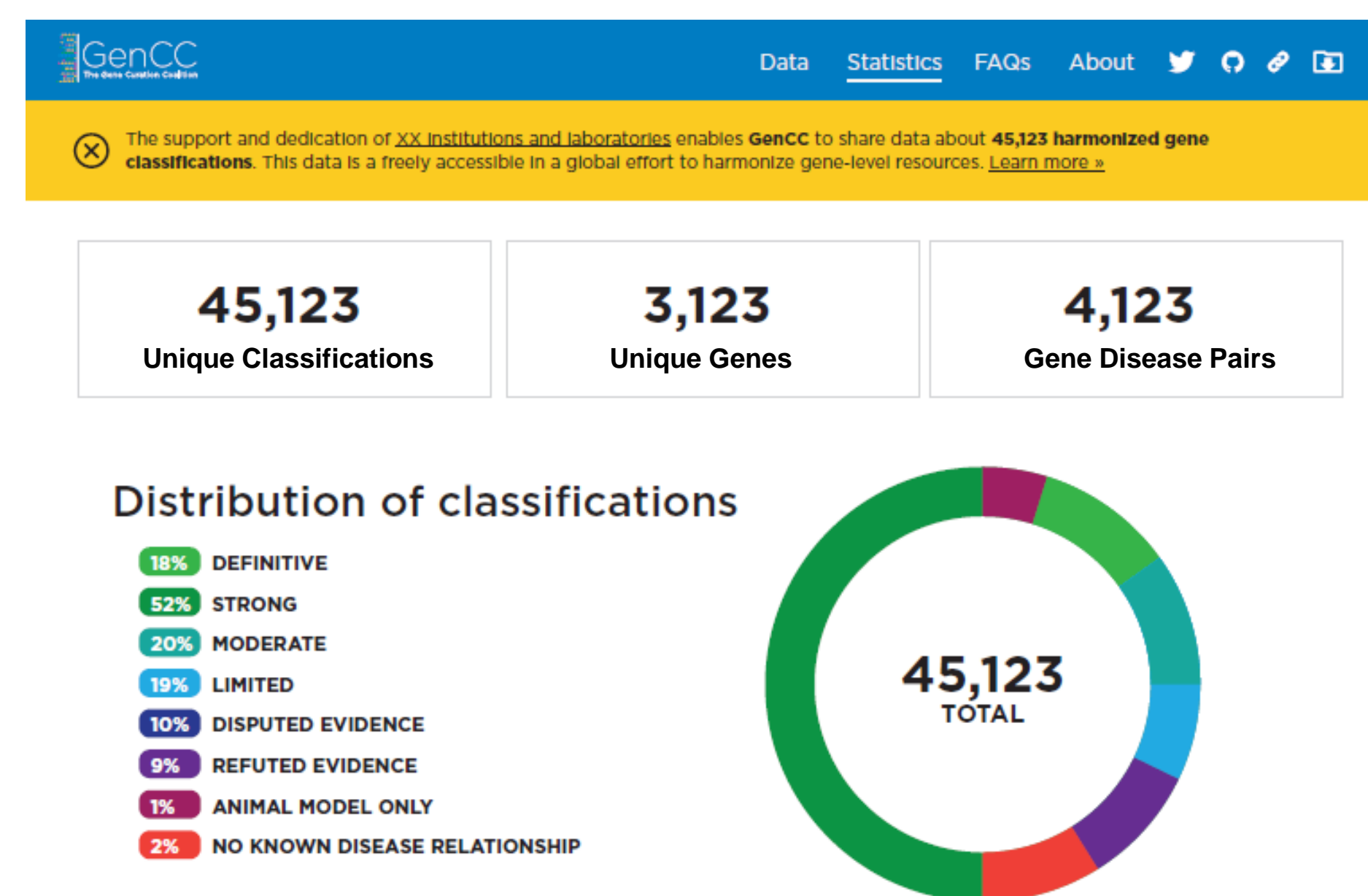


## GenCC Member Groups



## Validity Data Summary Mockup

NOTE: This is a MOCKUP and does not display real curation results from GenCC Members



**Figure 2: Mockup of Summary Data.** Users will see the number of unique classifications (a classification is attached to a gene, disease, a mode of inheritance, and a GenCC member group), unique genes, and unique diseases. Clinical validities are differentiated by color.

## Validity Gene List Mockup

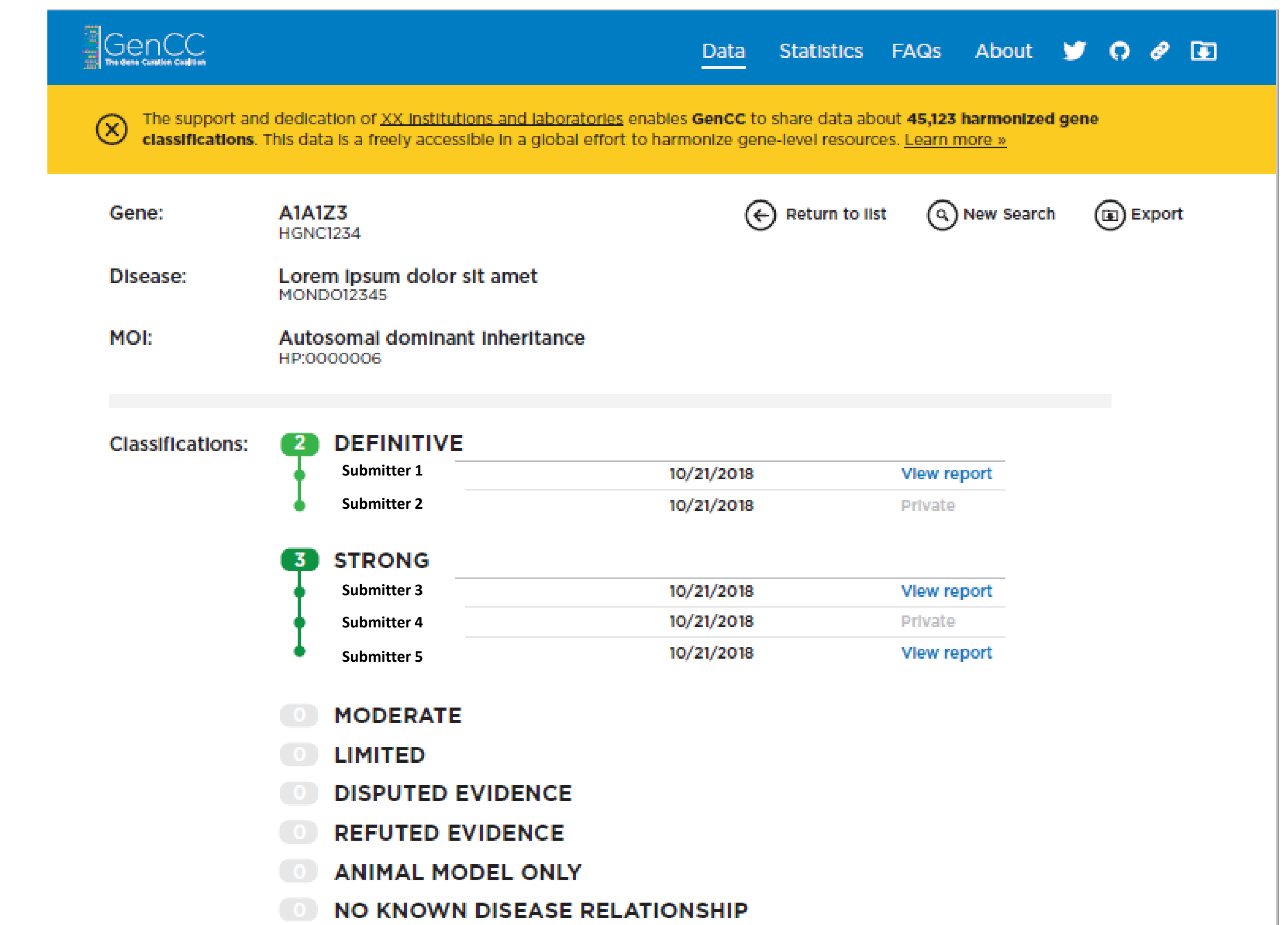
NOTE: This is a MOCKUP and does not display real curation results from GenCC Members

Gene	Disease	MOI	Classifications	Date
A1A1Z3	Lorem ipsum dolor sit amet		4 Definitive Classifications	12/12/2020
A2B1E4	Consectetur adipisicing elit	AD	4 4	12/12/2020
A3C4	Nulla porta arcu ante eros lectsed conetur...	AR	5 1 0	12/12/2020
A4D5A	Massa finibus vitae.	XLR	9 2 0	12/12/2020
A5E6G	Proin at eros lectus el dolor at odio	XL	6 2	12/12/2020
A6F9H	Aliquam tincidunt ipsum libero	AD	2 9 7 Disputed Evidence Classifications	12/12/2020
HGNC1234	Lorem ipsum dolor sit amet	AD	7 2 1	12/12/2020
A2B1E4	MONDO123456 - lectiscing elit	AD	4 4	12/12/2020
A3C4	Nulla porta arcu ante eros lectsed conetur...	AR	5 1 2	12/12/2020
A4D5A	Massa finibus vitae.	XLR	9 2 3	Last updated
A5E6G	Proin at eros lectus el dolor at odio	XL	6 9 10	12/12/2020
A6F9H	Aliquam tincidunt ipsum libero	AD	3 1	12/12/2020
A1A1Z3	Lorem ipsum dolor sit amet	AD	1 2 8	12/12/2020
A2B1E4	Consectetur adipisicing elit	AD	0 1 8	12/12/2020
A3C4	Nulla porta arcu ante eros lectsed conetur...	AR	5 1 2	12/12/2020

**Figure 3: Mockup of the gene list.** Curated genes will be displayed in a list format with the HGNC gene ID, the disease from the Monarch Disease Ontology (MONDO), the Mode of Inheritance (MOI), and the date of the most recent validity classification. Curations will be grouped and tallied by clinical validity with differing classifications for the same gene disease pair being displayed as different colors. The list will can be searched, filtered, and downloaded.

## Classification Page Mockup

NOTE: This is a MOCKUP and does not display real curation results from GenCC Members



**Figure 4: Classification Page Mockup.** Each page will display the gene, disease (MONDO), and mode of inheritance (MOI). Classifications will be sorted by clinical validity. Each submitter, the date curated, and a link to public evidence will be included. Each page can be exported.

## Conclusions and Future Directions

- The Gene Curation Coalition (GenCC) was formed to standardize nomenclature surrounding gene curation
- A Delphi survey was completed to standardize clinical validity terms and all GenCC members will adopt them
- An ongoing project is working with all members to publicly display thousands of gene curation results

## References

- 1) Strande NT, Rooney Riggs E, et al. Evaluating the clinical validity of gene-disease associations: an evidence-based framework developed by the Clinical Genome Resource. *bioRxiv*. doi: <https://doi.org/10.1101/111039>
- 2) Farwell hageman KD, Shinde DN, Mroske C, et al. Candidate-gene criteria for clinical reporting: diagnostic exome sequencing identifies altered candidate genes among 8% of patients with undiagnosed diseases. *Genet Med*. 2017;19(2):224-235.
- 3) Ceyhan-birsoy O, Machini K, Lebo MS, et al. A curated gene list for reporting results of newborn genomic sequencing. *Genet Med*. 2017;19(7):809-818.
- 4) Machini K, Ceyhan-birsoy O, Azzariti DR, et al. Analyzing and Reanalyzing the Genome: Findings from the MedSeq Project. *Am J Hum Genet*. 2019;105(1):177-188.

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