

NEWS IN BRIEF

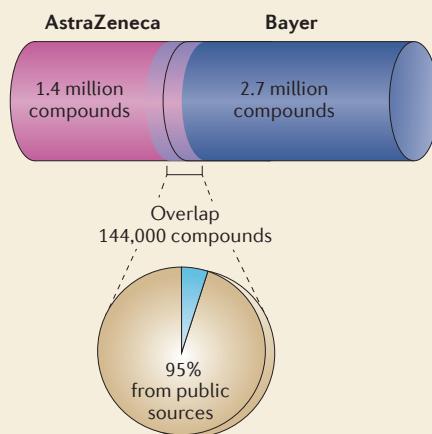
AstraZeneca and Bayer share their entire compound libraries

AstraZeneca and Bayer have agreed to make their entire compound libraries available to one another for high-throughput screening runs.

The lowdown: Peter Simpson, Director of Screening Sciences & Compound Management for AstraZeneca, announced the novel collaborative agreement — which effectively gives both companies access to around 4 million compounds — at the European Laboratory Robotics Interest Group (ELRIG) meeting in Manchester, UK, in September. Under the terms of the partnership, each company can act as an originator by nominating targets for screening runs. The partner then has the option of using the originator's assay or of developing its own assay before carrying out a high-throughput screening run of its library in-house. Hits are returned to the originator for further development. To avoid potential conflicts of interest, the companies are only using each other's libraries to screen against targets that are not within each other's therapeutic interests. The collaboration was announced in September, but has been in place for over 18 months.

Both companies have already run several screens for one another, but have not publicly disclosed the results of these.

The collaboration also provides interesting insight into how compound libraries differ between companies. Although many in the field thought that there was likely to be little overlap between compound libraries, their proprietary nature has made this assumption difficult to test. But, for AstraZeneca and Bayer at least, overlap is minimal (~3.5% of the combined library size) and is predominantly attributable to compounds obtained from publicly accessible sources including vendors (see figure).



fast-track designations and accelerated approvals] in the U.S. ... there was little difference in the approval times between products that had a special designation and those that did not," the authors also write.

Cytoskeletal motor protein researchers win Lasker award

This year's Albert Lasker Basic Medical Research Award went to three researchers for their study of cytoskeletal motor proteins, work that helped show the way to novel drug targets.

The lowdown: Michael Sheetz, of Columbia University, James Spudich, of Stanford University School of Medicine, and Ronald Vale, of the University of California, San Francisco, were recognized with the Lasker award for figuring out how to "reconstitute motility from its constituent parts in the laboratory" and for discovering "the motor protein kinesin and unveil[ing] key aspects of the process by which molecular engines convert chemical energy into mechanical work".

Because of the important role of motor proteins like myosin and kinesin in pathophysiology, the researchers' pioneering work has helped lay the foundation for several cytoskeletal motor protein-targeting drugs. Cytokinetics' and Amgen's omecamtiv mecarbil activates myosin, increasing cardiac contractility, and is in Phase II development for both acute and congestive heart failure. Kinesin-targeting drugs are in development as anticancer agents because kinesins have a key role in separating spindles during mitosis. Array's ARRY-520 is in Phase II trials in multiple myeloma, for example, and Lilly's litronesib (LY2523355) is in Phase II trials for eight different solid tumours.

The Lasker-DeBaKey Clinical Medical Research Award recognized Roy Calne, of the University of Cambridge, and Thomas Starzl, of the University of Pittsburgh, for their contributions to liver transplantation. During their studies they tested immunosuppressants including Astellas' tacrolimus, Wyeth's sirolimus (rapamycin) and Sanofi's alemtuzumab.

There is little ongoing active clinical development of new immunosuppressants for the prevention of liver transplant rejection, but Novartis's mammalian target of rapamycin (mTOR) inhibitor everolimus — which is approved for prevention of kidney (and, in the European Union, heart) transplant rejection — is under regulatory review for this indication on both sides of the Atlantic.

Total drug development timelines are getting shorter

The average total development and approval timeline for drugs in the United States is around 7 years and 5 months, down from a previous average of 8 years.

The lowdown: Drug development and approval timelines are down in the United States, shows an Impact Report from the [Tufts Center for the Study of Drug Development](#). When the investigators looked at the time from an investigational new drug (IND) application to approval for both new chemical entities (NCEs) and biologics license applications (BLAs), they found that the average development time for drugs approved from 2007–2011 was around 7 months shorter than for those approved from 2002–2006. Most of the gains came from drugs spending less time under review.

A deeper analysis of variation in US Food and Drug Administration (FDA) review times for oncology drugs compared with the rest of the pipeline also yielded some interesting differences. From 2007–2011, oncology drugs

tended to spend 10 months longer in clinical development than did non-oncology drugs, but 10 months less time under review. "Factors likely to account for these disparities include difficulties experienced during development for oncology drugs due to smaller patient populations for recruitment and longer periods for evaluation of treatment response," the authors write. From 2007–2011, it took the FDA around 7 months on average to review oncology drugs versus 17 months for non-oncology drugs.

Whereas the total development time for oncology small molecules stayed the same between 2002–2006 and 2007–2011 (at around 7.6 years), it dropped by almost 2.5 years for oncology biologics (from 8.9 years to 6.4 years).

The analysis also showed that from 2007–2011 the FDA was faster than the European Medicines Agency (EMA) at reviewing oncology drugs (7 months versus 15 months), but slower at reviewing non-oncology drugs (17 months versus 13 months).

"Moreover, while oncology products received a greater share of all special program designations [that is, orphan product and