

Desafíos futuros y oportunidades para la genética y la genómica en acuicultura

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- Araneda, M. E., & Miranda, R. (2013). Análisis y modelación bioeconómica: Una herramienta de gestión para decisiones de producción e inversión en acuicultura. www.aquainnovo.com
- Buckley, R. M., Harris, A. C., Wang, G. D., Whitaker, D. T., Zhang, Y. P., & Ostrander, E. A. (2022). Best practices for analyzing imputed genotypes from low-pass sequencing in dogs. *Mammalian Genome*, 33(1), 213–229. <https://doi.org/10.1007/s00335-021-09914-z>
- Chang, L.-Y., Toghiani, S., Aggrey, S. E., & Rekaya, R. (2019). Increasing accuracy of genomic selection in presence of high density marker panels through the prioritization of relevant polymorphisms. *BMC Genetics*, 20(1), 21. <https://doi.org/10.1186/s12863-019-0720-5>
- Dehler, C. E., Boudinot, P., Martin, S. A. M., & Collet, B. (2016). Development of an Efficient Genome Editing Method by CRISPR/Cas9 in a Fish Cell Line. *Marine Biotechnology*, 18(4), 449–452. <https://doi.org/10.1007/s10126-016-9708-6>
- Doudna, J. A., & Charpentier, E. (2014). The new frontier of genome engineering with CRISPR-Cas9. *Science*, 346(6213). <https://doi.org/10.1126/science.1258096>
- Drangsholt, T. M. K., Gjerde, B., Ødegård, J., Fridell, F., & Bentsen, H. B. (2011). Quantitative genetics of vaccine-induced side effects in farmed Atlantic salmon (*Salmo salar*). *Aquaculture*, 318(3–4), 316–324. <https://doi.org/10.1016/j.aquaculture.2011.05.044>
- Druet, T., Macleod, I. M., & Hayes, B. J. (2014). Toward genomic prediction from whole-genome sequence data: Impact of sequencing design on genotype imputation and accuracy of predictions. *Heredity*, 112(1), 39–47. <https://doi.org/10.1038/hdy.2013.13>
- Falconer, D. S., & Mackay, T. F. C. (1996). Introduction to Quantitative Genetics. (4th ed.).
- Gallardo-Hidalgo, J., Barría, A., Yoshida, G. M., & Yáñez, J. M. (2021). Genetics of growth and survival under chronic heat stress and trade-offs with growth- and robustness-related traits in rainbow trout. *Aquaculture*, 531 (March 2020), 735685. <https://doi.org/10.1016/j.aquaculture.2020.735685>
- Gjedrem, T. (2005). Selection and breeding programs in aquaculture. In T. Gjedrem (Ed.), Selection and Breeding Programs in Aquaculture. AKVAFORSK, Institute of Aquaculture Research AS, Norway. <https://doi.org/10.1007/1-4020-3342-7>
- Gjøen, H. M., Refstie, T., Ulla, O., & Gjerde, B. (1997). Genetic correlations between survival of Atlantic salmon in challenge and field tests. *Aquaculture*, 158(3–4), 277–288. [https://doi.org/10.1016/S0044-8486\(97\)00203-2](https://doi.org/10.1016/S0044-8486(97)00203-2)
- Gonzalez, C., Gallardo-Hidalgo, J., & Yáñez, J. M. (2022). Genotype-by-environment interaction for growth in seawater and freshwater in Atlantic salmon (*Salmo salar*). *Aquaculture*, 548, 737674. <https://doi.org/10.1016/j.aquaculture.2021.737674>
- Heidaritabar, M., Calus, M. P. L., Megens, H.-J., Vereijken, A., Groenen, M. A. M., & Bastiaansen, J. W. M. (2016). Accuracy of genomic prediction using imputed whole-genome sequence data in white layers. *Journal of Animal Breeding and Genetics*, 133(3), 167–179. <https://doi.org/10.1111/jbg.12199>
- Houston, R. D. (2017). Future directions in breeding for disease resistance in aquaculture species. *Revista Brasileira de Zootecnia*, 46(6), 545–551. <https://doi.org/10.1590/s1806-92902017000600010>
- Jenko, J., Gorjanc, G., Cleveland, M. A., Varshney, R. K., Whitelaw, C. B. A., Wooliams, J. A., & Hickey, J. M. (2015). Potential of promotion of alleles by genome editing to improve quantitative traits in livestock breeding programs. *Genetics Selection Evolution*, 47(1), 55. <https://doi.org/10.1186/s12711-015-0135-3>
- Kim, S., Shin, J. Y., Kwon, N. J., Kim, C. U., Kim, C., Lee, C. S., & Seo, J. S. (2021). Evaluation of low-pass genome sequencing in polygenic risk score calculation for Parkinson's disease. *Human Genomics*, 15(1), 1–12. <https://doi.org/10.1186/s40246-021-00357-w>
- Kolstad, K., Heuch, P. A., Gjerde, B., Gjedrem, T., & Salte, R. (2005). Genetic variation in resistance of Atlantic salmon (*Salmo salar*) to the salmon louse *Lepeophtheirus salmonis*. *Aquaculture*, 247(1–4), 145–151. <https://doi.org/10.1016/j.aquaculture.2005.02.009>
- Lhorente, J. P., Gallardo, J. A., Villanueva, B., Carabaño, M. J., & Neira, R. (2014). Disease Resistance in Atlantic Salmon (*Salmo salar*): Coinfection of the Intracellular Bacterial Pathogen *Piscirickettsia salmonis* and the Sea Louse *Caligus rogercresseyi*. *PLoS ONE*, 9(4), e95397. <https://doi.org/10.1371/journal.pone.0095397>
- Li, J. H., Mazur, C. A., Berisa, T., & Pickrell, J. K. (2021). Low-pass sequencing increases the power of GWAS and decreases measurement error of polygenic risk scores compared to genotyping arrays. *Genome Research*, 31(4), 529–537. <https://doi.org/10.1101/GR.266486.120>
- Lynch, M., & Walsh, B. (1998). Genetics and Analysis of Quantitative Traits. Sinauer Associates, Inc.
- Macqueen, D. J., Primmer, C. R., Houston, R. D., Nowak, B. F., Bernatchez, L., Bergseth, S., Davidson, W. S., Gallardo-Escárate, C., Goldammer, T., Guiguen, Y., Iturra, P., Kijas, J. W., Koop, B. F., Lien, S., Maass, A., Martin, S. A. M., McGinnity, P., Montecino, M., Naish, K. A., ... Consortium, T. F. (2017). Functional Annotation of All Salmonid Genomes (FAASG): an international initiative supporting future salmonid research, conservation and aquaculture. *BMC Genomics*, 18(1), 484. <https://doi.org/10.1186/s12864-017-3862-8>
- Mulder, H. A., & Bijma, P. (2005). Effects of genotype × environment interaction on genetic gain in breeding programs1. *Journal of Animal Science*, 83(1), 49–61. <https://doi.org/10.2527/2005.83149x>
- Nosková, A., Bhati, M., Kadri, N. K., Crysantho, D., Neuenschwander, S., Hofer, A., & Pausch, H. (2021). Characterization of a haplotype-reference panel for genotyping by low-pass sequencing in Swiss Large White pigs. *BMC Genomics*, 22(1), 1–14. <https://doi.org/10.1186/s12864-021-07610-5>
- Pérez-Enciso, M., Rincón, J. C., & Legarra, A. (2015). Sequence- vs. chip-assisted genomic selection: accurate biological information is advised. *Genetics Selection Evolution*, 47(1), 43. <https://doi.org/10.1186/s12711-015-0117-5>
- Ponzoni, R., James, J., Nguyen, N., Mekkawy, W., Khaw Authors Ponzoni, H. R., & Khaw, H. (2013). Strain comparisons in aquaculture species: a manual. http://pubs.iclairm.net/resource_centre/WF_3541.pdf