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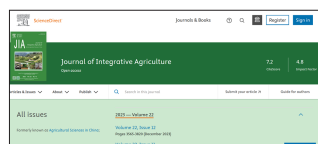
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Cover Story NADC34-like porcine reproductive and respiratory syndrome viruses (PRRSVs) cause significant economic losses to the global swine industry. This study analyzed 176 whole-genome sequences from the USA, China, and South Korea. It found that 56.8% of strains are recombinant variants and defined 12 consistent patterns (R1–R12). A temporal shift in recombination hotspots from structural genes to the ORF1ab region was identified in Chinese strains after 2020. Lineage 1.8 was the primary minor parent driving this genetic diversification. The cover image illustrates these evolutionary findings. The central 3D virus particle is surrounded by 12 Mosaic Bar-code ribbons representing the R1–R12 patterns. Orange segments show the NADC34-like backbone. Red segments highlight recombinant inputs primarily from Lineage 1.8. Circular charts represent the geographic distribution across different regions. The pig silhouette underscores the role of genomics in modern swine health surveillance. This image was produced by Zhengqin Ye and Prof. Xiangdong Li from Yangzhou University, China, with AI assistance. For details, see pages 3503–3507.