

Selected Publications

CIRB - Épidémiologie évolutive des maladies infectieuses

Wymant, C., Bezemer, D., Blanquart, F., Ferretti, L., Gall, A., Hall, M., Golubchik, T., Bakker, M., Ong, S. H., Zhao, L., Bonsall, D., de Cesare, M., MacIntyre-Cockett, G., Abeler-Dörner, L., Albert, J., Bannert, N., Fellay, J., Grabowski, M. K., Günsenheimer-Bartmeyer, B., Günthard, H. F., Kivelä, P., Kouyos, R. D., Laeyendecker, O., Meyer, L., Porter, K., Ristola, M., van Sighem, A., Berkhout, B., Kellam, P., Cornelissen, M., Reiss, P., Fraser, C., the Netherlands ATHENA HIV Observational Cohort, & THE BEEHIVE COLLABORATION (2022). A highly virulent variant of HIV-1 circulating in the Netherlands. *Science* 375, 540–545.

Blanquart, F., Hozé, N., Cowling, B. J., Débarre, F. & Cauchemez, S. (2022). Selection for infectivity profiles in slow and fast epidemics, and the rise of SARS-CoV-2 variants. *eLife* 11, e75791.

Gaymard, A., Bosetti, P., Feri, A., Destras, G., Enouf, V., Andronico, A., Burrel, S., Behillil, S., Sauvage, C., Bal, A., Morfin, F., Werf, S. V. D., Josset, L., Covid-19, A. M. A., Group, F. viro C., Blanquart, F., Coignard, B., Cauchemez, S. & Lina, B. (2021). Early assessment of diffusion and possible expansion of SARS-CoV-2 Lineage 20I/501Y.V1 (B.1.1.7, variant of concern 202012/01) in France, January to March 2021. *Eurosurveillance* 26, 2100133.

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Blanquart, F. (2019). Evolutionary epidemiology models to predict the dynamics of antibiotic resistance. *Evolutionary Applications*, 12(3): 365–383.

Blanquart, F., Lehtinen, S., Lipsitch, M., & Fraser, C. (2018). The evolution of antibiotic resistance in a structured host population. *Journal of The Royal Society Interface*, 15(143), 20180040.

Lehtinen, S., Blanquart, F., Croucher, N. J., Turner, P., Lipsitch, M. & Fraser, C. (2017). Evolution of antibiotic resistance is linked to any genetic mechanism affecting bacterial duration of carriage. *Proceedings of the National Academy of Sciences* 114, 1075–1080.

Blanquart F., Wymant C., Cornelissen M., Gall A., Bakker M., Bezemer D., Hall M., Hillebregt M., Ong S.H., Albert J., Bannert N., Fellay J., Fransen K., Gurlay A.J., Grabowski M.K., Günsenheimer-Bartmeyer B., Günthard H.F., Kivelä P., Kouyos R., Laeyendecker O., Liitsola K., Meyer L., Porter K., Ristola M., van Sighem A., Vanham G., Berkhout B., Kellam P., Reiss P., Fraser C., & the BEEHIVE collaboration. (2017). Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. *PLoS Biology* 15(6): e2001855.

Blanquart F., Grabowski M.K., Herbeck J., Nalugoda F., Serwadda D., Eller M.A., Robb M.L., Gray R., Kigozi G., Laeyendecker O., Lythgoe K.A., Nakigozi G., Quinn T.C., Reynolds S.J., Wawer M.J. & Fraser C. (2016). A transmission-virulence evolutionary trade-off explains the attenuation of HIV-1 in Uganda. *eLIFE* e20492.

Blanquart F., Kaltz O., Nuismer S. L. & Gandon S. (2013). A practical guide to measuring local adaptation. Ecology Letters 16: 1195-1205.